Supplementary material

Xin Yi, Ding-Sheng Jiang, Gaoke Feng, et al. An altered left ventricle protein profile in human ischemic cardiomyopathy revealed in comparative quantitative proteomics. Kardiol Pol. 2019; 77: 951-959. doi:10.33963/KP.14936.

Table S1. The information of normal donors and patients with severe ischemic cardiomyopathy (ICM).

Characteristics	**Normal donors**	**ICM patients**
No.	7	6
Age, y	27.7±7.43	59±5.4
Sex, male/total (%)	7/7 (100%)	6/6 (100%)
BMI (kg/m^2)	23.9±1.71	24.5±3.7
Medical history		
Hypertension	0 (0%)	3 (50%)
Diabetes mellitus	0 (0%)	2 (33.3%)
Drinking history	1 (14.3%)	2 (33.3%)
Cigarette smoker	1 (14.3%)	1 (16.7%)
LVEDD (mm)	42.3±1.8	67.8±14.1
LVEF (%)	61.4±1.7	30.4±7.2
Heart rate, bpm	77.3±7.0	78.7±9.8
Blood pressure, mmHg		
Systolic	N/A	106.5±25.8
Diastolic	N/A	58.5±25.7

Blood glucose, mmol/l	N/A	9.9±4.4

BMI: body mass index; LVEDD: left ventricular end-diastolic dimension; LVEF: left ventricular ejection fraction

Table S2. A total of 1,723 ventricle proteins were quantified in both experiments.

Name	Rep.01		Rep.02	
	CAD：Healthy	PVal CAD：Healthy	CAD：Healthy	PVal CAD：Healthy
Troponin C, slow skeletal and cardiac muscles OS=Homo sapiens GN=TNNC1 PE=1 SV=1	0.166226111	0.253135085	0.030317133	0.106427297
Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	0.488838587	0.680224478	0.042769532	0.175511107
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Homo sapiens GN=CHCHD2 PE=1 SV=1	0.165587282	0.287838191	0.068677826	0.024716711
Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	0.075120137	0.408163399	0.079888601	0.477288812
CapZ-interacting protein OS=Homo sapiens GN=RCSD1 PE=1 SV=1	0.081220847	0.187434196	0.080438098	0.034843419
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	0.10409499	0.209530905	0.093591245	0.195618197
Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2	1.103481298	0.937380075	0.159622548	0.220142901
Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2	0.37407497	0.06473399	0.200058496	0.219849899
Calsequestrin-2 OS=Homo sapiens GN=CASQ2 PE=1 SV=2	0.188715675	0.01236959	0.208691464	0.008588423
Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1	0.323540526	0.215387896	0.210389984	0.1013861
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	0.26753254	0.655063212	0.217696611	0.600547612
28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=1 SV=2	0.359143803	0.764469326	0.219418937	0.406949788
All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=1 SV=2	1.448366282	0.913184702	0.219419878	0.511036873
Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	0.279658487	0.127941504	0.226462412	0.510433316
Protein NipSnap homolog 3B OS=Homo sapiens GN=NIPSNAP3B PE=2 SV=1	0.205087323	0.583147585	0.227733274	0.486169994
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	0.188676726	0.361885488	0.231984275	0.198975801
Sarcoplasmic reticulum histidine-rich calcium-binding protein OS=Homo sapiens GN=HRC PE=1 SV=1	0.218838923	0.189348906	0.23562211	0.02349004
Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2	0.334038262	0.618803024	0.237917541	0.432160795
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	1.39258565	0.886226773	0.24378464	0.370292515
Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	3.023213229	0.562048376	0.245115089	0.647219598
High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	0.189139524	0.055180781	0.245870853	0.079076268
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1	0.503508186	0.543672979	0.246051725	0.631842017
GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1	0.314652808	0.656094313	0.255758338	0.62730968

Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1	0.618203643	0.700839877	0.268120164	0.656313777
Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2 PE=1 SV=1	1.248384551	0.484075308	0.268441744	0.267637014
Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1	0.29493017	0.128270805	0.274033795	0.003304357
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	0.792506688	0.91071701	0.277249011	0.674239218
Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	0.269412583	0.003911893	0.29019961	0.004820378
Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2	0.427150157	0.2361601	0.299824457	0.02552432
Coenzyme Q-binding protein COQ10 homolog A, mitochondrial OS=Homo sapiens GN=COQ10A PE=2 SV=2	0.507816065	0.560143471	0.300493507	0.248441204
Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	0.253274776	0.311740398	0.302343344	0.692371905
Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	0.255452968	0.213939205	0.305657564	0.005010913
Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3	0.305887388	3.06E-08	0.314303701	1.99707E-06
Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	1.053773342	0.914148629	0.320763365	0.335020214
Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1	0.583842041	0.578089178	0.334134593	0.063771613
Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	0.861878737	0.42884481	0.336053912	0.214845806
Inactive phospholipase C-like protein 1 OS=Homo sapiens GN=PLCL1 PE=1 SV=3	0.665449778	0.412378788	0.339237998	0.195502207
Troponin T, cardiac muscle OS=Homo sapiens GN=TNNT2 PE=1 SV=3	0.362060283	0.001056038	0.340711219	0.006877835
Dihydropyrimidine dehydrogenase [NADP(+)] OS=Homo sapiens GN=DPYD PE=1 SV=2	0.272484621	0.559552073	0.347082911	0.747576177
Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1	0.414620512	0.2439069	0.353923033	0.104249001
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0.846319413	0.746118784	0.355948664	0.568874598
Beta-lactamase-like protein 2 OS=Homo sapiens GN=LACTB2 PE=1 SV=2	0.339175753	0.66637671	0.355997426	0.555020571
Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	0.662962051	0.616657972	0.356521625	0.162975207
Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1	0.310180443	0.03284438	0.356970488	0.082461514
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2	0.519594149	0.369646311	0.359440962	0.538875103
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1 PE=1 SV=1	1.551410561	0.912825584	0.361649014	0.739825785
Ras-related protein Rab-12 OS=Homo sapiens GN=RAB12 PE=1 SV=3	0.275531128	0.437604606	0.367146145	0.134808496
5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens GN=NT5C PE=1 SV=2	1.216472377	0.779034197	0.369777753	0.7526021
Valacyclovir hydrolase OS=Homo sapiens GN=BPHL PE=1 SV=1	0.428004879	0.412714899	0.373733151	0.330944389
Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1	0.193730014	0.307939291	0.374925003	0.400296509
Ubiquitin fusion degradation protein 1 homolog OS=Homo sapiens GN=UFD1L PE=1 SV=3	0.185354584	0.036233589	0.377999534	0.203999296
Choline-phosphate cytidylyltransferase A OS=Homo sapiens GN=PCYT1A PE=1 SV=2	1.102320316	0.936207116	0.378849312	0.753828585

Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1	0.754910115	0.492122501	0.379497715	0.673936009
Coiled-coil domain-containing protein 90B, mitochondrial OS=Homo sapiens GN=CCDC90B PE=1 SV=2	0.494879945	0.687848985	0.380265144	0.578136504
Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	0.468129071	0.003966155	0.384156321	0.000169094
Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	1.009403632	0.984257221	0.386991353	0.233587101
N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1	1.17169451	0.931450725	0.387157672	0.048397481
Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	1.163591976	0.908771276	0.395041301	0.525968075
Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3	0.783622322	0.117488503	0.402673273	0.239861801
Protein phosphatase 1 regulatory subunit 12B OS=Homo sapiens GN=PPP1R12B PE=1 SV=2	0.817777833	0.918500602	0.403253289	0.534602284
Cullin-associated NEDD8-dissociated protein 2 OS=Homo sapiens GN=CAND2 PE=1 SV=3	0.461496193	0.273270011	0.403557747	0.077362411
Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2	0.519987541	0.619538128	0.404273655	0.444713086
Troponin I, cardiac muscle OS=Homo sapiens GN=TNNI3 PE=1 SV=3	0.437864038	0.262105614	0.409787206	0.3000516
NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens GN=NFU1 PE=1 SV=2	0.923009042	0.92807281	0.411527548	0.120451801
Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2	0.502056679	0.098330557	0.414262394	0.532865405
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	0.82952647	0.524800003	0.416371899	0.306084305
Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1	2.424748564	0.468859613	0.417350617	0.326602995
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	0.402603892	0.036581099	0.417784413	0.003164647
ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	0.516401166	0.035040699	0.418600232	0.125246301
Protein S100-A1 OS=Homo sapiens GN=S100A1 PE=1 SV=2	0.525570326	0.636476278	0.41874943	0.581884086
Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2	1.179889601	0.447654307	0.424265628	0.545615077
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	0.660592304	0.043470878	0.425410437	0.055731408
Plasminogen receptor (KT) OS=Homo sapiens GN=PLGRKT PE=1 SV=1	0.528742424	0.106640898	0.434333737	0.661131382
Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2	0.577819909	0.002746859	0.440576948	0.1293329
Ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=ANKRD2 PE=1 SV=3	0.350243683	0.00762907	0.442832317	0.07916601
Myosin light chain kinase 3 OS=Homo sapiens GN=MYLK3 PE=2 SV=3	0.96648795	0.966720521	0.443691542	0.274542511
Complex I assembly factor TIMMDC1, mitochondrial OS=Homo sapiens GN=TIMMDC1 PE=1 SV=2	0.482975373	0.053029291	0.445110139	0.07756336
Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	0.438131472	0.072042197	0.448681615	0.383934796
O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2	0.463673525	0.03346505	0.449243357	0.215259507
Fumarylacetoacetate hydrolase domain-containing protein 2A OS=Homo sapiens GN=FAHD2A PE=1 SV=1	0.465001423	0.231213793	0.452911864	0.249811396
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	0.460671763	0.0493536	0.454250421	0.031203309

Exocyst complex component 5 OS=Homo sapiens GN=EXOC5 PE=1 SV=1	1.384720091	0.074750938	0.454784827	0.376516014
Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	0.824838869	0.798847914	0.45638469	0.419265211
Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1	0.425469816	0.491823792	0.456505941	0.563231111
Leiomodin-2 OS=Homo sapiens GN=LMOD2 PE=1 SV=2	0.889468441	0.95558852	0.456821465	0.469814092
U8 snoRNA-decapping enzyme OS=Homo sapiens GN=NUDT16 PE=1 SV=2	0.47781369	0.046700951	0.458080983	0.170474604
Leucine-rich repeat-containing protein 20 OS=Homo sapiens GN=LRRC20 PE=1 SV=1	0.557436891	0.672773421	0.459751529	0.811183929
Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Homo sapiens GN=UQCC2 PE=1 SV=1	0.496297621	0.316656888	0.459952843	0.183768302
Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=1 SV=2	0.426538537	0.076142803	0.460700403	0.652257025
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	0.449003523	0.000127046	0.461638975	0.00057619
Protein NDRG4 OS=Homo sapiens GN=NDRG4 PE=1 SV=2	0.600150041	0.007549552	0.462901886	0.135386094
Mitofusin-2 OS=Homo sapiens GN=MFN2 PE=1 SV=3	0.431371763	0.185670406	0.464842799	0.209563002
Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3	0.556968103	0.000474877	0.465315176	0.016850449
ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2	2.257204897	0.483806014	0.465947629	0.107258402
Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2 PE=1 SV=2	0.63412144	0.313156188	0.466157413	0.045254041
Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2	0.798645486	0.828476727	0.466220473	0.400888205
[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Homo sapiens GN=BCKDK PE=1 SV=2	0.572177973	0.115315497	0.466380921	0.1460668
Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	0.812160299	0.957781911	0.466695448	0.587420583
Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1	0.54938443	0.019547051	0.46921789	0.462216586
ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1	0.565831375	0.133999601	0.469497679	0.130285203
39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	0.444480004	0.73425293	0.46959687	0.758048415
Myomesin-2 OS=Homo sapiens GN=MYOM2 PE=1 SV=2	0.509394236	2.14E-06	0.469766964	0.000771609
UPF0553 protein C9orf64 OS=Homo sapiens GN=C9orf64 PE=1 SV=1	0.820148056	0.867113888	0.470260268	0.26019749
Cysteine-rich with EGF-like domain protein 1 OS=Homo sapiens GN=CRELD1 PE=1 SV=3	0.360912204	0.742732584	0.471457053	0.417704999
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	0.865743879	0.928579271	0.473689869	0.559119523
Creatine kinase M-type OS=Homo sapiens GN=CKM PE=1 SV=2	0.497688479	0.09374135	0.475538525	0.181825697
28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2	0.442289421	0.197388306	0.476774176	0.039920289
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	0.597286658	0.193258196	0.477958688	0.444911599
Hormone-sensitive lipase OS=Homo sapiens GN=LIPE PE=1 SV=4	0.593762183	0.724335313	0.482491565	0.223822102
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	0.611187164	0.357162893	0.483105547	0.076065518

Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1	0.769508959	0.864579678	0.490371802	0.828393519
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2	0.30271063	0.26628089	0.490539209	0.222420096
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	0.52314333	0.463629097	0.49440627	0.496116787
Sideroflexin-4 OS=Homo sapiens GN=SFXN4 PE=1 SV=1	0.680858966	0.284204602	0.494867216	0.289510399
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	0.544118183	0.34683919	0.496123268	0.171556294
Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	0.899707766	0.848421216	0.496654045	0.310508996
Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	0.55866109	0.404158294	0.497324908	0.293620497
Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3	0.517501102	0.151729107	0.497538938	0.543415189
Gap junction alpha-1 protein OS=Homo sapiens GN=GJA1 PE=1 SV=2	0.50692717	0.535305917	0.498169236	0.59779942
Acetyl-coenzyme A synthetase 2-like, mitochondrial OS=Homo sapiens GN=ACSS1 PE=1 SV=2	0.440362965	0.01281658	0.498178644	0.064984933
Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1	0.60371601	0.123507097	0.502195359	0.697278619
Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2	0.656811862	0.604709923	0.506404484	0.351547599
NADH dehydrogenase [ubiquinone] complex I, assembly factor 7 OS=Homo sapiens GN=NDUFAF7 PE=1 SV=1	0.861978282	0.849354982	0.506979835	0.789770424
Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2	0.459037988	0.317001492	0.507155464	0.116909802
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2	0.624696248	0.343679607	0.508016763	0.041766521
Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	0.754882738	0.242928803	0.510703324	0.541612506
Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3	1.182310128	0.755065382	0.510956693	0.066430353
Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2	0.866073076	0.942366779	0.5128205	0.808814287
Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	1.289950884	0.544024289	0.514202528	0.426676303
Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	0.523861904	0.74691999	0.515096458	0.716830671
Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1	0.679327084	0.043569311	0.515629517	0.2413183
ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2	0.863318528	0.786388516	0.515772594	0.531659305
Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	0.565796149	0.036007781	0.520725392	0.032890599
Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	0.462235995	0.302488595	0.526202786	0.331067801
39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1	0.873894442	0.403232396	0.526774077	0.470267385
2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1	0.44983912	0.064665928	0.527659082	0.088373274
Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	0.686646231	0.777720094	0.528418349	0.235944197
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	0.570543106	0.089179367	0.529237195	0.070306167
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1	0.490333565	0.029189341	0.529491913	0.175681993

Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5	0.511618347	0.103324398	0.529611924	0.101290002
Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3	0.528975984	0.274229795	0.53128499	0.398225486
Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	0.606696363	0.247751296	0.531568798	0.493279815
Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	0.768159478	0.524940073	0.532573817	0.03794473
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	0.576781418	0.027594719	0.532704329	0.001516448
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUFB8 PE=1 SV=1	0.560454553	0.728344798	0.532767054	0.64496398
NADH-ubiquinone oxidoreductase chain 4 OS=Homo sapiens GN=MT-ND4 PE=1 SV=1	0.602243489	0.097101681	0.533226679	0.037475631
Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2	0.599261365	0.726225019	0.53366092	0.643812478
Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3	0.504823854	0.145857796	0.53805125	0.108374499
Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	0.549309602	0.134556398	0.538419182	0.061287839
BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1	0.897351902	0.937197924	0.538731873	0.585826874
Probable asparagine--tRNA ligase, mitochondrial OS=Homo sapiens GN=NARS2 PE=1 SV=3	0.850189748	0.384991795	0.540965109	0.362909913
Ryanodine receptor 2 OS=Homo sapiens GN=RYR2 PE=1 SV=3	0.658371174	0.007139492	0.541072823	0.000662373
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	0.63547745	0.804165304	0.54206243	0.692588091
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	0.603733868	0.01101408	0.543892398	0.046849359
Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2	0.527502402	0.368539512	0.544329074	0.44518289
NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=3	0.662695783	0.847292721	0.545025647	0.523317814
Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	0.546098349	0.333821297	0.54562994	0.220779806
Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2	0.548226982	0.003653145	0.545675194	0.004017875
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1	0.57075638	0.090669438	0.54740741	0.01561221
Serum deprivation-response protein OS=Homo sapiens GN=SDPR PE=1 SV=3	0.309477843	0.169651404	0.548738986	0.291915208
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	0.877654167	0.902539909	0.551393469	0.74930042
28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	0.48682906	0.089921817	0.551848377	0.111884803
Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	0.506821812	0.04156867	0.5543864	0.64081192
NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=1 SV=2	1.25012535	0.3283557	0.554444221	0.323561907
NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2	0.636810458	0.333876401	0.555709003	0.040633671
Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=ZAK PE=1 SV=3	0.466800004	0.068929464	0.55643938	0.006699705
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	0.484816036	0.137253493	0.55785983	0.74921459
Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	0.504995682	0.073639683	0.55807776	0.255946696

Transmembrane protein 65 OS=Homo sapiens GN=TMEM65 PE=1 SV=2	0.657927614	0.073494412	0.558125399	0.056885019
D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3	0.570232719	0.002676422	0.558261566	0.337052196
Probable cysteine--tRNA ligase, mitochondrial OS=Homo sapiens GN=CARS2 PE=1 SV=1	0.617102626	0.746666014	0.558637056	0.58482641
Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	1.272646397	0.848512828	0.558909622	0.827111185
Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3	0.649967705	0.110305101	0.563201946	0.088665813
Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	0.59127761	0.029859031	0.563565712	0.060052179
28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3	0.476789893	0.067615509	0.56443313	0.007980332
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	0.397525625	0.451044589	0.56475191	0.609875202
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	0.591279319	0.000505097	0.564848234	0.005775729
Transmembrane protein 245 OS=Homo sapiens GN=TMEM245 PE=1 SV=2	0.898498455	0.96078819	0.565177383	0.744836271
ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3	0.667699398	0.507513523	0.568068854	0.72249192
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3	0.526230217	0.314658195	0.569302963	0.58741802
Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2	0.954336901	0.65582788	0.569339245	0.495902508
28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1	0.996945323	0.995331705	0.569511754	0.368717611
Ribosyldihydronicotinamide dehydrogenase [quinone] OS=Homo sapiens GN=NQO2 PE=1 SV=5	0.530709519	0.038856551	0.570031186	0.052006532
Thiosulfate sulfurtransferase OS=Homo sapiens GN=TST PE=1 SV=4	0.592193579	0.178058803	0.570863582	0.334236294
Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	4.828895402	0.574355781	0.571113954	0.020849681
Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	0.396305499	0.332143903	0.571129936	0.406864405
Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	2.014001312	0.781113088	0.571952482	0.758472323
Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	0.558614587	0.470575601	0.572182539	0.345789105
Cadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4	0.670311347	0.314799696	0.572281415	0.231349006
Epimerase family protein SDR39U1 OS=Homo sapiens GN=SDR39U1 PE=1 SV=2	0.596523829	0.194400102	0.57301008	0.151228905
Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2	0.433930805	0.422607392	0.573908172	0.136921093
Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=1 SV=2	0.552396161	0.477260798	0.574422127	0.683899879
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	1.047635681	0.961683214	0.576284176	0.763075471
Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	0.714842247	0.588815689	0.579346083	0.171268895
Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1	0.591546922	0.03390092	0.580691108	0.057752959
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	0.554142789	0.0197716	0.580891442	0.00786454
Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	0.541127307	0.005067436	0.581499803	0.000942849

Protein NDRG2 OS=Homo sapiens GN=NDRG2 PE=1 SV=2	0.722404499	0.650429428	0.581808699	0.406011492
Uncharacterized protein C2orf47, mitochondrial OS=Homo sapiens GN=C2orf47 PE=1 SV=1	2.486727004	0.583637774	0.582330117	0.339404196
Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	0.949331357	0.893695593	0.583170305	0.03885068
Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR PE=1 SV=1	0.793398285	0.876261413	0.583227109	0.267366588
Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2	1.980667929	0.093468606	0.58378922	0.122458003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	0.564061605	0.073102079	0.584056876	0.02622992
Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	0.549392598	0.74217689	0.586147927	0.812177598
SPRY domain-containing protein 4 OS=Homo sapiens GN=SPRYD4 PE=1 SV=2	1.019377152	0.795500994	0.586586984	0.617427588
Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	0.921129248	0.847486913	0.587447778	0.680068374
PI-PLC X domain-containing protein 3 OS=Homo sapiens GN=PLCXD3 PE=2 SV=2	0.611424471	0.135935694	0.587576858	0.169040203
ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	0.573446759	0.868936479	0.587781313	0.875572205
Beta-1,3-glucosyltransferase OS=Homo sapiens GN=B3GLCT PE=1 SV=2	0.319294795	0.497220606	0.587956897	0.291452408
Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	0.470525994	0.052787151	0.588178566	0.156086996
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Homo sapiens GN=NDUFS8 PE=1 SV=1	0.658089581	0.466321409	0.588186855	0.655503094
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	0.98619231	0.98845458	0.590901301	0.495881408
Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	0.667033981	0.236386195	0.592354241	0.062869787
Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3	0.754674857	0.784604609	0.592556091	0.785391271
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	0.796581746	0.643652081	0.592860674	0.536730587
ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	0.780042767	0.459201813	0.592967161	0.314450711
Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	0.721658483	0.055303771	0.593567281	0.04536042
Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	0.594585468	0.032235142	0.593781895	0.194979593
Mth938 domain-containing protein OS=Homo sapiens GN=AAMDC PE=1 SV=1	0.705990851	0.505694807	0.594239918	0.301118612
Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2	0.559096175	0.0608836	0.594790951	0.068575412
Kelch-like protein 41 OS=Homo sapiens GN=KLHL41 PE=1 SV=2	0.947433559	0.952222228	0.595180339	0.662454307
Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1	0.569182095	0.00415076	0.596713547	0.007473676
Nexilin OS=Homo sapiens GN=NEXN PE=1 SV=1	0.536865174	0.166035503	0.598815662	0.108193301
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	0.70684463	0.046218801	0.5993109	0.038047459
Acyl carrier protein, mitochondrial OS=Homo sapiens GN=NDUFAB1 PE=1 SV=3	0.719105254	0.273442596	0.599332823	0.790870428
Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	1.102485907	0.82712239	0.599890815	0.64188832

Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1	0.63825822	0.008779767	0.600039499	0.001639653
3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2	0.56743321	1.17E-05	0.600453844	0.059402712
PGC-1 and ERR-induced regulator in muscle protein 1 OS=Homo sapiens GN=PERM1 PE=2 SV=4	0.438321578	0.380208611	0.60066336	0.596440613
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2	0.615333516	0.00108275	0.600951796	0.02680929
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens GN=NDUFB6 PE=1 SV=3	0.633085672	0.218435198	0.601122674	0.270691186
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1	0.511200656	0.593204319	0.601339554	0.189730495
Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 PE=1 SV=3	0.497556232	0.702930808	0.602955923	0.72467649
Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	0.749009808	0.424977988	0.604046748	0.618694723
Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1	1.010862246	0.957631528	0.604556562	0.126569897
Muscle-related coiled-coil protein OS=Homo sapiens GN=MURC PE=1 SV=2	0.676731443	0.430291504	0.607037755	0.323178589
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	0.708182682	0.132068798	0.607374387	0.01388148
NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1	0.591476224	0.099809848	0.607521216	0.35270679
Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2	2.09655029	0.417954594	0.608198131	0.511934817
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	0.898954757	0.852484822	0.608923273	0.159524903
Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3	0.59793451	0.223118097	0.609519735	0.082889497
SH3 domain-binding glutamic acid-rich protein OS=Homo sapiens GN=SH3BGR PE=2 SV=3	0.631754636	0.274179488	0.609937213	0.102096401
Alpha/beta hydrolase domain-containing protein 11 OS=Homo sapiens GN=ABHD11 PE=1 SV=1	0.404935335	0.123039097	0.611078484	0.526759624
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	0.968943388	0.911482513	0.611138229	0.048341431
Sulfite oxidase, mitochondrial OS=Homo sapiens GN=SUOX PE=1 SV=2	0.721978912	0.02607011	0.612031069	0.157702804
Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2	0.63154636	0.3917889	0.612313992	0.128968701
Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	0.593815059	0.27374211	0.612727833	0.244879395
Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	2.874101598	0.144714102	0.613566936	0.790483117
Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	0.623703491	0.107092202	0.61419214	0.01506041
Heat shock protein beta-7 OS=Homo sapiens GN=HSPB7 PE=1 SV=1	0.656444518	0.229115203	0.615136286	0.808361411
GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2	0.66988253	0.043094441	0.618449075	0.005404743
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	0.526958693	0.511104524	0.618606692	0.458854795
Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	0.651126861	0.710560679	0.619367994	0.703210592
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4 PE=1 SV=3	0.614153289	0.027461389	0.619672389	0.027441571
RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	1.197267579	0.933526874	0.620221175	0.895133972

Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	0.670761898	0.582594991	0.621344956	0.544675112
Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	0.639870583	0.424085289	0.621825578	0.066589363
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=1 SV=3	0.64075783	0.406361997	0.622895004	0.407302886
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	0.701939088	0.694314182	0.625413958	0.598370194
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	0.68523843	0.252942592	0.626139162	0.000381573
CDGSH iron-sulfur domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CISD3 PE=1 SV=1	0.607199937	0.414361209	0.626851152	0.141219601
COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	0.749733662	0.054471161	0.627120846	0.634673774
SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1	0.689368939	0.25099951	0.627682159	0.123090103
Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2	0.503399199	0.377536893	0.628425299	0.487808913
UPF0317 protein C14orf159, mitochondrial OS=Homo sapiens GN=C14orf159 PE=1 SV=2	0.872601871	0.778338909	0.629481098	0.534357429
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	0.632059711	0.385413408	0.629749089	0.392541289
Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3	0.790363912	0.741039515	0.630139172	0.478756309
Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2	0.599169423	0.097946607	0.631161704	0.190923303
Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	0.800749527	0.571678579	0.631380894	0.765788317
39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1	0.67901849	0.172972903	0.631574271	0.237591907
Regulator of microtubule dynamics protein 1 OS=Homo sapiens GN=RMDN1 PE=1 SV=1	1.048116925	0.983425379	0.631856041	0.155390605
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens GN=NDUFA6 PE=1 SV=3	0.658359496	0.002004592	0.631893166	0.002583307
Carnitine O-acetyltransferase OS=Homo sapiens GN=CRAT PE=1 SV=5	0.709203746	0.234171301	0.632076904	0.255424589
HD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1	0.707356148	0.277094096	0.632271138	0.298981994
Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1	2.015869375	0.73975569	0.632734788	0.390635997
Starch-binding domain-containing protein 1 OS=Homo sapiens GN=STBD1 PE=1 SV=1	2.799527105	0.541529	0.633491143	0.649664819
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	0.768514868	0.202644795	0.633788273	0.727697372
NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1	0.685895982	0.004676277	0.634224805	0.001349184
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1	0.692078895	0.003754991	0.6349037	0.033514708
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3	0.685842371	0.066899717	0.636010137	0.06131725
Creatine kinase S-type, mitochondrial OS=Homo sapiens GN=CKMT2 PE=1 SV=2	0.634829947	0.391509503	0.636510101	0.544969618
Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	0.524033222	0.191868395	0.636621542	0.155548602
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	0.524698347	0.190013707	0.636655992	0.137232304
ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3	0.701684967	0.283623308	0.637916231	0.651351273

Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1	0.892498534	0.914825678	0.639704824	0.544978023
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2	0.66238281	0.268013895	0.640114718	0.178573593
Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	0.77225447	0.874562621	0.640602275	0.160920694
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	0.794112106	0.458375514	0.64119951	0.042695072
Fatty acid-binding protein, heart OS=Homo sapiens GN=FABP3 PE=1 SV=4	0.652074969	0.401209414	0.641513777	0.186605603
Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2	0.692233151	0.01468813	0.644324929	0.037649211
Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	0.749676911	0.1785357	0.645196244	0.471308887
Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1	0.647383277	0.203127697	0.645395298	0.119440697
5-demethoxyubiquinone hydroxylase, mitochondrial OS=Homo sapiens GN=COQ7 PE=1 SV=3	0.758339823	0.667240381	0.645500286	0.281882793
Mimitin, mitochondrial OS=Homo sapiens GN=NDUFAF2 PE=1 SV=1	0.55523753	0.6145069	0.645601134	0.494980514
Pyridoxine-5'-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1	0.660725868	0.732458293	0.647477168	0.590125918
Redox-regulatory protein FAM213A OS=Homo sapiens GN=FAM213A PE=1 SV=3	0.773153642	0.530408919	0.64763188	0.159458697
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	0.728928853	0.329239309	0.648185999	0.02744858
39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2	0.547557875	0.248167202	0.650409066	0.144067302
Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6	0.700669681	0.098440118	0.65188155	0.069126368
ATP-dependent RNA helicase SUPV3L1, mitochondrial OS=Homo sapiens GN=SUPV3L1 PE=1 SV=1	0.986874625	0.974866986	0.652185538	0.149942905
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	0.681533163	0.4290905	0.6524315	0.540191472
NIF3-like protein 1 OS=Homo sapiens GN=NIF3L1 PE=1 SV=2	0.750662867	0.135819599	0.652595849	0.004355308
Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1	0.547294767	0.163102105	0.652723202	0.348820299
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	0.64922377	0.083201647	0.652776027	0.181331307
Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	0.599934361	0.133686706	0.65341456	0.193399593
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	0.457183219	0.000234804	0.653578539	0.281112701
Carnitine O-palmitoyltransferase 1, muscle isoform OS=Homo sapiens GN=CPT1B PE=1 SV=2	0.608198881	0.492148191	0.653701997	0.319886208
Coiled-coil domain-containing protein 22 OS=Homo sapiens GN=CCDC22 PE=1 SV=1	0.828261619	0.923392713	0.653757579	0.586597383
Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1	0.659149699	0.001317557	0.653757986	0.328146309
ADP-ribosylation factor-like protein 8A OS=Homo sapiens GN=ARL8A PE=1 SV=1	0.660927175	0.551815212	0.654367611	0.405366212
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	0.578636067	0.758148611	0.655260329	0.151805803
Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2	0.785144437	0.765757084	0.655931685	0.656170905
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	0.615916017	0.064739019	0.656194238	0.173149601

Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	0.582605257	0.259006411	0.656338508	0.512557328
Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3	0.665679224	0.209095299	0.657812923	0.765247285
Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1	0.673534486	0.000830362	0.658490402	0.002073576
39S ribosomal protein L1, mitochondrial OS=Homo sapiens GN=MRPL1 PE=1 SV=2	0.147946135	0.512018085	0.658615309	0.344909698
Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3	0.455149337	0.702074528	0.658644371	0.522849381
Telethonin OS=Homo sapiens GN=TCAP PE=1 SV=1	0.67785214	0.321237206	0.659172333	0.252841502
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	0.681067145	0.81346339	0.659846492	0.79391402
Phosphofurin acidic cluster sorting protein 1 OS=Homo sapiens GN=PACS1 PE=1 SV=2	0.897323777	0.907399178	0.660734611	0.152288198
Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	0.646535697	0.82866019	0.661608009	0.826523006
Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1	0.891337872	0.922755897	0.662103002	0.688745975
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	0.725319879	0.401592195	0.66258293	0.00313965
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	0.678080134	0.094371483	0.663169127	0.007647162
Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4	0.673245179	0.003560672	0.663319576	0.060525309
28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=1 SV=2	1.823928433	0.667626977	0.663660737	0.219557196
Metaxin-2 OS=Homo sapiens GN=MTX2 PE=1 SV=1	0.800877732	0.382254601	0.664074578	0.369100809
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	0.64373263	0.057982419	0.664323383	0.068057157
Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens GN=COQ9 PE=1 SV=1	0.745259752	0.529437184	0.664723039	0.334591508
Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2	0.693890779	0.032711051	0.664727885	0.169873402
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	1.306646021	0.806311488	0.665059899	0.339074701
Heat shock 70 kDa protein 12B OS=Homo sapiens GN=HSPA12B PE=1 SV=2	1.754887147	0.392292291	0.665121806	0.301385403
Branched-chain-amino-acid aminotransferase, mitochondrial OS=Homo sapiens GN=BCAT2 PE=1 SV=2	0.632451042	0.430612504	0.665479869	0.457910687
Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1	0.643396297	0.720844626	0.665975388	0.007821073
Fat storage-inducing transmembrane protein 1 OS=Homo sapiens GN=FITM1 PE=2 SV=1	0.820084875	0.296888113	0.66634014	0.038897268
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDUFA9 PE=1 SV=2	0.749590896	0.355665803	0.667342446	0.039939601
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=1 SV=3	0.570867817	0.462407887	0.668147721	0.64495492
Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2	0.730130052	0.893717229	0.668219626	0.863976777
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	1.822328862	0.538762987	0.668730376	0.463390112
Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1	0.721830929	0.661115587	0.669406769	0.126217797
Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1	0.639792401	0.002827191	0.669666322	0.123845898

[Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Homo sapiens GN=ADPRHL1 PE=2 SV=1	0.757734214	0.105764799	0.670460606	0.01157258
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1	0.767022893	0.515270829	0.670735779	0.361903995
NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens GN=NDUFS5 PE=1 SV=3	0.636957695	0.304315686	0.670888769	0.52390641
Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1	0.81172853	0.114373103	0.671130143	0.195684597
Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1	0.604059536	0.803892016	0.671195011	0.165543601
Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	0.628137925	0.167520106	0.671209887	0.301967114
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4	0.700190402	0.556736588	0.671256293	0.501155794
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV=2	0.704884052	0.172533795	0.671595291	0.116092198
Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1	0.526244346	0.394202292	0.672080039	0.52249378
Probable D-lactate dehydrogenase, mitochondrial OS=Homo sapiens GN=LDHD PE=1 SV=1	0.790627614	0.803986073	0.673077503	0.01297491
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	0.709534872	0.540625691	0.673262848	0.625543416
Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1	0.670760987	0.107169703	0.67371056	0.082083292
Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3	0.655197224	0.313081592	0.673956189	0.690886319
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	0.599899824	0.800768077	0.674818008	0.774688482
Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	0.664265991	0.04486379	0.67592137	0.094675288
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3	0.704260078	0.042671859	0.675941467	0.377436191
Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	0.434399188	0.357692689	0.676925252	0.71899128
Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	0.709763482	0.129179001	0.677105399	0.307882488
Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	0.745367558	0.714497983	0.67720215	0.074708194
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3	0.619352263	0.026437029	0.677417289	0.085890457
Methionine-R-sulfoxide reductase B2, mitochondrial OS=Homo sapiens GN=MSRB2 PE=1 SV=2	1.37957502	0.424517989	0.677476922	0.159161597
Cysteine desulfurase, mitochondrial OS=Homo sapiens GN=NFS1 PE=1 SV=3	0.638997666	0.01042419	0.677802518	0.00621328
Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2	0.673848075	0.01487102	0.678584392	0.016066991
Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1	0.873006348	0.110964097	0.679604079	0.662176192
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens GN=NDUFV1 PE=1 SV=4	0.74223127	0.3971228	0.679658096	0.001531734
Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1	0.864411062	0.843997121	0.679819811	0.524618506
Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1	1.015642337	0.969223022	0.680029725	0.515544713
Pterin-4-alpha-carbinolamine dehydratase 2 OS=Homo sapiens GN=PCBD2 PE=1 SV=4	0.823272223	0.522310019	0.680724099	0.04681294
Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3	0.69073889	0.009560392	0.681514614	0.022677639

Glycogenin-1 OS=Homo sapiens GN=GYG1 PE=1 SV=4	0.801028542	0.868975222	0.681635837	0.586608171
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	0.619664699	0.566092789	0.682503928	0.48258701
Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	0.782672287	0.319232702	0.682537025	0.532561481
Kelch-like protein 31 OS=Homo sapiens GN=KLHL31 PE=2 SV=1	0.387159602	0.01443988	0.682555185	0.323482394
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	0.985844265	0.965635121	0.682847881	0.348246902
Glycerol kinase OS=Homo sapiens GN=GK PE=1 SV=3	0.748545025	0.640592515	0.68320242	0.340440899
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	0.634463019	0.130343795	0.683266861	0.037636202
Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2	0.621190955	0.266470104	0.685120623	0.461524397
Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3	0.741865059	0.094761558	0.685306558	0.074021719
Fat storage-inducing transmembrane protein 2 OS=Homo sapiens GN=FITM2 PE=2 SV=1	0.706182284	0.576320112	0.685458762	0.660279512
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	0.716164125	0.619337916	0.685776043	0.605671287
NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 OS=Homo sapiens GN=NDUFAF6 PE=1 SV=2	0.640217554	0.01342608	0.685882803	0.194269195
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial OS=Homo sapiens GN=PDP1 PE=1 SV=3	0.79082394	0.168093204	0.686325786	0.098602757
Elongation factor Ts, mitochondrial OS=Homo sapiens GN=TSFM PE=1 SV=2	0.771312704	0.03778768	0.686697156	0.067008153
Thioredoxin reductase 2, mitochondrial OS=Homo sapiens GN=TXNRD2 PE=1 SV=3	0.687749397	0.107458398	0.686930691	0.01945498
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	0.679959445	0.752073526	0.688578591	0.727342188
Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens GN=MLYCD PE=1 SV=3	0.717720491	0.281195402	0.688581474	0.255551487
ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	0.749597661	0.184444696	0.688763128	0.044167899
LIM and cysteine-rich domains protein 1 OS=Homo sapiens GN=LMCD1 PE=1 SV=1	0.712326836	0.036861569	0.68896242	0.037302889
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3	1.145720808	0.869714022	0.689950166	0.04926366
Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5	0.626029818	0.131317198	0.690279288	0.246421203
EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	0.861118739	0.723177612	0.691592134	0.281403095
Frataxin, mitochondrial OS=Homo sapiens GN=FXN PE=1 SV=2	0.83785144	0.341267407	0.691609353	0.420099199
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	0.68828949	0.002011091	0.691812692	0.371125191
COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1	0.507509114	0.066886693	0.692299306	0.046236489
Calmegin OS=Homo sapiens GN=CLGN PE=1 SV=1	0.582927238	0.600823283	0.692577834	0.064337619
Cytosolic 5'-nucleotidase 1A OS=Homo sapiens GN=NT5C1A PE=2 SV=1	0.639084222	0.138662502	0.692804343	0.1703832
Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Homo sapiens GN=SDHC PE=1 SV=1	0.708120988	0.184500605	0.694214479	0.256409287
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	0.821488133	0.755454719	0.694477245	0.91842252

ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	0.898127997	0.962681115	0.695753837	0.0580016
Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	0.703568338	0.01214324	0.69662039	0.01290812
S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=1 SV=2	1.434891963	0.448179394	0.696665053	0.53760469
Triokinase/FMN cyclase OS=Homo sapiens GN=TKFC PE=1 SV=2	0.58682244	0.369804114	0.697332092	0.657527983
Alpha-aminoadipic semialdehyde synthase, mitochondrial OS=Homo sapiens GN=AASS PE=1 SV=1	0.577233558	0.058223169	0.697426419	0.371760398
Paraplegin OS=Homo sapiens GN=SPG7 PE=1 SV=2	0.804803681	0.511740088	0.697811876	0.411814511
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	0.800964372	0.721059918	0.697986238	0.578640103
AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	0.770362621	0.334334999	0.699018628	0.310350806
AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	0.741489379	0.32168901	0.699274318	0.2483145
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 OS=Homo sapiens GN=NDUFAF4 PE=1 SV=1	0.623188849	0.585072875	0.700211442	0.327619314
LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	0.717036083	0.072432421	0.70084155	0.049638972
Blood vessel epicardial substance OS=Homo sapiens GN=BVES PE=1 SV=1	0.4169401	0.573943675	0.701947017	0.471725196
Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1	0.81700812	0.817499876	0.701982497	0.651224375
KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1	1.282322664	0.653139174	0.70233155	0.222851098
COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4	0.636901693	0.054987941	0.702988692	0.184400201
Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	1.006839785	0.972081304	0.703812014	0.369325012
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	0.725591472	0.178311795	0.704006225	0.732081473
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	0.786295823	0.300538391	0.705909103	0.439797491
LYR motif-containing protein 4 OS=Homo sapiens GN=LYRM4 PE=1 SV=1	0.734112491	0.259410203	0.705987821	0.305396587
Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3	0.815763834	0.158591807	0.706262549	0.736105621
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	0.783883375	0.277282715	0.706490125	0.199082404
Alpha-1-syntrophin OS=Homo sapiens GN=SNTA1 PE=1 SV=1	0.773690811	0.133771107	0.706528029	0.09319298
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4	0.519747003	0.01294227	0.707739108	0.019886911
NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1	0.72679699	0.01750592	0.709368251	0.098031603
Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	0.612127358	0.08413142	0.710130958	0.453455687
Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	0.700469936	0.052387118	0.710356945	0.180125907
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens GN=NDUFA8 PE=1 SV=3	0.697348149	0.098421723	0.710803808	0.023217591
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	0.75456889	0.496739209	0.710805313	0.155899197
Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1	0.701961291	0.288861305	0.711728569	0.181841299

Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3	0.669358375	0.202649504	0.711902887	0.041009221
Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	0.765910855	0.084251873	0.71195509	0.076761022
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	0.644863834	0.601402283	0.713305968	0.648541093
Proline synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=1	0.749951835	0.221109301	0.713764688	0.156660095
Protein phosphatase 1 regulatory subunit 12C OS=Homo sapiens GN=PPP1R12C PE=1 SV=1	0.654923044	0.271123201	0.71380696	0.430452913
Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6	1.020808913	0.962696016	0.713829374	0.297081202
GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1	0.563387592	0.615031779	0.713863513	0.628890216
Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3	0.587300786	0.106972799	0.714033773	0.443266094
Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	0.73333243	0.207762599	0.714167875	0.624204874
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	1.257072091	0.852861702	0.715179148	0.870984018
Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens GN=TIMM21 PE=1 SV=1	0.584360965	0.67323643	0.715508739	0.476485014
Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	0.836153252	0.928657115	0.717102895	0.574383974
Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2	0.572978221	0.046454791	0.718250459	0.202816695
39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=1 SV=1	0.694136412	0.246569693	0.718962575	0.33082509
3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3	0.574246631	0.534824073	0.719238184	0.159178406
ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1	0.705312134	0.45524019	0.719834076	0.859903514
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	0.80646719	0.80586648	0.719841859	0.57417202
Perilipin-4 OS=Homo sapiens GN=PLIN4 PE=1 SV=2	0.752053856	0.326443404	0.720423717	0.154437304
Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	0.885782001	0.555999815	0.720438752	0.03359909
Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	0.824048366	0.700827599	0.722373208	0.681156814
D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3	0.728325213	0.047443628	0.722426958	0.06838388
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3	0.671642181	0.017333699	0.723002037	0.063438378
Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	0.765614744	0.67132169	0.723961956	0.622181296
Protein FAM210A OS=Homo sapiens GN=FAM210A PE=1 SV=2	0.90105756	0.765452623	0.724183203	0.067956388
Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	1.237390681	0.609437525	0.724315954	0.223225206
Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	0.757357746	0.142528296	0.724477534	0.120424703
Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	0.99205761	0.989171982	0.726168962	0.473747492
ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	0.664562214	0.195819095	0.726345647	0.338063508
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	0.774189785	0.211867094	0.726840883	0.126939401

Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1	0.965580939	0.865928113	0.727847593	0.473238409
Transport and Golgi organization protein 2 homolog OS=Homo sapiens GN=TANGO2 PE=2 SV=1	0.674609074	0.01412403	0.728033056	0.107071199
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	0.752890155	0.372868299	0.728715838	0.4214001
Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=1 SV=1	0.695331455	0.183131695	0.730285781	0.44879669
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	0.862576832	0.440978587	0.730917768	0.004537328
Acyl-CoA synthetase family member 2, mitochondrial OS=Homo sapiens GN=ACSF2 PE=1 SV=2	0.576340637	0.003235854	0.731360912	0.250505
Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=3	0.538927251	0.339556187	0.732943309	0.833137214
Carbonyl reductase family member 4 OS=Homo sapiens GN=CBR4 PE=1 SV=3	0.426652084	0.054453209	0.733944402	0.065419637
Protein FAM136A OS=Homo sapiens GN=FAM136A PE=1 SV=1	0.801053555	0.050695881	0.734344872	0.008873369
FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2	0.708314595	0.053122211	0.734402026	0.294856697
Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	0.713733108	0.002253971	0.734692305	0.00945647
Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3	1.556288458	0.156851605	0.735089791	0.53706038
Mitochondrial amidoxime reducing component 2 OS=Homo sapiens GN=MARC2 PE=1 SV=1	0.772838163	0.469125092	0.735334136	0.45859009
Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1	1.309420911	0.519632399	0.735712831	0.488766402
Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1	0.69250831	0.052392941	0.736084294	0.211745203
NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2	1.30631476	0.569412112	0.736088686	0.87689209
Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3	1.082807469	0.88082552	0.736159097	0.701943219
Uncharacterized protein C6orf136 OS=Homo sapiens GN=C6orf136 PE=2 SV=1	0.747126182	0.573371112	0.738375175	0.521520495
cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	0.762044089	0.057082061	0.738475537	0.506708503
Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1 PE=1 SV=2	1.652118065	0.899541974	0.739148031	0.822506487
Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	0.669096392	0.796909511	0.739352917	0.879606485
COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1	0.671428007	0.051897619	0.739740722	0.219677597
Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2	0.744860123	0.294842899	0.740006186	0.225643203
Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2	0.676179133	0.766197979	0.740253288	0.838372529
Mitochondrial inner membrane protein OXA1L OS=Homo sapiens GN=OXA1L PE=1 SV=3	0.544923504	0.191961795	0.740349196	0.598315775
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	0.351711661	0.735942781	0.740802218	0.801205575
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	0.654386447	0.108626097	0.742282498	0.075307287
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3	0.696350221	0.05701001	0.742948128	0.521669686
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	0.757157043	0.190084904	0.743107662	0.250914693

NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	0.591978691	0.275953412	0.743779192	0.529376686
Ketimine reductase mu-crystallin OS=Homo sapiens GN=CRYM PE=1 SV=1	0.767993086	0.744867682	0.743798053	0.589460373
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	0.863997334	0.308370113	0.744487416	0.128547102
Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4	0.75553408	0.042837661	0.745598704	0.0540714
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	1.167838028	0.946822226	0.746063749	0.79410708
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	0.903318734	0.68186152	0.747036893	0.450140297
Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2	0.583454396	0.110326	0.747269675	0.802271605
A-kinase anchor protein SPHKAP OS=Homo sapiens GN=SPHKAP PE=1 SV=1	0.709108184	0.658676684	0.747343972	0.746963024
Probable histidine--tRNA ligase, mitochondrial OS=Homo sapiens GN=HARS2 PE=1 SV=1	0.546675133	0.073878497	0.747648438	0.398281097
Mitochondrial intermediate peptidase OS=Homo sapiens GN=MIPEP PE=1 SV=2	0.415372625	0.409466207	0.748142933	0.747623384
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=1 SV=3	0.84187488	0.705552876	0.749114153	0.101353802
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 OS=Homo sapiens GN=NDUFB3 PE=1 SV=3	0.800623884	0.801116884	0.749367912	0.864470005
Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens GN=TIMM10 PE=1 SV=1	0.798197354	0.493908405	0.749748806	0.345759511
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	0.414438202	0.472351998	0.751427681	0.305982888
Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	0.714036812	0.006981411	0.752710522	0.031984281
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	0.734145386	0.475922287	0.75430651	0.53723228
Collagen alpha-1(XV) chain OS=Homo sapiens GN=COL15A1 PE=1 SV=2	0.870040349	0.769000411	0.754492064	0.655787528
Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Homo sapiens GN=HDHD2 PE=1 SV=1	0.682636724	0.268081695	0.755560347	0.250020713
Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	0.761789837	0.124346003	0.756967923	0.146826997
Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	0.81063294	0.318852991	0.756973592	0.088912033
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial OS=Homo sapiens GN=PDK2 PE=1 SV=2	0.948247503	0.941003084	0.757153011	0.599407315
Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial OS=Homo sapiens GN=SDHD PE=1 SV=1	0.729117022	0.512216508	0.757455812	0.623633981
Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	0.609798123	0.207615301	0.758236319	0.464375108
Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	0.711819281	0.373406589	0.758335229	0.565786004
UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	0.832859299	0.303308189	0.758365737	0.537485778
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	0.818835203	0.353443086	0.759205148	0.630931616
Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	0.700688819	0.125013396	0.759309535	0.319185108
Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2	0.827809052	0.584758818	0.759941347	0.477732211

N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	0.764858729	0.864655972	0.760193264	0.869065821
Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1	1.033864623	0.952640414	0.761468493	0.871450484
Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	0.706023234	0.482225686	0.761536929	0.559531212
Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3	0.759692555	0.286100894	0.762522881	0.463163108
3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2	0.702378889	0.800073326	0.762617713	0.889733911
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	0.751099819	0.302344799	0.76350562	0.522423387
Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2	0.629227636	0.308385402	0.763598959	0.295706391
Pterin-4-alpha-carbinolamine dehydratase OS=Homo sapiens GN=PCBD1 PE=1 SV=2	0.694741647	0.152361602	0.764664557	0.474017888
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	0.55973773	0.414141208	0.764731826	0.785004675
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	0.854162785	0.1463238	0.765474038	0.09076567
Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4	0.599517134	0.043248769	0.766458522	0.317832589
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4	0.691517049	0.173244298	0.766992316	0.383020312
ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens GN=ABCB7 PE=1 SV=2	1.021322954	0.964559376	0.76732192	0.621255815
NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1	0.737611652	0.053623632	0.767483246	0.002055767
Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	0.928315511	0.918749213	0.76752566	0.626864672
Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2	0.613366352	0.172358304	0.768615282	0.456092894
Sarcalumenin OS=Homo sapiens GN=SRL PE=2 SV=2	0.794249625	0.667828619	0.769130223	0.650058627
Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3	0.839501592	0.425984591	0.769514889	0.064871646
MICOS complex subunit MIC27 OS=Homo sapiens GN=APOOL PE=1 SV=1	0.91162527	0.493307889	0.771406118	0.088077463
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	0.827218771	0.153135598	0.771782412	0.217224598
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1	0.684563422	0.499897689	0.771850301	0.394543886
Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	0.705710812	0.615983486	0.772357	0.806819081
Echinoderm microtubule-associated protein-like 1 OS=Homo sapiens GN=EML1 PE=1 SV=3	0.672499005	0.234104604	0.772531835	0.398884594
Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C OS=Homo sapiens GN=PDE1C PE=1 SV=1	0.564502297	0.530481815	0.772735433	0.288026214
Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Homo sapiens GN=ECHDC3 PE=1 SV=2	0.622219473	0.105349898	0.772906237	0.799958527
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3	0.696367216	0.077700108	0.77358065	0.928744793
Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	0.794131051	0.257537901	0.773708723	0.2223479
NLR family member X1 OS=Homo sapiens GN=NLRX1 PE=1 SV=1	0.780465875	0.3832528	0.773968638	0.497060806

Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1	0.714049028	0.300564289	0.774003987	0.585251391
5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=2	0.436848921	0.108771697	0.774170566	0.905504584
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	0.775116892	0.547640085	0.774694125	0.133344501
Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Homo sapiens GN=COQ6 PE=1 SV=2	0.75334427	0.755834401	0.776627251	0.384624988
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	0.931387436	0.853608787	0.776872799	0.6366207
Acyl-coenzyme A thioesterase 13 OS=Homo sapiens GN=ACOT13 PE=1 SV=1	0.776885462	0.719931781	0.777001388	0.717472315
ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4	0.769075786	0.841255188	0.777067175	0.859206915
LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1	0.657353733	0.192811996	0.77718438	0.1957279
tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	0.504479517	0.057887461	0.777198277	0.312558889
Striatin OS=Homo sapiens GN=STRN PE=1 SV=4	0.808525723	0.875121415	0.777250198	0.832328975
39S ribosomal protein L15, mitochondrial OS=Homo sapiens GN=MRPL15 PE=1 SV=1	0.766613671	0.226651505	0.777293122	0.238164902
Optic atrophy 3 protein OS=Homo sapiens GN=OPA3 PE=1 SV=1	0.739602844	0.214743093	0.777386765	0.322175413
Acyl-coenzyme A thioesterase 11 OS=Homo sapiens GN=ACOT11 PE=1 SV=1	0.655736844	0.03840322	0.777941305	0.41673699
Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	0.716978474	0.097151779	0.778522142	0.314323604
Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens GN=TIMM9 PE=1 SV=1	0.755654	0.375616491	0.779020641	0.526339889
Dynein light chain 2, cytoplasmic OS=Homo sapiens GN=DYNLL2 PE=1 SV=1	0.5937911	0.088804439	0.779542308	0.581035376
Xin actin-binding repeat-containing protein 1 OS=Homo sapiens GN=XIRP1 PE=1 SV=1	0.705261908	0.430040807	0.780444527	0.536543012
NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1	0.683831763	0.391216308	0.780548736	0.28091079
Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Homo sapiens GN=ADHFE1 PE=1 SV=1	0.752584174	0.073043309	0.780679708	0.243114099
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1	0.976236509	0.964540482	0.781243906	0.658620715
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	0.796141594	0.320439309	0.781422132	0.320053101
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3	0.791382145	0.079467423	0.782212501	0.098183326
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	0.913001845	0.66745472	0.782702301	0.504752576
Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2	1.002561857	0.998969018	0.782940672	0.814068377
V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	0.877664176	0.663594902	0.78320617	0.200768605
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	0.715154089	0.618576229	0.78343936	0.639925003
Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	0.766471478	0.727195978	0.783571304	0.754979491
Ubiquinone biosynthesis O-methyltransferase, mitochondrial OS=Homo sapiens GN=COQ3 PE=1 SV=3	0.736323355	0.434681088	0.783755573	0.384770006
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2	0.509213715	0.306215793	0.783928866	0.632085919

Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2	0.824864013	0.2553536	0.784233157	0.359827101
Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1	0.723212223	0.696480572	0.784634329	0.252806097
Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	0.966388076	0.984391272	0.78499345	0.854206026
Protein unc-45 homolog B OS=Homo sapiens GN=UNC45B PE=1 SV=1	0.83112395	0.569212914	0.786174012	0.528316975
ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1	0.591507379	0.348171204	0.786675574	0.248907104
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	0.754221193	0.05932888	0.787223652	0.477847993
Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	0.726163682	0.422848791	0.787606814	0.534849882
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4	0.801727278	0.357004493	0.787660208	0.221358597
L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2	0.526774375	0.000408872	0.787895393	0.553910077
Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	0.788056825	0.825981379	0.787910933	0.765116394
GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4	0.660843296	0.264845401	0.788370554	0.168212697
Mitochondrial chaperone BCS1 OS=Homo sapiens GN=BCS1L PE=1 SV=1	0.632026138	0.078356333	0.789360701	0.2642726
Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	0.759530429	0.678415418	0.789510846	0.754622281
Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2	0.730679531	0.721307814	0.789699183	0.08452151
Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	0.763197409	0.004693672	0.790083494	0.003316286
Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1	0.934114096	0.683575571	0.79021709	0.411634505
Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3	0.795946395	0.453228503	0.790745144	0.366821885
Acylphosphatase-2 OS=Homo sapiens GN=ACYP2 PE=1 SV=2	0.999339421	0.998321772	0.790813875	0.456549704
Iron-sulfur cluster assembly enzyme ISCU, mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=2	0.864806553	0.382851601	0.790993437	0.321166694
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	0.858477439	0.59635812	0.791045352	0.761627197
Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens GN=MSRA PE=1 SV=1	0.845944229	0.343737692	0.791248154	0.260024697
Methylglutaconyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=AUH PE=1 SV=1	0.665398419	0.633242428	0.791659077	0.511710584
Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	0.474174779	0.477279097	0.792055994	0.452260107
Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4	0.911959457	0.749553382	0.792428829	0.918113112
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Homo sapiens GN=MYL2 PE=1 SV=3	0.791949961	0.757874489	0.795839318	0.761876285
Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	2.028706609	0.368925512	0.79604081	0.764709473
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	0.790408893	0.612102687	0.796404704	0.763556719
Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4	0.934805705	0.854576409	0.797371867	0.264187813
cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1	0.868056312	0.374899894	0.798083976	0.567614913

Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	0.766105661	0.145306602	0.798254093	0.062732741
ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	0.780991879	0.69870007	0.798313347	0.786610782
Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	0.76437519	0.418086201	0.798503248	0.556122422
Protein NipSnap homolog 3A OS=Homo sapiens GN=NIPSNAP3A PE=1 SV=2	0.885735705	0.748248577	0.799677559	0.129090905
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3	0.839823742	0.672167182	0.799872686	0.069729909
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	0.800128652	0.317986995	0.800630914	0.101579599
Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1	0.606572695	0.69079268	0.8009464	0.769640803
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial OS=Homo sapiens GN=COA3 PE=1 SV=1	1.145753592	0.851140082	0.800976532	0.157577902
Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens GN=RABGGTA PE=1 SV=2	1.130830566	0.862817585	0.801393108	0.815584719
SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1	0.806443776	0.478092313	0.80156012	0.403674394
Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2	0.837426958	0.36058709	0.802070623	0.130341202
Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	0.394085723	0.582869291	0.803023238	0.840082884
Protein phosphatase 1K, mitochondrial OS=Homo sapiens GN=PPM1K PE=1 SV=1	1.084484852	0.665804982	0.804102196	0.570029676
Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1	0.87620455	0.363191187	0.805741365	0.134360701
10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	0.89175204	0.653904915	0.80589982	0.396244496
Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1	0.532991383	0.019731849	0.806038199	0.473956496
Nucleoside diphosphate-linked moiety X motif 19, mitochondrial OS=Homo sapiens GN=NUDT19 PE=1 SV=1	0.892754325	0.711169302	0.806505571	0.136898905
Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	0.738071654	0.569610476	0.806788613	0.357403904
Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	0.977457876	0.947964728	0.807975687	0.911130786
Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	0.809767709	0.576011777	0.808015534	0.464194596
Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2	0.831362987	0.407519788	0.808040986	0.004828779
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens GN=NDUFA11 PE=1 SV=3	0.934501725	0.809519827	0.808487852	0.464362502
Mitochondrial pyruvate carrier 2 OS=Homo sapiens GN=MPC2 PE=1 SV=1	0.810258512	0.782819688	0.809737615	0.931422114
Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1	0.625599779	0.802903116	0.810200758	0.089955412
Retinol dehydrogenase 14 OS=Homo sapiens GN=RDH14 PE=1 SV=1	0.792949725	0.527022123	0.810327468	0.177407801
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens GN=NDUFA12 PE=1 SV=1	0.805238548	0.717513919	0.810630903	0.72401309
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2	0.735255763	0.253466994	0.810934644	0.461329907
Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14 PE=1 SV=3	0.922780792	0.507871389	0.810945149	0.189116105
Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1	1.227009034	0.425109595	0.811667896	0.661876321

Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2	0.581096704	0.694149196	0.812255297	0.286397398
Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3	0.879459555	0.8244524	0.812644719	0.606898189
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	0.902792697	0.618182778	0.813624606	0.417036593
Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	0.844643142	0.648375511	0.815519649	0.715041995
ATP synthase protein 8 OS=Homo sapiens GN=MT-ATP8 PE=1 SV=1	0.882988132	0.78810519	0.816509823	0.791605473
Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	0.769199409	0.4837161	0.818675616	0.660074115
Catenin alpha-3 OS=Homo sapiens GN=CTNNA3 PE=1 SV=2	0.835112149	0.560660422	0.819082657	0.532875478
Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1	0.828367946	0.536266208	0.819856926	0.330391109
28S ribosomal protein S28, mitochondrial OS=Homo sapiens GN=MRPS28 PE=1 SV=1	1.880285932	0.449968487	0.819873754	0.730805099
AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2	1.018481897	0.959393322	0.821452416	0.58642
Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 PE=1 SV=3	1.492518422	0.374526411	0.821506395	0.617826223
Transmembrane protein 120A OS=Homo sapiens GN=TMEM120A PE=1 SV=1	0.944403884	0.689582586	0.821889924	0.457793087
Myosin-binding protein C, cardiac-type OS=Homo sapiens GN=MYBPC3 PE=1 SV=4	0.910900258	0.876304924	0.822107483	0.608911812
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	0.76704176	0.279381514	0.822269055	0.359056085
Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	0.574052818	0.387273788	0.823031759	0.490031898
Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=3	1.364274378	0.295057386	0.823828403	0.945263028
DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2	1.443646454	0.682559788	0.824439701	0.614285171
ATP synthase subunit s, mitochondrial OS=Homo sapiens GN=ATP5S PE=1 SV=3	0.741469586	0.874774516	0.8245906	0.210344195
Protein FAM162A OS=Homo sapiens GN=FAM162A PE=1 SV=2	0.779499787	0.096456103	0.824620511	0.221069202
Ras-related protein Rab-4A OS=Homo sapiens GN=RAB4A PE=1 SV=3	1.596064999	0.374659806	0.82572427	0.66860491
Muscular LMNA-interacting protein OS=Homo sapiens GN=MLIP PE=1 SV=3	1.006141058	0.988249123	0.826074895	0.722241223
Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2	0.814366765	0.496452987	0.82790505	0.714442372
Succinate dehydrogenase assembly factor 2, mitochondrial OS=Homo sapiens GN=SDHAF2 PE=1 SV=1	0.848261317	0.300000697	0.82943633	0.281803906
CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1	0.884179509	0.374809414	0.829612528	0.477852494
Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5 PE=1 SV=3	1.126405177	0.882022023	0.82995193	0.780924916
Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	0.452745594	0.643024325	0.830648264	0.703730583
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens GN=FNTA PE=1 SV=1	0.954258519	0.742298782	0.831186126	0.356206805
Gamma-sarcoglycan OS=Homo sapiens GN=SGCG PE=1 SV=4	0.650309231	0.410885215	0.832721974	0.31550011
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2	0.931948163	0.915400028	0.833822511	0.060962819

Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRQ PE=1 SV=4	0.822035783	0.250050992	0.834590119	0.499463111
Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	0.851437727	0.016695021	0.83460191	0.008737793
Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	1.254926648	0.534368277	0.834687612	0.961304128
Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	0.808764412	0.292881399	0.835116306	0.471801609
Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	0.853595567	0.453870386	0.835257915	0.622175872
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	0.78453585	0.745899022	0.835446331	0.605234981
39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2	1.056677214	0.799319804	0.835673957	0.714139521
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	1.723216586	0.798627198	0.836142751	0.796547413
Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3	0.802881358	0.797255814	0.837145155	0.833395779
Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2	0.919094838	0.728883684	0.837347713	0.343545407
Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	0.68522438	0.129159197	0.837836712	0.574794173
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	0.882626543	0.95018512	0.838063466	0.961906791
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	0.861573603	0.651161194	0.83813799	0.675174773
Prostaglandin F2 receptor negative regulator OS=Homo sapiens GN=PTGFRN PE=1 SV=2	1.140114124	0.871913016	0.838476023	0.710506201
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	0.673933015	0.091109321	0.83850695	0.647033989
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	0.966252607	0.882701278	0.839777921	0.493514299
Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2	0.634257366	0.579787076	0.84091347	0.530305624
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	0.827404312	0.146892905	0.841491555	0.561025679
Laminin subunit alpha-2 OS=Homo sapiens GN=LAMA2 PE=1 SV=4	1.052251977	0.874190807	0.842277583	0.69729501
Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	0.906965276	0.183968693	0.84331748	0.855542123
Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	0.817737735	0.730710328	0.843917469	0.759485424
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Homo sapiens GN=NDUFS6 PE=1 SV=1	0.940390534	0.831673622	0.844395645	0.459654897
Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4	0.839434638	0.791749179	0.844698001	0.793378711
Lysophospholipase-like protein 1 OS=Homo sapiens GN=LYPLAL1 PE=1 SV=3	0.741124489	0.45647651	0.84492857	0.510286689
Methylmalonyl-CoA epimerase, mitochondrial OS=Homo sapiens GN=MCEE PE=1 SV=1	0.863095752	0.808865726	0.845726066	0.740049601
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	1.070575456	0.693020105	0.846298665	0.737436473
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	1.214654494	0.701956928	0.846944461	0.624873877
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	0.847944833	0.149258301	0.847858529	0.449644297
TOM1-like protein 2 OS=Homo sapiens GN=TOM1L2 PE=1 SV=1	0.850963889	0.349846303	0.848813563	0.504434824

Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	0.850890779	0.788104117	0.849007458	0.844533026
Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1 SV=2	1.035392094	0.860089123	0.849274949	0.44273439
Sarcolemmal membrane-associated protein OS=Homo sapiens GN=SLMAP PE=1 SV=1	0.867264313	0.527073383	0.849650168	0.267418087
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	0.897583879	0.783693373	0.851597289	0.672357023
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	0.805777122	0.634791613	0.852263496	0.704280615
6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	1.175589974	0.945040524	0.852354336	0.918461025
Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2	0.947641839	0.870572329	0.853353733	0.765522718
Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2	1.697478209	0.687213004	0.853912633	0.691799879
Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2	0.476306383	0.503535628	0.854671627	0.735924125
Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	0.761070353	0.598578215	0.855372744	0.1516532
C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4	0.769668311	0.257077903	0.855447325	0.197467104
Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2	0.940028132	0.924579203	0.855716009	0.734955013
Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2	1.14424028	0.770323813	0.855857357	0.466517687
Microtubule-associated protein RP/EB family member 2 OS=Homo sapiens GN=MAPRE2 PE=1 SV=1	0.604911645	0.716465116	0.856308077	0.839790583
Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	0.895461966	0.922847807	0.856308077	0.898022294
Alpha-parvin OS=Homo sapiens GN=PARVA PE=1 SV=1	1.339466093	0.392480791	0.857852891	0.659868419
Protein kinase C delta-binding protein OS=Homo sapiens GN=PRKCDBP PE=1 SV=3	1.371939925	0.361070991	0.857888948	0.795997381
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	0.870247765	0.273155212	0.858186385	0.240244195
5-oxoprolinase OS=Homo sapiens GN=OPLAH PE=1 SV=3	0.729539902	0.156100199	0.858399342	0.575874984
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	0.791097945	0.183535799	0.85900982	0.448261887
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	0.72804999	0.754951417	0.860540747	0.571487784
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	1.119832256	0.49195981	0.860548163	0.871023893
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	0.880872517	0.7153337	0.861382861	0.767945409
Myozenin-2 OS=Homo sapiens GN=MYOZ2 PE=1 SV=1	0.97469588	0.963521779	0.861650066	0.808763087
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	0.790282677	0.858776689	0.862151477	0.859413385
Synemin OS=Homo sapiens GN=SYNM PE=1 SV=2	1.232232924	0.648818612	0.862740597	0.340860486
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=Homo sapiens GN=COQ5 PE=1 SV=2	0.592554333	0.275739312	0.862795613	0.742409527
PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5	0.885819603	0.426990896	0.863385614	0.354703695
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	0.831000285	0.893737614	0.863487018	0.903432786

Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3	0.95059109	0.631075621	0.86522775	0.456026286
Myomesin-3 OS=Homo sapiens GN=MYOM3 PE=2 SV=1	0.911972743	0.734790385	0.86542395	0.718038678
Sorbin and SH3 domain-containing protein 2 OS=Homo sapiens GN=SORBS2 PE=1 SV=3	0.923917271	0.738538802	0.867225939	0.762013793
Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2	0.849759906	0.305546194	0.867395241	0.607388616
Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2	0.947484711	0.822358608	0.867438833	0.381381303
Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2	0.752622729	0.294966698	0.86878029	0.63510263
Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1	0.851405839	0.59286052	0.869092892	0.520800471
Haloacid dehalogenase-like hydrolase domain-containing protein 3 OS=Homo sapiens GN=HDHD3 PE=1 SV=1	0.778011509	0.633000076	0.869176728	0.791127205
Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2	1.04071483	0.724920571	0.871494613	0.32882151
60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	1.086435774	0.541631818	0.87295302	0.946822226
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	1.076142672	0.891126871	0.873159555	0.791820288
Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	0.826507733	0.60346508	0.873627233	0.785537004
LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4	0.796645821	0.305184513	0.874355889	0.862973392
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	1.050313941	0.731428921	0.874488238	0.617992699
Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2	0.451634856	0.710853219	0.875246732	0.786223412
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	0.870214453	0.466016203	0.875311849	0.393815994
Phosphomevalonate kinase OS=Homo sapiens GN=PMVK PE=1 SV=3	0.708508846	0.123897798	0.875750292	0.611359715
Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2	0.898592104	0.903847873	0.8762591	0.87382251
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	1.07239044	0.833216608	0.877242988	0.628608584
NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3	0.820330438	0.417201191	0.877257666	0.620361626
TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2	0.927970873	0.593492627	0.877550143	0.256897688
Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	0.779966105	0.84481442	0.878900704	0.886791825
Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4	0.809941514	0.487629712	0.880657695	0.372541785
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	0.805695938	0.757374704	0.881172963	0.85379678
Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	0.880586326	0.716640413	0.881419895	0.80106473
Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=6	1.013339402	0.990527987	0.882189725	0.944785774
Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3	0.843859741	0.797171116	0.882999099	0.853040516
Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=1 SV=1	0.945704296	0.954156876	0.883116041	0.67757529
Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2	0.883738825	0.488264889	0.88348901	0.449149013

Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	0.78398909	0.444968194	0.885667438	0.441756189
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	0.822707352	0.957861185	0.885833728	0.974329591
Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1	0.569558465	0.655644417	0.886763029	0.531805873
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	0.9191886	0.672447324	0.886991908	0.821923018
Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2	0.765324098	0.668381095	0.887081579	0.644245028
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	0.987015823	0.972308099	0.887256377	0.735628307
Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1	0.732707014	0.717645586	0.887576032	0.351062596
Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	1.057548639	0.924630523	0.888274629	0.643532217
COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=1 SV=1	0.753183875	0.2384018	0.888291184	0.895659387
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	0.738214938	0.254849404	0.889008997	0.597390711
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	0.969015693	0.916959584	0.889205009	0.509080708
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	0.827281751	0.919467092	0.8913983	0.956591785
Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	1.270924379	0.322129905	0.892148187	0.861579001
Protein-cysteine N-palmitoyltransferase HHAT-like protein OS=Homo sapiens GN=HHATL PE=2 SV=1	0.839892188	0.695582926	0.892273164	0.750211477
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	0.988227305	0.955275714	0.892741594	0.621870399
2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3	1.0155768	0.970808625	0.893529718	0.6001544
Adenylosuccinate synthetase isozyme 1 OS=Homo sapiens GN=ADSSL1 PE=1 SV=1	1.030156733	0.942199588	0.894868183	0.903367221
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1.020530545	0.990439177	0.895558234	0.551115096
Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	13.89481914	0.136748403	0.89673548	0.877492487
Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	1.003546012	0.987991393	0.897140193	0.625181496
26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	0.772476346	0.442908287	0.8980256	0.822215974
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	1.017701049	0.947670281	0.898388662	0.154293701
Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	0.793890853	0.1298884	0.898823086	0.548068285
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	0.986195208	0.948417783	0.898832813	0.576686502
Nebulette OS=Homo sapiens GN=NEBL PE=1 SV=1	0.989524867	0.958831012	0.899035589	0.336234987
Methionine-R-sulfoxide reductase B3 OS=Homo sapiens GN=MSRB3 PE=1 SV=2	1.021639579	0.872564673	0.899716644	0.606140792
MICOS complex subunit MIC26 OS=Homo sapiens GN=APOO PE=1 SV=1	0.918221389	0.94108212	0.899960369	0.967175484
Synaptojanin-2-binding protein OS=Homo sapiens GN=SYNJ2BP PE=1 SV=2	1.105789916	0.728383482	0.900301517	0.430604696
Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3	0.713666861	0.682405591	0.900978008	0.56049943

Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1	0.853163662	0.172011897	0.901163941	0.409516513
3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	1.140331723	0.901876926	0.903910639	0.920827687
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	0.736686248	0.201827303	0.904089696	0.748447716
Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	0.814186393	0.151745096	0.904793169	0.451589406
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	0.948360816	0.692653418	0.905979278	0.619710088
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	0.870971607	0.589443028	0.906158275	0.62551558
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	0.994839732	0.978610516	0.907900751	0.582151473
Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	0.666822682	0.714511693	0.908110982	0.754934371
ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	1.394845415	0.428700387	0.909392658	0.661094129
Reticulon-4-interacting protein 1, mitochondrial OS=Homo sapiens GN=RTN4IP1 PE=1 SV=2	0.665982948	0.625080287	0.909709524	0.871195793
Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1	0.914647784	0.888334274	0.909764971	0.764300704
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	1.10989815	0.764732778	0.909769904	0.706300318
1,4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=3	1.101764146	0.771675706	0.910484816	0.581255972
Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	0.933964021	0.670006812	0.910524545	0.795540571
Pyruvate dehydrogenase protein X component, mitochondrial OS=Homo sapiens GN=PDHX PE=1 SV=3	0.966420697	0.875513315	0.911277964	0.627550185
Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1	0.810156079	0.075104237	0.911559592	0.872690618
Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1	1.751821549	0.370818794	0.911695913	0.883231282
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	0.96360274	0.649353087	0.914055881	0.280982494
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	0.966261065	0.880851626	0.914505593	0.726047873
Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1	0.948107212	0.923294187	0.915563906	0.900659084
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	0.776699662	0.679247022	0.915806295	0.91413039
Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=1 SV=2	0.897693476	0.806576729	0.916268641	0.733679473
Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2	0.919297593	0.827779412	0.916743175	0.745281518
Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	1.082632716	0.799354374	0.916802088	0.832355618
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2	0.948586558	0.772362113	0.917474913	0.70473212
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	1.125537361	0.460741997	0.9175836	0.546408594
NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2	1.205383599	0.543465972	0.917783178	0.5638358
Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1	1.185921162	0.709558606	0.918833897	0.670089602
Coenzyme Q-binding protein COQ10 homolog B, mitochondrial OS=Homo sapiens GN=COQ10B PE=2 SV=1	0.674719657	0.832389474	0.918932639	0.848807812

Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	0.741626846	0.004067056	0.919547004	0.879453778
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	0.981484309	0.879618227	0.920074083	0.521128774
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	0.94740927	0.904469371	0.920560246	0.851018429
40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	0.9643936	0.777811885	0.920964611	0.800485015
Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	0.862814249	0.221006498	0.921439063	0.435529411
UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	0.890297564	0.835473299	0.922202144	0.880041122
39S ribosomal protein L13, mitochondrial OS=Homo sapiens GN=MRPL13 PE=1 SV=1	1.060270519	0.822171271	0.922883836	0.879333615
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	1.490458461	0.100213103	0.923251936	0.763411582
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	1.072958376	0.481106788	0.923905263	0.719408929
Myomesin-1 OS=Homo sapiens GN=MYOM1 PE=1 SV=2	0.85229692	0.3362571	0.924238333	0.701226771
Heat shock protein beta-6 OS=Homo sapiens GN=HSPB6 PE=1 SV=2	0.924123889	0.75840199	0.924563082	0.752619982
4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3	0.935231444	0.920359612	0.924957306	0.802246928
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	0.888373215	0.589768112	0.925142963	0.643941879
Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	1.252770928	0.790770113	0.925256843	0.94087261
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	1.274352566	0.729805827	0.925681689	0.808209479
Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	1.313799217	0.178453997	0.927747961	0.549007177
Oligoribonuclease, mitochondrial OS=Homo sapiens GN=REXO2 PE=1 SV=3	0.725249394	0.754022777	0.928034626	0.876180887
Protein quaking OS=Homo sapiens GN=QKI PE=1 SV=1	0.564346515	0.457564205	0.929708472	0.786671102
Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1	0.939434602	0.813811123	0.930126176	0.699022889
Dual specificity protein phosphatase 3 OS=Homo sapiens GN=DUSP3 PE=1 SV=1	0.844132577	0.325950503	0.930404819	0.805162013
Metalloendopeptidase OMA1, mitochondrial OS=Homo sapiens GN=OMA1 PE=1 SV=1	0.464655506	0.4270823	0.932115818	0.607613087
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	0.809298502	0.304404289	0.932424363	0.668072522
DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1	2.368842547	0.300518394	0.933006367	0.657192886
Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	0.89971346	0.763086379	0.934246738	0.695385516
Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3	0.924604966	0.317809403	0.934281699	0.582934201
Iron-sulfur protein NUBPL OS=Homo sapiens GN=NUBPL PE=1 SV=3	1.143732546	0.920450211	0.934331441	0.944166422
Protein phosphatase 1B OS=Homo sapiens GN=PPM1B PE=1 SV=1	1.023141283	0.966320097	0.934439683	0.670875072
60S ribosomal protein L3-like OS=Homo sapiens GN=RPL3L PE=2 SV=3	1.221555514	0.78935349	0.934447594	0.88973701
Poliovirus receptor OS=Homo sapiens GN=PVR PE=1 SV=2	0.841782712	0.196095303	0.936015879	0.625183105

Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	0.742210846	0.422730088	0.937034986	0.643028021
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	0.979056959	0.988161922	0.937172857	0.925760508
Dystrobrevin alpha OS=Homo sapiens GN=DTNA PE=1 SV=2	0.928956172	0.868264079	0.937937586	0.906119406
Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=4	0.437253099	0.140931994	0.938879019	0.963504076
Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3	0.381724251	0.181044295	0.939324358	0.905955315
Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2	0.405023081	0.53068769	0.940729374	0.949402213
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	1.14182818	0.878372908	0.941984137	0.929256976
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=1 SV=3	0.669043561	0.689208925	0.942246011	0.941898286
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	0.965568824	0.923930883	0.942696352	0.882625222
Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4	1.025370519	0.956058323	0.942784289	0.82512027
MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1	0.9966125	0.980638087	0.943240554	0.758896112
Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3	0.369277462	0.419116795	0.944699234	0.555205226
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	0.738542634	0.466881692	0.945454775	0.923397422
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	0.842860426	0.109407902	0.947392257	0.885433078
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	1.009678696	0.978867114	0.947421896	0.872196913
Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	0.830737269	0.408231288	0.947526021	0.751561522
Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2	2.065887758	0.242930502	0.947646335	0.845956326
Prostaglandin G/H synthase 1 OS=Homo sapiens GN=PTGS1 PE=1 SV=2	0.867031969	0.945866227	0.947838536	0.934581876
Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3	1.046303625	0.930126429	0.947973283	0.938574016
Trimethyllysine dioxygenase, mitochondrial OS=Homo sapiens GN=TMLHE PE=1 SV=1	0.79928386	0.1962789	0.948103676	0.852918923
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	1.006034812	0.98439312	0.94838955	0.818622589
Neural cell adhesion molecule 1 OS=Homo sapiens GN=NCAM1 PE=1 SV=3	3.248548415	0.502219081	0.950211743	0.963872612
Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	0.948683751	0.59921658	0.951350802	0.688799381
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	1.240538291	0.741546273	0.951735595	0.704569101
Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	0.727627257	0.167397201	0.952616878	0.880891025
Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1	0.996232216	0.984123528	0.952969025	0.769889712
Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1	0.488709121	0.163483605	0.954932024	0.892631829
Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4	0.623474816	0.755571425	0.955054225	0.919475377
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	0.925062571	0.682067096	0.957184175	0.864636481

Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	0.891175095	0.348534793	0.957582883	0.889388084
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	0.813015367	0.526687384	0.959882717	0.877772629
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	0.998556079	0.996990025	0.959899303	0.947936475
60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	1.121310282	0.47862491	0.960220913	0.902420878
Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2	0.898307176	0.485485703	0.960384162	0.889717519
EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	0.90271857	0.927861273	0.963416154	0.982276678
NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1	0.88765408	0.930942774	0.963690082	0.885202587
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	1.55761225	0.212056205	0.965322708	0.984892428
PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	1.335673086	0.560385406	0.965613505	0.956212521
S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	0.988658127	0.967913389	0.966857116	0.967720687
Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	0.965901697	0.778582692	0.966925321	0.823490918
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	0.711329096	0.347339809	0.967695413	0.895403028
39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1	1.108815961	0.865871906	0.967809737	0.938893616
Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1	0.898369323	0.837625384	0.968473329	0.937373817
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	0.997785951	0.98702991	0.968695661	0.822777689
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	0.930783281	0.844242871	0.968961295	0.920320213
Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3	0.911061316	0.755253911	0.969217669	0.802695811
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	0.99764557	0.997346103	0.969599234	0.960074782
EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	1.058719459	0.767448604	0.969870074	0.901658475
Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3	0.967047824	0.699201524	0.96999983	0.748930514
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	0.904595103	0.725199223	0.970717312	0.924136877
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	1.41507707	0.2744008	0.971041605	0.958988488
LIM domain-binding protein 3 OS=Homo sapiens GN=LDB3 PE=1 SV=2	0.896392336	0.792053878	0.973579922	0.974245906
BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	0.86020251	0.416938007	0.973999082	0.922986507
Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	1.745375859	0.833365917	0.975943026	0.993138015
Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	0.988618978	0.937708318	0.975975387	0.903586805
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	0.984570777	0.956080317	0.976282182	0.953429282
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	0.985155622	0.948560476	0.976562454	0.924804211
ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2	1.050320648	0.867399871	0.977283988	0.912576795

MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1	0.919238459	0.612033308	0.977349915	0.881784618
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	0.974792834	0.976732671	0.978055394	0.885433972
Sorting nexin-2 OS=Homo sapiens GN=SNX2 PE=1 SV=2	0.745519255	0.525578022	0.978268686	0.956396222
S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	1.091786949	0.840964317	0.978997543	0.976913571
Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2	0.607620888	0.39324379	0.979666045	0.953854203
Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2	1.35124304	0.889879584	0.980064471	0.992411971
Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3	0.781140748	0.086694077	0.980490151	0.984371424
Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=2	1.128892693	0.797310174	0.982307682	0.959729195
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	0.898515393	0.243775204	0.983694234	0.939567924
Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1	0.894175288	0.654539227	0.983775564	0.937289715
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	1.019546516	0.962427378	0.984093172	0.840431392
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	0.899517611	0.85973978	0.984198702	0.960913122
IST1 homolog OS=Homo sapiens GN=IST1 PE=1 SV=1	1.234932301	0.239889607	0.98428104	0.943383694
NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2	1.192758174	0.298044413	0.984913066	0.929104626
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	1.265058504	0.700169027	0.985214862	0.955109715
Tensin-1 OS=Homo sapiens GN=TNS1 PE=1 SV=2	1.312920064	0.362155706	0.986354768	0.964271486
Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5	0.984465167	0.924055874	0.98666035	0.954397082
Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	3.831131418	0.470331192	0.986840492	0.93220818
Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3	0.877206019	0.758831084	0.987376434	0.977256417
Ferrochelatase, mitochondrial OS=Homo sapiens GN=FECH PE=1 SV=2	1.171322714	0.729802787	0.98818528	0.972254515
Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	0.972710649	0.955337584	0.988195058	0.969861627
Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	0.918267726	0.887077391	0.9882145	0.986436486
Heat shock protein beta-3 OS=Homo sapiens GN=HSPB3 PE=1 SV=2	1.103986315	0.351752102	0.988254548	0.931861877
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	0.957656237	0.992114425	0.989580664	0.996940911
Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	1.210254504	0.482380509	0.989791305	0.961842418
Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1	1.682007186	0.748900712	0.98986477	0.934612811
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2	1.208279427	0.697501183	0.989952031	0.98067677
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	1.062971356	0.620467782	0.990348111	0.955396175
Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3	0.881845105	0.739859819	0.991192286	0.984974027

Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 PE=1 SV=1	0.850866872	0.777139187	0.991524428	0.946972072
Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	1.469951458	0.583634079	0.991668953	0.986222982
Sodium/calcium exchanger 1 OS=Homo sapiens GN=SLC8A1 PE=1 SV=3	0.962529695	0.910861015	0.992585376	0.970144987
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	1.005264855	0.971860528	0.992945132	0.930158019
26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	0.912824406	0.586815476	0.993380078	0.942566216
LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 PE=1 SV=4	0.453624575	0.576345086	0.993935042	0.965646088
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	0.863369263	0.327877402	0.994042694	0.975442529
Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1	0.914078491	0.612864196	0.996366282	0.981422305
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	1.03256994	0.822120607	0.996543002	0.987138391
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	1.061485051	0.879327416	0.996640325	0.979146123
Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1	0.919475139	0.688089013	0.997022935	0.985154688
4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	1.015466278	0.829841316	0.997169068	0.978947818
Transmembrane protein 143 OS=Homo sapiens GN=TMEM143 PE=2 SV=1	0.940433864	0.892204225	0.997403704	0.994841278
Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2	0.803647306	0.517300189	0.997416749	0.995226622
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	1.26609366	0.35519281	0.998832399	0.995711982
Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2	2.00894019	0.454421699	0.998885207	0.999780178
Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4	0.773466954	0.681236327	1.00050445	0.999633789
Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1	0.423811766	0.306141585	1.001236655	0.998685181
Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	0.92550429	0.934392512	1.001695044	0.989005506
PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1	0.943897528	0.547123194	1.001888377	0.992369771
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	0.876123928	0.331030011	1.002032947	0.992703378
Delta-sarcoglycan OS=Homo sapiens GN=SGCD PE=1 SV=2	0.875911415	0.898857176	1.002298859	0.998827696
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	0.843670396	0.096844308	1.002590675	0.99179858
Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2	1.018607857	0.975857019	1.004620464	0.990563393
B-cell receptor-associated protein 29 OS=Homo sapiens GN=BCAP29 PE=1 SV=2	0.918159781	0.605348229	1.005398773	0.977689385
Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2	0.892963208	0.631361127	1.005591489	0.982037723
Phosphoglucomutase-like protein 5 OS=Homo sapiens GN=PGM5 PE=1 SV=2	1.191772112	0.583854914	1.006902508	0.986163676
Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	1.311289181	0.568908572	1.008808334	0.996117473
Atypical kinase ADCK3, mitochondrial OS=Homo sapiens GN=ADCK3 PE=1 SV=1	1.031042858	0.955046713	1.008929425	0.987032175

6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2	1.277869859	0.69341898	1.009567146	0.980051279
60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	1.194428653	0.163871795	1.010523475	0.96136421
Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	1.047061622	0.920854986	1.01244714	0.975180209
Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	1.058696477	0.762626529	1.012727473	0.94510901
ADP-ribose pyrophosphatase, mitochondrial OS=Homo sapiens GN=NUDT9 PE=1 SV=1	2.186493918	0.419778109	1.014129445	0.965256214
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	1.50414938	0.758497179	1.016109584	0.979513407
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	1.09490113	0.632220984	1.016387208	0.929710984
Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1	0.964871026	0.938479722	1.016593461	0.970892787
E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3	2.489896067	0.141067997	1.016899948	0.993647575
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0.753501715	0.628000677	1.017258428	0.984783471
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5 OS=Homo sapiens GN=NDUFAF5 PE=1 SV=1	0.907955978	0.890820622	1.017511563	0.987558424
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	0.822242619	0.393250793	1.017788842	0.862197399
Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	0.84439352	0.784692585	1.019371516	0.960549176
Striatin-3 OS=Homo sapiens GN=STRN3 PE=1 SV=3	1.146868039	0.870565414	1.019492182	0.979569495
Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4	0.814082332	0.830127478	1.020393807	0.975289106
CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1	1.06669081	0.931161821	1.020488893	0.981792688
Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	0.994035744	0.987045586	1.020662166	0.938694417
BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1	0.938288723	0.927873671	1.021646671	0.9515149
ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Homo sapiens GN=CARKD PE=1 SV=1	1.45692163	0.242477	1.023320888	0.916222811
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	0.836246276	0.366148114	1.023549386	0.957744122
Serine/threonine-protein kinase Nek7 OS=Homo sapiens GN=NEK7 PE=1 SV=1	0.910824794	0.890040874	1.025813393	0.978004515
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	1.096456759	0.716453314	1.027328597	0.832270324
N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	1.039209926	0.93742162	1.028195999	0.97752893
Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	1.141070536	0.892526329	1.031274311	0.900276184
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	1.102318867	0.530225813	1.03149794	0.883225977
MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	0.682143124	0.332082987	1.032458865	0.914613426
Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5	1.580332354	0.369693995	1.032568351	0.968513429
Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2	0.831876201	0.767831683	1.032995713	0.990582287

Gamma-synuclein OS=Homo sapiens GN=SNCG PE=1 SV=2	0.834452886	0.696025193	1.034158537	0.966943502
Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	1.445794728	0.175001904	1.03450454	0.97525239
26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	1.19808794	0.85956037	1.03462167	0.9230088
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	0.973372397	0.853055298	1.035943958	0.820073307
Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4	0.985429435	0.874905407	1.036004026	0.668574095
Myosin light chain 3 OS=Homo sapiens GN=MYL3 PE=1 SV=3	1.029394646	0.969597518	1.037796473	0.955762088
CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=1 SV=2	1.005014404	0.99701041	1.037924109	0.902863681
60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	0.986414153	0.956588387	1.038130076	0.895343721
Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	1.188747116	0.409877002	1.039110998	0.912816823
Ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=ANKRD1 PE=1 SV=2	1.080653511	0.685101092	1.039684682	0.872677803
Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens GN=UFC1 PE=1 SV=3	1.197786426	0.759921014	1.039760778	0.908734083
cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2	0.661859825	0.363323987	1.040053735	0.933402181
Spermatogenesis-associated protein 20 OS=Homo sapiens GN=SPATA20 PE=2 SV=3	0.685839512	0.298353195	1.040076946	0.8964293
Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	0.8101614	0.937797427	1.041131584	0.965496719
Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	1.133256694	0.916002214	1.042618413	0.976578712
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	0.821290441	0.552029073	1.045176042	0.818272829
Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1	1.935447759	0.326778114	1.046349499	0.983210981
Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1	0.948671199	0.947144806	1.046878813	0.959656894
Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1	1.308029751	0.568020582	1.047483475	0.845887721
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	1.069586353	0.921031892	1.04765655	0.938310683
Scavenger receptor cysteine-rich type 1 protein M130 OS=Homo sapiens GN=CD163 PE=1 SV=2	1.351941978	0.114270397	1.048426927	0.927020609
Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2	2.162997009	0.349987686	1.048509158	0.954404891
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	1.054513305	0.83853972	1.048740324	0.85991317
Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3	1.704305701	0.329309702	1.050566495	0.705293775
Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	1.062714486	0.957047999	1.050842602	0.957262218
ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	0.541177682	0.103862897	1.051062815	0.816091776
Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1	1.199385195	0.431535989	1.051202298	0.86296469
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	1.139469564	0.384884089	1.051211321	0.754191816
Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1	0.953777112	0.700820684	1.051820933	0.831633627

Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	0.884880609	0.402227789	1.052095259	0.810914874
ATP synthase mitochondrial F1 complex assembly factor 2 OS=Homo sapiens GN=ATPAF2 PE=1 SV=1	1.064975897	0.977663219	1.053094301	0.988525391
28S ribosomal protein S36, mitochondrial OS=Homo sapiens GN=MRPS36 PE=1 SV=2	0.757036099	0.465952605	1.054062461	0.943734229
Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	0.905147757	0.722596884	1.055063984	0.787750423
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	1.156573748	0.692637384	1.055116204	0.791101992
Adenylyl cyclase-associated protein 2 OS=Homo sapiens GN=CAP2 PE=1 SV=1	0.994685435	0.998156786	1.055533085	0.973481178
Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	2.604800211	0.055666842	1.056073063	0.861611187
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	0.887790391	0.821231484	1.05649243	0.837307096
Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1	1.205209899	0.188221499	1.058952209	0.779090285
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	0.903262417	0.834742486	1.06375303	0.889020383
Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1	1.019887706	0.953986585	1.065092861	0.913673699
Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	0.768524303	0.215111405	1.067503165	0.80175668
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	0.979365695	0.96609652	1.067617084	0.904940128
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	1.010998147	0.971763909	1.068485627	0.599636972
Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1	1.890346232	0.321638614	1.068963404	0.813587487
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	1.138123176	0.660374284	1.069484966	0.753216326
Apolipoprotein L2 OS=Homo sapiens GN=APOL2 PE=1 SV=1	0.62593303	0.663605213	1.073390645	0.937558174
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4	1.016986308	0.973317325	1.074235044	0.906703591
Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	1.224565324	0.717964828	1.075157936	0.679970622
Radixin OS=Homo sapiens GN=RDX PE=1 SV=1	1.060056076	0.804775417	1.077884003	0.838141024
Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	1.130278004	0.775596023	1.078155257	0.885705888
MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1	1.062589362	0.69698292	1.079507465	0.672020018
NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1	1.168803919	0.799860597	1.080115856	0.701454818
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	1.160094989	0.397065997	1.081262846	0.618602872
GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1	1.030932619	0.92852819	1.082420586	0.570084512
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	1.151282012	0.781659901	1.082708172	0.858576894
Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	1.254565548	0.751160085	1.083064776	0.946692288
Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2	0.549651677	0.518976986	1.084196321	0.847481728
Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	1.736990495	0.296076387	1.08493032	0.818678796

Protein disulfide-isomerase TMX3 OS=Homo sapiens GN=TMX3 PE=1 SV=2	1.364846396	0.350678205	1.085170738	0.810118675
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	0.728199523	0.038775612	1.085368008	0.584651709
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	1.354388993	0.00380667	1.086848064	0.445853889
Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	1.862663193	0.641722202	1.08777612	0.798440576
Beta-taxilin OS=Homo sapiens GN=TXLNB PE=1 SV=3	0.750729913	0.595335484	1.087792483	0.784555614
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	1.100902444	0.417387813	1.088321572	0.699913621
PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP PE=1 SV=2	0.962391661	0.792539001	1.089837025	0.902186394
Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4	1.082124846	0.842137277	1.08985076	0.628298521
Long-chain fatty acid transport protein 6 OS=Homo sapiens GN=SLC27A6 PE=2 SV=1	1.179236925	0.798928022	1.089961285	0.893853784
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	1.170218208	0.594929516	1.091789933	0.49358511
Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1	1.107624574	0.680643797	1.094680808	0.566818714
Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	1.227854408	0.954601109	1.095189025	0.970662475
Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	1.054596891	0.90568608	1.095510905	0.418841809
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	1.07631437	0.4964706	1.096108398	0.366409093
Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	0.784209184	0.880936503	1.099714296	0.93874383
Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	0.806133087	0.759930372	1.100464843	0.831807971
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	0.927833952	0.767520785	1.101112774	0.818768382
ATP synthase mitochondrial F1 complex assembly factor 1 OS=Homo sapiens GN=ATPAF1 PE=1 SV=1	0.991845066	0.995470226	1.101564922	0.923133671
Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1	0.985882152	0.941398382	1.102178089	0.94919759
Alpha-2-macroglobulin receptor-associated protein OS=Homo sapiens GN=LRPAP1 PE=1 SV=1	0.814462912	0.478880793	1.105777234	0.404131204
Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2	0.807374875	0.325085908	1.106144313	0.78384608
6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	1.025068677	0.8860901	1.106687175	0.686676025
Histone-lysine N-methyltransferase SMYD1 OS=Homo sapiens GN=SMYD1 PE=1 SV=1	1.148522825	0.750040472	1.107666622	0.920276225
Beta-parvin OS=Homo sapiens GN=PARVB PE=1 SV=1	0.68357933	0.791953206	1.109051248	0.894015789
COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1	0.791059152	0.669108272	1.110275318	0.826147795
Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	0.995299249	0.992096782	1.113014607	0.788362384
Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1	1.271471175	0.42330429	1.113688198	0.742920697
Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	1.059370522	0.679742575	1.114192614	0.912854612
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	1.082558527	0.903187275	1.115386242	0.885142028

Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3	1.090017087	0.951326191	1.115396327	0.921464384
60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	1.109855345	0.206092402	1.116280877	0.365869701
Rab GTPase-binding effector protein 1 OS=Homo sapiens GN=RABEP1 PE=1 SV=2	2.570401269	0.382207394	1.116708701	0.940664709
SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	1.183491602	0.531445682	1.117201499	0.475300193
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	1.169359672	0.39588061	1.11722233	0.559383214
Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	0.612178328	0.837609589	1.118662439	0.97725898
Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2	0.905305908	0.898951411	1.121760571	0.933594584
Cardiomyopathy-associated protein 5 OS=Homo sapiens GN=CMYA5 PE=1 SV=3	1.134910408	0.84626168	1.12246184	0.926305115
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	1.133355833	0.583033621	1.122813555	0.110810302
Beta-sarcoglycan OS=Homo sapiens GN=SGCB PE=1 SV=1	1.109401503	0.929858983	1.123204817	0.908677697
Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2	1.04900688	0.753518701	1.124353641	0.261746198
Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1	0.834487667	0.623585284	1.12490774	0.917467177
Serine beta-lactamase-like protein LACTB, mitochondrial OS=Homo sapiens GN=LACTB PE=1 SV=2	0.973235978	0.938243985	1.125110971	0.798317373
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	1.299615899	0.589413583	1.125458308	0.815545619
Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=3 SV=2	1.707652305	0.165853694	1.127146418	0.826508999
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	1.101385002	0.748235822	1.127311599	0.439023793
Long-chain fatty acid transport protein 1 OS=Homo sapiens GN=SLC27A1 PE=2 SV=1	1.493252503	0.859871626	1.127974855	0.877782583
Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	1.230286195	0.06233687	1.128119418	0.208924904
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	1.302215111	0.350992411	1.129067809	0.669798911
Pantothenate kinase 4 OS=Homo sapiens GN=PANK4 PE=1 SV=1	1.436926981	0.574109316	1.129633106	0.882762372
ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	1.230245599	0.770614386	1.130521117	0.794668019
Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2	1.015505554	0.892223775	1.130620844	0.579142272
Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	1.272445148	0.206557497	1.131022676	0.604158819
Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1	0.795631665	0.835510314	1.132697554	0.704958797
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	1.163651375	0.131010905	1.13440064	0.270059586
V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4	0.746118296	0.823940516	1.134739309	0.523792088
Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	1.144003011	0.475370198	1.136423066	0.513595998
L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=3	0.884597218	0.837399125	1.136911771	0.81000638
Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1	1.113717105	0.229398996	1.138275526	0.339830101

Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	0.986363467	0.988461971	1.138569764	0.939603388
Cytochrome c oxidase subunit 7A1, mitochondrial OS=Homo sapiens GN=COX7A1 PE=1 SV=2	1.145514835	0.799057007	1.138753305	0.95933181
Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens GN=DNAJC19 PE=1 SV=3	1.017447882	0.994128585	1.139184376	0.865832627
Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=7	0.651419523	0.823304176	1.140613687	0.857773006
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	1.153187632	0.175275505	1.142742246	0.412490308
Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3	1.026636584	0.898170471	1.143272785	0.603238881
Trans-3-hydroxy-L-proline dehydratase OS=Homo sapiens GN=L3HYPDH PE=1 SV=2	0.750707944	0.93665272	1.143399321	0.664401472
3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	1.148965574	0.877465904	1.143975085	0.732632279
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	1.002094354	0.999190271	1.144669112	0.923990011
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	1.066068519	0.919092476	1.145324339	0.780862212
Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	1.219994091	0.352899402	1.145771746	0.488168597
KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	1.78118758	0.37133491	1.146126321	0.7609424
Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4	1.018772696	0.97792691	1.146492477	0.651639819
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	1.445818152	0.592916071	1.146875016	0.929402888
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	1.234366614	0.856051385	1.147163127	0.918013811
Xin actin-binding repeat-containing protein 2 OS=Homo sapiens GN=XIRP2 PE=1 SV=2	2.457750729	0.386728108	1.149439298	0.605510592
Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2	0.532666308	0.104678601	1.150060028	0.895932496
Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	1.029255144	0.798967123	1.150529527	0.379122108
Vacuolar protein-sorting-associated protein 36 OS=Homo sapiens GN=VPS36 PE=1 SV=1	0.79985217	0.434135914	1.1512403	0.750853717
Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	0.676885378	0.605223417	1.151519623	0.767737627
Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	1.626741474	0.468668789	1.152369092	0.765916288
Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	0.611567692	0.035108458	1.154690705	0.872145474
28S ribosomal protein S16, mitochondrial OS=Homo sapiens GN=MRPS16 PE=1 SV=1	1.45768924	0.701412916	1.15511667	0.931460798
Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2	0.861976865	0.752472579	1.156432164	0.836256206
Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3	0.922270177	0.244092897	1.157166453	0.483999491
Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	0.666662216	0.524818003	1.157213464	0.733915687
Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2	1.264522736	0.513898015	1.157294087	0.867667496
60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	1.090962838	0.693660319	1.160807353	0.164526999
Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1	0.444094286	0.366321087	1.162077408	0.635866225

Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	0.877616429	0.767814577	1.163932394	0.701931477
Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	1.575198099	0.790703177	1.164139228	0.80694592
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	1.125381456	0.437535197	1.166693672	0.39527601
ATP-binding cassette sub-family B member 10, mitochondrial OS=Homo sapiens GN=ABCB10 PE=1 SV=2	18.45525422	0.412307411	1.167438292	0.907572925
Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1	1.273109462	0.420358598	1.168100415	0.465460092
Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3	0.762148635	0.113820598	1.169933575	0.649368286
Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2	1.179285084	0.707249582	1.171235873	0.538027585
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2	0.993547855	0.983312488	1.171916637	0.719264925
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	1.197480192	0.711250126	1.172982281	0.913822293
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	1.139014847	0.540880322	1.173911608	0.472394586
Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2	1.002405395	0.994167984	1.17411502	0.859785914
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	1.168191835	0.1775188	1.174207383	0.897331774
Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	1.128110771	0.932856619	1.177422524	0.885239124
N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1	1.753520871	0.514681995	1.178013056	0.346982002
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	1.061887423	0.976285696	1.178036795	0.907666087
Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2	1.1602869	0.37471661	1.178237502	0.421931088
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	1.134231152	0.914245188	1.178767562	0.884853125
Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4	0.884281196	0.33984381	1.179579842	0.80785042
Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	1.165332239	0.74431181	1.181855299	0.730293095
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	1.575750529	0.131908	1.182625241	0.609717071
Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3	1.346885669	0.01346841	1.184094172	0.100499503
Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3	1.522514079	0.213152006	1.18540718	0.421213299
26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	0.930323406	0.864795625	1.186291799	0.329859614
Dynactin subunit 3 OS=Homo sapiens GN=DCTN3 PE=1 SV=1	1.38450389	0.221328601	1.188330247	0.230728805
Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2	1.230082066	0.29209131	1.191372408	0.485465586
Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	1.28735175	0.582427919	1.192551048	0.346677095
Guanylate-binding protein 1 OS=Homo sapiens GN=GBP1 PE=1 SV=2	1.517578245	0.271419615	1.19453887	0.323038697
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	1.059159319	0.891917884	1.195245042	0.61556989
Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	1.592719135	0.520310879	1.195481726	0.760145724

Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1	1.211461286	0.71769172	1.195496974	0.850740016
Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	0.831809056	0.841555178	1.198444564	0.71383357
OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1	1.358578254	0.35163179	1.19945688	0.618720472
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	1.030009879	0.937368274	1.199677992	0.339338213
Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1	0.377667171	0.513774991	1.200517381	0.665987074
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	1.028174575	0.989746094	1.202628502	0.692567587
Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=2	1.879576248	0.282875508	1.202914346	0.6076684
Cysteine and glycine-rich protein 3 OS=Homo sapiens GN=CSRP3 PE=1 SV=1	1.199260624	0.763286173	1.204555123	0.77397579
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	1.221657806	0.90220952	1.206938993	0.913522124
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	1.38332523	0.058513839	1.207305772	0.554305613
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	1.076995972	0.719014287	1.207639218	0.46773091
Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10 PE=1 SV=3	0.756387895	0.854875326	1.20807949	0.590300977
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	1.988241829	0.352799386	1.210428351	0.882402122
Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	0.622058072	0.35642159	1.211257584	0.845457315
N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3	1.256222892	0.303346515	1.21226951	0.304116696
Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	1.036235088	0.926549017	1.217723149	0.018977581
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2	1.335594721	0.602596223	1.219990986	0.801471829
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	1.471385142	0.692757726	1.221415091	0.765097082
Molybdenum cofactor biosynthesis protein 1 OS=Homo sapiens GN=MOCS1 PE=1 SV=3	0.915968193	0.82423389	1.223406617	0.794289112
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Homo sapiens GN=PPP2R5A PE=1 SV=1	0.833936571	0.79465121	1.224534399	0.687306225
Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	1.049106454	0.903242826	1.225462828	0.048516162
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	1.222667855	0.313469887	1.226496217	0.517544925
Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	0.847439686	0.835655689	1.22677271	0.320489407
Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2	1.275894558	0.77879101	1.229143116	0.843247414
WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1	0.942007197	0.695639908	1.229590829	0.85307312
Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1	1.268658519	0.000977822	1.230487955	0.005437331
Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens GN=MUT PE=1 SV=4	0.854544512	0.824585617	1.231146031	0.716878593
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	1.327785151	0.082484543	1.234581161	0.218331605
Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	1.331528989	0.178797394	1.237814468	0.372216791

Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2	0.490287654	0.636712015	1.239072748	0.961512804
39S ribosomal protein L27, mitochondrial OS=Homo sapiens GN=MRPL27 PE=1 SV=1	1.440836422	0.608603716	1.241443202	0.807016075
Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	0.786405287	0.659231007	1.243355854	0.617793918
Aminomethyltransferase, mitochondrial OS=Homo sapiens GN=AMT PE=1 SV=1	0.891217133	0.871574402	1.245688168	0.678794682
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	1.271497481	0.213076502	1.248155058	0.302498013
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	1.647085319	0.290310502	1.249024531	0.112748504
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	1.463125049	0.688189805	1.249282251	0.877488077
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	1.05398088	0.77552861	1.249681457	0.501114428
Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2	1.113735588	0.959890306	1.250956156	0.335938394
Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1	2.3150409	0.277078688	1.251591587	0.913833082
Microtubule-associated protein tau OS=Homo sapiens GN=MAPT PE=1 SV=5	0.808431596	0.672748506	1.251871104	0.701391995
Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	1.289456064	0.540102303	1.253801337	0.720793009
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	1.175827589	0.112365	1.253850063	0.023498051
Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1	1.522543647	0.882374585	1.254130122	0.911256671
Titin OS=Homo sapiens GN=TTN PE=1 SV=4	1.299733294	0.125541195	1.254582247	0.254709005
Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	1.291372715	0.097333059	1.255771087	0.394063413
Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2	1.922174971	0.282160014	1.256184798	0.482603788
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	0.834160556	0.798531413	1.256387616	0.722025394
Putative E3 ubiquitin-protein ligase SH3RF2 OS=Homo sapiens GN=SH3RF2 PE=1 SV=3	0.592472179	0.768096328	1.256898619	0.85982728
26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3	1.3586984	0.514845014	1.260306746	0.447274297
Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1	1.097583731	0.931900978	1.26055702	0.829658985
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	1.361089344	0.070557907	1.261356896	0.292153388
CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1	1.295075588	0.2327362	1.262485651	0.117662199
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	1.665127574	0.393591702	1.26424764	0.067634843
RelA-associated inhibitor OS=Homo sapiens GN=PPP1R13L PE=1 SV=4	0.831589795	0.759634614	1.268700347	0.842755497
Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	1.390623718	0.628097713	1.273075167	0.051299911
Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	1.340420578	0.676854372	1.274208646	0.64170748
Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	1.737366252	0.27588889	1.274453243	0.321341008
60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	1.153017001	0.579712629	1.276351057	0.414891392

Heat shock protein beta-2 OS=Homo sapiens GN=HSPB2 PE=1 SV=2	1.282996059	0.578208387	1.281015258	0.671258092
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	1.230255432	0.838645101	1.281935931	0.852201283
PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	1.321990277	0.253173798	1.282669619	0.294126511
Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	5.595457189	0.297713697	1.283008421	0.5718472
Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	1.271198055	0.521303177	1.285056321	0.590790272
Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1	1.163954681	0.33003059	1.28506577	0.175952002
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	0.787826502	0.592600822	1.286501213	0.214984402
Palmdelphin OS=Homo sapiens GN=PALMD PE=1 SV=1	0.854979994	0.660134375	1.287104449	0.63765341
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	1.350565698	0.706787527	1.287188189	0.620979607
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	1.070741555	0.570813179	1.287498753	0.190717101
Inactive phospholipase C-like protein 2 OS=Homo sapiens GN=PLCL2 PE=1 SV=2	0.482186101	0.201173902	1.290566394	0.321143299
Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	1.236475081	0.553202629	1.291433749	0.099082418
Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2	0.772904457	0.665927112	1.291579299	0.569184721
Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1	0.50358224	0.578335702	1.293007514	0.868487775
Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1	1.256294007	0.4133026	1.293838341	0.529103816
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	1.229919749	0.116151601	1.298465428	0.0560509
Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	1.4073979	0.634818196	1.299517449	0.840958774
Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	1.28572727	0.118946202	1.304256796	0.44713679
Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=2	0.973080747	0.971933722	1.304341667	0.879264712
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	1.578497262	0.34878841	1.305905189	0.564941883
Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	1.281489231	0.727109015	1.308941782	0.737276673
ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	1.016327731	0.991436183	1.309928619	0.333664
Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2	1.687948373	0.532937527	1.310260181	0.388256013
Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	1.436096989	0.153193504	1.312460651	0.072053231
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	0.931678218	0.865644991	1.312896125	0.595366001
Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Homo sapiens GN=ACSS3 PE=1 SV=1	1.488176569	0.438374102	1.313646353	0.652990282
Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	2.132817372	0.0263387	1.315347454	0.467161089
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	1.274270585	0.548841298	1.31798995	0.525318027
Carbonic anhydrase 3 OS=Homo sapiens GN=CA3 PE=1 SV=3	1.316433837	0.125974506	1.318843146	0.094164543

Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	0.954867239	0.950902224	1.322479112	0.777864516
von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	0.807225006	0.552488983	1.325362564	0.595343888
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	1.341935517	0.031402901	1.326933993	0.167346805
Retinol dehydrogenase 13 OS=Homo sapiens GN=RDH13 PE=1 SV=2	0.832907841	0.357642204	1.328299105	0.473284602
A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3	1.280561281	0.545400381	1.330079199	0.7811777
Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2	0.610559482	0.611265182	1.331133451	0.35554111
Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	1.285873311	0.629475474	1.33393304	0.514220417
ER membrane protein complex subunit 7 OS=Homo sapiens GN=EMC7 PE=1 SV=1	0.843834105	0.767608225	1.334158348	0.59329021
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	1.145953702	0.774043024	1.3356347	0.236567795
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	1.631517037	0.658465624	1.33565065	0.768870473
Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2	0.894945896	0.834716082	1.337985212	0.36258781
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	1.34123466	0.516670108	1.339917108	0.310705096
RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCA PE=1 SV=1	1.788390799	0.790970981	1.340411047	0.856324792
B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	1.266983148	0.093258306	1.34111844	0.01479769
Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=1 SV=3	1.434319944	0.293192714	1.342973395	0.693698525
Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	1.940050584	0.745403528	1.345880389	0.207320407
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	1.275289663	0.438301086	1.346564711	0.324472606
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	1.020228505	0.942472517	1.350337532	0.511108875
Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	1.264442015	0.289528698	1.351003548	0.244322196
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	1.297553582	0.817754328	1.351069588	0.910600305
Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	2.554318885	0.01539866	1.351370491	0.762556314
Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1	0.822016208	0.464169115	1.351875091	0.906122625
Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	1.062675849	0.945973098	1.35255691	0.33470431
Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	2.493722632	0.379640311	1.353761362	0.683308601
CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3	1.402667132	0.2411336	1.353984895	0.170056194
Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens GN=FAHD1 PE=1 SV=2	0.696314325	0.177967295	1.360537792	0.542437613
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	1.328568592	0.581551492	1.362777349	0.510107577
Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=3	1.323382183	0.249155805	1.365258671	0.490691304
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	1.339290306	0.446918696	1.366337516	0.470105499

Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	0.883367226	0.754784524	1.367343176	0.762992918
Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	1.370333803	0.775444984	1.369124833	0.583492398
Testin OS=Homo sapiens GN=TES PE=1 SV=1	0.955693139	0.89245069	1.369126844	0.02566603
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	1.171489155	0.824203372	1.37098474	0.680394173
Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	2.890478265	0.097998932	1.371118969	0.328176796
C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	1.671901377	0.678916097	1.372270177	0.557142198
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	0.777735027	0.760072529	1.372898464	0.784258723
Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2	1.433439193	0.05148587	1.372934865	0.303022414
Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	1.384848563	0.573016703	1.373067678	0.460950285
Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2	1.805073119	0.465837091	1.378617788	0.493946701
Mitochondrial Rho GTPase 1 OS=Homo sapiens GN=RHOT1 PE=1 SV=2	1.015935331	0.945758998	1.379466125	0.455257803
Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	1.47734267	0.00886816	1.381523284	0.786388218
Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	3.13042044	0.273086101	1.381571976	0.730640113
Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV=1	1.371058798	0.2618092	1.384658606	0.402301103
Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	1.530384868	0.123311102	1.386634788	0.049021911
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	1.264950246	0.361987889	1.388167836	0.194472
Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	0.994930822	0.997344077	1.388345085	0.55244571
Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1	1.058286306	0.853927016	1.388496295	0.417492598
Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	1.777466252	0.291114092	1.398848552	0.730846703
Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1	0.998069682	0.999454081	1.399549517	0.884061277
Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1 PE=1 SV=3	1.74517633	0.004623866	1.401576894	0.472772598
Perilipin-2 OS=Homo sapiens GN=PLIN2 PE=1 SV=2	1.689106686	0.782084882	1.402585868	0.870163321
Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	1.130964959	0.612666309	1.407211621	0.243898898
Prostaglandin reductase 2 OS=Homo sapiens GN=PTGR2 PE=1 SV=1	0.791604542	0.68538779	1.407989881	0.6405316
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	1.46339433	0.046511211	1.4146981	0.004485233
Laforin OS=Homo sapiens GN=EPM2A PE=1 SV=2	0.450466071	0.115192004	1.417447962	0.637066305
Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	1.406156501	0.145213395	1.421295454	0.053407609
Protein cordon-bleu OS=Homo sapiens GN=COBL PE=1 SV=2	2.021842414	0.135184899	1.421310505	0.589261115
Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3	2.207785802	0.178202197	1.423514266	0.737273276

Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3	0.996415871	0.995585024	1.423607274	0.085028186
Matrix-remodeling-associated protein 7 OS=Homo sapiens GN=MXRA7 PE=1 SV=1	1.506010905	0.165651202	1.423725304	0.231305405
AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2	0.79667563	0.387610614	1.430165403	0.751595616
Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1	1.182994488	0.340298086	1.430423053	0.501527786
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	1.571636306	0.119763397	1.431714408	0.546216786
Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1	1.569374643	0.317524701	1.432880324	0.4870525
Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2	1.595864294	0.02209292	1.432883628	0.161078006
Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2	1.636537799	0.310129791	1.43461982	0.456576586
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial OS=Homo sapiens GN=PDK3 PE=1 SV=1	0.964193741	0.987587214	1.435152179	0.436895609
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	1.968782231	0.319433004	1.435701273	0.535173178
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	1.335563144	0.454491794	1.435923191	0.513744116
Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=4	2.577963452	0.648087323	1.437938829	0.754512012
Septin-8 OS=Homo sapiens GN=SEPT8 PE=1 SV=4	1.441409069	0.188786298	1.440312079	0.188555405
Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1	0.854801654	0.924426198	1.441158464	0.79582721
Metaxin-1 OS=Homo sapiens GN=MTX1 PE=1 SV=2	1.07584987	0.877444685	1.442795904	0.332183987
Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	1.747393681	0.224153697	1.444477362	0.4712089
Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3	0.523042635	0.715749681	1.444943637	0.869442999
Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1	1.03213023	0.819967091	1.448602764	0.134343505
Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	1.230724269	0.680348694	1.448738736	0.48034659
Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1	1.719003116	0.739578128	1.448972713	0.829230726
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	1.547843878	0.142117798	1.449189239	0.256209314
Protein lunapark OS=Homo sapiens GN=LNP PE=1 SV=2	2.110212103	0.718313813	1.449759402	0.625805795
Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2	1.087389484	0.908926725	1.451185079	0.01443061
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1	1.450840849	0.242236495	1.451372887	0.266257197
Protein furry homolog OS=Homo sapiens GN=FRY PE=1 SV=1	1.067779072	0.825406492	1.453497011	0.567685783
Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	1.651626073	0.002624564	1.454867347	0.01270582
Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2	1.285785308	0.594474196	1.460114336	0.499139994
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	1.464526009	0.120105103	1.461638007	0.091606557

Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2	1.574368703	0.384777814	1.463663199	0.461547911
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	1.407639971	0.124679297	1.470541687	0.018194471
Sorting nexin-6 OS=Homo sapiens GN=SNX6 PE=1 SV=1	1.03565018	0.877971411	1.479096276	0.365583807
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	0.936424322	0.82283479	1.480897838	0.357076913
Integrin alpha-1 OS=Homo sapiens GN=ITGA1 PE=1 SV=2	1.526127398	0.043044969	1.487829346	0.541020274
Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2	1.68593785	0.522520483	1.490338508	0.7490291
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	1.316333132	0.341879189	1.491130346	0.660751224
3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens GN=BDH2 PE=1 SV=2	0.960911998	0.951364815	1.491500327	0.177294806
Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	0.822033769	0.89096421	1.492608317	0.635739982
Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3	3.169535071	0.05547544	1.494916485	0.774801016
UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1	1.671481125	0.341686308	1.496607676	0.430785805
Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	1.734923233	0.529537618	1.498842135	0.384241402
Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3	15.40278506	0.412070811	1.500669197	0.438821912
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	1.255054696	0.565605223	1.504416842	0.582035482
Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2	2.374843992	0.384564996	1.505255857	0.522631526
Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	1.422911093	0.362737209	1.50647447	0.346373498
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	1.411040219	0.1926402	1.507458937	0.227645203
Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1	0.941663948	0.968900979	1.509509554	0.774851918
Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2	1.653891993	0.130062103	1.515251213	0.148644701
Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=1 SV=4	1.662143493	0.374695688	1.515610396	0.458029985
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	1.675830091	0.259154111	1.516410821	0.337028205
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	1.58134346	0.408977687	1.51687656	0.40928629
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	1.869884799	0.00030376	1.517152272	0.119499497
Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	1.859750027	0.174422994	1.518094152	0.29598701
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	1.748408898	0.290895194	1.519230189	0.370135397
Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	1.447502669	0.209041595	1.519422951	0.579655588
Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	1.483949283	0.0150374	1.524054119	0.017402271
Syntaxin-binding protein 1 OS=Homo sapiens GN=STXBP1 PE=1 SV=1	0.210292115	0.505128384	1.525896431	0.526444316
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3	1.470755813	0.741443098	1.53064694	0.533191383

Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	0.887028862	0.665212512	1.534405095	0.2601749
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	1.16766791	0.570545614	1.535002586	0.525443614
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	0.706611409	0.598394275	1.539316144	0.406524897
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	1.258648058	0.493422806	1.547793756	0.363716304
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	1.568622787	0.80472821	1.550661197	0.752373219
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	1.474596519	0.585444689	1.552293635	0.752827287
Myopalladin OS=Homo sapiens GN=MYPN PE=1 SV=2	1.244878382	0.564730823	1.5550593	0.152529702
Protein SCO1 homolog, mitochondrial OS=Homo sapiens GN=SCO1 PE=1 SV=1	0.940167727	0.979142129	1.556147571	0.290138394
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	1.232917783	0.4750413	1.558200168	0.0380437
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	1.731295858	0.02102408	1.55999139	0.000225928
Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1	3.732192757	0.536340475	1.562802773	0.80605799
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	1.617603683	0.05084822	1.566252213	0.137440905
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	1.84355935	0.120477803	1.568828434	0.270443887
Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	1.350816454	0.206095606	1.570006882	0.732324123
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	1.692392101	0.629693985	1.572795387	0.040844399
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	1.058936502	0.949643075	1.574180359	0.588092685
Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2	1.521008035	0.375558406	1.574963574	0.39124921
EH domain-containing protein 3 OS=Homo sapiens GN=EHD3 PE=1 SV=2	1.080093256	0.907869577	1.578988848	0.149243593
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	1.279073523	0.25294441	1.579248953	0.137386993
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	1.29847789	0.312980294	1.588004281	0.233045802
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	1.203315534	0.503020406	1.590163086	0.458848506
Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=3	1.575268352	0.06597919	1.594000395	0.274759412
Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2	0.723316301	0.334869802	1.598743054	0.467433393
Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1	1.961053193	0.27365151	1.600086064	0.154944301
Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1	2.015943738	0.181061894	1.601738643	0.365876406
Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	1.571749531	0.033111371	1.602758501	0.094533801
Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2	2.513456979	0.236944407	1.604319338	0.570395589
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	1.485697172	0.505517781	1.605851246	0.184826896
Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	1.466810143	0.685511708	1.606602297	0.713205695

Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	1.434058927	0.286258906	1.606881121	5.29071E-05
Calcium/calmodulin-dependent protein kinase type II subunit beta OS=Homo sapiens GN=CAMK2B PE=1 SV=3	0.631990188	0.497274697	1.606984551	0.725361288
Sorting nexin-9 OS=Homo sapiens GN=SNX9 PE=1 SV=1	1.267924286	0.533914685	1.609387181	0.525769889
Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1	1.296644519	0.638188779	1.611158983	0.393971413
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	1.694390334	0.001255461	1.613635889	0.003302687
Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	0.844568223	0.863528013	1.615791542	0.423182309
Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1	0.563735346	0.05515578	1.617849987	0.580088317
Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	1.843801666	0.381175399	1.619685045	0.436957091
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	1.808712151	0.212649599	1.623555879	0.1620754
PDZ and LIM domain protein 3 OS=Homo sapiens GN=PDLIM3 PE=1 SV=1	1.307917888	0.915388525	1.62410675	0.867121994
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	0.784786425	0.445094407	1.626618296	0.77061832
Sorbin and SH3 domain-containing protein 1 OS=Homo sapiens GN=SORBS1 PE=1 SV=3	1.774946983	0.428566396	1.627575352	0.535238087
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	1.083723735	0.951730072	1.628461613	0.44133839
Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	1.952543913	0.666810811	1.631995692	0.532550693
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	2.596850865	0.425854892	1.634297976	0.147163302
2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2	2.481524477	0.256874114	1.642108857	0.554566085
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1	1.306903943	0.424203008	1.642884079	0.161246404
Alpha-sarcoglycan OS=Homo sapiens GN=SGCA PE=1 SV=1	1.254988228	0.590383589	1.645139933	0.589148223
Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1	1.390246095	0.740316927	1.645218821	0.58983469
Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4	1.460398908	0.801192105	1.64624668	0.312654614
Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	1.043313721	0.934294403	1.648998681	0.01308566
Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=5	1.850257971	0.518794417	1.650029161	0.216707706
RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2	1.242939131	0.706184506	1.652766967	0.267357111
NAD-dependent protein deacylase sirtuin-5, mitochondrial OS=Homo sapiens GN=SIRT5 PE=1 SV=2	1.523533739	0.332644403	1.659923732	0.177671194
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	3.35840733	0.007950985	1.664644651	0.308931112
Ribonuclease T2 OS=Homo sapiens GN=RNASET2 PE=1 SV=2	1.160389059	0.775385022	1.666184274	0.717768073
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	0.83211014	0.858211815	1.667836666	0.248944402
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	1.197199145	0.817477524	1.671528087	0.699310005
Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	0.527268219	0.743385196	1.673554783	0.256352514

Reticulon-2 OS=Homo sapiens GN=RTN2 PE=1 SV=1	0.091512992	0.506335914	1.673988104	0.190473303
Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	0.408649133	0.33141011	1.675953134	0.337349296
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	1.340849196	0.181028202	1.682774467	0.001616752
Complement component C1q receptor OS=Homo sapiens GN=CD93 PE=1 SV=3	1.870966634	0.364396304	1.689022002	0.047303569
Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	1.485454079	0.327468693	1.689863778	0.103958301
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	0.853947664	0.260481089	1.692043052	0.545777321
Serine/threonine-protein phosphatase 5 OS=Homo sapiens GN=PPP5C PE=1 SV=1	1.040024077	0.939781606	1.692828742	0.595488727
Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	1.674525266	0.469542593	1.694974405	0.122935303
Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	1.544388658	0.085909709	1.698890455	0.01604433
Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1	1.807467199	0.239466503	1.703119886	0.309812188
Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	1.048177365	0.992055118	1.708028864	0.596127927
Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	0.769063377	0.791360021	1.708955844	0.732784271
Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2	1.987275771	0.848271608	1.710583622	0.502310395
Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1	1.570883165	0.285474688	1.717501863	0.624304712
Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	1.726543413	0.229315996	1.723514519	0.413599402
Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	1.269714088	0.911318779	1.726848541	0.121883303
Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2	5.334485621	0.618353128	1.728461806	0.207716495
Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	2.508142126	0.002306582	1.729182593	0.499367505
Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3	1.119713124	0.653119683	1.729366538	0.272459686
Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=1 SV=2	0.813967714	0.561151505	1.729510227	0.320952088
Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	1.857605216	0.06776344	1.73156478	0.05998474
Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	2.549313934	0.457498491	1.734770033	0.301164389
Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	1.166032169	0.349470496	1.736450258	0.307031602
A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 PE=1 SV=2	1.254213189	0.78887248	1.739843044	0.460163504
Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1	1.718361538	0.700787902	1.742537911	0.886746228
Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	1.687773982	0.832435787	1.743921741	0.820657074
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	2.231699043	0.00700984	1.746975191	0.118960403
Integrin alpha-7 OS=Homo sapiens GN=ITGA7 PE=1 SV=3	0.873153466	0.903789997	1.747092348	0.592114985
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	1.762603472	7.67E-05	1.750174447	0.00011596

Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1	1.188808775	0.716879487	1.765708255	0.180643201
Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2	2.47309634	0.730905473	1.769620842	0.739096224
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3	1.579321203	0.603452325	1.77018883	0.787308097
Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4	1.622561173	0.04447262	1.770744287	0.251085013
Popeye domain-containing protein 2 OS=Homo sapiens GN=POPDC2 PE=2 SV=2	0.855122581	0.669993818	1.773529434	0.451984704
Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	1.281302007	0.363131106	1.774447252	0.153864294
Calponin-1 OS=Homo sapiens GN=CNN1 PE=1 SV=2	1.950296615	0.049431559	1.77732145	0.330933094
STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1	1.754447263	0.513094783	1.77977402	0.608105421
Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	1.479758867	0.690233588	1.78645337	0.731224775
Nestin OS=Homo sapiens GN=NES PE=1 SV=2	2.091237718	0.091413431	1.786730758	0.196283996
Phosphotriesterase-related protein OS=Homo sapiens GN=PTER PE=1 SV=1	1.47303525	0.2790775	1.792628361	0.109945796
A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	1.432769459	0.1268069	1.805189652	0.002057542
Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	1.858701095	0.613426685	1.811796341	0.718213499
Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2	2.583237152	0.55140841	1.814359764	0.412576407
ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2	1.742881671	0.619413614	1.816602102	0.196030498
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	1.228133132	0.289283812	1.824544125	0.49710539
Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	1.142245173	0.831387222	1.826891691	0.496880502
Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1	1.82834605	0.291893214	1.829409464	0.144230798
Myeloid-associated differentiation marker OS=Homo sapiens GN=MYADM PE=1 SV=2	1.870197043	0.113660201	1.831537408	0.222429499
Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	1.60730308	0.499563396	1.833244133	0.378256589
Fatty acid-binding protein, adipocyte OS=Homo sapiens GN=FABP4 PE=1 SV=3	1.762472561	0.636129677	1.840560396	0.456727386
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	1.593688932	0.168483198	1.842341035	0.263669789
Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	1.163650972	0.925093412	1.84366024	0.742272317
Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	2.1880593	0.005497242	1.854495444	0.037506599
Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	1.469540729	0.403567493	1.857231986	0.266780496
Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	1.99018125	0.324543715	1.862420029	0.571820676
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	2.288464172	0.001567722	1.864882515	0.000561166
Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	2.124897181	0.171545699	1.868084033	0.137106806
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	4.392764142	0.323952913	1.872361853	0.3345339

Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	0.845672438	0.937710583	1.873869865	0.261366904
28S ribosomal protein S35, mitochondrial OS=Homo sapiens GN=MRPS35 PE=1 SV=1	0.95094821	0.956040382	1.881202003	0.657402217
AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1	2.435730223	0.162148103	1.882006224	0.316244513
ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1	2.527945134	0.374666303	1.883848963	0.427325904
Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	1.166949213	0.538873613	1.887410659	0.107480302
Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	2.308605551	0.015985999	1.890196936	0.050586309
Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	1.951718705	0.0152134	1.894289249	0.000787229
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	1.350622017	0.871782482	1.89516978	0.805754483
SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2	2.038732255	0.03340438	1.899629262	0.016729631
ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	1.444424384	0.052543551	1.903438148	0.134306207
E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	1.064068505	0.928206503	1.905203465	0.053542349
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	0.96244168	0.97843349	1.9058049	0.402976096
Gamma-glutamyltransferase 5 OS=Homo sapiens GN=GGT5 PE=1 SV=2	1.792554238	0.022618709	1.90929503	0.01820273
Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	2.510539281	0.546577513	1.911302881	0.02363489
Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	1.33872551	0.788453698	1.919205212	0.652391016
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	1.483711486	0.819107711	1.923635067	0.675364673
Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	1.506744384	0.725564599	1.924536695	0.569418192
Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	1.735482627	0.700063586	1.92871292	0.692659795
Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1	1.189755512	0.218611807	1.928957736	0.497291088
Ig lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	2.530191605	0.073574603	1.94059274	0.504453719
Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	1.196410202	0.763985813	1.941661333	0.537326574
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	1.747929277	0.374805987	1.944484675	0.01599778
UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	1.257691878	0.655125082	1.947786028	0.070683964
Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	1.816237694	0.01349049	1.952572091	0.112862699
Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	1.703240572	0.039957762	1.954516515	0.04839325
CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	2.221642134	0.119401596	1.961463588	0.092733353
Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	1.710375577	0.103959396	1.962998246	0.124721996
GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2	1.379782762	0.042994902	1.966089984	0.097004861
Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	3.781367342	0.692197025	1.968812496	0.030827731

Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	1.811953077	0.100284196	1.971348892	0.054175898
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	2.053893285	0.000607699	1.971503869	0.000507982
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	2.037965285	0.000304832	1.977373817	0.063723259
Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	1.755911092	0.172372803	1.984545185	0.259359986
Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	1.948902178	0.106877103	1.985064819	0.224534303
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	1.103041863	0.794644892	1.991321478	0.237390906
Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	1.948502679	0.643159986	2.006046999	0.540496528
Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	2.59629388	0.189597204	2.013995268	0.60634762
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	1.000024379	1	2.014178182	0.650587082
Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	2.908182223	0.574812889	2.026569498	0.672347426
Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=2	2.412017521	0.145790696	2.027061656	0.377039492
CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	0.410090186	0.58273083	2.030423895	0.641815007
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial OS=Homo sapiens GN=PDK1 PE=1 SV=1	3.229337879	0.074842803	2.036122041	0.329310685
Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3	1.65710735	0.305343091	2.038311303	0.005685858
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	2.137487866	0.452238411	2.042410671	0.105403602
Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	2.058048941	0.762217879	2.04315051	0.76655668
Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	1.764788871	0.362631589	2.044873156	0.041018829
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	0.84883014	0.535799921	2.047635815	0.646537423
Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	2.347954645	0.620446384	2.047833763	0.124054998
Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	1.946983589	0.01105755	2.048817576	0.002920064
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	2.055524671	0.000381536	2.062357832	7.69527E-05
MICOS complex subunit MIC25 OS=Homo sapiens GN=CHCHD6 PE=1 SV=1	2.375606151	0.212688297	2.064113795	0.563501477
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	2.394321235	0.36656931	2.066046508	0.018641621
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	1.889912254	0.006528728	2.068073083	0.01274435
CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4	1.991281298	0.143990904	2.069652016	0.01702686
Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2	1.835117218	0.799848497	2.070186399	0.803283513
Actin-binding LIM protein 1 OS=Homo sapiens GN=ABLIM1 PE=1 SV=3	0.957864551	0.95232439	2.080199544	0.548726678
Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	2.552433369	0.364640802	2.087243464	0.410031408
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	2.156791879	0.331299096	2.094442185	0.357904196

Translin OS=Homo sapiens GN=TSN PE=1 SV=1	2.448208229	0.651557624	2.096139041	0.593912184
Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4	1.566272538	0.138023704	2.100559633	0.183817193
28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=1 SV=1	1.710011403	0.451734513	2.117783446	0.53147161
Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3	1.548949812	0.697575212	2.121713352	0.180849805
Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	4.648308987	0.0134454	2.128765633	0.33003971
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	1.491625639	0.076111957	2.131560719	0.068835393
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	2.504263552	0.140119404	2.132120644	0.147330701
Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	2.721669079	2.17E-05	2.135584377	0.004921414
S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	1.188389842	0.334967196	2.139215392	0.201907799
Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3	1.935062684	0.220324293	2.140608903	0.851557612
Corticosteroid-binding globulin OS=Homo sapiens GN=SERPINA6 PE=1 SV=1	2.018330881	0.27563861	2.149222283	0.083927803
Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	3.005322525	0.054217681	2.150467327	0.320969701
Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	2.687805703	0.528403401	2.154509348	0.502805114
Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1	1.793028195	0.248175204	2.161054239	0.181787193
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	2.294543708	0.001211877	2.163280929	0.000704373
Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	6.016474535	0.358274192	2.165501032	0.383541197
Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	1.773664993	0.802725911	2.174655781	0.208602205
Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	2.039416997	0.444226205	2.175230964	0.01168346
Arylsulfatase B OS=Homo sapiens GN=ARSB PE=1 SV=1	1.347563437	0.854148328	2.18866458	0.860333383
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	2.135941091	0.232313395	2.19334699	0.104848199
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	1.172612945	0.611965716	2.2072711	0.01254864
Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2	1.016378341	0.91988939	2.211462788	0.326595485
C-reactive protein OS=Homo sapiens GN=CRP PE=1 SV=1	0.623691017	0.297595888	2.21260679	0.840730906
Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	2.202345809	0.045092229	2.215572114	0.00243972
RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1	1.884647192	0.53990382	2.229833949	0.398137987
Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4	3.122231839	0.01393841	2.236948861	0.147967905
Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2	1.276660688	0.484901905	2.250160223	0.000180148
Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1	1.326256054	0.276648611	2.260270038	0.556745172
Mast cell carboxypeptidase A OS=Homo sapiens GN=CPA3 PE=1 SV=2	2.499455816	0.132718205	2.261131214	0.077924728

Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=4	1.065282222	0.90851748	2.27107243	0.199651703
Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2	1.132104892	0.759579182	2.273021806	0.263286293
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	1.413168298	0.885853887	2.280284343	0.722704589
60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2	0.979356205	0.968565881	2.286547906	0.48143971
Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=4	1.957058191	0.01456807	2.28689309	0.009523212
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	1.596549207	0.373478204	2.287043195	0.233441696
Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2	0.926848472	0.943063498	2.297114842	0.299510896
Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV=3	1.837498528	0.02711216	2.311360673	0.098798551
Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	1.575871008	0.610911787	2.314828808	0.370757997
Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	2.051338809	0.569605708	2.315904685	0.579368591
Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	2.879379049	0.514698923	2.329790783	0.603725612
Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4	4.163422594	0.153330296	2.342651643	0.347057909
SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	4.176437721	0.089747228	2.36790357	0.433354199
Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	1.417911926	0.311266512	2.385805712	0.020790709
Synaptopodin 2-like protein OS=Homo sapiens GN=SYNPO2L PE=2 SV=3	2.776387359	0.330309808	2.388405853	0.381384104
Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3	2.464119992	0.318556398	2.391948432	0.455773205
Synaptopodin-2 OS=Homo sapiens GN=SYNPO2 PE=1 SV=2	1.496762691	0.865336716	2.39623406	0.256738186
Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1	2.953720131	0.0122334	2.404194023	0.047113691
Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	2.409668713	0.461033195	2.404485353	0.322117805
Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	2.36223608	0.105181798	2.406636936	0.110900797
Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	1.381986678	0.846495509	2.407485797	0.435381591
Thymosin beta-4 OS=Homo sapiens GN=TMSB4X PE=1 SV=2	2.470473604	0.01250365	2.422165598	0.079084218
Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	1.386489828	0.701993585	2.428074941	0.121327497
Arsenite methyltransferase OS=Homo sapiens GN=AS3MT PE=1 SV=3	2.006851341	0.133707806	2.429065244	0.38332361
Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	2.159297389	0.003293055	2.433254034	0.000940557
Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	3.577704897	0.007831546	2.444010739	0.302646697
ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	2.005277935	0.09845522	2.446018259	0.193408906
Serine/threonine-protein kinase PAK 2 OS=Homo sapiens GN=PAK2 PE=1 SV=3	1.990066757	0.297426909	2.454716068	0.196151897
Perilipin-1 OS=Homo sapiens GN=PLIN1 PE=1 SV=2	2.845624525	0.000920325	2.461507041	0.038353499

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3	0.746703279	0.835803509	2.468956658	0.4413822
Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2	1.635416323	0.34607929	2.47341573	0.581277788
Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2	2.492114261	0.008570669	2.490003788	0.01996992
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	1.380703207	0.799700379	2.506017531	0.507223725
Membrane primary amine oxidase OS=Homo sapiens GN=AOC3 PE=1 SV=3	2.584956569	0.000192288	2.513990287	3.96782E-05
Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	2.614187672	0.065449849	2.521450691	0.088371433
Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	1.293032926	0.688593626	2.534701332	0.499089003
28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1	1.136562411	0.934243679	2.542533467	0.540297389
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	2.293415943	0.137644798	2.553098733	0.243090793
Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2	2.536456424	0.000256819	2.575639496	0.01555079
Complement C1q subcomponent subunit B OS=Homo sapiens GN=C1QB PE=1 SV=3	2.815446005	0.830767512	2.585537987	0.799131274
Heat shock 70 kDa protein 12A OS=Homo sapiens GN=HSPA12A PE=1 SV=2	2.1163139	0.485264897	2.586638198	0.236020699
Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	3.204246044	0.000501002	2.596565712	0.001634675
Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	2.943844051	0.01747906	2.604279831	0.38386181
Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2	3.382527776	0.070977382	2.607463385	0.126384899
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	2.642853514	0.146113902	2.607622453	0.468906701
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	2.655366035	0.002667488	2.608754321	0.002877688
Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	2.650034284	0.257418513	2.612370381	0.051003579
Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	2.262945729	0.197383106	2.62096536	0.007313928
ATP-binding cassette sub-family A member 8 OS=Homo sapiens GN=ABCA8 PE=1 SV=3	2.227942531	0.353955597	2.62704587	0.486532986
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	2.857084032	0.066910788	2.636327838	0.001475765
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2	2.269411848	0.428809285	2.659426584	0.26337859
Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	2.776809659	0.007730038	2.669047466	0.002363267
Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	3.202906691	0.333110988	2.673908988	0.061255459
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens GN=NDUFAF3 PE=1 SV=1	1.636978195	0.785403192	2.691168599	0.321038902
Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	2.542112005	0.165165201	2.691548747	0.4433752
Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	2.849805852	0.000547972	2.696692684	0.02942723
Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 SV=4	2.717981426	0.261593312	2.732935662	0.211158007
Desmin OS=Homo sapiens GN=DES PE=1 SV=3	1.817947134	0.098020427	2.734214827	0.01675621

14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	1.607855303	0.075470708	2.742925903	0.229325801
Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=2	2.9017359	0.373759687	2.752873358	0.603193879
Probable glutamate--tRNA ligase, mitochondrial OS=Homo sapiens GN=EARS2 PE=1 SV=2	4.371202466	0.356987387	2.753008423	0.393688589
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	3.126066798	0.397807091	2.77506821	0.262176603
Cx9C motif-containing protein 4 OS=Homo sapiens GN=CMC4 PE=1 SV=1	0.80958218	0.637503386	2.811838598	0.775547802
Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3	2.44104754	0.006473297	2.812449013	0.001892614
Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3	4.067821941	0.03132638	2.828202362	0.07316342
Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	2.82956274	0.01355026	2.836947138	0.03213777
Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	2.300025931	0.378323615	2.841242517	0.693128526
Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	2.697939657	0.004267934	2.845169456	0.001971648
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	1.564526832	0.316316307	2.856747867	0.35198459
Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	2.527345163	0.268960714	2.894806781	0.034105901
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	3.429343495	0.052379731	2.897305344	0.037975602
Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	3.28664002	0.000224752	2.900875689	0.009785079
Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1	0.269754014	0.630300581	2.918755367	0.124767996
Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	3.067460219	0.02179887	2.920470385	0.04263493
Protein FAM177A1 OS=Homo sapiens GN=FAM177A1 PE=1 SV=1	1.741595666	0.112224497	2.951719416	0.565894425
Prostacyclin synthase OS=Homo sapiens GN=PTGIS PE=1 SV=1	3.361614452	0.111336097	2.954692365	0.137125596
Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1	2.50413684	0.746671021	2.980620619	0.765427172
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	2.834178773	0.092586324	2.991335989	0.0583946
Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	2.115137543	0.02081559	2.991704577	0.032021411
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	2.178330339	0.529350579	3.000336029	0.289443612
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	3.495120082	0.00862292	3.008859045	0.019892169
Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	2.959883744	0.394007504	3.037750127	0.398611486
Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	3.088563515	0.000666379	3.048427251	0.005765616
Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3	1.226436146	0.336984485	3.069401668	0.456077904
Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	2.559991406	0.003124726	3.086339687	5.43365E-05
Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	1.557045296	0.394924611	3.143760301	0.423832089
LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	4.156808033	0.121205203	3.150969835	0.205784202

Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	4.097771266	0.009595795	3.160813873	0.00297504
Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	3.028141937	0.018745219	3.179327832	0.021778431
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	1.760577364	0.311956704	3.184267186	0.002701025
ADP-ribosylation factor-like protein 2 OS=Homo sapiens GN=ARL2 PE=1 SV=4	3.555106891	0.154608294	3.216317218	0.264789611
Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2	4.70958367	0.2131228	3.251734336	0.228666693
Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	5.303048052	0.009868966	3.290553808	0.327077001
Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens GN=PTRHD1 PE=1 SV=1	1.751098584	0.427248001	3.292848779	0.377221614
Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	0.646907946	0.598947585	3.329464388	0.079437517
Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	3.307009402	0.00198911	3.335988715	0.100683801
Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	1.091606799	0.970809996	3.344829387	0.303661793
Dermatopontin OS=Homo sapiens GN=DPT PE=1 SV=2	3.15917949	0.081260972	3.357888414	0.065583579
Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	2.877351656	0.139050603	3.387484399	0.104874499
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	1.835438037	0.621214271	3.455165851	0.006239873
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	4.814564667	0.229463995	3.457591161	0.077218883
Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	3.669048919	0.0062224	3.471391854	0.0180865
Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	4.158930992	6.33E-05	3.488281494	4.54155E-05
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	3.531112145	0.003442999	3.534751605	0.000236694
Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	1.230536781	0.653794229	3.545365224	0.36506179
Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	3.023337443	0.239436403	3.548267405	0.108184204
Prefoldin subunit 6 OS=Homo sapiens GN=PFDN6 PE=1 SV=1	1.902228936	0.503596485	3.559010032	0.715898573
Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	3.551759609	0.374321193	3.618888903	0.223010197
Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4	2.06480515	0.426021397	3.643147672	0.295708805
Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	6.199816321	0.286443502	3.752425419	0.068836197
Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1	4.049830841	0.01697248	3.799089041	0.019202581
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	4.442359525	0.01044344	3.799913367	0.143620104
ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	3.797548047	0.275877714	3.801328805	0.323268086
Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3	1.251295395	0.264803201	3.851774372	0.70556128
Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3	2.998767674	0.057954099	3.900649003	0.01222633
Target of Nesh-SH3 OS=Homo sapiens GN=ABI3BP PE=1 SV=1	2.984928502	0.004428824	3.900866669	0.085180767

60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	3.126408748	0.220682904	3.996748232	0.252316892
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	4.647615576	0.141556799	4.011240989	0.124105498
Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3	5.94266765	0.001937294	4.06532496	0.007026166
Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	4.986195709	0.274219096	4.073160568	0.431173891
UPF0160 protein MYG1, mitochondrial OS=Homo sapiens GN=C12orf10 PE=1 SV=2	2.172194111	0.202727407	4.236596888	0.111136198
Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	2.789408829	0.000165889	4.270885243	1.35427E-05
Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	4.093595912	0.056313392	4.32383446	0.01074463
Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2	4.117732449	0.284068495	4.330603521	0.089002587
NudC domain-containing protein 3 OS=Homo sapiens GN=NUDCD3 PE=1 SV=3	1.551635684	0.727097571	4.375992187	0.358155102
Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	3.109018651	7.84E-05	4.379505057	9.06807E-05
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	4.625458289	0.02048631	4.411310711	0.01151778
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	4.444987693	0.006178602	4.426664897	0.001038925
EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	4.372804333	0.417968392	4.467121436	0.410077304
UBX domain-containing protein 6 OS=Homo sapiens GN=UBXN6 PE=1 SV=1	1.037684656	0.948951781	4.535990834	0.661503613
Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	4.494345675	0.05153507	4.598988863	0.00100664
Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3	2.863728673	0.596832097	4.710364465	0.656389713
Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1	5.07469202	0.505734503	4.878358035	0.515476286
Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	5.49414934	1.69E-06	4.880824979	0.000415894
Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	5.873328598	0.005672461	4.903080796	0.219779
Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1	2.411086284	0.216654003	4.955170418	0.001420253
Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Homo sapiens GN=DHODH PE=1 SV=3	1.352330905	0.945236027	5.088400918	0.680948973
Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	2.26178797	0.503445625	5.110400065	0.2730501
Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	1.630840957	0.832286596	5.404856367	0.199229404
Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	5.314693551	0.045464989	5.487775407	0.04323253
Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=1 SV=3	6.982821199	0.03181912	5.540071052	0.069268487
Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5	6.728623725	0.125059098	5.581687099	0.037296671
Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	5.861410366	0.037946232	5.709806084	0.050659921
Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	1.529834907	0.364642411	5.714344687	0.186322793
Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	5.458503245	0.097694427	5.79090451	0.01223203

Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	9.411747282	0.01686869	5.839767164	0.003402783
Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2	0.942874045	0.674619973	5.947856156	0.597771704
SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2	0.649316939	0.163382396	5.965440748	0.290498793
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	5.65007518	0.000652791	6.074083165	0.003373662
SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	6.960133658	0.065864563	6.80895579	0.028926341
TBC1 domain family member 4 OS=Homo sapiens GN=TBC1D4 PE=1 SV=2	7.022545568	0.356984288	6.908620088	0.371125102
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	7.757115751	0.180538893	7.327220698	0.250395
Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	1.661786069	0.689796925	7.532701074	0.514012218
Signal transducer and activator of transcription 6 OS=Homo sapiens GN=STAT6 PE=1 SV=1	6.27908385	0.234502599	7.695634399	0.1494838
Switch-associated protein 70 OS=Homo sapiens GN=SWAP70 PE=1 SV=1	1.021131309	0.820005417	7.739057311	0.287163407
Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	8.038410622	0.024007181	8.198273801	0.03297
FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2	1.201802774	0.858720779	10.0973679	0.354990989
Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1	11.05471327	2.38E-06	10.12882113	2.07301E-06
Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1	10.64000685	0.353393704	10.84800716	0.497508287
Threonine synthase-like 1 OS=Homo sapiens GN=THNSL1 PE=1 SV=2	13.77922095	0.481973708	12.45834991	0.472389698
Dystonin OS=Homo sapiens GN=DST PE=1 SV=4	0.500113036	0.588713109	13.83557835	0.04128151
Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3	14.84031388	0.100722	14.76752884	0.333791703
GTP-binding protein RAD OS=Homo sapiens GN=RRAD PE=1 SV=2	2.530436031	0.805507302	16.58975386	0.538157701
Thioredoxin-related transmembrane protein 2 OS=Homo sapiens GN=TMX2 PE=1 SV=1	34.53483495	0.640312314	17.02575694	0.486936301
Adenylate cyclase type 5 OS=Homo sapiens GN=ADCY5 PE=1 SV=3	5.406901744	0.334143788	22.4633083	0.110302798
3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2	0.637161425	0.735376775	26.77640644	0.46231249
Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1	2.78795682	0.553674519	49.67675162	0.01713453

Table S3. A total of 167 differentially expressed proteins were found in the left ventricles of ICM patients compared with the normal samples.

Gene	**Average**	**Go**			**Function**
		Biological process	**Molecular function**	**Cellular component**	

FLII	0.08	actin cytoskeleton organization [GO:0030036]; actin filament severing [GO:0051014]; multicellular organism development [GO:0007275]; regulation of transcription, DNA-templated [GO:0006355]; transcription, DNA-templated [GO:0006351]	actin binding [GO:0003779]	brush border [GO:0005903]; cytoplasm [GO:0005737]; focal adhesion [GO:0005925]; microtubule organizing center [GO:0005815]; nucleoplasm [GO:0005654]	FUNCTION: May play a role as coactivator in transcriptional activation by hormone-activated nuclear receptors (NR) and acts in cooperation with NCOA2 and CARM1. Involved in estrogen hormone signaling. Involved in early embryonic development (By similarity). May play a role in regulation of cytoskeletal rearrangements involved in cytokinesis and cell migration, by inhibiting Rac1-dependent paxillin phosphorylation. {ECO:0000250, ECO:0000269|PubMed:14966289}.
RCSD1	0.08	cellular hyperosmotic response [GO:0071474]; skeletal muscle contraction [GO:0003009]	actin filament binding [GO:0051015]	actin filament [GO:0005884]	FUNCTION: Stress-induced phosphorylation of CAPZIP may regulate the ability of F-actin-capping protein to remodel actin filament assembly. {ECO:0000269|PubMed:15850461}.
TNNC1	0.10	cardiac muscle contraction [GO:0060048]; diaphragm contraction [GO:0002086]; muscle filament sliding [GO:0030049]; regulation of ATPase activity [GO:0043462]; regulation of muscle contraction [GO:0006937]; regulation of muscle filament sliding speed [GO:0032972]; response to metal ion [GO:0010038]; skeletal muscle contraction [GO:0003009]; transition between fast and slow fiber [GO:0014883]; ventricular cardiac muscle tissue morphogenesis [GO:0055010]	actin filament binding [GO:0051015]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; protein homodimerization activity [GO:0042803]; troponin I binding [GO:0031013]; troponin T binding [GO:0031014]	actin cytoskeleton [GO:0015629]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; nucleoplasm [GO:0005654]; troponin complex [GO:0005861]	FUNCTION: Troponin is the central regulatory protein of striated muscle contraction. Tn consists of three components: Tn-I which is the inhibitor of actomyosin ATPase, Tn-T which contains the binding site for tropomyosin and Tn-C. The binding of calcium to Tn-C abolishes the inhibitory action of Tn on actin filaments.

SLC3A2	0.10	amino acid transport [GO:0006865]; calcium ion transport [GO:0006816]; carbohydrate metabolic process [GO:0005975]; cell growth [GO:0016049]; leucine import [GO:0060356]; leukocyte migration [GO:0050900]; response to exogenous dsRNA [GO:0043330]; tryptophan transport [GO:0015827]	calcium:sodium antiporter activity [GO:0005432]; catalytic activity [GO:0003824]; double-stranded RNA binding [GO:0003725]; neutral amino acid transmembrane transporter activity [GO:0015175]; poly(A) RNA binding [GO:0044822]	apical plasma membrane [GO:0016324]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; melanosome [GO:0042470]; membrane [GO:0016020]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	FUNCTION: Required for the function of light chain amino-acid transporters. Involved in sodium-independent, high-affinity transport of large neutral amino acids such as phenylalanine, tyrosine, leucine, arginine and tryptophan. Involved in guiding and targeting of LAT1 and LAT2 to the plasma membrane. When associated with SLC7A6 or SLC7A7 acts as an arginine/glutamine exchanger, following an antiport mechanism for amino acid transport, influencing arginine release in exchange for extracellular amino acids. Plays a role in nitric oxide synthesis in human umbilical vein endothelial cells (HUVECs) via transport of L-arginine. Required for normal and neoplastic cell growth. When associated with SLC7A5/LAT1, is also involved in the transport of L-DOPA across the blood-brain barrier, and that of thyroid hormones triiodothyronine (T3) and thyroxine (T4) across the cell membrane in tissues such as placenta. Involved in the uptake of methylmercury (MeHg) when administered as the L-cysteine or D,L-homocysteine complexes, and hence plays a role in metal ion homeostasis and toxicity. When associated with SLC7A5 or SLC7A8, involved in the cellular activity of small molecular weight nitrosothiols, via the stereoselective transport of L-nitrosocysteine (L-CNSO) across the transmembrane. Together with ICAM1, regulates the transport activity LAT2 in polarized intestinal cells, by generating and delivering intracellular signals. When associated with SLC7A5, plays an important role in

					transporting L-leucine from the circulating blood to the retina across the inner blood-retinal barrier. {ECO:0000269|PubMed:10903140, ECO:0000269|PubMed:11311135, ECO:0000269|PubMed:11389679, ECO:0000269|PubMed:11557028, ECO:0000269|PubMed:11564694, ECO:0000269|PubMed:11742812, ECO:0000269|PubMed:12117417, ECO:0000269|PubMed:12225859, ECO:0000269|PubMed:12716892, ECO:0000269|PubMed:14603368, ECO:0000269|PubMed:15769744, ECO:0000269|PubMed:15980244, ECO:0000269|PubMed:9751058, ECO:0000269|PubMed:9829974, ECO:0000269|PubMed:9878049}.
CHCHD2	0.12	positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; regulation of cellular response to hypoxia [GO:1900037]; transcription, DNA-templated [GO:0006351]	sequence-specific DNA binding [GO:0043565]; transcription factor binding [GO:0008134]	mitochondrion [GO:0005739]; nucleus [GO:0005634]	FUNCTION: Transcription factor. Binds to the oxygen responsive element of COX4I2 and activates its transcription under hypoxia conditions (4% oxygen), as well as normoxia conditions (20% oxygen) (PubMed:23303788). {ECO:0000269|PubMed:23303788}.
CASQ2	0.20	cardiac muscle contraction [GO:0060048]; cellular response to caffeine [GO:0071313]; detection of calcium ion [GO:0005513]; ion transmembrane transport [GO:0034220]; negative regulation of potassium ion transmembrane transporter activity	calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; protein homodimerization activity [GO:0042803]	calcium channel complex [GO:0034704]; cytoplasm [GO:0005737]; intracellular [GO:0005622]; junctional membrane complex [GO:003031	FUNCTION: Calsequestrin is a high-capacity, moderate affinity, calcium-binding protein and thus acts as an internal calcium store in muscle. Calcium ions are bound by clusters of acidic residues at the protein surface, especially at the interface between subunits. Can bind around 60 Ca(2+) ions. Regulates the release of lumenal Ca(2+) via the calcium release channel RYR2; this plays an

		[GO:1901017]; negative regulation of potassium ion transport [GO:0043267]; negative regulation of ryanodine-sensitive calcium-release channel activity [GO:0060315]; protein polymerization [GO:0051258]; Purkinje myocyte to ventricular cardiac muscle cell signaling [GO:0086029]; regulation of cardiac conduction [GO:1903779]; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion [GO:0010881]; regulation of cell communication by electrical coupling [GO:0010649]; regulation of heart rate [GO:0002027]; regulation of membrane repolarization [GO:0060306]; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0010880]; sarcomere organization [GO:0045214]; sequestering of calcium ion [GO:0051208]; striated muscle contraction [GO:0006941]		4]; junctional sarcoplasmic reticulum membrane [GO:0014701]; sarcoplasmic reticulum [GO:0016529]; sarcoplasmic reticulum lumen [GO:0033018]; sarcoplasmic reticulum membrane [GO:0033017]; Z disc [GO:0030018]	important role in triggering muscle contraction. Plays a role in excitation-contraction coupling in the heart and in regulating the rate of heart beats. {ECO:0000269|PubMed:16908766, ECO:0000269|PubMed:17881003, ECO:0000269|PubMed:18399795, ECO:0000269|PubMed:21416293}.
TUBB	0.21	cell division [GO:0051301]; cellular process [GO:0009987]; cytoskeleton-dependent intracellular transport	GTPase activity [GO:0003924]; GTP binding [GO:0005525]; MHC	cell body [GO:0044297]; cytoplasmic ribonucleoprotein granule [GO:003646	FUNCTION: Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-

		[GO:0030705]; G2/M transition of mitotic cell cycle [GO:0000086]; microtubule-based process [GO:0007017]; movement of cell or subcellular component [GO:0006928]; natural killer cell mediated cytotoxicity [GO:0042267]; spindle assembly [GO:0051225]	class I protein binding [GO:0042288]; structural constituent of cytoskeleton [GO:0005200]; structural molecule activity [GO:0005198]; ubiquitin protein ligase binding [GO:0031625]	4]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; microtubule [GO:0005874]; nuclear envelope lumen [GO:0005641]; nucleus [GO:0005634]; protein complex [GO:0043234]	exchangeable site on the alpha chain.
NIPSNAP3B	0.22				
HMGB1	0.22	activation of innate immune response [GO:0002218]; apoptotic cell clearance [GO:0043277]; apoptotic DNA fragmentation [GO:0006309]; autophagy [GO:0006914]; base-excision repair [GO:0006284]; chromatin assembly [GO:0031497]; dendritic cell chemotaxis [GO:0002407]; DNA geometric change [GO:0032392]; DNA ligation involved in DNA repair [GO:0051103]; DNA recombination [GO:0006310]; DNA topological change [GO:0006265]; endothelial cell chemotaxis [GO:0035767]; endothelial cell proliferation [GO:0001935]; eye development	bubble DNA binding [GO:0000405]; calcium-dependent protein kinase regulator activity [GO:0010858]; chemoattractant activity [GO:0042056]; C-X-C chemokine binding [GO:0019958]; cytokine activity [GO:0005125]; damaged DNA binding [GO:0003684]; DNA binding, bending [GO:0008301]; DNA polymerase binding [GO:0070182]; double-	cell surface [GO:0009986]; condensed chromosome [GO:0000793]; early endosome [GO:0005769]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma	FUNCTION: Multifunctional redox sensitive protein with various roles in different cellular compartments. In the nucleus is one of the major chromatin-associated non-histone proteins and acts as a DNA chaperone involved in replication, transcription, chromatin remodeling, V(D)J recombination, DNA repair and genome stability. Proposed to be an universal biosensor for nucleic acids. Promotes host inflammatory response to sterile and infectious signals and is involved in the coordination and integration of innate and adaptive immune responses. In the cytoplasm functions as sensor and/or chaperone for immunogenic nucleic acids implicating the activation of TLR9-mediated immune responses, and mediates autophagy. Acts as danger associated molecular pattern (DAMP) molecule that amplifies immune responses during tissue injury. Released to the extracellular environment can bind DNA,

		[GO:0001654]; inflammatory response [GO:0006954]; inflammatory response to antigenic stimulus [GO:0002437]; innate immune response [GO:0045087]; lung development [GO:0030324]; macrophage activation involved in immune response [GO:0002281]; myeloid dendritic cell activation [GO:0001773]; negative regulation of apoptotic cell clearance [GO:2000426]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of CD4-positive, alpha-beta T cell differentiation [GO:0043371]; negative regulation of interferon-gamma production [GO:0032689]; negative regulation of RNA polymerase II transcriptional preinitiation complex assembly [GO:0017055]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; neuron projection development [GO:0031175]; neutrophil clearance [GO:0097350]; plasmacytoid dendritic cell activation [GO:0002270]; positive regulation of activated T cell	stranded DNA binding [GO:0003690]; double-stranded RNA binding [GO:0003725]; four-way junction DNA binding [GO:0000400]; lipopolysaccharide binding [GO:0001530]; lyase activity [GO:0016829]; phosphatidylserine binding [GO:0001786]; poly(A) RNA binding [GO:0044822]; protein kinase activator activity [GO:0030295]; RAGE receptor binding [GO:0050786]; repressing transcription factor binding [GO:0070491]; single-stranded DNA binding [GO:0003697]; single-stranded RNA binding [GO:0003727]; supercoiled DNA binding	membrane [GO:0005886]	nucleosomes, IL-1 beta, CXCL12, AGER isoform 2/sRAGE, lipopolysaccharide (LPS) and lipoteichoic acid (LTA), and activates cells through engagement of multiple surface receptors. In the extracellular compartment fully reduced HMGB1 (released by necrosis) acts as a chemokine, disulfide HMGB1 (actively secreted) as a cytokine, and sulfonyl HMGB1 (released from apoptotic cells) promotes immunological tolerance (PubMed:23519706, PubMed:23446148, PubMed:23994764, PubMed:25048472). Has proangiogdenic activity (By similarity). May be involved in platelet activation (By similarity). Binds to phosphatidylserine and phosphatidylethanolamide (By similarity). Bound to RAGE mediates signaling for neuronal outgrowth (By similarity). May play a role in accumulation of expanded polyglutamine (polyQ) proteins such as huntingtin (HTT) or TBP (PubMed:23303669, PubMed:25549101). {ECO:0000250|UniProtKB:P10103, ECO:0000250|UniProtKB:P12682, ECO:0000250|UniProtKB:P63158, ECO:0000250|UniProtKB:P63159, ECO:0000269|PubMed:23303669, ECO:0000269|PubMed:25549101, ECO:0000305|PubMed:23446148, ECO:0000305|PubMed:23519706, ECO:0000305|PubMed:23994764, ECO:0000305|PubMed:25048472}.; FUNCTION: Nuclear functions are attributed to fully reduced HGMB1. Associates with

		proliferation [GO:0042104]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043280]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; positive regulation of dendritic cell differentiation [GO:2001200]; positive regulation of DNA binding [GO:0043388]; positive regulation of DNA ligation [GO:0051106]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of glycogen catabolic process [GO:0045819]; positive regulation of interferon-alpha production [GO:0032727]; positive regulation of interferon-beta production [GO:0032728]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-12 production [GO:0032735]; positive regulation of interleukin-1 beta secretion [GO:0050718]; positive regulation of interleukin-1 secretion [GO:0050716]; positive regulation of interleukin-6 secretion	[GO:0097100]; transcription factor activity, sequence-specific DNA binding [GO:0003700]; transcription factor binding [GO:0008134]		chromatin and binds DNA with a preference to non-canonical DNA structures such as single-stranded DNA, DNA-containing cruciforms or bent structures, supercoiled DNA and ZDNA. Can bent DNA and enhance DNA flexibility by looping thus providing a mechanism to promote activities on various gene promoters by enhancing transcription factor binding and/or bringing distant regulatory sequences into close proximity (PubMed:20123072). May have an enhancing role in nucleotide excision repair (NER) (By similarity). However, effects in NER using in vitro systems have been reported conflictingly (PubMed:19446504, PubMed:19360789). May be involved in mismatch repair (MMR) and base excision repair (BER) pathways (PubMed:15014079, PubMed:16143102, PubMed:17803946). May be involved in double strand break repair such as non-homologous end joining (NHEJ) (By similarity). Involved in V(D)J recombination by acting as a cofactor of the RAG complex: acts by stimulating cleavage and RAG protein binding at the 23 bp spacer of conserved recombination signal sequences (RSS) (By similarity). In vitro can displace histone H1 from highly bent DNA (By similarity). Can restructure the canonical nucleosome leading to relaxation of structural constraints for transcription factor-binding (By similarity). Enhances binding of sterol regulatory element-binding proteins (SREBPs) such as SREBF1 to their cognate DNA sequences and increases their transcriptional activities (By similarity). Facilitates

		[GO:2000778]; positive regulation of JNK cascade [GO:0046330]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of mismatch repair [GO:0032425]; positive regulation of monocyte chemotaxis [GO:0090026]; positive regulation of myeloid cell differentiation [GO:0045639]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of toll-like receptor 2 signaling pathway [GO:0034137]; positive regulation of toll-like receptor 4 signaling pathway [GO:0034145]; positive regulation of toll-like receptor 9 signaling pathway [GO:0034165]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of tumor necrosis factor production [GO:0032760]; positive regulation of wound healing [GO:0090303]; regulation of autophagy [GO:0010506]; regulation of nucleotide-excision repair [GO:2000819]; regulation of restriction endodeoxyribonuclea			binding of TP53 to DNA (PubMed:23063560). Proposed to be involved in mitochondrial quality control and autophagy in a transcription-dependent fashion implicating HSPB1; however, this function has been questioned (By similarity). Can modulate the activity of the telomerase complex and may be involved in telomere maintenance (By similarity). {ECO:0000250|UniProtKB:P10103, ECO:0000250|UniProtKB:P63158, ECO:0000250|UniProtKB:P63159, ECO:0000269|PubMed:15014079, ECO:0000269|PubMed:16143102, ECO:0000269|PubMed:17803946, ECO:0000269|PubMed:19446504, ECO:0000269|PubMed:23063560, ECO:0000305|PubMed:19360789, ECO:0000305|PubMed:20123072}.; FUNCTION: In the cytoplasm proposed to dissociate the BECN1:BCL2 complex via competitive interaction with BECN1 leading to autophagy activation (PubMed:20819940). Involved in oxidative stress-mediated autophagy (PubMed:21395369). Can protect BECN1 and ATG5 from calpain-mediated cleavage and thus proposed to control their proautophagic and proapoptotic functions and to regulate the extent and severity of inflammation-associated cellular injury (By similarity). In myeloid cells has a protective role against endotoxemia and bacterial infection by promoting autophagy (By similarity). Involved in endosomal translocation and activation

		se activity [GO:0032072]; regulation of T cell mediated immune response to tumor cell [GO:0002840]; regulation of tolerance induction [GO:0002643]; regulation of transcription from RNA polymerase II promoter [GO:0006357]; response to glucocorticoid [GO:0051384]; T-helper 1 cell activation [GO:0035711]; T-helper 1 cell differentiation [GO:0045063]; tumor necrosis factor secretion [GO:1990774]; V(D)J recombination [GO:0033151]			of TLR9 in response to CpG-DNA in macrophages (By similarity). {ECO:0000250|UniProtKB:P63158, ECO:0000269|PubMed:20819940, ECO:0000269|PubMed:21395369}.; FUNCTION: In the extracellular compartment (following either active secretion or passive release) involved in regulation of the inflammatory response. Fully reduced HGMB1 (which subsequently gets oxidized after release) in association with CXCL12 mediates the recruitment of inflammatory cells during the initial phase of tissue injury; the CXCL12:HMGB1 complex triggers CXCR4 homodimerization (PubMed:22370717). Induces the migration of monocyte-derived immature dendritic cells and seems to regulate adhesive and migratory functions of neutrophils implicating AGER/RAGE and ITGAM (By similarity). Can bind to various types of DNA and RNA including microbial unmethylated CpG-DNA to enhance the innate immune response to nucleic acids. Proposed to act in promiscuous DNA/RNA sensing which cooperates with subsequent discriminative sensing by specific pattern recognition receptors (By similarity). Promotes extracellular DNA-induced AIM2 inflammasome activation implicating AGER/RAGE (PubMed:24971542). Disulfide HMGB1 binds to transmembrane receptors, such as AGER/RAGE, TLR2, TLR4 and probably TREM1, thus activating their signal transduction pathways. Mediates the release of cytokines/chemokines such

					as TNF, IL-1, IL-6, IL-8, CCL2, CCL3, CCL4 and CXCL10 (PubMed:12765338, PubMed:18354232, PubMed:19264983, PubMed:20547845, PubMed:24474694). Promotes secretion of interferon-gamma by macrophage-stimulated natural killer (NK) cells in concert with other cytokines like IL-2 or IL-12 (PubMed:15607795). TLR4 is proposed to be the primary receptor promoting macrophage activation and signaling through TLR4 seems to implicate LY96/MD-2 (PubMed:20547845). In bacterial LPS- or LTA-mediated inflammatory responses binds to the endotoxins and transfers them to CD14 for signaling to the respective TLR4:LY96 and TLR2 complexes (PubMed:18354232, PubMed:21660935, PubMed:25660311). Contributes to tumor proliferation by association with ACER/RAGE (By similarity). Can bind to IL1-beta and signals through the IL1R1:IL1RAP receptor complex (PubMed:18250463). Binding to class A CpG activates cytokine production in plasmacytoid dendritic cells implicating TLR9, MYD88 and AGER/RAGE and can activate autoreactive B cells. Via HMGB1-containing chromatin immune complexes may also promote B cell responses to endogenous TLR9 ligands through a B-cell receptor (BCR)-dependent and ACER/RAGE-independent mechanism (By similarity). Inhibits phagocytosis of apoptotic cells by macrophages; the function is

<table>
<tr><td></td><td></td><td></td><td></td><td></td><td>dependent on poly-ADP-ribosylation and involves binding to phosphatidylserine on the cell surface of apoptotic cells (By similarity). In adaptive immunity may be involved in enhancing immunity through activation of effector T cells and suppression of regulatory T (TReg) cells (PubMed:15944249, PubMed:22473704). In contrast, without implicating effector or regulatory T-cells, required for tumor infiltration and activation of T-cells expressing the lymphotoxin LTA:LTB heterotrimer thus promoting tumor malignant progression (By similarity). Also reported to limit proliferation of T-cells (By similarity). Released HMGB1:nucleosome complexes formed during apoptosis can signal through TLR2 to induce cytokine production (PubMed:19064698). Involved in induction of immunological tolerance by apoptotic cells; its pro-inflammatory activities when released by apoptotic cells are neutralized by reactive oxygen species (ROS)-dependent oxidation specifically on Cys-106 (PubMed:18631454). During macrophage activation by activated lymphocyte-derived self apoptotic DNA (ALD-DNA) promotes recruitment of ALD-DNA to endosomes (By similarity). {ECO:0000250|UniProtKB:P10103, ECO:0000250|UniProtKB:P63158, ECO:0000250|UniProtKB:P63159, ECO:0000269|PubMed:12765338, ECO:0000269|PubMed:15607795, ECO:0000269|PubMed:15944249, ECO:0000269|PubMed:1825</td></tr>
</table>

					0463, ECO:0000269|PubMed:18354232, ECO:0000269|PubMed:18631454, ECO:0000269|PubMed:19064698, ECO:0000269|PubMed:19264983, ECO:0000269|PubMed:20547845, ECO:0000269|PubMed:21660935, ECO:0000269|PubMed:22370717, ECO:0000269|PubMed:22473704, ECO:0000269|PubMed:24474694, ECO:0000269|PubMed:24971542, ECO:0000269|PubMed:25660311, ECO:0000269|Ref.8}.
HRC	0.23	muscle contraction [GO:0006936]; negative regulation of cytosolic calcium ion concentration [GO:0051481]; positive regulation of heart contraction [GO:0045823]; positive regulation of heart rate [GO:0010460]; positive regulation of relaxation of cardiac muscle [GO:1901899]; regulation of calcium ion transmembrane transport [GO:1903169]; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion [GO:0010881]; regulation of cell communication by electrical coupling involved in cardiac conduction [GO:1901844]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of heart	ATPase binding [GO:0051117]; calcium ion binding [GO:0005509]; ion channel binding [GO:0044325]	sarcoplasmic reticulum lumen [GO:0033018]; sarcoplasmic reticulum membrane [GO:0033017]; Z disc [GO:0030018]	FUNCTION: May play a role in the regulation of calcium sequestration or release in the SR of skeletal and cardiac muscle.

		rate [GO:0002027]; regulation of peptidyl-serine phosphorylation [GO:0033135]; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0010880]; regulation of ryanodine-sensitive calcium-release channel activity [GO:0060314]			
DNAJA1	0.24	androgen receptor signaling pathway [GO:0030521]; DNA damage response, detection of DNA damage [GO:0042769]; negative regulation of apoptotic process [GO:0043066]; negative regulation of JUN kinase activity [GO:0043508]; negative regulation of protein ubiquitination [GO:0031397]; positive regulation of apoptotic process [GO:0043065]; protein folding [GO:0006457]; protein localization to mitochondrion [GO:0070585]; regulation of protein transport [GO:0051223]; response to heat [GO:0009408]; response to unfolded protein [GO:0006986]; spermatogenesis [GO:0007283]; sperm motility [GO:0030317]; toxin transport [GO:1901998]	ATP binding [GO:0005524]; C3HC4-type RING finger domain binding [GO:0055131]; chaperone binding [GO:0051087]; G-protein coupled receptor binding [GO:0001664]; Hsp70 protein binding [GO:0030544]; low-density lipoprotein particle receptor binding [GO:0050750]; metal ion binding [GO:0046872]; ubiquitin protein ligase binding [GO:0031625]	cytoplasmic side of endoplasmic reticulum membrane [GO:0098554]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]	FUNCTION: Co-chaperone for HSPA8/Hsc70 (PubMed:10816573). Stimulates ATP hydrolysis, but not the folding of unfolded proteins mediated by HSPA1A (in vitro) (PubMed:24318877). Plays a role in protein transport into mitochondria via its role as co-chaperone. Functions as co-chaperone for HSPA1B and negatively regulates the translocation of BAX from the cytosol to mitochondria in response to cellular stress, thereby protecting cells against apoptosis (PubMed:14752510). Promotes apoptosis in response to cellular stress mediated by exposure to anisomycin or UV (PubMed:24512202). {ECO:0000269|PubMed:10816573, ECO:0000269|PubMed:14752510, ECO:0000269|PubMed:24318877, ECO:0000269|PubMed:24512202, ECO:0000269|PubMed:9192730}.
NCKAP1	0.25	apoptotic process [GO:0006915]; central nervous	protein complex binding	cytosol [GO:0005829];	FUNCTION: Part of the WAVE complex that regulates lamellipodia

		system development [GO:0007417]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; positive regulation of Arp2/3 complex-mediated actin nucleation [GO:2000601]; positive regulation of lamellipodium assembly [GO:0010592]; Rac protein signal transduction [GO:0016601]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]; viral process [GO:0016032]	[GO:0032403]	extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; integral component of membrane [GO:0016021]; lamellipodium membrane [GO:0031258]; SCAR complex [GO:0031209]	formation. The WAVE complex regulates actin filament reorganization via its interaction with the Arp2/3 complex. Actin remodeling activity is regulated by RAC1.
HDLBP	0.27	cholesterol metabolic process [GO:0008203]; lipid transport [GO:0006869]	lipid binding [GO:0008289]; poly(A) RNA binding [GO:0044822]	cytoplasm [GO:0005737]; high-density lipoprotein particle [GO:0034364]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	FUNCTION: Appears to play a role in cell sterol metabolism. It may function to protect cells from over-accumulation of cholesterol.
ABHD10	0.27	cellular glucuronidation [GO:0052695]; glucuronoside catabolic process [GO:0019391]	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]	cytosol [GO:0005829]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	FUNCTION: Catalyzes the deglucuronidation of mycophenolic acid acyl-glucuronide, a metabolite of the immunosuppressant drug mycophenolate. {ECO:0000269|PubMed:22294686}.
SDCBP	0.28	actin cytoskeleton organization [GO:0030036]; ephrin receptor signaling pathway [GO:0048013]; intracellular signal transduction [GO:0035556]; negative regulation	cytoskeletal adaptor activity [GO:0008093]; frizzled binding [GO:0005109]; identical protein binding	adherens junction [GO:0005912]; blood microparticle [GO:0072562]; cytoplasm [GO:000573	FUNCTION: Multifunctional adapter protein involved in diverse array of functions including trafficking of transmembrane proteins, neuro and immunomodulation, exosome biogenesis, and tumorigenesis (PubMed:26291527).

		of proteasomal ubiquitin-dependent protein catabolic process [GO:0032435]; negative regulation of receptor internalization [GO:0002091]; positive regulation of cell growth [GO:0030307]; positive regulation of cell migration [GO:0030335]; positive regulation of cell proliferation [GO:0008284]; positive regulation of epithelial to mesenchymal transition [GO:0010718]; positive regulation of exosomal secretion [GO:1903543]; positive regulation of extracellular exosome assembly [GO:1903553]; positive regulation of JNK cascade [GO:0046330]; positive regulation of pathway-restricted SMAD protein phosphorylation [GO:0010862]; positive regulation of phosphorylation [GO:0042327]; positive regulation of transforming growth factor beta receptor signaling pathway [GO:0030511]; protein targeting to membrane [GO:0006612]; Ras protein signal transduction [GO:0007265]; regulation of mitotic cell cycle [GO:0007346]; substrate-dependent cell migration, cell extension [GO:0006930];	[GO:0042802]; interleukin-5 receptor binding [GO:0005137]; protein heterodimerization activity [GO:0046982]; protein N-terminus binding [GO:0047485]; syndecan binding [GO:0045545]	7]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; endoplasmic reticulum membrane [GO:0005789]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; focal adhesion [GO:0005925]; interleukin-5 receptor complex [GO:0005895]; melanosome [GO:0042470]; membrane [GO:0016020]; membrane raft [GO:0045121]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	Positively regulates TGFB1-mediated SMAD2/3 activation and TGFB1-induced epithelial-to-mesenchymal transition (EMT) and cell migration in various cell types. May increase TGFB1 signaling by enhancing cell-surface expression of TGFR1 by preventing the interaction between TGFR1 and CAV1 and subsequent CAV1-dependent internalization and degradation of TGFR1 (PubMed:25893292). In concert with SDC1/4 and PDCD6IP, regulates exosome biogenesis (PubMed:22660413). Regulates migration, growth, proliferation, and cell cycle progression in a variety of cancer types (PubMed:26539120). In adherens junctions may function to couple syndecans to cytoskeletal proteins or signaling components. Seems to couple transcription factor SOX4 to the IL-5 receptor (IL5RA) (PubMed:11498591). May also play a role in vesicular trafficking (PubMed:11179419). Seems to be required for the targeting of TGFA to the cell surface in the early secretory pathway (PubMed:10230395). {ECO:0000269|PubMed:10230395, ECO:0000269|PubMed:11179419, ECO:0000269|PubMed:11498591, ECO:0000269|PubMed:22660413, ECO:0000269|PubMed:25893292, ECO:0000269|PubMed:26539120, ECO:0000303|PubMed:26291527}.

		synaptic transmission [GO:0007268]			
TGM2	0.28	apoptotic cell clearance [GO:0043277]; branching involved in salivary gland morphogenesis [GO:0060445]; negative regulation of endoplasmic reticulum calcium ion concentration [GO:0032471]; peptide cross-linking [GO:0018149]; phospholipase C-activating G-protein coupled receptor signaling pathway [GO:0007200]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cell adhesion [GO:0045785]; positive regulation of mitochondrial calcium ion concentration [GO:0051561]; salivary gland cavitation [GO:0060662]	metal ion binding [GO:0046872]; protein-glutamine gamma-glutamyltransferase activity [GO:0003810]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; intrinsic component of plasma membrane [GO:0031226]; mitochondrion [GO:0005739]	FUNCTION: Catalyzes the cross-linking of proteins and the conjugation of polyamines to proteins.
ANXA7	0.28	autophagy [GO:0006914]; cell proliferation [GO:0008283]; cellular calcium ion homeostasis [GO:0006874]; cellular water homeostasis [GO:0009992]; epithelial cell differentiation [GO:0030855]; hemostasis [GO:0007599]; membrane fusion [GO:0061025]; negative regulation of gene expression [GO:0010629]; regulation of cell shape [GO:0008360]; response to calcium ion [GO:0051592];	calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; integrin binding [GO:0005178]; poly(A) RNA binding [GO:0044822]	cytosol [GO:0005829]; endoplasmic reticulum membrane [GO:0005789]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; nuclear envelope [GO:0005635]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.

		response to organic cyclic compound [GO:0014070]; response to salt stress [GO:0009651]; social behavior [GO:0035176]			
UFD1L	0.28	ER-associated misfolded protein catabolic process [GO:0071712]; error-free translesion synthesis [GO:0070987]; retrograde protein transport, ER to cytosol [GO:0030970]; skeletal system development [GO:0001501]; ubiquitin-dependent protein catabolic process [GO:0006511]	thiol-dependent ubiquitin-specific protease activity [GO:0004843]	cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; UFD1-NPL4 complex [GO:0036501]; VCP-NPL4-UFD1 AAA ATPase complex [GO:0034098]	FUNCTION: Essential component of the ubiquitin-dependent proteolytic pathway which degrades ubiquitin fusion proteins. The ternary complex containing UFD1L, VCP and NPLOC4 binds ubiquitinated proteins and is necessary for the export of misfolded proteins from the ER to the cytoplasm, where they are degraded by the proteasome. The NPLOC4-UFD1L-VCP complex regulates spindle disassembly at the end of mitosis and is necessary for the formation of a closed nuclear envelope. It may be involved in the development of some ectoderm-derived structures.
ANXA11	0.28	cell cycle [GO:0007049]; cell division [GO:0051301]; phagocytosis [GO:0006909]; response to calcium ion [GO:0051592]	calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; MHC class II protein complex binding [GO:0023026]; phosphatidylethanolamine binding [GO:0008429]; poly(A) RNA binding [GO:0044822]; S100 protein binding	azurophil granule [GO:0042582]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; melanosome [GO:0042470]; membrane [GO:0016020]; midbody [GO:0030496]; nuclear envelope [GO:0005635]; nucleoplasm [GO:0005654]; phagocytic vesicle [GO:0045335]; specific granule [GO:004258	FUNCTION: Binds specifically to calcyclin in a calcium-dependent manner (By similarity). Required for midbody formation and completion of the terminal phase of cytokinesis. {ECO:0000250, ECO:0000269|PubMed:15197175}.

			[GO:0044548]	1]; spindle [GO:0005819]	
XPNPEP3	0.28	glomerular filtration [GO:0003094]; protein processing [GO:0016485]	aminopeptidase activity [GO:0004177]; manganese ion binding [GO:0030145]; metallopeptidase activity [GO:0008237]	extracellular exosome [GO:0070062]; mitochondrion [GO:0005739]	
TSTA3	0.29	'de novo' GDP-L-fucose biosynthetic process [GO:0042351]; cytolysis [GO:0019835]; GDP-mannose metabolic process [GO:0019673]; leukocyte cell-cell adhesion [GO:0007159]	coenzyme binding [GO:0050662]; electron carrier activity [GO:0009055]; GDP-4-dehydro-D-rhamnose reductase activity [GO:0042356]; GDP-L-fucose synthase activity [GO:0050577]; isomerase activity [GO:0016853]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]	FUNCTION: Catalyzes the two-step NADP-dependent conversion of GDP-4-dehydro-6-deoxy-D-mannose to GDP-fucose, involving an epimerase and a reductase reaction. {ECO:0000269|PubMed:8910301}.
MECR	0.29	fatty acid biosynthetic process [GO:0006633]; fatty acid metabolic process [GO:0006631]	trans-2-enoyl-CoA reductase (NADPH) activity [GO:0019166]; zinc ion binding [GO:0008270]	mitochondrion [GO:0005739]; nucleus [GO:0005634]	FUNCTION: Oxidoreductase with a preference for short and medium chain substrates, including trans-2-hexenoyl-CoA (C6), trans-2-decenoyl-CoA (C10), and trans-2-hexadecenoyl-CoA (C16). May play a role in mitochondrial fatty acid synthesis. {ECO:0000269|PubMed:18479707}.
PSMF1	0.29	anaphase-promoting complex-dependent catabolic process [GO:0031145]; antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-	endopeptidase inhibitor activity [GO:0004866]; proteasome binding [GO:0070628]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; membrane [GO:001602	FUNCTION: Plays an important role in control of proteasome function. Inhibits the hydrolysis of protein and peptide substrates by the 20S proteasome. Also inhibits the activation of the proteasome by the proteasome regulatory proteins PA700 and PA28.

		dependent [GO:0002479]; Fc-epsilon receptor signaling pathway [GO:0038095]; MAPK cascade [GO:0000165]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of proteasomal protein catabolic process [GO:1901799]; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle [GO:0051436]; NIK/NF-kappaB signaling [GO:0038061]; positive regulation of canonical Wnt signaling pathway [GO:0090263]; positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition [GO:0051437]; proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]; protein polyubiquitination [GO:0000209]; regulation of cellular amino acid metabolic process [GO:0006521]; regulation of mRNA stability [GO:0043488]; stimulatory C-type lectin receptor signaling pathway [GO:0002223]; T cell receptor signaling pathway [GO:0050852]; tumor necrosis factor-mediated		0]; nucleoplasm [GO:0005654]; proteasome core complex [GO:0005839]	{ECO:0000269|PubMed:10764772}.

		signaling pathway [GO:0033209]; ubiquitin-dependent protein catabolic process [GO:0006511]; Wnt signaling pathway, planar cell polarity pathway [GO:0060071]			
MRPS23	0.29	mitochondrial translational elongation [GO:0070125]; mitochondrial translational termination [GO:0070126]	poly(A) RNA binding [GO:0044822]; structural constituent of ribosome [GO:0003735]	intermediate filament cytoskeleton [GO:0045111]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; nuclear membrane [GO:0031965]; ribosome [GO:0005840]	
DPYD	0.31	beta-alanine biosynthetic process [GO:0019483]; purine nucleobase catabolic process [GO:0006145]; pyrimidine nucleobase catabolic process [GO:0006208]; pyrimidine nucleoside catabolic process [GO:0046135]; thymidine catabolic process [GO:0006214]; thymine catabolic process [GO:0006210]; uracil catabolic process [GO:0006212]	4 iron, 4 sulfur cluster binding [GO:0051539]; dihydropyrimidine dehydrogenase (NADP+) activity [GO:0017113]; flavin adenine dinucleotide binding [GO:0050660]; metal ion binding [GO:0046872]; NADP binding [GO:0050661]; protein homodimerization activity [GO:0042803]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	FUNCTION: Involved in pyrimidine base degradation. Catalyzes the reduction of uracil and thymine. Also involved the degradation of the chemotherapeutic drug 5-fluorouracil.
FHL2	0.31	androgen receptor signaling pathway [GO:0030521]; atrial	androgen receptor binding	actin cytoskeleton [GO:001562	FUNCTION: May function as a molecular transmitter linking various signaling

		cardiac muscle cell development [GO:0055014]; heart trabecula formation [GO:0060347]; negative regulation of apoptotic process [GO:0043066]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; osteoblast differentiation [GO:0001649]; positive regulation of transcription, DNA-templated [GO:0045893]; response to hormone [GO:0009725]; transcription, DNA-templated [GO:0006351]; ventricular cardiac muscle cell development [GO:0055015]	[GO:0050681]; identical protein binding [GO:0042802]; transcription coactivator activity [GO:0003713]; transcription factor binding [GO:0008134]; zinc ion binding [GO:0008270]	9]; focal adhesion [GO:0005925]; M band [GO:0031430]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; Z disc [GO:0030018]	pathways to transcriptional regulation. Negatively regulates the transcriptional repressor E4F1 and may function in cell growth. Inhibits the transcriptional activity of FOXO1 and its apoptotic function by enhancing the interaction of FOXO1 with SIRT1 and FOXO1 deacetylation. {ECO:0000269|PubMed:15692560, ECO:0000269|PubMed:16652157, ECO:0000269|PubMed:18853468}.
RAB12	0.32	autophagy [GO:0006914]; cellular protein catabolic process [GO:0044257]; endosome to lysosome transport [GO:0008333]; positive regulation of macroautophagy [GO:0016239]; protein transport [GO:0015031]; small GTPase mediated signal transduction [GO:0007264]	GDP binding [GO:0019003]; GTP binding [GO:0005525]	autophagosome [GO:0005776]; cytoplasmic vesicle [GO:0031410]; Golgi membrane [GO:0000139]; lysosomal membrane [GO:0005765]; lysosome [GO:0005764]; recycling endosome membrane [GO:0055038]	FUNCTION: The small GTPases Rab are key regulators of intracellular membrane trafficking, from the formation of transport vesicles to their fusion with membranes. Rabs cycle between an inactive GDP-bound form and an active GTP-bound form that is able to recruit to membranes different set of downstream effectors directly responsible for vesicle formation, movement, tethering and fusion. That Rab may play a role in protein transport from recycling endosomes to lysosomes regulating, for instance, the degradation of the transferrin receptor. Involved in autophagy (By similarity). {ECO:0000250}.
GCDH	0.33	fatty acid beta-oxidation using acyl-CoA dehydrogenase [GO:0033539]; fatty-acyl-CoA biosynthetic process [GO:0046949]; lipid homeostasis	electron carrier activity [GO:0009055]; fatty-acyl-CoA binding [GO:000006	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	FUNCTION: Catalyzes the oxidative decarboxylation of glutaryl-CoA to crotonyl-CoA and CO(2) in the degradative pathway of L-lysine, L-hydroxylysine, and L-tryptophan metabolism. It uses electron transfer

		[GO:0055088]; lysine catabolic process [GO:0006554]; tryptophan metabolic process [GO:0006568]	2]; flavin adenine dinucleotide binding [GO:0050660]; glutaryl-CoA dehydrogenase activity [GO:0004361]; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor [GO:0052890]		flavoprotein as its electron acceptor. Isoform Short is inactive. {ECO:0000269|PubMed:17176108, ECO:0000269|PubMed:6423663, ECO:0000269|PubMed:8541831}.
TNNT2	0.35	actin crosslink formation [GO:0051764]; cardiac muscle contraction [GO:0060048]; muscle filament sliding [GO:0030049]; negative regulation of ATPase activity [GO:0032780]; positive regulation of ATPase activity [GO:0032781]; protein heterooligomerization [GO:0051291]; regulation of heart contraction [GO:0008016]; regulation of muscle filament sliding speed [GO:0032972]; response to calcium ion [GO:0051592]; ventricular cardiac muscle tissue morphogenesis [GO:0055010]	actin binding [GO:0003779]; tropomyosin binding [GO:0005523]; troponin C binding [GO:0030172]; troponin I binding [GO:0031013]	cytosol [GO:0005829]; sarcomere [GO:0030017]; striated muscle thin filament [GO:0005865]; troponin complex [GO:0005861]	FUNCTION: Troponin T is the tropomyosin-binding subunit of troponin, the thin filament regulatory complex which confers calcium-sensitivity to striated muscle actomyosin ATPase activity.
NPM1	0.41	cell aging [GO:0007569]; CENP-A containing nucleosome assembly [GO:0034080]; centrosome cycle [GO:0007098]; DNA	histone binding [GO:0042393]; NF-kappaB binding [GO:0051059]; poly(A)	centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; focal	FUNCTION: Involved in diverse cellular processes such as ribosome biogenesis, centrosome duplication, protein chaperoning, histone assembly, cell proliferation, and regulation of tumor suppressors p53/TP53 and

		damage response, signal transduction by p53 class mediator resulting in cell cycle arrest [GO:0006977]; DNA repair [GO:0006281]; intracellular protein transport [GO:0006886]; negative regulation of apoptotic process [GO:0043066]; negative regulation of cell proliferation [GO:0008285]; negative regulation of centrosome duplication [GO:0010826]; negative regulation of protein kinase activity by regulation of protein phosphorylation [GO:0044387]; nucleocytoplasmic transport [GO:0006913]; nucleosome assembly [GO:0006334]; positive regulation of cell cycle G2/M phase transition [GO:1902751]; positive regulation of cell proliferation [GO:0008284]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of translation [GO:0045727]; protein localization [GO:0008104]; protein oligomerization [GO:0051259]; regulation of centriole replication [GO:0046599];	RNA binding [GO:0044822]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; protein kinase binding [GO:0019901]; protein kinase inhibitor activity [GO:0004860]; ribosomal large subunit binding [GO:0043023]; ribosomal small subunit binding [GO:0043024]; RNA binding [GO:0003723]; Tat protein binding [GO:0030957]; transcription coactivator activity [GO:0003713]; unfolded protein binding [GO:0051082]	adhesion [GO:0005925]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; spindle pole centrosome [GO:0031616]	ARF. Binds ribosome presumably to drive ribosome nuclear export. Associated with nucleolar ribonucleoprotein structures and bind single-stranded nucleic acids. Acts as a chaperonin for the core histones H3, H2B and H4. Stimulates APEX1 endonuclease activity on apurinic/apyrimidinic (AP) double-stranded DNA but inhibits APEX1 endonuclease activity on AP single-stranded RNA. May exert a control of APEX1 endonuclease activity within nucleoli devoted to repair AP on rDNA and the removal of oxidized rRNA molecules. In concert with BRCA2, regulates centrosome duplication. Regulates centriole duplication: phosphorylation by PLK2 is able to trigger centriole replication. Negatively regulates the activation of EIF2AK2/PKR and suppresses apoptosis through inhibition of EIF2AK2/PKR autophosphorylation. Antagonizes the inhibitory effect of ATF5 on cell proliferation and relieves ATF5-induced G2/M blockade (PubMed:22528486). {ECO:0000269|PubMed:12882984, ECO:0000269|PubMed:16107701, ECO:0000269|PubMed:17015463, ECO:0000269|PubMed:18809582, ECO:0000269|PubMed:19188445, ECO:0000269|PubMed:20352051, ECO:0000269|PubMed:21084279, ECO:0000269|PubMed:22002061, ECO:0000269|PubMed:22528486}.

		regulation of eIF2 alpha phosphorylation by dsRNA [GO:0060735]; regulation of endodeoxyribonuclease activity [GO:0032071]; regulation of endoribonuclease activity [GO:0060699]; response to stress [GO:0006950]; ribosome assembly [GO:0042255]; signal transduction [GO:0007165]; viral process [GO:0016032]			
ACAT1	0.43	adipose tissue development [GO:0060612]; brain development [GO:0007420]; branched-chain amino acid catabolic process [GO:0009083]; ketone body biosynthetic process [GO:0046951]; ketone body catabolic process [GO:0046952]; liver development [GO:0001889]; metanephric proximal convoluted tubule development [GO:0072229]; protein homooligomerization [GO:0051260]; response to hormone [GO:0009725]; response to organic cyclic compound [GO:0014070]; response to starvation [GO:0042594]	acetyl-CoA C-acetyltransferase activity [GO:0003985]; coenzyme binding [GO:0050662]; metal ion binding [GO:0046872]	extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	FUNCTION: Plays a major role in ketone body metabolism.
HSP90AA1	0.46	cardiac muscle cell apoptotic process [GO:0010659]; chaperone-mediated autophagy [GO:0061684]; chaperone-mediated	ATPase activity [GO:0016887]; ATP binding [GO:0005524]; CTP	apical plasma membrane [GO:0016324]; basolateral plasma	FUNCTION: Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved for instance in cell cycle control

		protein complex assembly [GO:0051131]; ERBB2 signaling pathway [GO:0038128]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; G2/M transition of mitotic cell cycle [GO:0000086]; mitochondrial transport [GO:0006839]; neuron migration [GO:0001764]; positive regulation of cardiac muscle contraction [GO:0060452]; positive regulation of cell size [GO:0045793]; positive regulation of lamellipodium assembly [GO:0010592]; positive regulation of nitric oxide biosynthetic process [GO:0045429]; positive regulation of protein import into nucleus, translocation [GO:0033160]; protein import into mitochondrial outer membrane [GO:0045040]; protein refolding [GO:0042026]; protein stabilization [GO:0050821]; protein unfolding [GO:0043335]; receptor-mediated endocytosis [GO:0006898]; regulation of cellular response to heat [GO:1900034]; regulation of nitric-oxide synthase activity [GO:0050999]; regulation of protein	binding [GO:0002135]; dATP binding [GO:0032564]; GTPase binding [GO:0051020]; GTP binding [GO:0005525]; histone deacetylase binding [GO:0042826]; identical protein binding [GO:0042802]; MHC class II protein complex binding [GO:0023026]; mRNA binding [GO:0003729]; nitric-oxide synthase regulator activity [GO:0030235]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; protein homodimerization activity [GO:0042803]; protein tyrosine kinase activity [GO:0004713]; TPR domain binding [GO:0030911]; UTP binding [GO:0002134]	membrane [GO:0016323]; brush border membrane [GO:0031526]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; endocytic vesicle lumen [GO:0071682]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; lysosomal lumen [GO:0043202]; melanosome [GO:0042470]; membrane [GO:0016020]; myelin sheath [GO:0043209]; neuronal cell body [GO:0043025]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma	and signal transduction. Undergoes a functional cycle that is linked to its ATPase activity. This cycle probably induces conformational changes in the client proteins, thereby causing their activation. Interacts dynamically with various co-chaperones that modulate its substrate recognition, ATPase cycle and chaperone function. Binds bacterial lipopolysaccharide (LPS) et mediates LPS-induced inflammatory response, including TNF secretion by monocytes. {ECO:0000269|PubMed:11274138, ECO:0000269|PubMed:11276205, ECO:0000269|PubMed:15577939, ECO:0000269|PubMed:15937123}.

		complex assembly [GO:0043254]; regulation of protein ubiquitination [GO:0031396]; response to antibiotic [GO:0046677]; response to cold [GO:0009409]; response to estrogen [GO:0043627]; response to heat [GO:0009408]; response to salt stress [GO:0009651]; response to unfolded protein [GO:0006986]; signal transduction [GO:0007165]; skeletal muscle contraction [GO:0003009]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]		membrane [GO:0005886]; protein complex [GO:0043234]; ruffle membrane [GO:0032587]	
ANXA5	0.46	blood coagulation [GO:0007596]; cellular response to gonadotropin-releasing hormone [GO:0097211]; cellular response to lead ion [GO:0071284]; mitophagy in response to mitochondrial depolarization [GO:0098779]; negative regulation of apoptotic process [GO:0043066]; negative regulation of blood coagulation [GO:0030195]; negative regulation of prolactin secretion [GO:1902721]; positive regulation of apoptotic process [GO:0043065]; positive regulation of defense response to virus by host [GO:0002230]; protein homooligomerization	calcium-dependent phospholipid binding [GO:0005544]; calcium ion binding [GO:0005509]; calcium-transporting ATPase activity [GO:0005388]; peptide hormone binding [GO:0017046]; phospholipase inhibitor activity [GO:0004859]; phospholipid binding [GO:0005543]	axon terminus [GO:0043679]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; endothelial microparticle [GO:0072563]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925];	FUNCTION: This protein is an anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade.

		[GO:0051260]; regulation of sperm motility [GO:1901317]; response to calcium ion [GO:0051592]; response to thyroid hormone [GO:0097066]; signal transduction [GO:0007165]; xenophagy [GO:0098792]		intercalated disc [GO:0014704]; intracellular [GO:0005622]; membrane [GO:0016020]; nucleus [GO:0005634]; perikaryon [GO:0043204]; sarcolemma [GO:0042383]; synaptic vesicle [GO:0008021]; Z disc [GO:0030018]	
MYOM2	0.49	muscle contraction [GO:0006936]	structural constituent of muscle [GO:0008307]	M band [GO:0031430]; mitochondrion [GO:0005739]; myosin filament [GO:0032982]	FUNCTION: Major component of the vertebrate myofibrillar M band. Binds myosin, titin, and light meromyosin. This binding is dose dependent.
GPT	0.51	cellular amino acid biosynthetic process [GO:0008652]; L-alanine catabolic process [GO:0042853]	L-alanine:2-oxoglutarate aminotransferase activity [GO:0004021]; pyridoxal phosphate binding [GO:0030170]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]	FUNCTION: Catalyzes the reversible transamination between alanine and 2-oxoglutarate to form pyruvate and glutamate. Participates in cellular nitrogen metabolism and also in liver gluconeogenesis starting with precursors transported from skeletal muscles (By similarity). {ECO:0000250}.
TIMM44	0.54	protein import into mitochondrial matrix [GO:0030150]; protein targeting to mitochondrion [GO:0006626]	ATP binding [GO:0005524]; chaperone binding [GO:0051087]	mitochondrial inner membrane [GO:0005743]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	FUNCTION: Essential component of the PAM complex, a complex required for the translocation of transit peptide-containing proteins from the inner membrane into the mitochondrial matrix in an ATP-dependent manner. Recruits mitochondrial HSP70 to drive protein translocation into the matrix using ATP as an energy source.

DBI	0.55	phosphatidylcholine acyl-chain remodeling [GO:0036151]; transport [GO:0006810]	benzodiazepine receptor binding [GO:0030156]; lipid binding [GO:0008289]; long-chain fatty acyl-CoA binding [GO:0036042]; protein dimerization activity [GO:0046983]	endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; perinuclear endoplasmic reticulum [GO:0097038]	FUNCTION: Binds medium- and long-chain acyl-CoA esters with very high affinity and may function as an intracellular carrier of acyl-CoA esters. It is also able to displace diazepam from the benzodiazepine (BZD) recognition site located on the GABA type A receptor. It is therefore possible that this protein also acts as a neuropeptide to modulate the action of the GABA receptor.
WARS	0.56	angiogenesis [GO:0001525]; negative regulation of cell proliferation [GO:0008285]; regulation of angiogenesis [GO:0045765]; translation [GO:0006412]; tRNA aminoacylation for protein translation [GO:0006418]; tryptophanyl-tRNA aminoacylation [GO:0006436]	ATP binding [GO:0005524]; tryptophan-tRNA ligase activity [GO:0004830]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	FUNCTION: Isoform 1, isoform 2 and T1-TrpRS have aminoacylation activity while T2-TrpRS lacks it. Isoform 2, T1-TrpRS and T2-TrpRS possess angiostatic activity whereas isoform 1 lacks it. T2-TrpRS inhibits fluid shear stress-activated responses of endothelial cells. Regulates ERK, Akt, and eNOS activation pathways that are associated with angiogenesis, cytoskeletal reorganization and shear stress-responsive gene expression. {ECO:0000269|PubMed:11773625, ECO:0000269|PubMed:11773626, ECO:0000269|PubMed:1373391, ECO:0000269|PubMed:14630953}.
IDH2	0.56	2-oxoglutarate metabolic process [GO:0006103]; carbohydrate metabolic process [GO:0005975]; glyoxylate cycle [GO:0006097]; isocitrate metabolic process [GO:0006102]; tricarboxylic acid cycle [GO:0006099]	isocitrate dehydrogenase (NADP+) activity [GO:0004450]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743]; mitochondrial matrix [GO:0005759]; mitochondri	FUNCTION: Plays a role in intermediary metabolism and energy production. It may tightly associate or interact with the pyruvate dehydrogenase complex.

				on [GO:0005739]; peroxisome [GO:0005777]	
NCL	0.57	angiogenesis [GO:0001525]; cellular response to lipopolysaccharide [GO:0071222]; endocytosis [GO:0006897]; liver regeneration [GO:0097421]; negative regulation of apoptotic process [GO:0043066]; positive regulation of interleukin-6 secretion [GO:2000778]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter [GO:1901838]; positive regulation of tumor necrosis factor production [GO:0032760]; regulation of rRNA processing [GO:2000232]; spermatogenesis [GO:0007283]	calcium ion binding [GO:0005509]; identical protein binding [GO:0042802]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; protein C-terminus binding [GO:0008022]; RNA binding [GO:0003723]; rRNA primary transcript binding [GO:0042134]; selenocysteine insertion sequence binding [GO:0035368]; single-stranded DNA binding [GO:0003697]; telomeric DNA binding [GO:0042162]	cell cortex [GO:0005938]; cell surface [GO:0009986]; cytoplasmic ribonucleoprotein granule [GO:0036464]; dense fibrillar component [GO:0001651]; extracellular exosome [GO:0070062]; fibrillar center [GO:0001650]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	FUNCTION: Nucleolin is the major nucleolar protein of growing eukaryotic cells. It is found associated with intranucleolar chromatin and pre-ribosomal particles. It induces chromatin decondensation by binding to histone H1. It is thought to play a role in pre-rRNA transcription and ribosome assembly. May play a role in the process of transcriptional elongation. Binds RNA oligonucleotides with 5'-UUAGGG-3' repeats more tightly than the telomeric single-stranded DNA 5'-TTAGGG-3' repeats. {ECO:0000269|PubMed:10393184}.
HADHA	0.57	cardiolipin acyl-chain remodeling [GO:0035965]; fatty acid beta-oxidation [GO:0006635]; response to drug [GO:0042493]; response to insulin [GO:0032868]	3-hydroxyacyl-CoA dehydrogenase activity [GO:0003857]; acetyl-CoA C-acetyltransferase activity [GO:000398	mitochondrial fatty acid beta-oxidation multienzyme complex [GO:0016507]; mitochondrial inner membrane	FUNCTION: Bifunctional subunit.

			5]; enoyl-CoA hydratase activity [GO:0004300]; fatty-acyl-CoA binding [GO:0000062]; long-chain-3-hydroxyacyl-CoA dehydrogenase activity [GO:0016509]; long-chain-enoyl-CoA hydratase activity [GO:0016508]; NAD binding [GO:0051287]	[GO:0005743]; mitochondrial nucleoid [GO:0042645]; mitochondrion [GO:0005739]	
IDH3B	0.58	2-oxoglutarate metabolic process [GO:0006103]; isocitrate metabolic process [GO:0006102]; NADH metabolic process [GO:0006734]; tricarboxylic acid cycle [GO:0006099]	electron carrier activity [GO:0009055]; isocitrate dehydrogenase (NAD+) activity [GO:0004449]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	
ACSL1	0.58	adiponectin-activated signaling pathway [GO:0033211]; alpha-linolenic acid metabolic process [GO:0036109]; linoleic acid metabolic process [GO:0043651]; lipid biosynthetic process [GO:0008610]; long-chain fatty acid import [GO:0044539]; long-chain fatty acid metabolic process [GO:0001676]; long-	ATP binding [GO:0005524]; long-chain fatty acid-CoA ligase activity [GO:0004467]	endoplasmic reticulum membrane [GO:0005789]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; mitochondrial outer membrane [GO:000574	FUNCTION: Activation of long-chain fatty acids for both synthesis of cellular lipids, and degradation via beta-oxidation. Preferentially uses palmitoleate, oleate and linoleate.

		chain fatty-acyl-CoA biosynthetic process [GO:0035338]; positive regulation of protein serine/threonine kinase activity [GO:0071902]; response to drug [GO:0042493]; response to nutrient [GO:0007584]; response to oleic acid [GO:0034201]; response to organic cyclic compound [GO:0014070]; triglyceride metabolic process [GO:0006641]; xenobiotic catabolic process [GO:0042178]		1]; mitochondrion [GO:0005739]; peroxisomal membrane [GO:0005778]; plasma membrane [GO:0005886]	
RYR2	0.60	BMP signaling pathway [GO:0030509]; calcium ion transport [GO:0006816]; calcium ion transport into cytosol [GO:0060402]; calcium-mediated signaling [GO:0019722]; calcium-mediated signaling using intracellular calcium source [GO:0035584]; canonical Wnt signaling pathway [GO:0060070]; cardiac muscle contraction [GO:0060048]; cardiac muscle hypertrophy [GO:0003300]; cell communication by electrical coupling involved in cardiac conduction [GO:0086064]; cellular calcium ion homeostasis [GO:0006874]; cellular response to caffeine [GO:0071313]; cellular response to	calcium channel activity [GO:0005262]; calcium-induced calcium release activity [GO:0048763]; calcium ion binding [GO:0005509]; calcium-release channel activity [GO:0015278]; calmodulin binding [GO:0005516]; enzyme binding [GO:0019899]; identical protein binding [GO:0042802]; ion channel binding [GO:0044325]; protein kinase A catalytic subunit	calcium channel complex [GO:0034704]; extracellular exosome [GO:0070062]; junctional sarcoplasmic reticulum membrane [GO:0014701]; membrane [GO:0016020]; plasma membrane [GO:0005886]; protein complex [GO:0043234]; sarcoplasmic reticulum [GO:0016529]; sarcoplasmic reticulum membrane [GO:0033017]; smooth endoplasmic reticulum [GO:0005790]; Z disc	FUNCTION: Calcium channel that mediates the release of Ca(2+) from the sarcoplasmic reticulum into the cytoplasm and thereby plays a key role in triggering cardiac muscle contraction. Aberrant channel activation can lead to cardiac arrhythmia. In cardiac myocytes, calcium release is triggered by increased Ca(2+) levels due to activation of the L-type calcium channel CACNA1C. The calcium channel activity is modulated by formation of heterotetramers with RYR3. Required for cellular calcium ion homeostasis. Required for embryonic heart development. {ECO:0000269|PubMed:10830164, ECO:0000269|PubMed:20056922}.

		epinephrine stimulus [GO:0071872]; detection of calcium ion [GO:0005513]; embryonic heart tube morphogenesis [GO:0003143]; establishment of protein localization to endoplasmic reticulum [GO:0072599]; ion transmembrane transport [GO:0034220]; left ventricular cardiac muscle tissue morphogenesis [GO:0003220]; positive regulation of calcium-transporting ATPase activity [GO:1901896]; positive regulation of heart rate [GO:0010460]; positive regulation of sequestering of calcium ion [GO:0051284]; positive regulation of the force of heart contraction [GO:0098735]; Purkinje myocyte to ventricular cardiac muscle cell signaling [GO:0086029]; regulation of atrial cardiac muscle cell action potential [GO:0098910]; regulation of AV node cell action potential [GO:0098904]; regulation of cardiac conduction [GO:1903779]; regulation of cardiac muscle contraction [GO:0055117]; regulation of cardiac muscle contraction by calcium ion signaling [GO:0010882]; regulation of cardiac muscle contraction by regulation of the	binding [GO:0034236]; protein kinase A regulatory subunit binding [GO:0034237]; ryanodine-sensitive calcium-release channel activity [GO:0005219]; suramin binding [GO:0043924]	[GO:0030018]	

		release of sequestered calcium ion [GO:0010881]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of heart rate [GO:0002027]; regulation of SA node cell action potential [GO:0098907]; regulation of ventricular cardiac muscle cell action potential [GO:0098911]; release of sequestered calcium ion into cytosol [GO:0051209]; release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0014808]; response to caffeine [GO:0031000]; response to hypoxia [GO:0001666]; response to muscle activity [GO:0014850]; response to muscle stretch [GO:0035994]; response to redox state [GO:0051775]; sarcoplasmic reticulum calcium ion transport [GO:0070296]; type B pancreatic cell apoptotic process [GO:0097050]; ventricular cardiac muscle cell action potential [GO:0086005]			
ALDH6A1	0.61	beta-alanine catabolic process [GO:0019484]; branched-chain amino acid catabolic process [GO:0009083]; brown fat cell differentiation	aldehyde dehydrogenase (NAD) activity [GO:0004029]; fatty-acyl-CoA binding [GO:000006	extracellular exosome [GO:0070062]; mitochondrial matrix [GO:0005759]; mitochondri	FUNCTION: Plays a role in valine and pyrimidine metabolism. Binds fatty acyl-CoA.

		[GO:0050873]; thymine catabolic process [GO:0006210]; thymine metabolic process [GO:0019859]; valine catabolic process [GO:0006574]; valine metabolic process [GO:0006573]	2]; malonate-semialdehyde dehydrogenase (acetylating) activity [GO:0018478]; methylmalonate-semialdehyde dehydrogenase (acylating) activity [GO:0004491]; poly(A) RNA binding [GO:0044822]; thiolester hydrolase activity [GO:0016790]	on [GO:0005739]; nucleoplasm [GO:0005654]	
PCCA	0.61	biotin metabolic process [GO:0006768]; short-chain fatty acid catabolic process [GO:0019626]	ATP binding [GO:0005524]; biotin binding [GO:0009374]; biotin carboxylase activity [GO:0004075]; enzyme binding [GO:0019899]; metal ion binding [GO:0046872]; propionyl-CoA carboxylase activity [GO:0004658]	cytosol [GO:0005829]; mitochondrial matrix [GO:0005759]	
NDUFB4	0.62	mitochondrial electron transport, NADH to ubiquinone [GO:0006120]; mitochondrial respiratory chain complex I assembly [GO:0032981]; response to oxidative stress [GO:0006979]	NADH dehydrogenase (ubiquinone) activity [GO:0008137]	extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; mitochondri	FUNCTION: Accessory subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I), that is believed not to be involved in catalysis. Complex I functions in the transfer of electrons from NADH to the respiratory chain. The

				al inner membrane [GO:0005743]; mitochondrial respiratory chain complex I [GO:0005747]; mitochondrion [GO:0005739]; nuclear membrane [GO:0031965]; nucleoplasm [GO:0005654]	immediate electron acceptor for the enzyme is believed to be ubiquinone.
TMOD1	0.62	actin filament organization [GO:0007015]; adult locomotory behavior [GO:0008344]; lens fiber cell development [GO:0070307]; muscle contraction [GO:0006936]; muscle filament sliding [GO:0030049]; myofibril assembly [GO:0030239]; pointed-end actin filament capping [GO:0051694]	tropomyosin binding [GO:0005523]	cortical cytoskeleton [GO:0030863]; cytosol [GO:0005829]; membrane [GO:0016020]; nucleus [GO:0005634]; striated muscle thin filament [GO:0005865]	FUNCTION: Blocks the elongation and depolymerization of the actin filaments at the pointed end. The Tmod/TM complex contributes to the formation of the short actin protofilament, which in turn defines the geometry of the membrane skeleton. May play an important role in regulating the organization of actin filaments by preferentially binding to a specific tropomyosin isoform at its N-terminus. {ECO:0000269|PubMed:8002995}.
GRPEL1	0.64	protein folding [GO:0006457]	adenyl-nucleotide exchange factor activity [GO:0000774]; unfolded protein binding [GO:0051082]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	FUNCTION: Essential component of the PAM complex, a complex required for the translocation of transit peptide-containing proteins from the inner membrane into the mitochondrial matrix in an ATP-dependent manner. Seems to control the nucleotide-dependent binding of mitochondrial HSP70 to substrate proteins.
NDUFA6	0.65	mitochondrial electron transport, NADH to ubiquinone [GO:0006120]; mitochondrial respiratory chain complex I assembly [GO:0032981];	NADH dehydrogenase (ubiquinone) activity [GO:0008137]	mitochondrial inner membrane [GO:0005743]; mitochondrial membrane [GO:003196	FUNCTION: Accessory subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I), that is believed to be not involved in catalysis. Complex I functions in the transfer of

		response to oxidative stress [GO:0006979]		6]; mitochondrial respiratory chain complex I [GO:0005747]	electrons from NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone.
NUDC	0.65	cell division [GO:0051301]; cell proliferation [GO:0008283]; mitotic nuclear division [GO:0007067]; multicellular organism development [GO:0007275]; sister chromatid cohesion [GO:0007062]		cytoplasm [GO:0005737]; cytosol [GO:0005829]; microtubule [GO:0005874]; nucleoplasm [GO:0005654]	FUNCTION: Plays a role in neurogenesis and neuronal migration (By similarity). Necessary for correct formation of mitotic spindles and chromosome separation during mitosis. Necessary for cytokinesis and cell proliferation. {ECO:0000250, ECO:0000269|PubMed:12679384, ECO:0000269|PubMed:12852857}.
NFS1	0.66	[2Fe-2S] cluster assembly [GO:0044571]; iron incorporation into metallo-sulfur cluster [GO:0018283]; molybdopterin cofactor biosynthetic process [GO:0032324]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; protein complex assembly [GO:0006461]; small molecule metabolic process [GO:0044281]; sulfur amino acid metabolic process [GO:0000096]	cysteine desulfurase activity [GO:0031071]; iron-sulfur cluster binding [GO:0051536]; metal ion binding [GO:0046872]; protein homodimerization activity [GO:0042803]; pyridoxal phosphate binding [GO:0030170]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; intracellular membrane-bounded organelle [GO:0043231]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	FUNCTION: Catalyzes the removal of elemental sulfur from cysteine to produce alanine. It supplies the inorganic sulfur for iron-sulfur (Fe-S) clusters. May be involved in the biosynthesis of molybdenum cofactor. {ECO:0000269|PubMed:18650437}.
ME2	0.66	malate metabolic process [GO:0006108]; regulation of NADP metabolic process [GO:1902031]	electron carrier activity [GO:0009055]; malate dehydrogenase (decarboxylating) (NAD+) activity [GO:000447	intracellular membrane-bounded organelle [GO:0043231]; mitochondrial matrix [GO:0005759]; mitochondrion	

			1]; malic enzyme activity [GO:0004470]; metal ion binding [GO:0046872]; NAD binding [GO:0051287]; oxaloacetate decarboxylase activity [GO:0008948]	[GO:0005739]	
IDH3G	0.66	2-oxoglutarate metabolic process [GO:0006103]; carbohydrate metabolic process [GO:0005975]; isocitrate metabolic process [GO:0006102]; NADH metabolic process [GO:0006734]; negative regulation of growth [GO:0045926]; tricarboxylic acid cycle [GO:0006099]	ATP binding [GO:0005524]; isocitrate dehydrogenase (NAD+) activity [GO:0004449]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	
GBAS	0.67	ATP biosynthetic process [GO:0006754]; negative regulation of ATP citrate synthase activity [GO:2000984]; oxidative phosphorylation [GO:0006119]		integral component of plasma membrane [GO:0005887]; membrane [GO:0016020]; mitochondrion [GO:0005739]	
COX5B	0.67	mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]; respiratory gaseous exchange [GO:0007585]	cytochrome-c oxidase activity [GO:0004129]; metal ion binding [GO:0046872]	extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.

TPP1	0.68	bone resorption [GO:0045453]; central nervous system development [GO:0007417]; epithelial cell differentiation [GO:0030855]; IRE1-mediated unfolded protein response [GO:0036498]; lipid metabolic process [GO:0006629]; lysosome organization [GO:0007040]; nervous system development [GO:0007399]; neuromuscular process controlling balance [GO:0050885]; peptide catabolic process [GO:0043171]; protein catabolic process [GO:0030163]; proteolysis [GO:0006508]	endopeptidase activity [GO:0004175]; metal ion binding [GO:0046872]; peptidase activity [GO:0008233]; peptide binding [GO:0042277]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]; tripeptidyl-peptidase activity [GO:0008240]	extracellular exosome [GO:0070062]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]; melanosome [GO:0042470]; mitochondrion [GO:0005739]	FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity). {ECO:0000250}.
ATP1A3	0.69	adult locomotory behavior [GO:0008344]; ATP hydrolysis coupled proton transport [GO:0015991]; cardiac muscle contraction [GO:0060048]; cell communication by electrical coupling involved in cardiac conduction [GO:0086064]; cellular potassium ion homeostasis [GO:0030007]; cellular response to steroid hormone stimulus [GO:0071383]; cellular sodium ion homeostasis [GO:0006883]; ionotropic glutamate receptor signaling pathway [GO:0035235]; ion	ATP binding [GO:0005524]; chaperone binding [GO:0051087]; metal ion binding [GO:0046872]; sodium:potassium-exchanging ATPase activity [GO:0005391]; sodium:potassium-exchanging ATPase activity involved in regulation of cardiac muscle cell membrane potential	axon [GO:0030424]; dendritic spine head [GO:0044327]; dendritic spine neck [GO:0044326]; endoplasmic reticulum [GO:0005783]; extracellular vesicle [GO:1903561]; Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021]; myelin sheath [GO:0043209]; nucleus	FUNCTION: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients.

		transmembrane transport [GO:0034220]; memory [GO:0007613]; potassium ion import [GO:0010107]; regulation of cardiac conduction [GO:1903779]; response to drug [GO:0042493]; response to glycoside [GO:1903416]; sodium ion export from cell [GO:0036376]; visual learning [GO:0008542]	[GO:0086037]; steroid hormone binding [GO:1990239]	[GO:0005634]; plasma membrane [GO:0005886]; sarcolemma [GO:0042383]; sodium:potassium-exchanging ATPase complex [GO:0005890]; synapse [GO:0045202]	
COX6B1	0.70	mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]; substantia nigra development [GO:0021762]	cytochrome-c oxidase activity [GO:0004129]	mitochondrial inner membrane [GO:0005743]; mitochondrial intermembrane space [GO:0005758]; mitochondrion [GO:0005739]	FUNCTION: Connects the two COX monomers into the physiological dimeric form. {ECO:0000250}.
LMCD1	0.70	cellular protein metabolic process [GO:0044267]; mitophagy in response to mitochondrial depolarization [GO:0098779]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; positive regulation of calcineurin-NFAT signaling cascade [GO:0070886]; positive regulation of defense response to virus by host [GO:0002230]; regulation of cardiac muscle hypertrophy [GO:0010611]; transcription, DNA-templated	transcription corepressor activity [GO:0003714]; zinc ion binding [GO:0008270]	cytoplasm [GO:0005737]; extracellular space [GO:0005615]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	FUNCTION: Transcriptional cofactor that restricts GATA6 function by inhibiting DNA-binding, resulting in repression of GATA6 transcriptional activation of downstream target genes. Represses GATA6-mediated trans activation of lung- and cardiac tissue-specific promoters. Inhibits DNA-binding by GATA4 and GATA1 to the cTNC promoter (By similarity). Plays a critical role in the development of cardiac hypertrophy via activation of calcineurin/nuclear factor of activated T-cells signaling pathway. {ECO:0000250, ECO:0000269|PubMed:20026769}.

		[GO:0006351]; xenophagy [GO:0098792]			
ST13	0.72	chaperone cofactor-dependent protein refolding [GO:0070389]; negative regulation of protein refolding [GO:0061084]; protein folding [GO:0006457]; protein homooligomerization [GO:0051260]	dATP binding [GO:0032564]; protein binding, bridging [GO:0030674]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; protein complex [GO:0043234]	FUNCTION: One HIP oligomer binds the ATPase domains of at least two HSC70 molecules dependent on activation of the HSC70 ATPase by HSP40. Stabilizes the ADP state of HSC70 that has a high affinity for substrate protein. Through its own chaperone activity, it may contribute to the interaction of HSC70 with various target proteins (By similarity). {ECO:0000250}.
FLNC	0.73	cell junction assembly [GO:0034329]; muscle fiber development [GO:0048747]	ankyrin binding [GO:0030506]; cytoskeletal protein binding [GO:0008092]	costamere [GO:0043034]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; focal adhesion [GO:0005925]; plasma membrane [GO:0005886]; sarcolemma [GO:0042383]; sarcoplasm [GO:0016528]; Z disc [GO:0030018]	FUNCTION: Muscle-specific filamin, which plays a central role in muscle cells, probably by functioning as a large actin-cross-linking protein. May be involved in reorganizing the actin cytoskeleton in response to signaling events, and may also display structural functions at the Z lines in muscle cells. Critical for normal myogenesis and for maintaining the structural integrity of the muscle fibers.
STIP1	0.78	response to stress [GO:0006950]	poly(A) RNA binding [GO:0044822]	Golgi apparatus [GO:0005794]; myelin sheath [GO:0043209]; nucleus [GO:0005634]; protein complex [GO:0043234]	FUNCTION: Mediates the association of the molecular chaperones HSC70 and HSP90 (HSPCA and HSPCB).
DDX39B	1.25	liver development [GO:0001889]; mRNA 3'-end processing [GO:0031124];	ATPase activity [GO:0016887]; ATP binding	cytoplasm [GO:0005737]; nuclear matrix [GO:001636	FUNCTION: Involved in nuclear export of spliced and unspliced mRNA. Assembling component of the TREX complex which is

		mRNA export from nucleus [GO:0006406]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation of DNA damage checkpoint [GO:2000002]; positive regulation of cell growth involved in cardiac muscle cell development [GO:0061051]; positive regulation of DNA biosynthetic process [GO:2000573]; positive regulation of DNA-templated transcription, elongation [GO:0032786]; positive regulation of translation [GO:0045727]; positive regulation of vascular smooth muscle cell proliferation [GO:1904707]; RNA export from nucleus [GO:0006405]; RNA secondary structure unwinding [GO:0010501]; RNA splicing [GO:0008380]; spliceosomal complex assembly [GO:0000245]; termination of RNA polymerase II transcription [GO:0006369]; viral mRNA export from host cell nucleus [GO:0046784]	[GO:0005524]; ATP-dependent protein binding [GO:0043008]; ATP-dependent RNA helicase activity [GO:0004004]; poly(A) RNA binding [GO:0044822]; RNA-dependent ATPase activity [GO:0008186]; U4 snRNA binding [GO:0030621]; U6 snRNA binding [GO:0017070]	3]; nuclear speck [GO:0016607]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; transcription export complex [GO:0000346]	thought to couple mRNA transcription, processing and nuclear export, and specifically associates with spliced mRNA and not with unspliced pre-mRNA. TREX is recruited to spliced mRNAs by a transcription-independent mechanism, binds to mRNA upstream of the exon-junction complex (EJC) and is recruited in a splicing- and cap-dependent manner to a region near the 5' end of the mRNA where it functions in mRNA export to the cytoplasm via the TAP/NFX1 pathway. May undergo several rounds of ATP hydrolysis during assembly of TREX to drive subsequent loading of components such as ALYREF/THOC and CHTOP onto mRNA. The TREX complex is essential for the export of Kaposi's sarcoma-associated herpesvirus (KSHV) intronless mRNAs and infectious virus production. Also associates with pre-mRNA independent of ALYREF/THOC4 and the THO complex. Involved in the nuclear export of intronless mRNA; the ATP-bound form is proposed to recruit export adapter ALYREF/THOC4 to intronless mRNA; its ATPase activity is cooperatively stimulated by RNA and ALYREF/THOC4 and ATP hydrolysis is thought to trigger the dissociation from RNA to allow the association of ALYREF/THOC4 and the NXF1-NXT1 heterodimer. Involved in transcription elongation and genome stability.; FUNCTION: Splice factor that is required for the first ATP-dependent step in spliceosome assembly and for the interaction of U2 snRNP with the branchpoint. Has both RNA-stimulated ATP

					binding/hydrolysis activity and ATP-dependent RNA unwinding activity. Even with the stimulation of RNA, the ATPase activity is weak. Can only hydrolyze ATP but not other NTPs. The RNA stimulation of ATPase activity does not have a strong preference for the sequence and length of the RNA. However, ssRNA stimulates the ATPase activity much more strongly than dsRNA. Can unwind 5' or 3' overhangs or blunt end RNA duplexes in vitro. The ATPase and helicase activities are not influenced by U2AF2; the effect of ALYREF/THOC4 is reported conflictingly with [PubMed:23299939] reporting a stimulatory effect.
VAT1	1.44	negative regulation of mitochondrial fusion [GO:0010637]	oxidoreductase activity [GO:0016491]; zinc ion binding [GO:0008270]	extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; mitochondrial outer membrane [GO:0005741]	FUNCTION: Possesses ATPase activity (By similarity). Plays a part in calcium-regulated keratinocyte activation in epidermal repair mechanisms. Has no effect on cell proliferation. Negatively regulates mitochondrial fusion in cooperation with mitofusin proteins (MFN1-2). {ECO:0000250, ECO:0000269|PubMed:12898150, ECO:0000269|PubMed:17105775, ECO:0000269|PubMed:19508442}.
FGG	1.50	blood coagulation [GO:0007596]; blood coagulation, fibrin clot formation [GO:0072378]; cell-matrix adhesion [GO:0007160]; cellular protein complex assembly [GO:0043623]; extracellular matrix organization [GO:0030198]; fibrinolysis [GO:0042730]; negative regulation	cell adhesion molecule binding [GO:0050839]; metal ion binding [GO:0046872]; receptor binding [GO:0005102]; structural molecule activity [GO:0005198]	blood microparticle [GO:0072562]; cell cortex [GO:0005938]; cell surface [GO:0009986]; external side of plasma membrane [GO:0009897];	FUNCTION: Together with fibrinogen alpha (FGA) and fibrinogen beta (FGB), polymerizes to form an insoluble fibrin matrix. Has a major function in hemostasis as one of the primary components of blood clots. In addition, functions during the early stages of wound repair to stabilize the lesion and guide cell migration during re-epithelialization. Was originally thought to be essential for platelet aggregation, based on in

		of endothelial cell apoptotic process [GO:2000352]; negative regulation of extrinsic apoptotic signaling pathway via death domain receptors [GO:1902042]; plasminogen activation [GO:0031639]; platelet aggregation [GO:0070527]; platelet degranulation [GO:0002576]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of exocytosis [GO:0045921]; positive regulation of heterotypic cell-cell adhesion [GO:0034116]; positive regulation of peptide hormone secretion [GO:0090277]; positive regulation of protein secretion [GO:0050714]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; positive regulation of vasoconstriction [GO:0045907]; protein polymerization [GO:0051258]; protein secretion [GO:0009306]; response to calcium ion [GO:0051592]; signal transduction [GO:0007165]		extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex [GO:0005577]; plasma membrane [GO:0005886]; platelet alpha granule [GO:0031091]; platelet alpha granule lumen [GO:0031093]	vitro studies using anticoagulated blood. However, subsequent studies have shown that it is not absolutely required for thrombus formation in vivo. Enhances expression of SELP in activated platelets via an ITGB3-dependent pathway. Maternal fibrinogen is essential for successful pregnancy. Fibrin deposition is also associated with infection, where it protects against IFNG-mediated hemorrhage. May also facilitate the antibacterial immune response via both innate and T-cell mediated pathways. {ECO:0000250|UniProtKB: E9PV24}.
ARHGAP1	1.55	regulation of small GTPase mediated signal transduction [GO:0051056]; Rho protein signal transduction [GO:0007266]; small GTPase mediated	GTPase activator activity [GO:0005096]; SH3/SH2 adaptor activity	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:007006	FUNCTION: GTPase activator for the Rho, Rac and Cdc42 proteins, converting them to the putatively inactive GDP-bound state. Cdc42 seems to be the preferred substrate.

		signal transduction [GO:0007264]	[GO:0005070]	2]; perinuclear region of cytoplasm [GO:0048471]	
HYOU1	1.65	cellular response to hypoxia [GO:0071456]; ER to Golgi vesicle-mediated transport [GO:0006888]; IRE1-mediated unfolded protein response [GO:0036498]; negative regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic signaling pathway [GO:1903382]; negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway [GO:1903298]; receptor-mediated endocytosis [GO:0006898]; response to endoplasmic reticulum stress [GO:0034976]; response to ischemia [GO:0002931]	ATP binding [GO:0005524]; chaperone binding [GO:0051087]	endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum chaperone complex [GO:0034663]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; focal adhesion [GO:0005925]; membrane [GO:0016020]; smooth endoplasmic reticulum [GO:0005790]	FUNCTION: Has a pivotal role in cytoprotective cellular mechanisms triggered by oxygen deprivation. May play a role as a molecular chaperone and participate in protein folding. {ECO:0000269|PubMed:10037731}.
HNRNPU	1.65	cellular response to dexamethasone stimulus [GO:0071549]; circadian regulation of gene expression [GO:0032922]; CRD-mediated mRNA stabilization [GO:0070934]; gene expression [GO:0010467]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation	ATP binding [GO:0005524]; core promoter binding [GO:0001047]; DNA binding [GO:0003677]; enhancer binding [GO:0035326]; poly(A) RNA binding [GO:004482	catalytic step 2 spliceosome [GO:0071013]; cell surface [GO:0009986]; CRD-mediated mRNA stability complex [GO:0070937]; cytoplasmic ribonucleopr	FUNCTION: Component of the CRD-mediated complex that promotes MYC mRNA stabilization. Binds to pre-mRNA. Has high affinity for scaffold-attached region (SAR) DNA. Binds to double- and single-stranded DNA and RNA. Plays a role in the circadian regulation of the core clock component ARNTL/BMAL1 transcription (By similarity). {ECO:0000250|UniProtKB: Q8VEK3,

		of telomere maintenance via telomerase [GO:0032211]; osteoblast differentiation [GO:0001649]; positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity [GO:2000373]; positive regulation of gene expression [GO:0010628]; RNA processing [GO:0006396]	2]; poly(G) binding [GO:0034046]; ribonucleoprotein complex binding [GO:0043021]; RNA binding [GO:0003723]; telomerase RNA binding [GO:0070034]	otein granule [GO:0036464]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	ECO:0000269|PubMed:19029303}.
C3	1.76	blood coagulation [GO:0007596]; complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; fatty acid metabolic process [GO:0006631]; G-protein coupled receptor signaling pathway [GO:0007186]; immune response [GO:0006955]; inflammatory response [GO:0006954]; positive regulation of activation of membrane attack complex [GO:0001970]; positive regulation of angiogenesis [GO:0045766]; positive regulation of apoptotic cell clearance [GO:2000427]; positive regulation of developmental growth [GO:0048639]; positive regulation of	C5L2 anaphylatoxin chemotactic receptor binding [GO:0031715]; cofactor binding [GO:0048037]; endopeptidase inhibitor activity [GO:0004866]; lipid binding [GO:0008289]; receptor binding [GO:0005102]; serine-type endopeptidase activity [GO:0004252]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	FUNCTION: C3 plays a central role in the activation of the complement system. Its processing by C3 convertase is the central reaction in both classical and alternative complement pathways. After activation C3b can bind covalently, via its reactive thioester, to cell surface carbohydrates or immune aggregates.; FUNCTION: Derived from proteolytic degradation of complement C3, C3a anaphylatoxin is a mediator of local inflammatory process. In chronic inflammation, acts as a chemoattractant for neutrophils (By similarity). It induces the contraction of smooth muscle, increases vascular permeability and causes histamine release from mast cells and basophilic leukocytes. {ECO:0000250}.; FUNCTION: C3-beta-c: Acts as a chemoattractant for neutrophils in chronic inflammation. {ECO:0000250}.; FUNCTION: Acylation stimulating protein: adipogenic hormone that stimulates triglyceride (TG) synthesis and glucose transport in adipocytes, regulating fat storage and playing a role in postprandial TG clearance. Appears to

		ERK1 and ERK2 cascade [GO:0070374]; positive regulation of glucose transport [GO:0010828]; positive regulation of G-protein coupled receptor protein signaling pathway [GO:0045745]; positive regulation of lipid storage [GO:0010884]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of type IIa hypersensitivity [GO:0001798]; positive regulation of vascular endothelial growth factor production [GO:0010575]; regulation of complement activation [GO:0030449]; regulation of immune response [GO:0050776]; regulation of triglyceride biosynthetic process [GO:0010866]; response to estradiol [GO:0032355]; response to glucocorticoid [GO:0051384]; response to magnesium ion [GO:0032026]; response to progesterone [GO:0032570]; signal transduction [GO:0007165]; tolerance induction [GO:0002507]			stimulate TG synthesis via activation of the PLC, MAPK and AKT signaling pathways. Ligand for C5AR2. Promotes the phosphorylation, ARRB2-mediated internalization and recycling of C5AR2 (PubMed:8376604, PubMed:2909530, PubMed:9059512, PubMed:10432298, PubMed:15833747, PubMed:16333141, PubMed:19615750). {ECO:0000269|PubMed:10432298, ECO:0000269|PubMed:15833747, ECO:0000269|PubMed:16333141, ECO:0000269|PubMed:19615750, ECO:0000269|PubMed:2909530, ECO:0000269|PubMed:8376604, ECO:0000269|PubMed:9059512}.
C7	1.83	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957];		extracellular exosome [GO:0070062]; extracellular region [GO:000557	FUNCTION: Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target

		complement activation, classical pathway [GO:0006958]; cytolysis [GO:0019835]; regulation of complement activation [GO:0030449]		6]; membrane attack complex [GO:0005579]	cells. C7 serves as a membrane anchor.
GGT5	1.85	cellular amino acid metabolic process [GO:0006520]; glutathione biosynthetic process [GO:0006750]; glutathione metabolic process [GO:0006749]; inflammatory response [GO:0006954]; leukotriene biosynthetic process [GO:0019370]; leukotriene metabolic process [GO:0006691]	gamma-glutamyltransferase activity [GO:0003840]; glutathione hydrolase activity [GO:0036374]	anchored component of external side of plasma membrane [GO:0031362]; integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	FUNCTION: Cleaves the gamma-glutamyl peptide bond of glutathione conjugates, but maybe not glutathione itself. Converts leukotriene C4 (LTC4) to leukotriene D4 (LTD4).
C9	1.92	complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; hemolysis by symbiont of host erythrocytes [GO:0019836]; regulation of complement activation [GO:0030449]		blood microparticle [GO:0072562]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; integral component of plasma membrane [GO:0005887]; membrane attack complex [GO:0005579]; plasma membrane [GO:0005886]	FUNCTION: Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target cells. C9 is the pore-forming subunit of the MAC.
SPARCL1	1.97	signal transduction [GO:0007165]	calcium ion binding	extracellular exosome [GO:007006	

			[GO:0005509]	2]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	
RCN1	1.98	camera-type eye development [GO:0043010]; in utero embryonic development [GO:0001701]	calcium ion binding [GO:0005509]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]	FUNCTION: May regulate calcium-dependent activities in the endoplasmic reticulum lumen or post-ER compartment.
G6PD	2.00	cellular response to oxidative stress [GO:0034599]; cholesterol biosynthetic process [GO:0006695]; erythrocyte maturation [GO:0043249]; glucose 6-phosphate metabolic process [GO:0051156]; glucose metabolic process [GO:0006006]; glutathione metabolic process [GO:0006749]; lipid metabolic process [GO:0006629]; NADPH regeneration [GO:0006740]; NADP metabolic process [GO:0006739]; negative regulation of protein glutathionylation [GO:0010734]; oxidation-reduction process [GO:0055114]; pentose biosynthetic process [GO:0019322]; pentose-phosphate shunt [GO:0006098]; pentose-phosphate shunt, oxidative	glucose-6-phosphate dehydrogenase activity [GO:0004345]; glucose binding [GO:0005536]; identical protein binding [GO:0042802]; NADP binding [GO:0050661]; protein homodimerization activity [GO:0042803]	centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; intracellular membrane-bounded organelle [GO:0043231]; membrane [GO:0016020]; microtubule organizing center [GO:0005815]; nucleus [GO:0005634]	FUNCTION: Catalyzes the rate-limiting step of the oxidative pentose-phosphate pathway, which represents a route for the dissimilation of carbohydrates besides glycolysis. The main function of this enzyme is to provide reducing power (NADPH) and pentose phosphates for fatty acid and nucleic acid synthesis. {ECO:0000269|PubMed:15858258, ECO:0000269|PubMed:24769394}.

		branch [GO:0009051]; regulation of neuron apoptotic process [GO:0043523]; response to ethanol [GO:0045471]; response to food [GO:0032094]; response to organic cyclic compound [GO:0014070]; ribose phosphate biosynthetic process [GO:0046390]; substantia nigra development [GO:0021762]			
FBLN1	2.01	blood coagulation, fibrin clot formation [GO:0072378]; embryo implantation [GO:0007566]; extracellular matrix organization [GO:0030198]; negative regulation of cell adhesion [GO:0007162]; negative regulation of cell motility [GO:2000146]; negative regulation of ERK1 and ERK2 cascade [GO:0070373]; negative regulation of protein phosphorylation [GO:0001933]; negative regulation of stem cell proliferation [GO:2000647]; negative regulation of substrate adhesion-dependent cell spreading [GO:1900025]; negative regulation of transformation of host cell by virus [GO:1904188]; negative regulation of transforming growth factor-beta secretion [GO:2001202]; positive regulation of fibroblast	calcium ion binding [GO:0005509]; extracellular matrix structural constituent [GO:0005201]; fibrinogen binding [GO:0070051]; fibronectin binding [GO:0001968]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; peptidase activator activity [GO:0016504]; protein complex binding [GO:0032403]; protein C-terminus binding [GO:0008022]	basement membrane [GO:0005604]; elastic fiber [GO:0071953]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	FUNCTION: Incorporated into fibronectin-containing matrix fibers. May play a role in cell adhesion and migration along protein fibers within the extracellular matrix (ECM). Could be important for certain developmental processes and contribute to the supramolecular organization of ECM architecture, in particular to those of basement membranes. Has been implicated in a role in cellular transformation and tumor invasion, it appears to be a tumor suppressor. May play a role in haemostasis and thrombosis owing to its ability to bind fibrinogen and incorporate into clots. Could play a significant role in modulating the neurotrophic activities of APP, particularly soluble APP. {ECO:0000269|PubMed:11792823, ECO:0000269|PubMed:9393974, ECO:0000269|PubMed:9466671}.

		proliferation [GO:0048146]; positive regulation of gene expression [GO:0010628]; positive regulation of substrate-dependent cell migration, cell attachment to substrate [GO:1904237]; viral process [GO:0016032]			
SERPING1	2.02	aging [GO:0007568]; blood circulation [GO:0008015]; blood coagulation, intrinsic pathway [GO:0007597]; complement activation, classical pathway [GO:0006958]; fibrinolysis [GO:0042730]; innate immune response [GO:0045087]; negative regulation of complement activation, lectin pathway [GO:0001869]; platelet degranulation [GO:0002576]	serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	FUNCTION: Activation of the C1 complex is under control of the C1-inhibitor. It forms a proteolytically inactive stoichiometric complex with the C1r or C1s proteases. May play a potentially crucial role in regulating important physiological pathways including complement activation, blood coagulation, fibrinolysis and the generation of kinins. Very efficient inhibitor of FXIIa. Inhibits chymotrypsin and kallikrein. {ECO:0000269|PubMed:8495195}.
TKT	2.06	glyceraldehyde-3-phosphate biosynthetic process [GO:0046166]; pentose-phosphate shunt [GO:0006098]; pentose-phosphate shunt, non-oxidative branch [GO:0009052]; regulation of growth [GO:0040008]; xylulose biosynthetic process [GO:0005999]	cofactor binding [GO:0048037]; metal ion binding [GO:0046872]; protein homodimerization activity [GO:0042803]; transketolase activity [GO:0004802]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; myelin sheath [GO:0043209]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; peroxisome [GO:0005777]; vesicle [GO:0031982]	FUNCTION: Catalyzes the transfer of a two-carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate.
ANXA1	2.08	actin cytoskeleton reorganization [GO:0031532]; adaptive immune	annealing helicase activity [GO:003631	apical plasma membrane [GO:001632	FUNCTION: Plays important roles in the innate immune response as effector of glucocorticoid-mediated

		response [GO:0002250]; alpha-beta T cell differentiation [GO:0046632]; arachidonic acid secretion [GO:0050482]; cell surface receptor signaling pathway [GO:0007166]; cellular response to glucocorticoid stimulus [GO:0071385]; cellular response to hydrogen peroxide [GO:0070301]; DNA duplex unwinding [GO:0032508]; DNA rewinding [GO:0036292]; endocrine pancreas development [GO:0031018]; estrous cycle [GO:0044849]; gliogenesis [GO:0042063]; G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger [GO:0007187]; granulocyte chemotaxis [GO:0071621]; hepatocyte differentiation [GO:0070365]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; insulin secretion [GO:0030073]; keratinocyte differentiation [GO:0030216]; monocyte chemotaxis [GO:0002548]; myoblast migration involved in skeletal muscle regeneration [GO:0014839]; negative regulation	0]; calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; double-stranded DNA-dependent ATPase activity [GO:0033676]; helicase activity [GO:0004386]; phospholipase A2 inhibitor activity [GO:0019834]; phospholipid binding [GO:0005543]; protein binding, bridging [GO:0030674]; receptor binding [GO:0005102]; single-stranded DNA binding [GO:0003697]; single-stranded RNA binding [GO:0003727]; structural molecule activity [GO:0005198]	4]; basolateral plasma membrane [GO:0016323]; cell surface [GO:0009986]; cornified envelope [GO:0001533]; cytoplasm [GO:0005737]; cytoplasmic vesicle membrane [GO:0030659]; early endosome membrane [GO:0031901]; endosome [GO:0005768]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of endosome membrane [GO:0031313]; extrinsic component of external side of plasma membrane [GO:0031232]; extrinsic component of membrane [GO:0019898]; focal adhesion [GO:0005925]; lateral plasma	responses and regulator of the inflammatory process. Has anti-inflammatory activity (PubMed:8425544). Plays a role in glucocorticoid-mediated down-regulation of the early phase of the inflammatory response (By similarity). Promotes resolution of inflammation and wound healing (PubMed:25664854). Functions at least in part by activating the formyl peptide receptors and downstream signaling cascades (PubMed:15187149, PubMed:25664854). Promotes chemotaxis of granulocytes and monocytes via activation of the formyl peptide receptors (PubMed:15187149). Contributes to the adaptive immune response by enhancing signaling cascades that are triggered by T-cell activation, regulates differentiation and proliferation of activated T-cells (PubMed:17008549). Promotes the differentiation of T-cells into Th1 cells and negatively regulates differentiation into Th2 cells (PubMed:17008549). Has no effect on unstimulated T cells (PubMed:17008549). Promotes rearrangement of the actin cytoskeleton, cell polarization and cell migration (PubMed:15187149). Negatively regulates hormone exocytosis via activation of the formyl peptide receptors and reorganization of the actin cytoskeleton (PubMed:19625660). Has high affinity for Ca(2+) and can bind up to eight Ca(2+) ions (By similarity). Displays Ca(2+)-dependent binding to phospholipid membranes (PubMed:2532504, PubMed:8557678). Plays a role in the formation of

		of apoptotic process [GO:0043066]; negative regulation of exocytosis [GO:0045920]; negative regulation of interleukin-8 secretion [GO:2000483]; negative regulation of phospholipase A2 activity [GO:1900138]; negative regulation of T-helper 2 cell differentiation [GO:0045629]; neutrophil clearance [GO:0097350]; neutrophil homeostasis [GO:0001780]; peptide cross-linking [GO:0018149]; phagocytosis [GO:0006909]; positive regulation of G1/S transition of mitotic cell cycle [GO:1900087]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of neutrophil apoptotic process [GO:0033031]; positive regulation of prostaglandin biosynthetic process [GO:0031394]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of T-helper 1 cell differentiation [GO:0045627]; positive regulation of vesicle fusion [GO:0031340]; positive regulation of wound healing [GO:0090303]; prolactin secretion [GO:0070459]; prostate gland development [GO:0030850];		membrane [GO:0016328]; mast cell granule [GO:0042629]; mitochondrial membrane [GO:0031966]; motile cilium [GO:0031514]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; phagocytic cup [GO:0001891]; plasma membrane [GO:0005886]; protein complex [GO:0043234]; sarcolemma [GO:0042383]; vesicle [GO:0031982]	phagocytic cups and phagosomes. Plays a role in phagocytosis by mediating the Ca(2+)-dependent interaction between phagosomes and the actin cytoskeleton (By similarity). {ECO:0000250|UniProtKB:P10107, ECO:0000250|UniProtKB:P19619, ECO:0000269|PubMed:15187149, ECO:0000269|PubMed:17008549, ECO:0000269|PubMed:19625660, ECO:0000269|PubMed:2532504, ECO:0000269|PubMed:25664854, ECO:0000269|PubMed:2936963, ECO:0000269|PubMed:8425544, ECO:0000269|PubMed:8557678}.

		regulation of cell shape [GO:0008360]; regulation of hormone secretion [GO:0046883]; regulation of inflammatory response [GO:0050727]; regulation of interleukin-1 production [GO:0032652]; regulation of leukocyte migration [GO:0002685]; response to drug [GO:0042493]; response to estradiol [GO:0032355]; response to interleukin-1 [GO:0070555]; response to peptide hormone [GO:0043434]; response to X-ray [GO:0010165]; signal transduction [GO:0007165]			
LMNB2	2.12		structural molecule activity [GO:0005198]	lamin filament [GO:0005638]; nuclear inner membrane [GO:0005637]	FUNCTION: Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin.
CA2	2.21	angiotensin-activated signaling pathway [GO:0038166]; bicarbonate transport [GO:0015701]; carbon dioxide transport [GO:0015670]; cellular response to fluid shear stress [GO:0071498]; kidney development [GO:0001822]; morphogenesis of an epithelium [GO:0002009]; odontogenesis of dentin-containing tooth [GO:0042475]; one-carbon	arylesterase activity [GO:0004064]; carbonate dehydratase activity [GO:0004089]; zinc ion binding [GO:0008270]	apical part of cell [GO:0045177]; axon [GO:0030424]; basolateral plasma membrane [GO:0016323]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062];	FUNCTION: Essential for bone resorption and osteoclast differentiation (By similarity). Reversible hydration of carbon dioxide. Can hydrate cyanamide to urea. Involved in the regulation of fluid secretion into the anterior chamber of the eye. Contributes to intracellular pH regulation in the duodenal upper villous epithelium during proton-coupled peptide absorption. Stimulates the chloride-bicarbonate exchange activity of SLC26A6. {ECO:0000250, ECO:0000269|PubMed:10550681,

		metabolic process [GO:0006730]; positive regulation of bone resorption [GO:0045780]; positive regulation of cellular pH reduction [GO:0032849]; positive regulation of dipeptide transmembrane transport [GO:2001150]; positive regulation of osteoclast differentiation [GO:0045672]; positive regulation of synaptic transmission, GABAergic [GO:0032230]; regulation of anion transport [GO:0044070]; regulation of chloride transport [GO:2001225]; regulation of intracellular pH [GO:0051453]; response to estrogen [GO:0043627]; response to pH [GO:0009268]; response to zinc ion [GO:0010043]; secretion [GO:0046903]		extracellular space [GO:0005615]; microvillus [GO:0005902]; myelin sheath [GO:0043209]; plasma membrane [GO:0005886]	ECO:0000269|PubMed:11831900, ECO:0000269|PubMed:15990874}.
FLNA	2.23	actin crosslink formation [GO:0051764]; actin cytoskeleton reorganization [GO:0031532]; adenylate cyclase-inhibiting dopamine receptor signaling pathway [GO:0007195]; cell junction assembly [GO:0034329]; cilium assembly [GO:0042384]; cytoplasmic sequestering of protein [GO:0051220]; establishment of protein localization	actin filament binding [GO:0051015]; Fc-gamma receptor I complex binding [GO:0034988]; glycoprotein binding [GO:0001948]; G-protein coupled receptor binding [GO:0001664]; GTPase binding	actin cytoskeleton [GO:0015629]; actin filament [GO:0005884]; apical dendrite [GO:0097440]; cell-cell junction [GO:0005911]; cortical cytoskeleton [GO:0030863]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendritic	FUNCTION: Promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. Interaction with FLNA may allow neuroblast migration from the ventricular zone into the cortical plate. Tethers cell surface-localized furin, modulates its rate of internalization and directs its intracellular trafficking (By similarity). Involved in ciliogenesis. Plays a role in

		[GO:0045184]; mitotic spindle assembly [GO:0090307]; mRNA transcription from RNA polymerase II promoter [GO:0042789]; negative regulation of apoptotic process [GO:0043066]; negative regulation of protein catabolic process [GO:0042177]; negative regulation of sequence-specific DNA binding transcription factor activity [GO:0043433]; negative regulation of transcription from RNA polymerase I promoter [GO:0016479]; platelet activation [GO:0030168]; platelet aggregation [GO:0070527]; platelet degranulation [GO:0002576]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of integrin-mediated signaling pathway [GO:2001046]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; positive regulation of transcription factor import into nucleus [GO:0042993]; protein localization to cell surface [GO:0034394]; protein stabilization [GO:0050821]; receptor clustering [GO:0043113]; regulation of cell migration	[GO:0051020]; kinase binding [GO:0019900]; poly(A) RNA binding [GO:0044822]; protein homodimerization activity [GO:0042803]; Rac GTPase binding [GO:0048365]; Ral GTPase binding [GO:0017160]; Rho GTPase binding [GO:0017048]; signal transducer activity [GO:0004871]; small GTPase binding [GO:0031267]; transcription factor binding [GO:0008134]	shaft [GO:0043198]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; focal adhesion [GO:0005925]; membrane [GO:0016020]; Myb complex [GO:0031523]; neuronal cell body [GO:0043025]; nucleolus [GO:0005730]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]	cell-cell contacts and adherens junctions during the development of blood vessels, heart and brain organs. Plays a role in platelets morphology through interaction with SYK that regulates ITAM- and ITAM-like-containing receptor signaling, resulting in by platelet cytoskeleton organization maintainance (By similarity). {ECO:0000250, ECO:0000250|UniProtKB:Q8BTM8, ECO:0000269|PubMed:22121117}.

		[GO:0030334]; semaphorin-plexin signaling pathway [GO:0071526]; wound healing, spreading of cells [GO:0044319]			
ITIH2	2.30	hyaluronan metabolic process [GO:0030212]	endopeptidase inhibitor activity [GO:0004866]; serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	FUNCTION: May act as a carrier of hyaluronan in serum or as a binding protein between hyaluronan and other matrix protein, including those on cell surfaces in tissues to regulate the localization, synthesis and degradation of hyaluronan which are essential to cells undergoing biological processes.
APOB	2.43	artery morphogenesis [GO:0048844]; cellular protein catabolic process [GO:0044257]; cellular response to prostaglandin stimulus [GO:0071379]; cellular response to tumor necrosis factor [GO:0071356]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; cholesterol transport [GO:0030301]; fertilization [GO:0009566]; in utero embryonic development [GO:0001701]; leukocyte migration [GO:0050900]; lipoprotein biosynthetic process [GO:0042158]; lipoprotein catabolic process [GO:0042159]; lipoprotein metabolic process [GO:0042157]; lipoprotein transport [GO:0042953]; low-	cholesterol transporter activity [GO:0017127]; heparin binding [GO:0008201]; lipase binding [GO:0035473]; low-density lipoprotein particle receptor binding [GO:0050750]; phospholipid binding [GO:0005543]	actin cytoskeleton [GO:0015629]; chylomicron [GO:0042627]; chylomicron remnant [GO:0034360]; clathrin-coated endocytic vesicle membrane [GO:0030669]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; early endosome [GO:0005769]; endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum lumen [GO:0005788]; endoplasmic reticulum membrane [GO:0005789]; endosome	FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.

		density lipoprotein particle clearance [GO:0034383]; low-density lipoprotein particle remodeling [GO:0034374]; nervous system development [GO:0007399]; positive regulation of cholesterol storage [GO:0010886]; positive regulation of gene expression [GO:0010628]; positive regulation of lipid storage [GO:0010884]; positive regulation of macrophage derived foam cell differentiation [GO:0010744]; post-embryonic development [GO:0009791]; receptor-mediated endocytosis [GO:0006898]; regulation of cholesterol biosynthetic process [GO:0045540]; response to carbohydrate [GO:0009743]; response to lipopolysaccharide [GO:0032496]; response to selenium ion [GO:0010269]; response to virus [GO:0009615]; retinoid metabolic process [GO:0001523]; spermatogenesis [GO:0007283]; sperm motility [GO:0030317]; triglyceride catabolic process [GO:0019433]; triglyceride mobilization [GO:0006642]; very-low-density lipoprotein particle assembly [GO:0034379]		lumen [GO:0031904]; endosome membrane [GO:0010008]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; intermediate-density lipoprotein particle [GO:0034363]; intracellular membrane-bounded organelle [GO:0043231]; low-density lipoprotein particle [GO:0034362]; mature chylomicron [GO:0034359]; neuronal cell body [GO:0043025]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	

ITGB2	2.49	aging [GO:0007568]; apoptotic process [GO:0006915]; cell adhesion [GO:0007155]; cell-cell signaling [GO:0007267]; cell-matrix adhesion [GO:0007160]; cellular extravasation [GO:0045123]; cellular response to low-density lipoprotein particle stimulus [GO:0071404]; endodermal cell differentiation [GO:0035987]; endothelial cell migration [GO:0043542]; extracellular matrix organization [GO:0030198]; heterotypic cell-cell adhesion [GO:0034113]; inflammatory response [GO:0006954]; integrin-mediated signaling pathway [GO:0007229]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; leukocyte migration involved in inflammatory response [GO:0002523]; natural killer cell activation [GO:0030101]; neutrophil chemotaxis [GO:0030593]; positive regulation of angiogenesis [GO:0045766]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of nitric oxide	cell adhesion molecule binding [GO:0050839]; glycoprotein binding [GO:0001948]; ICAM-3 receptor activity [GO:0030369]; metal ion binding [GO:0046872]; protein kinase binding [GO:0019901]	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; extracellular vesicle [GO:1903561]; integrin alphaL-beta2 complex [GO:0034687]; integrin complex [GO:0008305]; membrane [GO:0016020]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]; secretory granule [GO:0030141]	FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. Integrins alpha-M/beta-2 and alpha-X/beta-2 are receptors for the iC3b fragment of the third complement component and for fibrinogen. Integrin alpha-X/beta-2 recognizes the sequence G-P-R in fibrinogen alpha-chain. Integrin alpha-M/beta-2 recognizes P1 and P2 peptides of fibrinogen gamma chain. Integrin alpha-M/beta-2 is also a receptor for factor X. Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. Contributes to natural killer cell cytotoxicity (PubMed:15356110). Involved in leukocyte adhesion and transmigration of leukocytes including T-cells and neutrophils (PubMed:11812992). Triggers neutrophil transmigration during lung injury through PTK2B/PYK2-mediated activation (PubMed:18587400). Integrin alpha-L/beta-2 in assosiation with ICAM3, contributes to apoptotic neutrophil phagocytosis by macrophages (PubMed:23775590). {ECO:0000269|PubMed:11812992, ECO:0000269|PubMed:15356110, ECO:0000269|PubMed:18587400, ECO:0000269|PubMed:23775590}.

		biosynthetic process [GO:0045429]; receptor clustering [GO:0043113]; receptor internalization [GO:0031623]; regulation of cell shape [GO:0008360]; regulation of immune response [GO:0050776]; regulation of peptidyl-tyrosine phosphorylation [GO:0050730]; toll-like receptor 4 signaling pathway [GO:0034142]			
AOC3	2.55	amine metabolic process [GO:0009308]; cell adhesion [GO:0007155]; inflammatory response [GO:0006954]; response to antibiotic [GO:0046677]; xenobiotic metabolic process [GO:0006805]	aliphatic-amine oxidase activity [GO:0052595]; aminoacetone:oxygen oxidoreductase(deaminating) activity [GO:0052594]; calcium ion binding [GO:0005509]; copper ion binding [GO:0005507]; phenethylamine:oxygen oxidoreductase (deaminating) activity [GO:0052596]; primary amine oxidase activity [GO:0008131]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity	cell surface [GO:0009986]; cytoplasm [GO:0005737]; early endosome [GO:0005769]; endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021]; microvillus [GO:0005902]; plasma membrane [GO:0005886]	FUNCTION: Cell adhesion protein that participates in lymphocyte extravasation and recirculation by mediating the binding of lymphocytes to peripheral lymph node vascular endothelial cells in an L-selectin-independent fashion. Has semicarbazide-sensitive (SSAO) monoamine oxidase activity. May play a role in adipogenesis. {ECO:0000269|PubMed:17400359, ECO:0000269|PubMed:19588076, ECO:0000269|PubMed:23349812, ECO:0000269|PubMed:9653080}.

			[GO:0042803]; quinone binding [GO:0048038]; tryptamine:oxygen oxidoreductase (deaminating) activity [GO:0052593]		
ITIH1	2.55	hyaluronan metabolic process [GO:0030212]	calcium ion binding [GO:0005509]; serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	FUNCTION: May act as a carrier of hyaluronan in serum or as a binding protein between hyaluronan and other matrix protein, including those on cell surfaces in tissues to regulate the localization, synthesis and degradation of hyaluronan which are essential to cells undergoing biological processes.; FUNCTION: Contains a potential peptide which could stimulate a broad spectrum of phagocytotic cells.
GUSB	2.56	carbohydrate metabolic process [GO:0005975]; glycosaminoglycan catabolic process [GO:0006027]; hyaluronan catabolic process [GO:0030214]	beta-glucuronidase activity [GO:0004566]; protein domain specific binding [GO:0019904]; receptor binding [GO:0005102]	extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; intracellular membrane-bounded organelle [GO:0043231]; lysosomal lumen [GO:0043202]; membrane [GO:0016020]	FUNCTION: Plays an important role in the degradation of dermatan and keratan sulfates.
F12	2.63	blood coagulation, intrinsic pathway [GO:0007597]; Factor XII activation [GO:0002542]; fibrinolysis [GO:0042730]; innate immune response	calcium ion binding [GO:0005509]; misfolded protein binding [GO:0051787]; serine-	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular	FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin. Prekallikrein is cleaved by factor XII to form kallikrein, which then

		[GO:0045087]; plasma kallikrein-kinin cascade [GO:0002353]; positive regulation of blood coagulation [GO:0030194]; positive regulation of fibrinolysis [GO:0051919]; positive regulation of plasminogen activation [GO:0010756]; protein autoprocessing [GO:0016540]; protein processing [GO:0016485]; response to misfolded protein [GO:0051788]; zymogen activation [GO:0031638]	type endopeptidase activity [GO:0004252]	space [GO:0005615]; plasma membrane [GO:0005886]	cleaves factor XII first to alpha-factor XIIa and then trypsin cleaves it to beta-factor XIIa. Alpha-factor XIIa activates factor XI to factor XIa. {ECO:0000269|PubMed:21304106}.
ALB	2.63	bile acid and bile salt transport [GO:0015721]; cellular response to starvation [GO:0009267]; hemolysis by symbiont of host erythrocytes [GO:0019836]; lipoprotein metabolic process [GO:0042157]; maintenance of mitochondrion location [GO:0051659]; negative regulation of apoptotic process [GO:0043066]; negative regulation of programmed cell death [GO:0043069]; platelet degranulation [GO:0002576]; positive regulation of circadian sleep/wake cycle, non-REM sleep [GO:0046010]; receptor-mediated endocytosis [GO:0006898]; response to mercury ion [GO:0046689]; response to nutrient	antioxidant activity [GO:0016209]; chaperone binding [GO:0051087]; copper ion binding [GO:0005507]; DNA binding [GO:0003677]; drug binding [GO:0008144]; fatty acid binding [GO:0005504]; identical protein binding [GO:0042802]; pyridoxal phosphate binding [GO:0030170]; toxic substance binding [GO:0015643]; zinc ion binding [GO:0008270]	basement membrane [GO:0005604]; blood microparticle [GO:0072562]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; myelin sheath [GO:0043209]; nucleus [GO:0005634]; platelet alpha granule lumen [GO:003109	FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood. Major zinc transporter in plasma, typically binds about 80% of all plasma zinc. {ECO:0000269|PubMed:19021548}.

		[GO:0007584]; response to organic substance [GO:0010033]; response to platinum ion [GO:0070541]; retina homeostasis [GO:0001895]; sodium-independent organic anion transport [GO:0043252]; transport [GO:0006810]		3]; protein complex [GO:0043234]	
PLIN1	2.65	lipid metabolic process [GO:0006629]	lipid binding [GO:0008289]	endoplasmic reticulum [GO:0005783]; lipid particle [GO:0005811]	FUNCTION: Modulator of adipocyte lipid metabolism. Coats lipid storage droplets to protect them from breakdown by hormone-sensitive lipase (HSL). Its absence may result in leanness. Plays a role in unilocular lipid droplet formation by activating CIDEC. Their interaction promotes lipid droplet enlargement and directional net neutral lipid transfer. May modulate lipolysis and triglyceride levels. {ECO:0000269|PubMed:23399566}.
TPSAB1	2.68	defense response [GO:0006952]; extracellular matrix disassembly [GO:0022617]	serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type. May play a role in innate immunity. Isoform 2 cleaves large substrates, such as fibronectin, more efficiently than isoform 1, but seems less efficient toward small substrates (PubMed:18854315). {ECO:0000250, ECO:0000250|UniProtKB:P21845, ECO:0000269|PubMed:18854315}.
S100A8	2.72	activation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0006919]; acute inflammatory response [GO:0002526];	arachidonic acid binding [GO:0050544]; calcium ion binding [GO:0005509]; microtubule binding	cytoskeleton [GO:0005856]; cytosol [GO:0005829]; extracellular exosome [GO:0070062];	FUNCTION: S100A8 is a calcium- and zinc-binding protein which plays a prominent role in the regulation of inflammatory processes and immune response. It can induce neutrophil chemotaxis and adhesion. Predominantly

		astrocyte development [GO:0014002]; autophagy [GO:0006914]; chemokine production [GO:0032602]; chronic inflammatory response [GO:0002544]; cytokine production [GO:0001816]; defense response to bacterium [GO:0042742]; defense response to fungus [GO:0050832]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; leukocyte migration involved in inflammatory response [GO:0002523]; neutrophil aggregation [GO:0070488]; neutrophil chemotaxis [GO:0030593]; peptidyl-cysteine S-nitrosylation [GO:0018119]; positive regulation of cell growth [GO:0030307]; positive regulation of inflammatory response [GO:0050729]; positive regulation of intrinsic apoptotic signaling pathway [GO:2001244]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of peptide secretion [GO:0002793]; regulation of	[GO:0008017]; RAGE receptor binding [GO:0050786]; Toll-like receptor 4 binding [GO:0035662]; zinc ion binding [GO:0008270]	extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	found as calprotectin (S100A8/A9) which has a wide plethora of intra- and extracellular functions. The intracellular functions include: facilitating leukocyte arachidonic acid trafficking and metabolism, modulation of the tubulin-dependent cytoskeleton during migration of phagocytes and activation of the neutrophilic NADPH-oxidase. Activates NADPH-oxidase by facilitating the enzyme complex assembly at the cell membrane, transferring arachidonic acid, an essential cofactor, to the enzyme complex and S100A8 contributes to the enzyme assembly by directly binding to NCF2/P67PHOX. The extracellular functions involve proinfammatory, antimicrobial, oxidant-scavenging and apoptosis-inducing activities. Its proinflammatory activity includes recruitment of leukocytes, promotion of cytokine and chemokine production, and regulation of leukocyte adhesion and migration. Acts as an alarmin or a danger associated molecular pattern (DAMP) molecule and stimulates innate immune cells via binding to pattern recognition receptors such as Toll-like receptor 4 (TLR4) and receptor for advanced glycation endproducts (AGER). Binding to TLR4 and AGER activates the MAP-kinase and NF-kappa-B signaling pathways resulting in the amplification of the proinflammatory cascade. Has antimicrobial activity towards bacteria and fungi and exerts its antimicrobial activity probably via chelation of Zn(2+) which is essential for microbial growth. Can induce cell death via autophagy and apoptosis and this occurs through the

		cytoskeleton organization [GO:0051493]; response to ethanol [GO:0045471]; response to lipopolysaccharide [GO:0032496]; response to zinc ion [GO:0010043]; sequestering of zinc ion [GO:0032119]; wound healing [GO:0042060]			cross-talk of mitochondria and lysosomes via reactive oxygen species (ROS) and the process involves BNIP3. Can regulate neutrophil number and apoptosis by an anti-apoptotic effect; regulates cell survival via ITGAM/ITGB and TLR4 and a signaling mechanism involving MEK-ERK. Its role as an oxidant scavenger has a protective role in preventing exaggerated tissue damage by scavenging oxidants. Can act as a potent amplifier of inflammation in autoimmunity as well as in cancer development and tumor spread. The iNOS-S100A8/A9 transnitrosylase complex directs selective inflammatory stimulus-dependent S-nitrosylation of GAPDH and probably multiple targets such as ANXA5, EZR, MSN and VIM by recognizing a [IL]-x-C-x-x-[DE] motif; S100A8 seems to contribute to S-nitrosylation site selectivity. {ECO:0000269|PubMed:12626582, ECO:0000269|PubMed:15331440, ECO:0000269|PubMed:15598812, ECO:0000269|PubMed:15642721, ECO:0000269|PubMed:16258195, ECO:0000269|PubMed:19087201, ECO:0000269|PubMed:19122197, ECO:0000269|PubMed:19935772, ECO:0000269|PubMed:21487906, ECO:0000269|PubMed:22363402, ECO:0000269|PubMed:22808130, ECO:0000269|PubMed:25417112}.
TF	2.77	cellular iron ion homeostasis [GO:0006879]; cellular response to iron ion	ferric iron binding [GO:0008199]; ferric iron	apical plasma membrane [GO:0016324]; basal part	FUNCTION: Transferrins are iron binding transport proteins which can bind two Fe(3+) ions in association with the binding of an anion,

		[GO:0071281]; ferrous iron import into cell [GO:0097460]; iron ion homeostasis [GO:0055072]; platelet degranulation [GO:0002576]; positive regulation of receptor-mediated endocytosis [GO:0048260]; regulation of protein stability [GO:0031647]; retina homeostasis [GO:0001895]; transferrin transport [GO:0033572]	transmembrane transporter activity [GO:0015091]; ferrous iron binding [GO:0008198]; transferrin receptor binding [GO:1990459]	of cell [GO:0045178]; basal plasma membrane [GO:0009925]; blood microparticle [GO:0072562]; cell surface [GO:0009986]; coated pit [GO:0005905]; cytoplasmic, membrane-bounded vesicle [GO:0016023]; early endosome [GO:0005769]; endocytic vesicle [GO:0030139]; endosome membrane [GO:0010008]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of external side of plasma membrane [GO:0031232]; HFE-transferrin receptor complex [GO:1990712]; late endosome [GO:0005770];	usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation.

				perinuclear region of cytoplasm [GO:0048471]; recycling endosome [GO:0055037]; secretory granule lumen [GO:0034774]; vesicle [GO:0031982]	
F2	2.77	acute-phase response [GO:0006953]; blood coagulation [GO:0007596]; blood coagulation, intrinsic pathway [GO:0007597]; cell surface receptor signaling pathway [GO:0007166]; cellular protein metabolic process [GO:0044267]; cellular response to mechanical stimulus [GO:0071260]; ER to Golgi vesicle-mediated transport [GO:0006888]; fibrinolysis [GO:0042730]; leukocyte migration [GO:0050900]; multicellular organism development [GO:0007275]; negative regulation of astrocyte differentiation [GO:0048712]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of platelet activation [GO:0010544]; negative regulation of proteolysis [GO:0045861]; peptidyl-glutamic acid carboxylation [GO:0017187]; platelet activation [GO:0030168]; positive regulation of	calcium ion binding [GO:0005509]; growth factor activity [GO:0008083]; receptor binding [GO:0005102]; serine-type endopeptidase activity [GO:0004252]; thrombospondin receptor activity [GO:0070053]	blood microparticle [GO:0072562]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi lumen [GO:0005796]; plasma membrane [GO:0005886]	FUNCTION: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombomodulin, protein C. Functions in blood homeostasis, inflammation and wound healing. {ECO:0000269|PubMed:2856554}.

		blood coagulation [GO:0030194]; positive regulation of cell growth [GO:0030307]; positive regulation of cell proliferation [GO:0008284]; positive regulation of collagen biosynthetic process [GO:0032967]; positive regulation of phosphatidylinositol 3-kinase signaling [GO:0014068]; positive regulation of phospholipase C-activating G-protein coupled receptor signaling pathway [GO:1900738]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of reactive oxygen species metabolic process [GO:2000379]; positive regulation of release of sequestered calcium ion into cytosol [GO:0051281]; proteolysis [GO:0006508]; regulation of blood coagulation [GO:0030193]; regulation of cell shape [GO:0008360]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of gene expression [GO:0010468]; response to inactivity [GO:0014854]; response to wounding [GO:0009611]; signal peptide processing [GO:0006465]			

SERPIND1	2.82	bioluminescence [GO:0008218]; blood coagulation [GO:0007596]; chemotaxis [GO:0006935]	endopeptidase inhibitor activity [GO:0004866]; heparin binding [GO:0008201]; serine-type endopeptidase inhibitor activity [GO:0004867]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	FUNCTION: Thrombin inhibitor activated by the glycosaminoglycans, heparin or dermatan sulfate. In the presence of the latter, HC-II becomes the predominant thrombin inhibitor in place of antithrombin III (AT-III). Also inhibits chymotrypsin, but in a glycosaminoglycan-independent manner. {ECO:0000269|PubMed:1939083}.; FUNCTION: Peptides at the N-terminal of HC-II have chemotactic activity for both monocytes and neutrophils. {ECO:0000269|PubMed:1939083}.
MFGE8	2.83	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cellular protein metabolic process [GO:0044267]; phagocytosis, engulfment [GO:0006911]; phagocytosis, recognition [GO:0006910]; positive regulation of apoptotic cell clearance [GO:2000427]; positive regulation of cell proliferation [GO:0008284]; response to estrogen [GO:0043627]; single fertilization [GO:0007338]; viral process [GO:0016032]	phosphatidylethanolamine binding [GO:0008429]; phosphatidylserine binding [GO:0001786]	external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; extrinsic component of plasma membrane [GO:0019897]; membrane [GO:0016020]	FUNCTION: Plays an important role in the maintenance of intestinal epithelial homeostasis and the promotion of mucosal healing. Promotes VEGF-dependent neovascularization (By similarity). Contributes to phagocytic removal of apoptotic cells in many tissues. Specific ligand for the alpha-v/beta-3 and alpha-v/beta-5 receptors. Also binds to phosphatidylserine-enriched cell surfaces in a receptor-independent manner. Zona pellucida-binding protein which may play a role in gamete interaction. Binds specifically to rotavirus and inhibits its replication. {ECO:0000250, ECO:0000269|PubMed:19204935}.; FUNCTION: Medin is the main constituent of aortic medial amyloid. {ECO:0000269|PubMed:19204935}.
COL6A3	2.90	cell adhesion [GO:0007155]; collagen catabolic process [GO:0030574]; extracellular matrix organization [GO:0030198]; muscle organ development [GO:0007517]	serine-type endopeptidase inhibitor activity [GO:0004867]	collagen type VI trimer [GO:0005589]; endoplasmic reticulum lumen [GO:0005788]; extracellular	FUNCTION: Collagen VI acts as a cell-binding protein.

				exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; proteinaceous extracellular matrix [GO:0005578]; sarcolemma [GO:0042383]	
IGHM	2.99	adaptive immune response [GO:0002250]; antibacterial humoral response [GO:0019731]; B cell receptor signaling pathway [GO:0050853]; complement activation, classical pathway [GO:0006958]; defense response to Gram-negative bacterium [GO:0050829]; innate immune response [GO:0045087]; phagocytosis, engulfment [GO:0006911]; phagocytosis, recognition [GO:0006910]; positive regulation of B cell activation [GO:0050871]	antigen binding [GO:0003823]	blood microparticle [GO:0072562]; cell surface [GO:0009986]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; hexameric IgM immunoglobulin complex [GO:0071757]; integral component of membrane [GO:0016021];	FUNCTION: IgM antibodies play an important role in primary defense mechanisms. They have been shown to be involved in early recognition of external invaders like bacteria and viruses, cellular waste and modified self, as well as in recognition and elimination of precancerous and cancerous lesions. The membrane-bound form is found in the majority of normal B-cells alongside with IgD. Membrane-bound IgM induces the phosphorylation of CD79A and CD79B by the Src family of protein tyrosine kinases. It may cause death of cells by apoptosis. It is also found in soluble form, which represents about 30% of the total serum immunoglobulins where it is found almost exclusively as a homopentamer. After the antigen binds to the B-cell receptor, the secreted form is secreted in large amounts.

				pentameric IgM immunoglobulin complex [GO:0071756]; plasma membrane [GO:0005886]	{ECO:0000269|PubMed:3137579}.
MPO	3.07	aging [GO:0007568]; defense response [GO:0006952]; defense response to fungus [GO:0050832]; hydrogen peroxide catabolic process [GO:0042744]; hypochlorous acid biosynthetic process [GO:0002149]; low-density lipoprotein particle remodeling [GO:0034374]; negative regulation of apoptotic process [GO:0043066]; negative regulation of growth of symbiont in host [GO:0044130]; oxidation-reduction process [GO:0055114]; removal of superoxide radicals [GO:0019430]; respiratory burst involved in defense response [GO:0002679]; response to food [GO:0032094]; response to gold nanoparticle [GO:1990268]; response to lipopolysaccharide [GO:0032496]; response to mechanical stimulus [GO:0009612]; response to oxidative stress [GO:0006979]; response to yeast [GO:0001878]	chromatin binding [GO:0003682]; heme binding [GO:0020037]; heparin binding [GO:0008201]; metal ion binding [GO:0046872]; peroxidase activity [GO:0004601]	azurophil granule [GO:0042582]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; lysosome [GO:0005764]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; secretory granule [GO:0030141]	FUNCTION: Part of the host defense system of polymorphonuclear leukocytes. It is responsible for microbicidal activity against a wide range of organisms. In the stimulated PMN, MPO catalyzes the production of hypohalous acids, primarily hypochlorous acid in physiologic situations, and other toxic intermediates that greatly enhance PMN microbicidal activity.
VTN	3.09	cell adhesion [GO:0007155]; cell adhesion mediated by integrin	extracellular matrix binding [GO:005084	alphav-beta3 integrin-vitronectin complex	FUNCTION: Vitronectin is a cell adhesion and spreading factor found in serum and tissues. Vitronectin interact

		[GO:0033627]; cell-matrix adhesion [GO:0007160]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; immune response [GO:0006955]; negative regulation of blood coagulation [GO:0030195]; negative regulation of endopeptidase activity [GO:0010951]; oligodendrocyte differentiation [GO:0048709]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of protein binding [GO:0032092]; positive regulation of receptor-mediated endocytosis [GO:0048260]; positive regulation of smooth muscle cell migration [GO:0014911]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; positive regulation of wound healing [GO:0090303]; regulation of complement activation [GO:0030449]; smooth muscle cell-matrix adhesion [GO:0061302]	0]; heparin binding [GO:0008201]; integrin binding [GO:0005178]; polysaccharide binding [GO:0030247]; scavenger receptor activity [GO:0005044]	[GO:0071062]; blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	with glycosaminoglycans and proteoglycans. Is recognized by certain members of the integrin family and serves as a cell-to-substrate adhesion molecule. Inhibitor of the membrane-damaging effect of the terminal cytolytic complement pathway.; FUNCTION: Somatomedin-B is a growth hormone-dependent serum factor with protease-inhibiting activity.
SLC4A1	3.10	anion transport [GO:0006820]; bicarbonate transport [GO:0015701];	anion:anion antiporter activity [GO:001530	basolateral plasma membrane [GO:001632	FUNCTION: Functions both as a transporter that mediates electroneutral anion exchange across the cell

		cellular ion homeostasis [GO:0006873]; chloride transmembrane transport [GO:1902476]; chloride transport [GO:0006821]; regulation of intracellular pH [GO:0051453]	1]; anion transmembrane transporter activity [GO:0008509]; ankyrin binding [GO:0030506]; bicarbonate transmembrane transporter activity [GO:0015106]; chloride transmembrane transporter activity [GO:0015108]; inorganic anion exchanger activity [GO:0005452]; protein anchor [GO:0043495]; protein homodimerization activity [GO:0042803]	3]; blood microparticle [GO:0072562]; cortical cytoskeleton [GO:0030863]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; Z disc [GO:0030018]	membrane and as a structural protein. Major integral membrane glycoprotein of the erythrocyte membrane; required for normal flexibility and stability of the erythrocyte membrane and for normal erythrocyte shape via the interactions of its cytoplasmic domain with cytoskeletal proteins, glycolytic enzymes, and hemoglobin. Functions as a transporter that mediates the 1:1 exchange of inorganic anions across the erythrocyte membrane. Mediates chloride-bicarbonate exchange in the kidney, and is required for normal acidification of the urine. {ECO:0000269|PubMed:10926824, ECO:0000269|PubMed:14734552, ECO:0000269|PubMed:1538405, ECO:0000269|PubMed:20151848, ECO:0000269|PubMed:24121512}.
COL6A1	3.25	cell adhesion [GO:0007155]; cellular response to amino acid stimulus [GO:0071230]; collagen catabolic process [GO:0030574]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; osteoblast differentiation [GO:0001649]; protein heterotrimerization [GO:0070208]	platelet-derived growth factor binding [GO:0048407]	collagen type VI trimer [GO:0005589]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; lysosomal membrane	FUNCTION: Collagen VI acts as a cell-binding protein.

				[GO:0005765]; membrane [GO:0016020]; protein complex [GO:0043234]; sarcolemma [GO:0042383]	
ARL2	3.39	bicellular tight junction assembly [GO:0070830]; cell cycle [GO:0007049]; centrosome organization [GO:0051297]; maintenance of protein location in nucleus [GO:0051457]; negative regulation of GTPase activity [GO:0034260]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of microtubule polymerization [GO:0031116]; regulation of insulin secretion [GO:0050796]; regulation of microtubule polymerization [GO:0031113]; small GTPase mediated signal transduction [GO:0007264]; tubulin complex assembly [GO:0007021]	GTPase activity [GO:0003924]; GTPase inhibitor activity [GO:0005095]; GTP binding [GO:0005525]	centrosome [GO:0005813]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; lateral plasma membrane [GO:0016328]; mitochondrial intermembrane space [GO:0005758]; mitochondrial matrix [GO:0005759]; nucleus [GO:0005634]	FUNCTION: Small GTP-binding protein which cycles between an inactive GDP-bound and an active GTP-bound form, and the rate of cycling is regulated by guanine nucleotide exchange factors (GEF) and GTPase-activating proteins (GAP). GTP-binding protein that does not act as an allosteric activator of the cholera toxin catalytic subunit. Regulates formation of new microtubules and centrosome integrity. Prevents the TBCD-induced microtubule destruction. Participates in association with TBCD, in the disassembly of the apical junction complexes. Antagonizes the effect of TBCD on epithelial cell detachment and tight and adherens junctions disassembly. Together with ARL2, plays a role in the nuclear translocation, retention and transcriptional activity of STAT3. Component of a regulated secretory pathway involved in Ca(2+)-dependent release of acetylcholine. Required for normal progress through the cell cycle. {ECO:0000269|PubMed:10831612, ECO:0000269|PubMed:16525022, ECO:0000269|PubMed:18234692, ECO:0000269|PubMed:18588884, ECO:0000269|PubMed:20740604}.
PON1	3.39	aromatic compound catabolic process	acyl-L-homoserine-	blood microparticl	FUNCTION: Hydrolyzes the toxic metabolites of a variety

		[GO:0019439]; carboxylic acid catabolic process [GO:0046395]; cholesterol metabolic process [GO:0008203]; organophosphate catabolic process [GO:0046434]; phosphatidylcholine metabolic process [GO:0046470]; positive regulation of binding [GO:0051099]; positive regulation of cholesterol efflux [GO:0010875]; positive regulation of transporter activity [GO:0032411]; response to external stimulus [GO:0009605]; response to fatty acid [GO:0070542]; response to fluoride [GO:1902617]; response to nutrient levels [GO:0031667]; response to toxic substance [GO:0009636]	lactone lactonohydrolase activity [GO:0102007]; aryldialkylphosphatase activity [GO:0004063]; arylesterase activity [GO:0004064]; calcium ion binding [GO:0005509]; phospholipid binding [GO:0005543]; protein homodimerization activity [GO:0042803]	e [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; intracellular membrane-bounded organelle [GO:0043231]; spherical high-density lipoprotein particle [GO:0034366]	of organophosphorus insecticides. Capable of hydrolyzing a broad spectrum of organophosphate substrates and lactones, and a number of aromatic carboxylic acid esters. Mediates an enzymatic protection of low density lipoproteins against oxidative modification and the consequent series of events leading to atheroma formation. {ECO:0000269|PubMed:10479665, ECO:0000269|PubMed:15772423}.
ABI3BP	3.44	extracellular matrix organization [GO:0030198]; positive regulation of cell-substrate adhesion [GO:0010811]	heparin binding [GO:0008201]	extracellular space [GO:0005615]; interstitial matrix [GO:0005614]	
COL14A1	3.45	collagen fibril organization [GO:0030199]; extracellular matrix organization [GO:0030198]; single organismal cell-cell adhesion [GO:0016337]	collagen binding [GO:0005518]; extracellular matrix structural constituent [GO:0005201]; poly(A) RNA binding [GO:0044822]; protein binding, bridging	collagen trimer [GO:0005581]; collagen type XIV trimer [GO:0005596]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062];	FUNCTION: Plays an adhesive role by integrating collagen bundles. It is probably associated with the surface of interstitial collagen fibrils via COL1. The COL2 domain may then serve as a rigid arm which sticks out from the fibril and protrudes the large N-terminal globular domain into the extracellular space, where it might interact with other matrix molecules or cell surface receptors (By similarity). {ECO:0000250,

			[GO:0030674]	extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	ECO:0000269|PubMed:2187872}.
GSTM1	3.45	cellular detoxification of nitrogen compound [GO:0070458]; glutathione derivative biosynthetic process [GO:1901687]; glutathione metabolic process [GO:0006749]; nitrobenzene metabolic process [GO:0018916]; xenobiotic catabolic process [GO:0042178]	enzyme binding [GO:0019899]; glutathione binding [GO:0043295]; glutathione transferase activity [GO:0004364]; protein homodimerization activity [GO:0042803]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	FUNCTION: Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. {ECO:0000269|PubMed:16548513}.
CFHR1	3.52	complement activation [GO:0006956]		blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]	FUNCTION: Involved in complement regulation. The dimerized forms have avidity for tissue-bound complement fragments and efficiently compete with the physiological complement inhibitor CFH. Can associate with lipoproteins and may play a role in lipid metabolism. {ECO:0000269|PubMed:23487775}.
APOA4	3.53	cellular protein metabolic process [GO:0044267]; cholesterol biosynthetic process [GO:0006695]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; chylomicron	antioxidant activity [GO:0016209]; cholesterol binding [GO:0015485]; cholesterol transporter activity [GO:0017127]; copper ion binding [GO:000550	blood microparticle [GO:0072562]; chylomicron [GO:0042627]; cytosol [GO:0005829]; early endosome [GO:0005769]; endoplasmic reticulum	FUNCTION: May have a role in chylomicrons and VLDL secretion and catabolism. Required for efficient activation of lipoprotein lipase by ApoC-II; potent activator of LCAT. Apoa-IV is a major component of HDL and chylomicrons.

		assembly [GO:0034378]; chylomicron remodeling [GO:0034371]; high-density lipoprotein particle assembly [GO:0034380]; high-density lipoprotein particle remodeling [GO:0034375]; hydrogen peroxide catabolic process [GO:0042744]; innate immune response in mucosa [GO:0002227]; leukocyte cell-cell adhesion [GO:0007159]; lipid homeostasis [GO:0055088]; lipid transport [GO:0006869]; lipoprotein biosynthetic process [GO:0042158]; lipoprotein metabolic process [GO:0042157]; multicellular organism lipid catabolic process [GO:0044240]; negative regulation of plasma lipoprotein particle oxidation [GO:0034445]; neuron projection regeneration [GO:0031102]; phosphatidylcholine metabolic process [GO:0046470]; phospholipid efflux [GO:0033700]; positive regulation of cholesterol esterification [GO:0010873]; positive regulation of fatty acid biosynthetic process [GO:0045723]; positive regulation of lipoprotein lipase activity [GO:0051006]; positive regulation of triglyceride catabolic	7]; lipid binding [GO:0008289]; lipid transporter activity [GO:0005319]; phosphatidylcholine binding [GO:0031210]; phosphatidylcholine-sterol O-acyltransferase activator activity [GO:0060228]; protein homodimerization activity [GO:0042803]	lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; very-low-density lipoprotein particle [GO:0034361]	

		process [GO:0010898]; protein-lipid complex assembly [GO:0065005]; regulation of cholesterol transport [GO:0032374]; regulation of intestinal cholesterol absorption [GO:0030300]; removal of superoxide radicals [GO:0019430]; response to lipid hydroperoxide [GO:0006982]; response to stilbenoid [GO:0035634]; retinoid metabolic process [GO:0001523]; reverse cholesterol transport [GO:0043691]; triglyceride homeostasis [GO:0070328]; very-low-density lipoprotein particle remodeling [GO:0034372]			
ITGA5	3.53	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cell-cell adhesion mediated by integrin [GO:0033631]; cell-substrate adhesion [GO:0031589]; cell-substrate junction assembly [GO:0007044]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules [GO:0007157]; heterotypic cell-cell adhesion [GO:0034113];	metal ion binding [GO:0046872]; platelet-derived growth factor receptor binding [GO:0005161]; vascular endothelial growth factor receptor 2 binding [GO:0043184]; virus receptor activity [GO:0001618]	alphav-beta3 integrin-vitronectin complex [GO:0071062]; cell surface [GO:0009986]; cytoplasmic vesicle [GO:0031410]; endoplasmic reticulum [GO:0005783]; external side of plasma membrane [GO:0009897]; focal adhesion [GO:0005925]; Golgi apparatus	FUNCTION: Integrin alpha-5/beta-1 is a receptor for fibronectin and fibrinogen. It recognizes the sequence R-G-D in its ligands. ITGA5:ITGB1 binds to PLA2G2A via a site (site 2) which is distinct from the classical ligand-binding site (site 1) and this induces integrin conformational changes and enhanced ligand binding to site 1 (PubMed:18635536, PubMed:25398877). {ECO:0000269|PubMed:18635536, ECO:0000269|PubMed:25398877}.; FUNCTION: (Microbial infection) Integrin ITGA5:ITGB1 acts as a receptor for human metapneumovirus (PubMed:12907437). Integrin ITGA2:ITGB1 acts as a receptor for human

		integrin-mediated signaling pathway [GO:0007229]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; memory [GO:0007613]; negative regulation of anoikis [GO:2000811]; positive regulation of cell migration [GO:0030335]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; wound healing, spreading of epidermal cells [GO:0035313]		[GO:0005794]; integrin complex [GO:0008305]; plasma membrane [GO:0005886]; ruffle [GO:0001726]; synapse [GO:0045202]	parvovirus B19 (PubMed:24478423). In case of HIV-1 infection, the interaction with extracellular viral Tat protein seems to enhance angiogenesis in Kaposi's sarcoma lesions (PubMed:10397733). {ECO:0000269|PubMed:10397733, ECO:0000269|PubMed:12907437, ECO:0000269|PubMed:24478423}.
FN1	3.53	acute-phase response [GO:0006953]; angiogenesis [GO:0001525]; calcium-independent cell-matrix adhesion [GO:0007161]; cell activation [GO:0001775]; cell adhesion [GO:0007155]; cell-substrate junction assembly [GO:0007044]; cellular response to BMP stimulus [GO:0071773]; cellular response to glucose stimulus [GO:0071333]; cellular response to interleukin-1	collagen binding [GO:0005518]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; mercury ion binding [GO:0045340]; peptidase activator activity [GO:0016504]; protease binding	apical plasma membrane [GO:0016324]; basal lamina [GO:0005605]; blood microparticle [GO:0072562]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; extracellular exosome	FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape. Involved in osteoblast compaction through the fibronectin fibrillogenesis cell-mediated matrix assembly process, essential for osteoblast mineralization. Participates in the regulation of type I collagen deposition by osteoblasts.; FUNCTION: Anastellin binds fibronectin and induces fibril formation. This fibronectin polymer,

		[GO:0071347]; cellular response to lipopolysaccharide [GO:0071222]; cellular response to mercury ion [GO:0071288]; cellular response to platelet-derived growth factor stimulus [GO:0036120]; cellular response to prostaglandin E stimulus [GO:0071380]; cellular response to transforming growth factor beta stimulus [GO:0071560]; cellular response to vascular endothelial growth factor stimulus [GO:0035924]; endodermal cell differentiation [GO:0035987]; extracellular matrix disassembly [GO:0022617]; extracellular matrix organization [GO:0030198]; glial cell migration [GO:0008347]; integrin activation [GO:0033622]; leukocyte migration [GO:0050900]; negative regulation of apoptotic process [GO:0043066]; negative regulation of transforming growth factor-beta secretion [GO:2001202]; peptide cross-linking [GO:0018149]; platelet degranulation [GO:0002576]; positive regulation of axon extension [GO:0045773]; positive regulation of cell proliferation [GO:0008284]; positive regulation of	[GO:0002020]	[GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex [GO:0005577]; platelet alpha granule lumen [GO:0031093]	named superfibronectin, exhibits enhanced adhesive properties. Both anastellin and superfibronectin inhibit tumor growth, angiogenesis and metastasis. Anastellin activates p38 MAPK and inhibits lysophospholipid signaling.

		chemotaxis [GO:0050921]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of gene expression [GO:0010628]; positive regulation of substrate-dependent cell migration, cell attachment to substrate [GO:1904237]; regulation of cell shape [GO:0008360]; regulation of ERK1 and ERK2 cascade [GO:0070372]; regulation of protein phosphorylation [GO:0001932]; response to glucocorticoid [GO:0051384]; response to ischemia [GO:0002931]; response to ozone [GO:0010193]; response to wounding [GO:0009611]; substrate adhesion-dependent cell spreading [GO:0034446]; wound healing [GO:0042060]			
EARS2	3.56	glutamyl-tRNA aminoacylation [GO:0006424]; tRNA aminoacylation for mitochondrial protein translation [GO:0070127]	ATP binding [GO:0005524]; glutamate-tRNA(Gln) ligase activity [GO:0050561]; glutamate-tRNA ligase activity [GO:0004818]; RNA binding [GO:0003723]; tRNA binding [GO:0000049]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	FUNCTION: Catalyzes the attachment of glutamate to tRNA(Glu) in a two-step reaction: glutamate is first activated by ATP to form Glu-AMP and then transferred to the acceptor end of tRNA(Glu). {ECO:0000250}.

RPL9	3.56	cytoplasmic translation [GO:0002181]; nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]; SRP-dependent cotranslational protein targeting to membrane [GO:0006614]; translation [GO:0006412]; translational initiation [GO:0006413]; viral transcription [GO:0019083]	RNA binding [GO:0003723]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; cytosolic large ribosomal subunit [GO:0022625]; focal adhesion [GO:0005925]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleus [GO:0005634]; ribosome [GO:0005840]	
COL6A2	3.57	cell adhesion [GO:0007155]; collagen catabolic process [GO:0030574]; extracellular matrix organization [GO:0030198]; protein heterotrimerization [GO:0070208]; response to glucose [GO:0009749]		collagen trimer [GO:0005581]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; proteinaceous extracellular matrix [GO:0005578]; protein complex [GO:0043234];	FUNCTION: Collagen VI acts as a cell-binding protein.

				sarcolemma [GO:0042383]	
APOD	3.59	aging [GO:0007568]; angiogenesis [GO:0001525]; brain development [GO:0007420]; glucose metabolic process [GO:0006006]; lipid metabolic process [GO:0006629]; negative regulation of cytokine production involved in inflammatory response [GO:1900016]; negative regulation of focal adhesion assembly [GO:0051895]; negative regulation of lipoprotein lipid oxidation [GO:0060588]; negative regulation of monocyte chemotactic protein-1 production [GO:0071638]; negative regulation of platelet-derived growth factor receptor signaling pathway [GO:0010642]; negative regulation of protein import into nucleus [GO:0042308]; negative regulation of smooth muscle cell-matrix adhesion [GO:2000098]; negative regulation of smooth muscle cell proliferation [GO:0048662]; negative regulation of T cell migration [GO:2000405]; peripheral nervous system axon regeneration [GO:0014012]; response to axon injury [GO:0048678];	cholesterol binding [GO:0015485]; lipid transporter activity [GO:0005319]	cytosolic ribosome [GO:0022626]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; neuronal cell body [GO:0043025]; perinuclear region of cytoplasm [GO:0048471]	FUNCTION: APOD occurs in the macromolecular complex with lecithin-cholesterol acyltransferase. It is probably involved in the transport and binding of bilin. Appears to be able to transport a variety of ligands in a number of different contexts.

		response to drug [GO:0042493]; response to reactive oxygen species [GO:0000302]; tissue regeneration [GO:0042246]			
ARPC1B	3.62	Arp2/3 complex-mediated actin nucleation [GO:0034314]; ephrin receptor signaling pathway [GO:0048013]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; movement of cell or subcellular component [GO:0006928]	structural constituent of cytoskeleton [GO:0005200]	actin cytoskeleton [GO:0015629]; Arp2/3 protein complex [GO:0005885]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]	FUNCTION: Functions as component of the Arp2/3 complex which is involved in regulation of actin polymerization and together with an activating nucleation-promoting factor (NPF) mediates the formation of branched actin networks.
APOE	3.63	AMPA glutamate receptor clustering [GO:0097113]; artery morphogenesis [GO:0048844]; cellular calcium ion homeostasis [GO:0006874]; cGMP-mediated signaling [GO:0019934]; cholesterol catabolic process [GO:0006707]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; chylomicron remnant clearance [GO:0034382]; cytoskeleton organization [GO:0007010]; fatty acid homeostasis [GO:0055089]; G-protein coupled receptor signaling pathway [GO:0007186]; high-density lipoprotein particle assembly	antioxidant activity [GO:0016209]; beta-amyloid binding [GO:0001540]; cholesterol binding [GO:0015485]; cholesterol transporter activity [GO:0017127]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; lipid binding [GO:0008289]; lipid transporter activity [GO:0005319]; lipoprotein particle binding [GO:0071813]; low-	blood microparticle [GO:0072562]; chylomicron [GO:0042627]; cytoplasm [GO:0005737]; dendrite [GO:0030425]; early endosome [GO:0005769]; endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576];	FUNCTION: Mediates the binding, internalization, and catabolism of lipoprotein particles. It can serve as a ligand for the LDL (apo B/E) receptor and for the specific apo-E receptor (chylomicron remnant) of hepatic tissues. {ECO:0000303|PubMed:3283935}.

		[GO:0034380]; high-density lipoprotein particle clearance [GO:0034384]; high-density lipoprotein particle remodeling [GO:0034375]; intracellular transport [GO:0046907]; lipoprotein biosynthetic process [GO:0042158]; lipoprotein catabolic process [GO:0042159]; lipoprotein metabolic process [GO:0042157]; long-chain fatty acid transport [GO:0015909]; low-density lipoprotein particle remodeling [GO:0034374]; maintenance of location in cell [GO:0051651]; negative regulation of beta-amyloid formation [GO:1902430]; negative regulation of blood coagulation [GO:0030195]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of cholesterol biosynthetic process [GO:0045541]; negative regulation of cholesterol efflux [GO:0090370]; negative regulation of dendritic spine development [GO:0061000]; negative regulation of dendritic spine maintenance [GO:1902951]; negative regulation of endothelial cell	density lipoprotein particle receptor binding [GO:0050750]; metal chelating activity [GO:0046911]; phosphatidylcholine-sterol O-acyltransferase activator activity [GO:0060228]; phospholipid binding [GO:0005543]; protein homodimerization activity [GO:0042803]; tau protein binding [GO:0048156]; very-low-density lipoprotein particle receptor binding [GO:0070326]	extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; Golgi apparatus [GO:0005794]; high-density lipoprotein particle [GO:0034364]; intermediate-density lipoprotein particle [GO:0034363]; low-density lipoprotein particle [GO:0034362]; membrane [GO:0016020]; neuronal cell body [GO:0043025]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	

		proliferation [GO:0001937]; negative regulation of inflammatory response [GO:0050728]; negative regulation of lipid biosynthetic process [GO:0051055]; negative regulation of lipid transport across blood brain barrier [GO:1903001]; negative regulation of MAP kinase activity [GO:0043407]; negative regulation of neuron apoptotic process [GO:0043524]; negative regulation of neuron death [GO:1901215]; negative regulation of phospholipid efflux [GO:1902999]; negative regulation of platelet activation [GO:0010544]; negative regulation of postsynaptic membrane organization [GO:1901627]; negative regulation of presynaptic membrane organization [GO:1901630]; neuron projection regeneration [GO:0031102]; nitric oxide mediated signal transduction [GO:0007263]; NMDA glutamate receptor clustering [GO:0097114]; phospholipid efflux [GO:0033700]; positive regulation by host of viral process [GO:0044794]; positive regulation of beta-amyloid			

		formation [GO:1902004]; positive regulation of cGMP biosynthetic process [GO:0030828]; positive regulation of cholesterol efflux [GO:0010875]; positive regulation of cholesterol esterification [GO:0010873]; positive regulation of dendritic spine development [GO:0060999]; positive regulation of dendritic spine maintenance [GO:1902952]; positive regulation of lipid biosynthetic process [GO:0046889]; positive regulation of lipid transport across blood brain barrier [GO:1903002]; positive regulation of low-density lipoprotein particle receptor catabolic process [GO:0032805]; positive regulation of membrane protein ectodomain proteolysis [GO:0051044]; positive regulation of neurofibrillary tangle assembly [GO:1902998]; positive regulation of neuron death [GO:1901216]; positive regulation of nitric-oxide synthase activity [GO:0051000]; positive regulation of phospholipid efflux [GO:1902995]; positive regulation of postsynaptic membrane organization [GO:1901628]; positive regulation of			

		presynaptic membrane organization [GO:1901631]; protein import [GO:0017038]; receptor-mediated endocytosis [GO:0006898]; regulation of axon extension [GO:0030516]; regulation of beta-amyloid clearance [GO:1900221]; regulation of Cdc42 protein signal transduction [GO:0032489]; regulation of gene expression [GO:0010468]; regulation of neuronal synaptic plasticity [GO:0048168]; regulation of neuron death [GO:1901214]; regulation of tau-protein kinase activity [GO:1902947]; response to dietary excess [GO:0002021]; response to reactive oxygen species [GO:0000302]; retinoid metabolic process [GO:0001523]; reverse cholesterol transport [GO:0043691]; synaptic transmission, cholinergic [GO:0007271]; triglyceride catabolic process [GO:0019433]; triglyceride metabolic process [GO:0006641]; vasodilation [GO:0042311]; very-low-density lipoprotein particle clearance [GO:0034447]; very-			

		low-density lipoprotein particle remodeling [GO:0034372]; virion assembly [GO:0019068]			
LASP1	3.65	ion transport [GO:0006811]	ion transmembrane transporter activity [GO:0015075]; SH3/SH2 adaptor activity [GO:0005070]; zinc ion binding [GO:0008270]	cortical actin cytoskeleton [GO:0030864]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]	FUNCTION: Plays an important role in the regulation of dynamic actin-based, cytoskeletal activities. Agonist-dependent changes in LASP1 phosphorylation may also serve to regulate actin-associated ion transport activities, not only in the parietal cell but also in certain other F-actin-rich secretory epithelial cell types (By similarity). {ECO:0000250}.
AEBP1	3.68	muscle organ development [GO:0007517]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; peptide metabolic process [GO:0006518]; protein processing [GO:0016485]; skeletal system development [GO:0001501]; transcription, DNA-templated [GO:0006351]	carboxypeptidase activity [GO:0004180]; metallocarboxypeptidase activity [GO:0004181]; RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977]; serine-type carboxypeptidase activity [GO:0004185]; transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding [GO:0001227]; transcription corepressor activity	cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; nucleus [GO:0005634]	FUNCTION: May positively regulate MAP-kinase activity in adipocytes, leading to enhanced adipocyte proliferation and reduced adipocyte differentiation. May also positively regulate NF-kappa-B activity in macrophages by promoting the phosphorylation and subsequent degradation of I-kappa-B-alpha (NFKBIA), leading to enhanced macrophage inflammatory responsiveness. Can act as a transcriptional repressor. {ECO:0000250}.

			[GO:0003714]; transcription factor activity, sequence-specific DNA binding [GO:0003700]; zinc ion binding [GO:0008270]		
ACSL4	3.69	dendritic spine development [GO:0060996]; embryonic process involved in female pregnancy [GO:0060136]; fatty acid transport [GO:0015908]; lipid biosynthetic process [GO:0008610]; lipid metabolic process [GO:0006629]; long-chain fatty-acyl-CoA biosynthetic process [GO:0035338]; negative regulation of prostaglandin secretion [GO:0032307]; positive regulation of cell growth [GO:0030307]; response to interleukin-15 [GO:0070672]; response to nutrient [GO:0007584]; triglyceride metabolic process [GO:0006641]	arachidonate-CoA ligase activity [GO:0047676]; ATP binding [GO:0005524]; long-chain fatty acid-CoA ligase activity [GO:0004467]; very long-chain fatty acid-CoA ligase activity [GO:0031957]	cytoplasm [GO:0005737]; endoplasmic reticulum membrane [GO:0005789]; ER-mitochondrion membrane contact site [GO:0044233]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; lipid particle [GO:0005811]; membrane [GO:0016020]; mitochondrial outer membrane [GO:0005741]; neuronal cell body [GO:0043025]; peroxisomal membrane [GO:0005778]	FUNCTION: Activation of long-chain fatty acids for both synthesis of cellular lipids, and degradation via beta-oxidation. Preferentially uses arachidonate and eicosapentaenoate as substrates.
TGFBI	3.74	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cell proliferation	collagen binding [GO:0005518]; extracellular	basement membrane [GO:0005604]; extracellular	FUNCTION: Plays a role in cell adhesion (PubMed:8024701). May play a role in cell-collagen interactions (By similarity).

		[GO:0008283]; cellular protein metabolic process [GO:0044267]; chondrocyte differentiation [GO:0002062]; extracellular matrix organization [GO:0030198]; negative regulation of cell adhesion [GO:0007162]; response to stimulus [GO:0050896]; visual perception [GO:0007601]	matrix binding [GO:0050840]; integrin binding [GO:0005178]	exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]; proteinaceous extracellular matrix [GO:0005578]; trans-Golgi network [GO:0005802]	{ECO:0000250|UniProtKB:O11780, ECO:0000269|PubMed:8024701}.
XPO7	3.79	mRNA transport [GO:0051028]; protein export from nucleus [GO:0006611]	nuclear export signal receptor activity [GO:0005049]; Ran GTPase binding [GO:0008536]	cytoplasm [GO:0005737]; nuclear pore [GO:0005643]; nucleus [GO:0005634]	FUNCTION: Mediates the nuclear export of proteins (cargos) with broad substrate specificity. In the nucleus binds cooperatively to its cargo and to the GTPase Ran in its active GTP-bound form. Docking of this trimeric complex to the nuclear pore complex (NPC) is mediated through binding to nucleoporins. Upon transit of a nuclear export complex into the cytoplasm, disassembling of the complex and hydrolysis of Ran-GTP to Ran-GDP (induced by RANBP1 and RANGAP1, respectively) cause release of the cargo from the export receptor. XPO7 then return to the nuclear compartment and mediate another round of transport. The directionality of nuclear export is thought to be conferred by an asymmetric distribution of the GTP- and GDP-bound forms of Ran between the cytoplasm and nucleus. {ECO:0000269|PubMed:11024021, ECO:0000269|PubMed:15282546}.

ARF4	3.80	activation of phospholipase D activity [GO:0031584]; apical protein localization [GO:0045176]; brain development [GO:0007420]; cell migration [GO:0016477]; dendritic spine development [GO:0060996]; epidermal growth factor receptor signaling pathway [GO:0007173]; ER to Golgi vesicle-mediated transport [GO:0006888]; establishment or maintenance of epithelial cell apical/basal polarity [GO:0045197]; learning [GO:0007612]; negative regulation of apoptotic process [GO:0043066]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; protein ADP-ribosylation [GO:0006471]; protein localization to cilium [GO:0061512]; protein transport [GO:0015031]; regulation of reactive oxygen species metabolic process [GO:2000377]; response to axon injury [GO:0048678]; retrograde vesicle-mediated transport, Golgi to ER [GO:0006890]; small GTPase mediated signal transduction [GO:0007264]	ARF guanyl-nucleotide exchange factor activity [GO:0005086]; epidermal growth factor receptor binding [GO:0005154]; GTPase activity [GO:0003924]; GTP binding [GO:0005525]	cytosol [GO:0005829]; dendritic spine [GO:0043197]; extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; membrane [GO:0016020]; ruffle membrane [GO:0032587]	FUNCTION: GTP-binding protein that functions as an allosteric activator of the cholera toxin catalytic subunit, an ADP-ribosyltransferase. Involved in protein trafficking; may modulate vesicle budding and uncoating within the Golgi apparatus.
AFM	3.82	vitamin transport [GO:0051180]	vitamin E binding	blood microparticl	FUNCTION: Vitamin E binding protein. May

			[GO:0008431]	e [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	transport vitamin E in body fluids under conditions where the lipoprotein system is not sufficient. May be involved in the regulation and transport of vitamin E at the blood-brain barrier. {ECO:0000269|PubMed:12463752, ECO:0000269|PubMed:15952736, ECO:0000269|PubMed:19046407}.
APOC1	3.92	cholesterol efflux [GO:0033344]; cholesterol metabolic process [GO:0008203]; chylomicron remnant clearance [GO:0034382]; high-density lipoprotein particle remodeling [GO:0034375]; lipid metabolic process [GO:0006629]; lipoprotein metabolic process [GO:0042157]; negative regulation of cholesterol transport [GO:0032375]; negative regulation of fatty acid biosynthetic process [GO:0045717]; negative regulation of lipid catabolic process [GO:0050995]; negative regulation of lipid metabolic process [GO:0045833]; negative regulation of lipoprotein lipase activity [GO:0051005]; negative regulation of phosphatidylcholine catabolic process [GO:0010900]; negative regulation of receptor-mediated endocytosis [GO:0048261];	fatty acid binding [GO:0005504]; lipase inhibitor activity [GO:0055102]; phosphatidylcholine binding [GO:0031210]; phosphatidylcholine-sterol O-acyltransferase activator activity [GO:0060228]; phospholipase inhibitor activity [GO:0004859]	chylomicron [GO:0042627]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; high-density lipoprotein particle [GO:0034364]; very-low-density lipoprotein particle [GO:0034361]	FUNCTION: Inhibitor of lipoprotein binding to the low density lipoprotein (LDL) receptor, LDL receptor-related protein, and very low density lipoprotein (VLDL) receptor. Associates with high density lipoproteins (HDL) and the triacylglycerol-rich lipoproteins in the plasma and makes up about 10% of the protein of the VLDL and 2% of that of HDL. Appears to interfere directly with fatty acid uptake and is also the major plasma inhibitor of cholesteryl ester transfer protein (CETP). Binds free fatty acids and reduces their intracellular esterification. Modulates the interaction of APOE with beta-migrating VLDL and inhibits binding of beta-VLDL to the LDL receptor-related protein. {ECO:0000269|PubMed:17339654, ECO:0000303|PubMed:25160599}.

		negative regulation of very-low-density lipoprotein particle clearance [GO:0010916]; phospholipid efflux [GO:0033700]; plasma lipoprotein particle remodeling [GO:0034369]; positive regulation of cholesterol esterification [GO:0010873]; regulation of cholesterol transport [GO:0032374]; triglyceride metabolic process [GO:0006641]; very-low-density lipoprotein particle assembly [GO:0034379]; very-low-density lipoprotein particle clearance [GO:0034447]			
RPA1	3.98	base-excision repair [GO:0006284]; DNA damage response, detection of DNA damage [GO:0042769]; DNA-dependent DNA replication [GO:0006261]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]; double-strand break repair via homologous recombination [GO:0000724]; error-free translesion synthesis [GO:0070987]; error-prone translesion synthesis [GO:0042276]; G1/S transition of mitotic cell cycle [GO:0000082]; interstrand cross-link repair [GO:0036297];	damaged DNA binding [GO:0003684]; metal ion binding [GO:0046872]; single-stranded DNA binding [GO:0003697]	DNA replication factor A complex [GO:0005662]; nuclear chromosome, telomeric region [GO:0000784]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; PML body [GO:0016605]	FUNCTION: As part of the heterotrimeric replication protein A complex (RPA/RP-A), binds and stabilizes single-stranded DNA intermediates, that form during DNA replication or upon DNA stress. It prevents their reannealing and in parallel, recruits and activates different proteins and complexes involved in DNA metabolism. Thereby, it plays an essential role both in DNA replication and the cellular response to DNA damage (PubMed:9430682). In the cellular response to DNA damage, the RPA complex controls DNA repair and DNA damage checkpoint activation. Through recruitment of ATRIP activates the ATR kinase a master regulator of the DNA damage response (PubMed:24332808). It is required for the recruitment of the DNA double-strand break repair factors RAD51 and RAD52 to chromatin in response to DNA damage

		mismatch repair [GO:0006298]; nucleotide-excision repair [GO:0006289]; nucleotide-excision repair, DNA gap filling [GO:0006297]; nucleotide-excision repair, DNA incision [GO:0033683]; nucleotide-excision repair, DNA incision, 3'-to lesion [GO:0006295]; nucleotide-excision repair, DNA incision, 5'-to lesion [GO:0006296]; nucleotide-excision repair, preincision complex assembly [GO:0006294]; nucleotide-excision repair, preincision complex stabilization [GO:0006293]; protein sumoylation [GO:0016925]; regulation of cellular response to heat [GO:1900034]; regulation of signal transduction by p53 class mediator [GO:1901796]; telomere maintenance [GO:0000723]; telomere maintenance via recombination [GO:0000722]; transcription-coupled nucleotide-excision repair [GO:0006283]; translesion synthesis [GO:0019985]			(PubMed:17765923). Also recruits to sites of DNA damage proteins like XPA and XPG that are involved in nucleotide excision repair and is required for this mechanism of DNA repair (PubMed:7697716). Plays also a role in base excision repair (BER) probably through interaction with UNG (PubMed:9765279). Through RFWD3 may activate CHEK1 and play a role in replication checkpoint control. Also recruits SMARCAL1/HARP, which is involved in replication fork restart, to sites of DNA damage. May also play a role in telomere maintenance (PubMed:17959650). As part of the alternative replication protein A complex, aRPA, binds single-stranded DNA and probably plays a role in DNA repair. Compared to the RPA2-containing, canonical RPA complex, may not support chromosomal DNA replication and cell cycle progression through S-phase. The aRPA may not promote efficient priming by DNA polymerase alpha but could support DNA synthesis by polymerase delta in presence of PCNA and replication factor C (RFC), the dual incision/excision reaction of nucleotide excision repair and RAD51-dependent strand exchange (PubMed:19996105). {ECO:0000269|PubMed:12791985, ECO:0000269|PubMed:17765923, ECO:0000269|PubMed:17959650, ECO:0000269|PubMed:19116208, ECO:0000269|PubMed:19996105, ECO:0000269|PubMed:24332808, ECO:0000269|PubMed:7697716, ECO:0000269|PubMed:7700

					386, ECO:0000269|PubMed:9430682, ECO:0000269|PubMed:9765279}.
ROCK1	4.09	actin cytoskeleton organization [GO:0030036]; apical constriction [GO:0003383]; bleb assembly [GO:0032060]; cellular component disassembly involved in execution phase of apoptosis [GO:0006921]; cortical actin cytoskeleton organization [GO:0030866]; ephrin receptor signaling pathway [GO:0048013]; establishment of protein localization to plasma membrane [GO:0090002]; I-kappaB kinase/NF-kappaB signaling [GO:0007249]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; leukocyte tethering or rolling [GO:0050901]; membrane to membrane docking [GO:0022614]; myoblast migration [GO:0051451]; negative regulation of angiogenesis [GO:0016525]; negative regulation of bicellular tight junction assembly [GO:1903347]; negative regulation of myosin-light-chain-phosphatase activity [GO:0035509]; negative regulation of neuron apoptotic process [GO:0043524];	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; protein kinase activity [GO:0004672]; protein serine/threonine kinase activity [GO:0004674]	bleb [GO:0032059]; centriole [GO:0005814]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; Golgi membrane [GO:0000139]; lamellipodium [GO:0030027]; plasma membrane [GO:0005886]; ruffle [GO:0001726]	FUNCTION: Protein kinase which is a key regulator of actin cytoskeleton and cell polarity. Involved in regulation of smooth muscle contraction, actin cytoskeleton organization, stress fiber and focal adhesion formation, neurite retraction, cell adhesion and motility via phosphorylation of DAPK3, GFAP, LIMK1, LIMK2, MYL9/MLC2, PFN1 and PPP1R12A. Phosphorylates FHOD1 and acts synergistically with it to promote SRC-dependent non-apoptotic plasma membrane blebbing. Phosphorylates JIP3 and regulates the recruitment of JNK to JIP3 upon UVB-induced stress. Acts as a suppressor of inflammatory cell migration by regulating PTEN phosphorylation and stability. Acts as a negative regulator of VEGF-induced angiogenic endothelial cell activation. Required for centrosome positioning and centrosome-dependent exit from mitosis. Plays a role in terminal erythroid differentiation. May regulate closure of the eyelids and ventral body wall by inducing the assembly of actomyosin bundles. Promotes keratinocyte terminal differentiation. Involved in osteoblast compaction through the fibronectin fibrillogenesis cell-mediated matrix assembly process, essential for osteoblast mineralization. {ECO:0000269|PubMed:10436159, ECO:0000269|PubMed:10652353, ECO:0000269|PubMed:11018042, ECO:0000269|PubMed:11283607,

		negative regulation of protein binding [GO:0032091]; positive regulation of focal adhesion assembly [GO:0051894]; protein phosphorylation [GO:0006468]; regulation of actin cytoskeleton organization [GO:0032956]; regulation of cell adhesion [GO:0030155]; regulation of cell motility [GO:2000145]; regulation of establishment of cell polarity [GO:2000114]; regulation of establishment of endothelial barrier [GO:1903140]; regulation of focal adhesion assembly [GO:0051893]; regulation of keratinocyte differentiation [GO:0045616]; regulation of stress fiber assembly [GO:0051492]; Rho protein signal transduction [GO:0007266]; signal transduction [GO:0007165]; smooth muscle contraction [GO:0006939]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]			ECO:0000269|PubMed:17158456, ECO:0000269|PubMed:18573880, ECO:0000269|PubMed:18694941, ECO:0000269|PubMed:19036714, ECO:0000269|PubMed:19131646, ECO:0000269|PubMed:19181962, ECO:0000269|PubMed:19997641, ECO:0000269|PubMed:21072057, ECO:0000269|PubMed:8617235, ECO:0000269|PubMed:9722579}.
AHSG	4.12	acute-phase response [GO:0006953]; negative regulation of biomineral tissue development [GO:0070168]; negative regulation of bone mineralization	cysteine-type endopeptidase inhibitor activity [GO:0004869]; endopeptidase inhibitor	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062];	FUNCTION: Promotes endocytosis, possesses opsonic properties and influences the mineral phase of bone. Shows affinity for calcium and barium ions.

		[GO:0030502]; negative regulation of insulin receptor signaling pathway [GO:0046627]; ossification [GO:0001503]; pinocytosis [GO:0006907]; platelet degranulation [GO:0002576]; positive regulation of phagocytosis [GO:0050766]; regulation of bone mineralization [GO:0030500]; regulation of inflammatory response [GO:0050727]; skeletal system development [GO:0001501]	activity [GO:0004866]; kinase inhibitor activity [GO:0019210]	extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	
THBS1	4.14	activation of MAPK activity [GO:0000187]; behavioral response to pain [GO:0048266]; cell adhesion [GO:0007155]; cell cycle arrest [GO:0007050]; cell migration [GO:0016477]; cellular response to heat [GO:0034605]; chronic inflammatory response [GO:0002544]; engulfment of apoptotic cell [GO:0043652]; extracellular matrix organization [GO:0030198]; immune response [GO:0006955]; inflammatory response [GO:0006954]; negative regulation of angiogenesis [GO:0016525]; negative regulation of antigen processing and presentation of	calcium ion binding [GO:0005509]; collagen V binding [GO:0070052]; fibrinogen binding [GO:0070051]; fibroblast growth factor binding [GO:0017134]; fibronectin binding [GO:0001968]; glycoprotein binding [GO:0001948]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; laminin binding	cell surface [GO:0009986]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex	FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Binds heparin. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp (By similarity). Ligand for CD36 mediating antiangiogenic properties. Plays a role in ER stress response, via its interaction with the activating transcription factor 6 alpha (ATF6) which produces adaptive ER stress response factors (By similarity). {ECO:0000250, ECO:0000269|PubMed:11134179, ECO:0000269|PubMed:15014436}.

		peptide or polysaccharide antigen via MHC class II [GO:0002581]; negative regulation of apoptotic process [GO:0043066]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of cell-matrix adhesion [GO:0001953]; negative regulation of cGMP-mediated signaling [GO:0010754]; negative regulation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0043154]; negative regulation of dendritic cell antigen processing and presentation [GO:0002605]; negative regulation of endothelial cell chemotaxis [GO:2001027]; negative regulation of endothelial cell migration [GO:0010596]; negative regulation of endothelial cell proliferation [GO:0001937]; negative regulation of extrinsic apoptotic signaling pathway [GO:2001237]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of fibroblast growth factor receptor signaling pathway [GO:0040037]; negative regulation of focal adhesion assembly [GO:0051895];	[GO:0043236]; low-density lipoprotein particle binding [GO:0030169]; phosphatidylserine binding [GO:0001786]; proteoglycan binding [GO:0043394]; transforming growth factor beta binding [GO:0050431]	[GO:0005577]; platelet alpha granule [GO:0031091]; platelet alpha granule lumen [GO:0031093]; sarcoplasmic reticulum [GO:0016529]; secretory granule [GO:0030141]	

		negative regulation of interleukin-12 production [GO:0032695]; negative regulation of nitric oxide mediated signal transduction [GO:0010751]; negative regulation of plasma membrane long-chain fatty acid transport [GO:0010748]; negative regulation of plasminogen activation [GO:0010757]; peptide cross-linking [GO:0018149]; platelet degranulation [GO:0002576]; positive regulation of angiogenesis [GO:0045766]; positive regulation of blood coagulation [GO:0030194]; positive regulation of blood vessel endothelial cell migration [GO:0043536]; positive regulation of cell migration [GO:0030335]; positive regulation of chemotaxis [GO:0050921]; positive regulation of endothelial cell apoptotic process [GO:2000353]; positive regulation of endothelial cell migration [GO:0010595]; positive regulation of extrinsic apoptotic signaling pathway via death domain receptors [GO:1902043]; positive regulation of fibroblast migration [GO:0010763]; positive regulation of macrophage activation			

		[GO:0043032]; positive regulation of macrophage chemotaxis [GO:0010759]; positive regulation of phosphorylation [GO:0042327]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of reactive oxygen species metabolic process [GO:2000379]; positive regulation of transforming growth factor beta1 production [GO:0032914]; positive regulation of transforming growth factor beta receptor signaling pathway [GO:0030511]; positive regulation of translation [GO:0045727]; positive regulation of tumor necrosis factor biosynthetic process [GO:0042535]; protein O-linked fucosylation [GO:0036066]; regulation of cGMP metabolic process [GO:0030823]; response to calcium ion [GO:0051592]; response to drug [GO:0042493]; response to endoplasmic reticulum stress [GO:0034976]; response to glucose [GO:0009749]; response to hypoxia [GO:0001666]; response to magnesium ion [GO:0032026]; response to progesterone [GO:0032570]; response to unfolded protein			

		[GO:0006986]; sprouting angiogenesis [GO:0002040]			
TAGLN	4.21	epithelial cell differentiation [GO:0030855]; muscle organ development [GO:0007517]		cytoplasm [GO:0005737]	FUNCTION: Actin cross-linking/gelling protein (By similarity). Involved in calcium interactions and contractile properties of the cell that may contribute to replicative senescence. {ECO:0000250}.
SLC2A1	4.22	cellular response to glucose starvation [GO:0042149]; glucose transport [GO:0015758]; lactose biosynthetic process [GO:0005989]; L-ascorbic acid metabolic process [GO:0019852]; protein complex assembly [GO:0006461]; regulation of insulin secretion [GO:0050796]; response to osmotic stress [GO:0006970]	dehydroascorbic acid transporter activity [GO:0033300]; D-glucose transmembrane transporter activity [GO:0055056]; glucose transmembrane transporter activity [GO:0005355]; identical protein binding [GO:0042802]; protein self-association [GO:0043621]; xenobiotic transporter activity [GO:0042910]	apical plasma membrane [GO:0016324]; basolateral plasma membrane [GO:0016323]; blood microparticle [GO:0072562]; caveola [GO:0005901]; cell-cell junction [GO:0005911]; cortical actin cytoskeleton [GO:0030864]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; female pronucleus [GO:0001939]; Golgi membrane [GO:0000139]; integral component of plasma membrane [GO:0005887]; melanosome [GO:0042470]; membrane [GO:0016020]; midbody [GO:0030496]; plasma	FUNCTION: Facilitative glucose transporter. This isoform may be responsible for constitutive or basal glucose uptake. Has a very broad substrate specificity; can transport a wide range of aldoses including both pentoses and hexoses. {ECO:0000269|PubMed:18245775, ECO:0000269|PubMed:19449892}.

				membrane [GO:0005886]	
CTSG	4.30	angiotensin maturation [GO:0002003]; cellular protein metabolic process [GO:0044267]; defense response to fungus [GO:0050832]; extracellular matrix disassembly [GO:0022617]; immune response [GO:0006955]; negative regulation of growth of symbiont in host [GO:0044130]; neutrophil mediated killing of gram-positive bacterium [GO:0070946]; positive regulation of immune response [GO:0050778]; protein phosphorylation [GO:0006468]; protein processing [GO:0016485]; proteolysis [GO:0006508]; response to lipopolysaccharide [GO:0032496]	heparin binding [GO:0008201]; peptidase activity [GO:0008233]; serine-type endopeptidase activity [GO:0004252]	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; secretory granule [GO:0030141]	FUNCTION: Serine protease with trypsin- and chymotrypsin-like specificity. Cleaves complement C3. Has antibacterial activity against the Gram-negative bacterium P.aeruginosa, antibacterial activity is inhibited by LPS from P.aeruginosa, Z-Gly-Leu-Phe-CH2Cl and phenylmethylsulfonyl fluoride. {ECO:0000269|PubMed:1861080, ECO:0000269|PubMed:1937776, ECO:0000269|PubMed:8194606}.
SLC1A5	4.33	amino acid transport [GO:0006865]; glutamine transport [GO:0006868]; neutral amino acid transport [GO:0015804]	amino acid transmembrane transporter activity [GO:0015171]; L-glutamine transmembrane transporter activity [GO:0015186]; neutral amino acid transmembrane transporter activity [GO:0015175]; receptor activity	extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; integral component of plasma membrane [GO:0005887]; melanosome [GO:0042470]; membrane [GO:0016020]; plasma membrane [GO:0005886]	FUNCTION: Sodium-dependent amino acids transporter that has a broad substrate specificity, with a preference for zwitterionic amino acids. It accepts as substrates all neutral amino acids, including glutamine, asparagine, and branched-chain and aromatic amino acids, and excludes methylated, anionic, and cationic amino acids. May also be activated by insulin. Through binding of the fusogenic protein syncytin-1/ERVW-1 may mediate trophoblasts syncytialization, the spontaneous fusion of their plasma membranes, an essential process in placental development

			[GO:0004872]; symporter activity [GO:0015293]; virus receptor activity [GO:0001618]		(PubMed:10708449, PubMed:23492904). Acts as a cell surface receptor for feline endogenous virus RD114, baboon M7 endogenous virus and type D simian retroviruses (PubMed:10051606, PubMed:10196349). {ECO:0000269|PubMed:10051606, ECO:0000269|PubMed:10196349, ECO:0000269|PubMed:10708449, ECO:0000269|PubMed:23492904}.
EFEMP1	4.42	camera-type eye development [GO:0043010]; embryonic eye morphogenesis [GO:0048048]; epidermal growth factor receptor signaling pathway [GO:0007173]; negative regulation of chondrocyte differentiation [GO:0032331]; negative regulation of neuron projection development [GO:0010977]; peptidyl-tyrosine phosphorylation [GO:0018108]; positive regulation of cell projection organization [GO:0031346]; positive regulation of cell proliferation [GO:0008284]; post-embryonic eye morphogenesis [GO:0048050]; regulation of glial cell migration [GO:1903975]; regulation of transcription, DNA-templated [GO:0006355]; visual perception [GO:0007601]	calcium ion binding [GO:0005509]; epidermal growth factor-activated receptor activity [GO:0005006]; epidermal growth factor receptor binding [GO:0005154]	basement membrane [GO:0005604]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	FUNCTION: Binds EGFR, the EGF receptor, inducing EGFR autophosphorylation and the activation of downstream signaling pathways. May play a role in cell adhesion and migration. May function as a negative regulator of chondrocyte differentiation. In the olfactory epithelium, it may regulate glial cell migration, differentiation and the ability of glial cells to support neuronal neurite outgrowth. {ECO:0000269|PubMed:19804359, ECO:0000269|PubMed:19887559, ECO:0000269|PubMed:20005202}.
HBA1	4.44	bicarbonate transport [GO:0015701]; cellular oxidant	heme binding [GO:002003	blood microparticle	FUNCTION: Involved in oxygen transport from the

		detoxification [GO:0098869]; hydrogen peroxide catabolic process [GO:0042744]; oxygen transport [GO:0015671]; positive regulation of cell death [GO:0010942]; protein heterooligomerization [GO:0051291]; receptor-mediated endocytosis [GO:0006898]; response to hydrogen peroxide [GO:0042542]	7]; iron ion binding [GO:0005506]; oxygen binding [GO:0019825]; oxygen transporter activity [GO:0005344]	[GO:0072562]; cytosol [GO:0005829]; cytosolic small ribosomal subunit [GO:0022627]; endocytic vesicle lumen [GO:0071682]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; haptoglobin-hemoglobin complex [GO:0031838]; hemoglobin complex [GO:0005833]; membrane [GO:0016020]	lung to the various peripheral tissues.
LUM	4.52	cartilage development [GO:0051216]; collagen fibril organization [GO:0030199]; extracellular matrix organization [GO:0030198]; keratan sulfate biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of transforming growth factor beta1 production [GO:0032914]; response to growth factor	collagen binding [GO:0005518]; extracellular matrix structural constituent [GO:0005201]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrillar collagen trimer [GO:0005583]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix	

		[GO:0070848]; response to organic cyclic compound [GO:0014070]; visual perception [GO:0007601]		[GO:0005578]	
HNRNPR	4.53	circadian rhythm [GO:0007623]; gene expression [GO:0010467]; mRNA destabilization [GO:0061157]; mRNA processing [GO:0006397]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation of catalytic activity [GO:0043086]; positive regulation of mRNA catabolic process [GO:0061014]	mRNA 3'-UTR binding [GO:0003730]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; RNA binding [GO:0003723]	axon terminus [GO:0043679]; catalytic step 2 spliceosome [GO:0071013]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; growth cone [GO:0030426]; intracellular ribonucleoprotein complex [GO:0030529]; nucleoplasm [GO:0005654]; spliceosomal complex [GO:0005681]	FUNCTION: Component of ribonucleosomes, which are complexes of at least 20 other different heterogenious nuclear ribonucleoproteins (hnRNP). hnRNP play an important role in processing of precursor mRNA in the nucleus.
H3F3A	4.55	blood coagulation [GO:0007596]; brain development [GO:0007420]; cellular protein metabolic process [GO:0044267]; chromatin silencing at rDNA [GO:0000183]; DNA replication-independent nucleosome assembly [GO:0006336]; gene silencing by RNA [GO:0031047]; negative regulation of gene expression, epigenetic [GO:0045814]; nucleosome assembly [GO:0006334];	histone binding [GO:0042393]; nucleosomal DNA binding [GO:0031492]; RNA polymerase II core promoter sequence-specific DNA binding [GO:0000979]; RNA polymerase II distal enhancer sequence-specific DNA	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; nuclear chromosome [GO:0000228]; nuclear chromosome, telomeric region [GO:0000784]; nuclear nucleosome [GO:0000788]; nucleoplasm [GO:0005654]; nucleosome [GO:000078	FUNCTION: Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active genes. Constitutes the predominant form of histone H3 in non-dividing cells and is incorporated into chromatin independently of DNA synthesis. Deposited at sites of nucleosomal displacement throughout transcribed genes, suggesting that it represents an epigenetic imprint of transcriptionally active chromatin. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation,

		positive regulation of cell growth [GO:0030307]; positive regulation of gene expression, epigenetic [GO:0045815]; response to hormone [GO:0009725]; telomere organization [GO:0032200]	binding [GO:0000980]	6]; nucleus [GO:0005634]; protein complex [GO:0043234]	DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling. {ECO:0000269|PubMed:14718166, ECO:0000269|PubMed:15776021, ECO:0000269|PubMed:16258499}.
MYH10	4.60	actin filament-based movement [GO:0030048]; actomyosin structure organization [GO:0031032]; adult heart development [GO:0007512]; aorta development [GO:0035904]; axon guidance [GO:0007411]; cardiac myofibril assembly [GO:0055003]; cardiac septum development [GO:0003279]; cell adhesion [GO:0007155]; cell proliferation [GO:0008283]; cerebellar Purkinje cell layer development [GO:0021680]; coronary vasculature development [GO:0060976]; exocytosis [GO:0006887]; fourth ventricle development [GO:0021592]; in utero embryonic development [GO:0001701]; lateral ventricle development [GO:0021670]; mitotic cytokinesis [GO:0000281]; neuromuscular process controlling balance [GO:0050885];	actin binding [GO:0003779]; actin-dependent ATPase activity [GO:0030898]; actin filament binding [GO:0051015]; ADP binding [GO:0043531]; ATP binding [GO:0005524]; microfilament motor activity [GO:0000146]	actin cytoskeleton [GO:0015629]; actomyosin [GO:0042641]; axon [GO:0030424]; brush border [GO:0005903]; cell cortex [GO:0005938]; cleavage furrow [GO:0032154]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendritic spine [GO:0043197]; extracellular exosome [GO:0070062]; growth cone [GO:0030426]; lamellipodium [GO:0030027]; midbody [GO:0030496]; mitochondrion [GO:0005739]; myosin complex [GO:0016459]; myosin II	FUNCTION: Cellular myosin that appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Involved with LARP6 in the stabilization of type I collagen mRNAs for CO1A1 and CO1A2. During cell spreading, plays an important role in cytoskeleton reorganization, focal contacts formation (in the central part but not the margins of spreading cells), and lamellipodial extension; this function is mechanically antagonized by MYH9. {ECO:0000269|PubMed:20052411, ECO:0000269|PubMed:20603131}.

		neuron migration [GO:0001764]; nuclear migration [GO:0007097]; plasma membrane repair [GO:0001778]; regulation of cell shape [GO:0008360]; retina development in camera-type eye [GO:0060041]; substrate-dependent cell migration, cell extension [GO:0006930]; third ventricle development [GO:0021678]; ventricular cardiac muscle cell development [GO:0055015]		complex [GO:0016460]; myosin II filament [GO:0097513]; neuromuscular junction [GO:0031594]; neuronal cell body [GO:0043025]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; spindle [GO:0005819]; stress fiber [GO:0001725]	
C1R	4.98	complement activation [GO:0006956]; complement activation, classical pathway [GO:0006958]; immune response [GO:0006955]; innate immune response [GO:0045087]	calcium ion binding [GO:0005509]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	FUNCTION: C1r B chain is a serine protease that combines with C1q and C1s to form C1, the first component of the classical pathway of the complement system.
LPL	4.98	cholesterol homeostasis [GO:0042632]; chylomicron remodeling [GO:0034371]; fatty acid biosynthetic process [GO:0006633]; lipoprotein metabolic process [GO:0042157]; phospholipid metabolic process [GO:0006644]; positive regulation of chemokine secretion [GO:0090197]; positive regulation of cholesterol storage [GO:0010886]; positive regulation of	apolipoprotein binding [GO:0034185]; heparin binding [GO:0008201]; lipoprotein lipase activity [GO:0004465]; phospholipase activity [GO:0004620]; receptor binding [GO:0005102]; triglyceride binding [GO:001712	anchored component of membrane [GO:0031225]; cell surface [GO:0009986]; chylomicron [GO:0042627]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region	FUNCTION: The primary function of this lipase is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (VLDL). Binding to heparin sulfate proteogylcans at the cell surface is vital to the function. The apolipoprotein, APOC2, acts as a coactivator of LPL activity in the presence of lipids on the luminal surface of vascular endothelium (By similarity). {ECO:0000250}.

		inflammatory response [GO:0050729]; positive regulation of macrophage derived foam cell differentiation [GO:0010744]; positive regulation of sequestering of triglyceride [GO:0010890]; response to cold [GO:0009409]; response to drug [GO:0042493]; response to glucose [GO:0009749]; retinoid metabolic process [GO:0001523]; triglyceride biosynthetic process [GO:0019432]; triglyceride catabolic process [GO:0019433]; triglyceride homeostasis [GO:0070328]; triglyceride metabolic process [GO:0006641]; very-low-density lipoprotein particle remodeling [GO:0034372]	9]; triglyceride lipase activity [GO:0004806]	[GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	
VCAN	5.00	cell adhesion [GO:0007155]; cell recognition [GO:0008037]; central nervous system development [GO:0007417]; chondroitin sulfate biosynthetic process [GO:0030206]; chondroitin sulfate catabolic process [GO:0030207]; dermatan sulfate biosynthetic process [GO:0030208]; extracellular matrix organization [GO:0030198]; glial cell migration [GO:0008347]; glycosaminoglycan metabolic process	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; extracellular matrix structural constituent [GO:0005201]; glycosaminoglycan binding [GO:0005539]; hyaluronic acid binding [GO:0005540]	extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi lumen [GO:0005796]; intracellular membrane-bounded organelle [GO:0043231]; lysosomal lumen	FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.

		[GO:0030203]; multicellular organism development [GO:0007275]; osteoblast differentiation [GO:0001649]; skeletal system development [GO:0001501]		[GO:0043202]; membrane [GO:0016020]; proteinaceous extracellular matrix [GO:0005578]	
PRELP	5.19	cell aging [GO:0007569]; keratan sulfate biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; skeletal system development [GO:0001501]	extracellular matrix structural constituent [GO:0005201]; heparin binding [GO:0008201]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix [GO:0005578]	FUNCTION: May anchor basement membranes to the underlying connective tissue. {ECO:0000250}.
ENO2	5.39	canonical glycolysis [GO:0061621]; gluconeogenesis [GO:0006094]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0004634]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; myelin sheath [GO:0043209]; perikaryon [GO:0043204]; phosphopyruvate hydratase	FUNCTION: Has neurotrophic and neuroprotective properties on a broad spectrum of central nervous system (CNS) neurons. Binds, in a calcium-dependent manner, to cultured neocortical neurons and promotes cell survival (By similarity). {ECO:0000250}.

				complex [GO:0000015]; photoreceptor inner segment [GO:0001917]; plasma membrane [GO:0005886]	
BASP1	5.40	diaphragm development [GO:0060539]; glomerular visceral epithelial cell differentiation [GO:0072112]; gonad development [GO:0008406]; mesenchymal to epithelial transition [GO:0060231]; metanephric mesenchyme development [GO:0072075]; negative regulation of transcription, DNA-templated [GO:0045892]; positive regulation of heart growth [GO:0060421]; positive regulation of metanephric ureteric bud development [GO:2001076]; substantia nigra development [GO:0021762]; thorax and anterior abdomen determination [GO:0007356]	protein domain specific binding [GO:0019904]; transcription corepressor activity [GO:0003714]; transcription regulatory region DNA binding [GO:0044212]	cell junction [GO:0030054]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; growth cone [GO:0030426]; nuclear speck [GO:0016607]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; vesicle [GO:0031982]	
ELANE	5.63	acute inflammatory response to antigenic stimulus [GO:0002438]; cellular calcium ion homeostasis [GO:0006874]; defense response to bacterium [GO:0042742]; extracellular matrix disassembly [GO:0022617]; leukocyte migration [GO:0050900];	cytokine binding [GO:0019955]; endopeptidase activity [GO:0004175]; heparin binding [GO:0008201]; peptidase activity [GO:0008233]; protease binding	cell surface [GO:0009986]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular	FUNCTION: Modifies the functions of natural killer cells, monocytes and granulocytes. Inhibits C5a-dependent neutrophil enzyme release and chemotaxis. {ECO:0000269|PubMed:15140022}.

		negative regulation of chemokine biosynthetic process [GO:0045079]; negative regulation of chemotaxis [GO:0050922]; negative regulation of growth of symbiont in host [GO:0044130]; negative regulation of inflammatory response [GO:0050728]; negative regulation of interleukin-8 biosynthetic process [GO:0045415]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; neutrophil mediated killing of fungus [GO:0070947]; phagocytosis [GO:0006909]; positive regulation of immune response [GO:0050778]; positive regulation of interleukin-8 biosynthetic process [GO:0045416]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of smooth muscle cell proliferation [GO:0048661]; protein catabolic process [GO:0030163]; proteolysis [GO:0006508]; response to lipopolysaccharide [GO:0032496]; response to UV [GO:0009411]; response to yeast [GO:0001878]	[GO:0002020]; RNA polymerase II transcription corepressor activity [GO:0001106]; serine-type endopeptidase activity [GO:0004252]	space [GO:0005615]; secretory granule [GO:0030141]; transcriptional repressor complex [GO:0017053]	
C1QC	5.79	complement activation [GO:0006956]; complement activation, classical	serine-type endopeptidase activity [GO:0004252]	blood microparticle [GO:0072562]; collagen	FUNCTION: C1q associates with the proenzymes C1r and C1s to yield C1, the first component of the serum complement system. The

		pathway [GO:0006958]; immune response [GO:0006955]; innate immune response [GO:0045087]; negative regulation of granulocyte differentiation [GO:0030853]; negative regulation of macrophage differentiation [GO:0045650]		trimer [GO:0005581]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	collagen-like regions of C1q interact with the Ca(2+)-dependent C1r(2)C1s(2) proenzyme complex, and efficient activation of C1 takes place on interaction of the globular heads of C1q with the Fc regions of IgG or IgM antibody present in immune complexes.
SERPINC1	5.86	blood coagulation [GO:0007596]; negative regulation of inflammatory response [GO:0050728]; regulation of blood coagulation, intrinsic pathway [GO:2000266]; response to nutrient [GO:0007584]	heparin binding [GO:0008201]; protease binding [GO:0002020]; serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	FUNCTION: Most important serine protease inhibitor in plasma that regulates the blood coagulation cascade. AT-III inhibits thrombin, matriptase-3/TMPRSS7, as well as factors IXa, Xa and XIa. Its inhibitory activity is greatly enhanced in the presence of heparin. {ECO:0000269|PubMed:15853774}.
CFD	6.16	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; platelet degranulation [GO:0002576]; proteolysis [GO:0006508]	serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	FUNCTION: Factor D cleaves factor B when the latter is complexed with factor C3b, activating the C3bbb complex, which then becomes the C3 convertase of the alternate pathway. Its function is homologous to that of C1s in the classical pathway.
LTBP2	6.26	extracellular fibril organization [GO:0043206]; protein secretion [GO:0009306]; protein targeting [GO:0006605]; transforming growth	calcium ion binding [GO:0005509]; heparin binding [GO:0008201]	extracellular exosome [GO:0070062]; extracellular space [GO:0005615];	FUNCTION: May play an integral structural role in elastic-fiber architectural organization and/or assembly.

		factor beta receptor signaling pathway [GO:0007179]		intracellular [GO:0005622]; proteinaceous extracellular matrix [GO:0005578]	
SUN2	6.89	centrosome localization [GO:0051642]; cytoskeletal anchoring at nuclear membrane [GO:0090286]; mitotic spindle organization [GO:0007052]; nuclear envelope organization [GO:0006998]; nuclear matrix anchoring at nuclear membrane [GO:0090292]; nuclear migration [GO:0007097]; nuclear migration along microfilament [GO:0031022]; positive regulation of cell migration [GO:0030335]	identical protein binding [GO:0042802]; lamin binding [GO:0005521]; microtubule binding [GO:0008017]	condensed nuclear chromosome [GO:0000794]; endosome membrane [GO:0010008]; integral component of nuclear inner membrane [GO:0005639]; LINC complex [GO:0034993]; nuclear chromosome, telomeric region [GO:0000784]; nuclear envelope [GO:0005635]; nuclear membrane [GO:0031965]	FUNCTION: Component of SUN-protein-containing multivariate complexes also called LINC complexes which link the nucleoskeleton and cytoskeleton by providing versatile outer nuclear membrane attachment sites for cytoskeletal filaments. Specifically, SYNE2 and SUN2 assemble in arrays of transmembrane actin-associated nuclear (TAN) lines which are bound to F-actin cables and couple the nucleus to retrograde actin flow during actin-dependent nuclear movement. Required for interkinetic nuclear migration (INM) and essential for nucleokinesis and centrosome-nucleus coupling during radial neuronal migration in the cerebral cortex and during glial migration. Anchors chromosome movement in the prophase of meiosis and is involved in selective gene expression of coding and non-coding RNAs needed for gametogenesis. Required for telomere attachment to nuclear envelope and gametogenesis. May also function on endocytic vesicles as a receptor for RAB5-GDP and participate in the activation of RAB5. {ECO:0000269|PubMed:18396275}.
TBC1D4	6.97	activation of GTPase activity [GO:0090630]; cellular response to insulin stimulus [GO:0032869]; intracellular protein transport [GO:0006886];	GTPase activator activity [GO:0005096]; Rab GTPase binding [GO:0017137]	cytoplasm [GO:0005737]; cytoplasmic vesicle membrane [GO:0030659]; endomembra	FUNCTION: May act as a GTPase-activating protein for RAB2A, RAB8A, RAB10 and RAB14. Isoform 2 promotes insulin-induced glucose transporter SLC2A4/GLUT4 translocation at the plasma membrane, thus increasing

		membrane organization [GO:0061024]; negative regulation of vesicle fusion [GO:0031339]; regulation of vesicle fusion [GO:0031338]; vesicle-mediated transport [GO:0016192]		ne system [GO:0012505]; extracellular exosome [GO:0070062]; intracellular [GO:0005622]	glucose uptake. {ECO:0000269|PubMed:15971998, ECO:0000269|PubMed:18771725, ECO:0000269|PubMed:22908308}.
STAT6	6.99	cellular response to hydrogen peroxide [GO:0070301]; cellular response to reactive nitrogen species [GO:1902170]; interleukin-4-mediated signaling pathway [GO:0035771]; mammary gland epithelial cell proliferation [GO:0033598]; mammary gland morphogenesis [GO:0060443]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; negative regulation of type 2 immune response [GO:0002829]; positive regulation of isotype switching to IgE isotypes [GO:0048295]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of type I interferon production [GO:0032481]; regulation of cell proliferation [GO:0042127]; regulation of transcription from RNA polymerase II promoter [GO:0006357];	identical protein binding [GO:0042802]; protein phosphatase binding [GO:0019903]; RNA polymerase II core promoter sequence-specific DNA binding [GO:0000979]; signal transducer activity [GO:0004871]; transcription factor activity, sequence-specific DNA binding [GO:0003700]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; membrane raft [GO:0045121]; nuclear chromatin [GO:0000790]; nucleoplasm [GO:0005654]	FUNCTION: Carries out a dual function: signal transduction and activation of transcription. Involved in IL4/interleukin-4- and IL3/interleukin-3-mediated signaling. {ECO:0000269|PubMed:17210636}.

		signal transduction [GO:0007165]; T-helper 1 cell lineage commitment [GO:0002296]; transcription, DNA-templated [GO:0006351]			
CNN2	7.54	actomyosin structure organization [GO:0031032]; cellular response to mechanical stimulus [GO:0071260]; cytoskeleton organization [GO:0007010]; regulation of actin filament-based process [GO:0032970]	actin binding [GO:0003779]	cell-cell junction [GO:0005911]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; membrane [GO:0016020]; stress fiber [GO:0001725]	FUNCTION: Thin filament-associated protein that is implicated in the regulation and modulation of smooth muscle contraction. It is capable of binding to actin, calmodulin, troponin C and tropomyosin. The interaction of calponin with actin inhibits the actomyosin Mg-ATPase activity.
VIM	7.63	astrocyte development [GO:0014002]; Bergmann glial cell differentiation [GO:0060020]; intermediate filament organization [GO:0045109]; lens fiber cell development [GO:0070307]; movement of cell or subcellular component [GO:0006928]; muscle filament sliding [GO:0030049]; negative regulation of neuron projection development [GO:0010977]; positive regulation of gene expression [GO:0010628]; SMAD protein signal transduction [GO:0060395]; viral process [GO:0016032]	double-stranded RNA binding [GO:0003725]; glycoprotein binding [GO:0001948]; identical protein binding [GO:0042802]; keratin filament binding [GO:1990254]; protein C-terminus binding [GO:0008022]; scaffold protein binding [GO:0097110]; structural constituent of cytoskeleton [GO:0005200]; structural constituent	cell leading edge [GO:0031252]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; intermediate filament [GO:0005882]; intermediate filament cytoskeleton [GO:0045111]; neuron projection [GO:0043005]; peroxisome	FUNCTION: Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells. Vimentin is attached to the nucleus, endoplasmic reticulum, and mitochondria, either laterally or terminally. {ECO:0000269|PubMed:21746880}.; FUNCTION: Involved with LARP6 in the stabilization of type I collagen mRNAs for CO1A1 and CO1A2. {ECO:0000269|PubMed:21746880}.

			of eye lens [GO:0005212]	[GO:0005777]; plasma membrane [GO:0005886]	
APOH	8.12	aging [GO:0007568]; blood coagulation, intrinsic pathway [GO:0007597]; negative regulation of angiogenesis [GO:0016525]; negative regulation of blood coagulation [GO:0030195]; negative regulation of endothelial cell migration [GO:0010596]; negative regulation of endothelial cell proliferation [GO:0001937]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of myeloid cell apoptotic process [GO:0033033]; negative regulation of respiratory burst [GO:0060268]; negative regulation of smooth muscle cell apoptotic process [GO:0034392]; organ regeneration [GO:0031100]; plasminogen activation [GO:0031639]; platelet degranulation [GO:0002576]; positive regulation of blood coagulation [GO:0030194]; positive regulation of lipoprotein lipase activity [GO:0051006]; positive regulation of triglyceride catabolic process [GO:0010898]; regulation of fibrinolysis [GO:0051917]; response to	glycoprotein binding [GO:0001948]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; lipid binding [GO:0008289]; lipoprotein lipase activator activity [GO:0060230]; phospholipid binding [GO:0005543]	cell surface [GO:0009986]; chylomicron [GO:0042627]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; plasma membrane [GO:0005886]; platelet dense granule lumen [GO:0031089]; very-low-density lipoprotein particle [GO:0034361]	FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.

		triglyceride [GO:0034014]; triglyceride metabolic process [GO:0006641]; triglyceride transport [GO:0034197]			
C8B	8.45	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; cytolysis [GO:0019835]; immune response [GO:0006955]; regulation of complement activation [GO:0030449]		extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; membrane [GO:0016020]; membrane attack complex [GO:0005579]	FUNCTION: Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target cells.
RRAD	9.56	negative regulation of cell growth [GO:0030308]; small GTPase mediated signal transduction [GO:0007264]	GTPase activity [GO:0003924]; GTP binding [GO:0005525]	intracellular [GO:0005622]; plasma membrane [GO:0005886]	FUNCTION: May play an important role in cardiac antiarrhythmia via the strong suppression of voltage-gated L-type Ca(2+) currents. Regulates voltage-dependent L-type calcium channel subunit alpha-1C trafficking to the cell membrane (By similarity). Inhibits cardiac hypertrophy through the calmodulin-dependent kinase II (CaMKII) pathway. Inhibits phosphorylation and activation of CAMK2D. {ECO:0000250, ECO:0000269|PubMed:18056528}.
OGN	10.59	axonogenesis [GO:0007409]; keratan sulfate biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; negative regulation of smooth muscle	heparin binding [GO:0008201]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:000561	FUNCTION: Induces bone formation in conjunction with TGF-beta-1 or TGF-beta-2.

		cell proliferation [GO:0048662]		5]; extracellular vesicle [GO:1903561]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix [GO:0005578]	
EEF1E1	10.74	glutathione metabolic process [GO:0006749]; negative regulation of cell proliferation [GO:0008285]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cellular senescence [GO:2000774]; positive regulation of DNA damage response, signal transduction by p53 class mediator [GO:0043517]; tRNA aminoacylation for protein translation [GO:0006418]	glutathione transferase activity [GO:0004364]; translation elongation factor activity [GO:0003746]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	FUNCTION: Positive modulator of ATM response to DNA damage.
THNSL1	13.12		pyridoxal phosphate binding [GO:0030170]	cytoplasm [GO:0005737]; mitochondrion [GO:0005739]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	
ADCY5	13.94	activation of adenylate cyclase activity [GO:0007190]; activation of protein kinase A activity [GO:0034199]; adenosine receptor	adenylate cyclase activity [GO:0004016]; adenylate cyclase binding [GO:000817	integral component of membrane [GO:0016021]; intracellular [GO:000562	FUNCTION: Catalyzes the formation of the signaling molecule cAMP in response to G-protein signaling (PubMed:15385642, PubMed:26206488, PubMed:24700542). Mediates signaling

		signaling pathway [GO:0001973]; adenylate cyclase-activating dopamine receptor signaling pathway [GO:0007191]; adenylate cyclase-activating G-protein coupled receptor signaling pathway [GO:0007189]; adenylate cyclase-inhibiting dopamine receptor signaling pathway [GO:0007195]; adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway [GO:0007193]; cAMP biosynthetic process [GO:0006171]; cAMP-mediated signaling [GO:0019933]; cellular response to forskolin [GO:1904322]; cellular response to glucagon stimulus [GO:0071377]; locomotory behavior [GO:0007626]; neuromuscular process controlling balance [GO:0050885]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; regulation of insulin secretion involved in cellular response to glucose stimulus [GO:0061178]; renal water homeostasis [GO:0003091]	9]; ATP binding [GO:0005524]; metal ion binding [GO:0046872]; protein heterodimerization activity [GO:0046982]	2]; plasma membrane [GO:0005886]; primary cilium [GO:0072372]	downstream of ADRB1 (PubMed:24700542). Regulates the increase of free cytosolic Ca(2+) in response to increased blood glucose levels and contributes to the regulation of Ca(2+)-dependent insulin secretion (PubMed:24740569). {ECO:0000269|PubMed:15385642, ECO:0000269|PubMed:24700542, ECO:0000269|PubMed:24740569, ECO:0000269|PubMed:26206488}.
AZU1	14.80	antimicrobial humoral response [GO:0019730]; calcium-mediated signaling using intracellular calcium source [GO:0035584]; cell chemotaxis	heparan sulfate proteoglycan binding [GO:0043395]; heparin binding [GO:0008201]; peptidase	azurophil granule [GO:0042582]; azurophil granule membrane [GO:0035577]; extracellular	FUNCTION: This is a neutrophil granule-derived antibacterial and monocyte- and fibroblast-specific chemotactic glycoprotein. Binds heparin. The cytotoxic action is limited to many species of Gram-negative bacteria; this specificity may

		[GO:0060326]; cellular extravasation [GO:0045123]; defense response to Gram-negative bacterium [GO:0050829]; defense response to virus [GO:0051607]; glial cell migration [GO:0008347]; induction of positive chemotaxis [GO:0050930]; inflammatory response [GO:0006954]; macrophage chemotaxis [GO:0048246]; microglial cell activation [GO:0001774]; monocyte activation [GO:0042117]; negative regulation of apoptotic process [GO:0043066]; neutrophil mediated killing of bacterium [GO:0070944]; positive regulation of cell adhesion [GO:0045785]; positive regulation of fractalkine biosynthetic process [GO:0050754]; positive regulation of gene expression [GO:0010628]; positive regulation of interleukin-1 beta biosynthetic process [GO:0050725]; positive regulation of MHC class II biosynthetic process [GO:0045348]; positive regulation of peptidyl-threonine phosphorylation [GO:0010800]; positive regulation of phagocytosis [GO:0050766]; positive regulation of protein kinase activity [GO:0045860];	activity [GO:0008233]; serine-type endopeptidase activity [GO:0004252]; toxic substance binding [GO:0015643]	exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of membrane [GO:0019898]	be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope. It may play a role in mediating recruitment of monocytes in the second wave of inflammation. Has antibacterial activity against the Gram-nagative bacterium P.aeruginosa, this activity is inhibited by LPS from P.aeruginosa. Acting alone, it does not have antimicrobial activity against the Gram-negative bacteria A.actinomycetemcomitans ATCC 29532, A.actinomycetemcomitans NCTC 9709, A.actinomycetemcomitans FDC-Y4, H.aphrophilus ATCC 13252, E.corrodens ATCC 23834, C.sputigena ATCC 33123, Capnocytophaga sp ATCC 33124, Capnocytophaga sp ATCC 27872 or E.coli ML-35. Has antibacterial activity against C.sputigena ATCC 33123 when acting synergistically with either elastase or cathepsin G. {ECO:0000269|PubMed:1399008, ECO:0000269|PubMed:1937776, ECO:0000269|PubMed:2312733}.

		positive regulation of tumor necrosis factor biosynthetic process [GO:0042535]; protein kinase C-activating G-protein coupled receptor signaling pathway [GO:0007205]; protein kinase C signaling [GO:0070528]; protein processing [GO:0016485]; proteolysis [GO:0006508]; regulation of vascular permeability [GO:0043114]			
TMX2	25.78	cell redox homeostasis [GO:0045454]		cell [GO:0005623]; integral component of membrane [GO:0016021]	
EIF3K	26.23	formation of translation preinitiation complex [GO:0001731]; regulation of translational initiation [GO:0006446]; translational initiation [GO:0006413]	ribosome binding [GO:0043022]; translation initiation factor activity [GO:0003743]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; eukaryotic 43S preinitiation complex [GO:0016282]; eukaryotic 48S preinitiation complex [GO:0033290]; eukaryotic translation initiation factor 3 complex [GO:0005852]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; nucleus [GO:0005634]	FUNCTION: Component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is required for several steps in the initiation of protein synthesis. The eIF-3 complex associates with the 40S ribosome and facilitates the recruitment of eIF-1, eIF-1A, eIF-2:GTP:methionyl-tRNAi and eIF-5 to form the 43S preinitiation complex (43S PIC). The eIF-3 complex stimulates mRNA recruitment to the 43S PIC and scanning of the mRNA for AUG recognition. The eIF-3 complex is also required for disassembly and recycling of post-termination ribosomal complexes and subsequently prevents premature joining of the 40S and 60S ribosomal subunits prior to initiation.

Table S4. All the proteins involved in the network analysis were summarized.

Gene	Clusters	Go			Function
		Biological process	Molecular function	Cellular component	
RCSD1	cardiac muscle contraction	cellular hyperosmotic response [GO:0071474]; skeletal muscle contraction [GO:0003009]	actin filament binding [GO:0051015]	actin filament [GO:0005884]	Stress-induced phosphorylation of CAPZIP may regulate the ability of F-actin-capping protein to remodel actin filament assembly. {ECO:0000269|PubMed:15850461}.
TNNC1	cardiac muscle contraction	cardiac muscle contraction [GO:0060048]; diaphragm contraction [GO:0002086]; muscle filament sliding [GO:0030049]; regulation of ATPase activity [GO:0043462]; regulation of muscle contraction [GO:0006937]; regulation of muscle filament sliding speed [GO:0032972]; response to metal ion [GO:0010038]; skeletal muscle contraction [GO:0003009]; transition between fast and slow fiber [GO:0014883]; ventricular cardiac muscle tissue morphogenesis [GO:0055010]	actin filament binding [GO:0051015]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; protein homodimerization activity [GO:0042803]; troponin I binding [GO:0031013]; troponin T binding [GO:0031014]	actin cytoskeleton [GO:0015629]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; nucleoplasm [GO:0005654]; troponin complex [GO:0005861]	Troponin is the central regulatory protein of striated muscle contraction. Tn consists of three components: Tn-I which is the inhibitor of actomyosin ATPase, Tn-T which contains the binding site for tropomyosin and Tn-C. The binding of calcium to Tn-C abolishes the inhibitory action of Tn on actin filaments.
CASQ2	cardiac muscle contraction	cardiac muscle contraction [GO:0060048]; cellular response to caffeine [GO:0071313]; detection of calcium ion [GO:0005513]; ion transmembrane transport	calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; protein homodimeriz	calcium channel complex [GO:0034704]; cytoplasm [GO:0005737]; intracellular [GO:0005622]; junctional membrane	Calsequestrin is a high-capacity, moderate affinity, calcium-binding protein and thus acts as an internal calcium store in muscle. Calcium ions are bound by clusters of acidic residues at the protein surface, especially at the interface between

		[GO:0034220]; negative regulation of potassium ion transmembrane transporter activity [GO:1901017]; negative regulation of potassium ion transport [GO:0043267]; negative regulation of ryanodine-sensitive calcium-release channel activity [GO:0060315]; protein polymerization [GO:0051258]; Purkinje myocyte to ventricular cardiac muscle cell signaling [GO:0086029]; regulation of cardiac conduction [GO:1903779]; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion [GO:0010881]; regulation of cell communication by electrical coupling [GO:0010649]; regulation of heart rate [GO:0002027]; regulation of membrane repolarization [GO:0060306]; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0010880]; sarcomere organization [GO:0045214]; sequestering of calcium ion [GO:0051208]; striated muscle contraction [GO:0006941]	ation activity [GO:0042803]	complex [GO:0030314]; junctional sarcoplasmic reticulum membrane [GO:0014701]; sarcoplasmic reticulum [GO:0016529]; sarcoplasmic reticulum lumen [GO:0033018]; sarcoplasmic reticulum membrane [GO:0033017]; Z disc [GO:0030018]	subunits. Can bind around 60 Ca(2+) ions. Regulates the release of lumenal Ca(2+) via the calcium release channel RYR2; this plays an important role in triggering muscle contraction. Plays a role in excitation-contraction coupling in the heart and in regulating the rate of heart beats. {ECO:0000269|PubMed:16908766, ECO:0000269|PubMed:17881003, ECO:0000269|PubMed:18399795, ECO:0000269|PubMed:21416293}.
HRC	cardiac muscle	muscle contraction [GO:0006936];	ATPase binding	sarcoplasmic reticulum	May play a role in the regulation of calcium

	contraction	negative regulation of cytosolic calcium ion concentration [GO:0051481]; positive regulation of heart contraction [GO:0045823]; positive regulation of heart rate [GO:0010460]; positive regulation of relaxation of cardiac muscle [GO:1901899]; regulation of calcium ion transmembrane transport [GO:1903169]; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion [GO:0010881]; regulation of cell communication by electrical coupling involved in cardiac conduction [GO:1901844]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of heart rate [GO:0002027]; regulation of peptidyl-serine phosphorylation [GO:0033135]; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0010880]; regulation of ryanodine-sensitive calcium-release channel activity [GO:0060314]	[GO:0051117]; calcium ion binding [GO:0005509]; ion channel binding [GO:0044325]	lumen [GO:0033018]; sarcoplasmic reticulum membrane [GO:0033017]; Z disc [GO:0030018]	sequestration or release in the SR of skeletal and cardiac muscle.
FHL2	cardiac muscle contraction	androgen receptor signaling pathway [GO:0030521]; atrial cardiac muscle cell development [GO:0055014]; heart trabecula formation [GO:0060347];	androgen receptor binding [GO:0050681]; identical protein binding [GO:0042802	actin cytoskeleton [GO:0015629]; focal adhesion [GO:0005925]; M band [GO:0031430]; nucleoplasm	May function as a molecular transmitter linking various signaling pathways to transcriptional regulation. Negatively regulates the transcriptional repressor E4F1 and may function in

		negative regulation of apoptotic process [GO:0043066]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; osteoblast differentiation [GO:0001649]; positive regulation of transcription, DNA-templated [GO:0045893]; response to hormone [GO:0009725]; transcription, DNA-templated [GO:0006351]; ventricular cardiac muscle cell development [GO:0055015]	]; transcription coactivator activity [GO:0003713]; transcription factor binding [GO:0008134]; zinc ion binding [GO:0008270]	[GO:0005654]; nucleus [GO:0005634]; Z disc [GO:0030018]	cell growth. Inhibits the transcriptional activity of FOXO1 and its apoptotic function by enhancing the interaction of FOXO1 with SIRT1 and FOXO1 deacetylation. {ECO:0000269|PubMed:15692560, ECO:0000269|PubMed:16652157, ECO:0000269|PubMed:18853468}.
TNNT2	cardiac muscle contraction	actin crosslink formation [GO:0051764]; cardiac muscle contraction [GO:0060048]; muscle filament sliding [GO:0030049]; negative regulation of ATPase activity [GO:0032780]; positive regulation of ATPase activity [GO:0032781]; protein heterooligomerization [GO:0051291]; regulation of heart contraction [GO:0008016]; regulation of muscle filament sliding speed [GO:0032972]; response to calcium ion [GO:0051592]; ventricular cardiac muscle tissue morphogenesis [GO:0055010]	actin binding [GO:0003779]; tropomyosin binding [GO:0005523]; troponin C binding [GO:0030172]; troponin I binding [GO:0031013]	cytosol [GO:0005829]; sarcomere [GO:0030017]; striated muscle thin filament [GO:0005865]; troponin complex [GO:0005861]	Troponin T is the tropomyosin-binding subunit of troponin, the thin filament regulatory complex which confers calcium-sensitivity to striated muscle actomyosin ATPase activity.
MYOM2	cardiac muscle contraction	muscle contraction [GO:0006936]	structural constituent of muscle [GO:0008307]	M band [GO:0031430]; mitochondrion [GO:0005739]; myosin	Major component of the vertebrate myofibrillar M band. Binds myosin, titin, and light meromyosin.

				filament [GO:0032982]	This binding is dose dependent.
RYR2	cardiac muscle contraction	BMP signaling pathway [GO:0030509]; calcium ion transport [GO:0006816]; calcium ion transport into cytosol [GO:0060402]; calcium-mediated signaling [GO:0019722]; calcium-mediated signaling using intracellular calcium source [GO:0035584]; canonical Wnt signaling pathway [GO:0060070]; cardiac muscle contraction [GO:0060048]; cardiac muscle hypertrophy [GO:0003300]; cell communication by electrical coupling involved in cardiac conduction [GO:0086064]; cellular calcium ion homeostasis [GO:0006874]; cellular response to caffeine [GO:0071313]; cellular response to epinephrine stimulus [GO:0071872]; detection of calcium ion [GO:0005513]; embryonic heart tube morphogenesis [GO:0003143]; establishment of protein localization to endoplasmic reticulum [GO:0072599]; ion transmembrane transport [GO:0034220]; left ventricular cardiac muscle tissue morphogenesis [GO:0003220]; positive regulation of calcium-transporting	calcium channel activity [GO:0005262]; calcium-induced calcium release activity [GO:0048763]; calcium ion binding [GO:0005509]; calcium-release channel activity [GO:0015278]; calmodulin binding [GO:0005516]; enzyme binding [GO:0019899]; identical protein binding [GO:0042802]; ion channel binding [GO:0044325]; protein kinase A catalytic subunit binding [GO:0034236]; protein kinase A regulatory subunit binding [GO:0034237]; ryanodine-sensitive calcium-release channel activity [GO:0005219]; suramin binding [GO:0043924]	calcium channel complex [GO:0034704]; extracellular exosome [GO:0070062]; junctional sarcoplasmic reticulum membrane [GO:0014701]; membrane [GO:0016020]; plasma membrane [GO:0005886]; protein complex [GO:0043234]; sarcoplasmic reticulum [GO:0016529]; sarcoplasmic reticulum membrane [GO:0033017]; smooth endoplasmic reticulum [GO:0005790]; Z disc [GO:0030018]	Calcium channel that mediates the release of Ca(2+) from the sarcoplasmic reticulum into the cytoplasm and thereby plays a key role in triggering cardiac muscle contraction. Aberrant channel activation can lead to cardiac arrhythmia. In cardiac myocytes, calcium release is triggered by increased Ca(2+) levels due to activation of the L-type calcium channel CACNA1C. The calcium channel activity is modulated by formation of heterotetramers with RYR3. Required for cellular calcium ion homeostasis. Required for embryonic heart development. {ECO:0000269|PubMed:10830164, ECO:0000269|PubMed:20056922}.

		ATPase activity [GO:1901896]; positive regulation of heart rate [GO:0010460]; positive regulation of sequestering of calcium ion [GO:0051284]; positive regulation of the force of heart contraction [GO:0098735]; Purkinje myocyte to ventricular cardiac muscle cell signaling [GO:0086029]; regulation of atrial cardiac muscle cell action potential [GO:0098910]; regulation of AV node cell action potential [GO:0098904]; regulation of cardiac conduction [GO:1903779]; regulation of cardiac muscle contraction [GO:0055117]; regulation of cardiac muscle contraction by calcium ion signaling [GO:0010882]; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion [GO:0010881]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of heart rate [GO:0002027]; regulation of SA node cell action potential [GO:0098907]; regulation of ventricular cardiac muscle cell action potential [GO:0098911]; release of sequestered calcium ion into cytosol			

		[GO:0051209]; release of sequestered calcium ion into cytosol by sarcoplasmic reticulum [GO:0014808]; response to caffeine [GO:0031000]; response to hypoxia [GO:0001666]; response to muscle activity [GO:0014850]; response to muscle stretch [GO:0035994]; response to redox state [GO:0051775]; sarcoplasmic reticulum calcium ion transport [GO:0070296]; type B pancreatic cell apoptotic process [GO:0097050]; ventricular cardiac muscle cell action potential [GO:0086005]			
TMOD1	cardiac muscle contraction	actin filament organization [GO:0007015]; adult locomotory behavior [GO:0008344]; lens fiber cell development [GO:0070307]; muscle contraction [GO:0006936]; muscle filament sliding [GO:0030049]; myofibril assembly [GO:0030239]; pointed-end actin filament capping [GO:0051694]	tropomyosin binding [GO:0005523]	cortical cytoskeleton [GO:0030863]; cytosol [GO:0005829]; membrane [GO:0016020]; nucleus [GO:0005634]; striated muscle thin filament [GO:0005865]	Blocks the elongation and depolymerization of the actin filaments at the pointed end. The Tmod/TM complex contributes to the formation of the short actin protofilament, which in turn defines the geometry of the membrane skeleton. May play an important role in regulating the organization of actin filaments by preferentially binding to a specific tropomyosin isoform at its N-terminus. {ECO:0000269|PubMed:8002995}.
ATP1A3	cardiac muscle contraction	adult locomotory behavior [GO:0008344]; ATP hydrolysis coupled proton transport [GO:0015991]; cardiac muscle contraction [GO:0060048]; cell communication by electrical coupling	ATP binding [GO:0005524]; chaperone binding [GO:0051087]; metal ion binding [GO:0046872]; sodium:potassium-	axon [GO:0030424]; dendritic spine head [GO:0044327]; dendritic spine neck [GO:0044326]; endoplasmic reticulum [GO:0005783];	This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium

		involved in cardiac conduction [GO:0086064]; cellular potassium ion homeostasis [GO:0030007]; cellular response to steroid hormone stimulus [GO:0071383]; cellular sodium ion homeostasis [GO:0006883]; ionotropic glutamate receptor signaling pathway [GO:0035235]; ion transmembrane transport [GO:0034220]; memory [GO:0007613]; potassium ion import [GO:0010107]; regulation of cardiac conduction [GO:1903779]; response to drug [GO:0042493]; response to glycoside [GO:1903416]; sodium ion export from cell [GO:0036376]; visual learning [GO:0008542]	exchanging ATPase activity [GO:0005391]; sodium:potassium-exchanging ATPase activity involved in regulation of cardiac muscle cell membrane potential [GO:0086037]; steroid hormone binding [GO:1990239]	extracellular vesicle [GO:1903561]; Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021]; myelin sheath [GO:0043209]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; sarcolemma [GO:0042383]; sodium:potassium-exchanging ATPase complex [GO:0005890]; synapse [GO:0045202]	ions, providing the energy for active transport of various nutrients.
FLNC	cardiac muscle contraction	cell junction assembly [GO:0034329]; muscle fiber development [GO:0048747]	ankyrin binding [GO:0030506]; cytoskeletal protein binding [GO:0008092]	costamere [GO:0043034]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; focal adhesion [GO:0005925]; plasma membrane [GO:0005886]; sarcolemma [GO:0042383]; sarcoplasm [GO:0016528]; Z disc [GO:0030018]	Muscle-specific filamin, which plays a central role in muscle cells, probably by functioning as a large actin-cross-linking protein. May be involved in reorganizing the actin cytoskeleton in response to signaling events, and may also display structural functions at the Z lines in muscle cells. Critical for normal myogenesis and for maintaining the structural integrity of the muscle fibers.
RRAD	cardiac muscle contraction	negative regulation of cell growth [GO:0030308]; small GTPase mediated	GTPase activity [GO:0003924]; GTP binding	intracellular [GO:0005622]; plasma membrane [GO:0005886]	May play an important role in cardiac antiarrhythmia via the strong suppression of voltage-gated L-type

		signal transduction [GO:0007264]	[GO:0005525]		Ca(2+) currents. Regulates voltage-dependent L-type calcium channel subunit alpha-1C trafficking to the cell membrane (By similarity). Inhibits cardiac hypertrophy through the calmodulin-dependent kinase II (CaMKII) pathway. Inhibits phosphorylation and activation of CAMK2D. {ECO:0000250, ECO:0000269|PubMed:18056528}.
FLII	cytoskeleton organization	actin cytoskeleton organization [GO:0030036]; actin filament severing [GO:0051014]; multicellular organism development [GO:0007275]; regulation of transcription, DNA-templated [GO:0006355]; transcription, DNA-templated [GO:0006351]	actin binding [GO:0003779]	brush border [GO:0005903]; cytoplasm [GO:0005737]; focal adhesion [GO:0005925]; microtubule organizing center [GO:0005815]; nucleoplasm [GO:0005654]	May play a role as coactivator in transcriptional activation by hormone-activated nuclear receptors (NR) and acts in cooperation with NCOA2 and CARM1. Involved in estrogen hormone signaling. Involved in early embryonic development (By similarity). May play a role in regulation of cytoskeletal rearrangements involved in cytokinesis and cell migration, by inhibiting Rac1-dependent paxillin phosphorylation. {ECO:0000250, ECO:0000269|PubMed:14966289}.
TUBB	cytoskeleton organization	cell division [GO:0051301]; cellular process [GO:0009987]; cytoskeleton-dependent intracellular transport [GO:0030705]; G2/M transition of mitotic cell cycle [GO:0000086]; microtubule-based process [GO:0007017]; movement of cell or subcellular component [GO:0006928]; natural killer cell mediated cytotoxicity	GTPase activity [GO:0003924]; GTP binding [GO:0005525]; MHC class I protein binding [GO:0042288]; structural constituent of cytoskeleton [GO:0005200]; structural molecule activity [GO:0005198]; ubiquitin protein ligase binding	cell body [GO:0044297]; cytoplasmic ribonucleoprotein granule [GO:0036464]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; microtubule [GO:0005874]; nuclear envelope lumen [GO:0005641]; nucleus	Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain.

		[GO:0042267]; spindle assembly [GO:0051225]	[GO:0031625]	[GO:0005634]; protein complex [GO:0043234]	
NCKAP1	cytoskeleton organization	apoptotic process [GO:0006915]; central nervous system development [GO:0007417]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; positive regulation of Arp2/3 complex-mediated actin nucleation [GO:2000601]; positive regulation of lamellipodium assembly [GO:0010592]; Rac protein signal transduction [GO:0016601]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]; viral process [GO:0016032]	protein complex binding [GO:0032403]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; integral component of membrane [GO:0016021]; lamellipodium membrane [GO:0031258]; SCAR complex [GO:0031209]	Part of the WAVE complex that regulates lamellipodia formation. The WAVE complex regulates actin filament reorganization via its interaction with the Arp2/3 complex. Actin remodeling activity is regulated by RAC1.
SDCBP	cytoskeleton organization	actin cytoskeleton organization [GO:0030036]; ephrin receptor signaling pathway [GO:0048013]; intracellular signal transduction [GO:0035556]; negative regulation of proteasomal ubiquitin-dependent protein catabolic process [GO:0032435]; negative regulation of receptor internalization [GO:0002091]; positive regulation of cell growth [GO:0030307]; positive regulation of cell migration [GO:0030335]; positive regulation of cell proliferation	cytoskeletal adaptor activity [GO:0008093]; frizzled binding [GO:0005109]; identical protein binding [GO:0042802]; interleukin-5 receptor binding [GO:0005137]; protein heterodimerization activity [GO:0046982]; protein N-terminus binding [GO:0047485]; syndecan binding [GO:0045545]	adherens junction [GO:0005912]; blood microparticle [GO:0072562]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; endoplasmic reticulum membrane [GO:0005789]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; focal adhesion [GO:0005925];	Multifunctional adapter protein involved in diverse array of functions including trafficking of transmembrane proteins, neuro and immunomodulation, exosome biogenesis, and tumorigenesis (PubMed:26291527). Positively regulates TGFB1-mediated SMAD2/3 activation and TGFB1-induced epithelial-to-mesenchymal transition (EMT) and cell migration in various cell types. May increase TGFB1 signaling by enhancing cell-surface expression of TGFR1 by preventing the interaction between TGFR1 and CAV1 and subsequent CAV1-dependent internalization and degradation of TGFR1

		[GO:0008284]; positive regulation of epithelial to mesenchymal transition [GO:0010718]; positive regulation of exosomal secretion [GO:1903543]; positive regulation of extracellular exosome assembly [GO:1903553]; positive regulation of JNK cascade [GO:0046330]; positive regulation of pathway-restricted SMAD protein phosphorylation [GO:0010862]; positive regulation of phosphorylation [GO:0042327]; positive regulation of transforming growth factor beta receptor signaling pathway [GO:0030511]; protein targeting to membrane [GO:0006612]; Ras protein signal transduction [GO:0007265]; regulation of mitotic cell cycle [GO:0007346]; substrate-dependent cell migration, cell extension [GO:0006930]; synaptic transmission [GO:0007268]		interleukin-5 receptor complex [GO:0005895]; melanosome [GO:0042470]; membrane [GO:0016020]; membrane raft [GO:0045121]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	(PubMed:25893292). In concert with SDC1/4 and PDCD6IP, regulates exosome biogenesis (PubMed:22660413). Reg
FLNA	cytoskeleton organization	actin crosslink formation [GO:0051764]; actin cytoskeleton reorganization [GO:0031532]; adenylate cyclase-inhibiting dopamine receptor signaling pathway [GO:0007195]; cell junction assembly [GO:0034329]; cilium assembly [GO:0042384]; cytoplasmic	actin filament binding [GO:0051015]; Fc-gamma receptor I complex binding [GO:0034988]; glycoprotein binding [GO:0001948]; G-protein coupled receptor binding	actin cytoskeleton [GO:0015629]; actin filament [GO:0005884]; apical dendrite [GO:0097440]; cell-cell junction [GO:0005911]; cortical cytoskeleton [GO:0030863]; cytoplasm [GO:0005737]; cytosol	Promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. Interaction with FLNA may allow neuroblast migration from the ventricular zone into the cortical plate. Tethers cell surface-localized

		sequestering of protein [GO:0051220]; establishment of protein localization [GO:0045184]; mitotic spindle assembly [GO:0090307]; mRNA transcription from RNA polymerase II promoter [GO:0042789]; negative regulation of apoptotic process [GO:0043066]; negative regulation of protein catabolic process [GO:0042177]; negative regulation of sequence-specific DNA binding transcription factor activity [GO:0043433]; negative regulation of transcription from RNA polymerase I promoter [GO:0016479]; platelet activation [GO:0030168]; platelet aggregation [GO:0070527]; platelet degranulation [GO:0002576]; positive regulation of I-kappaB kinase/NF-kappaB signaling [GO:0043123]; positive regulation of integrin-mediated signaling pathway [GO:2001046]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; positive regulation of transcription factor import into nucleus [GO:0042993]; protein localization to cell surface [GO:0034394]; protein stabilization	[GO:0001664]; GTPase binding [GO:0051020]; kinase binding [GO:0019900]; poly(A) RNA binding [GO:0044822]; protein homodimerization activity [GO:0042803]; Rac GTPase binding [GO:0048365]; Ral GTPase binding [GO:0017160]; Rho GTPase binding [GO:0017048]; signal transducer activity [GO:0004871]; small GTPase binding [GO:0031267]; transcription factor binding [GO:0008134]	[GO:0005829]; dendritic shaft [GO:0043198]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; focal adhesion [GO:0005925]; membrane [GO:0016020]; Myb complex [GO:0031523]; neuronal cell body [GO:0043025]; nucleolus [GO:0005730]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]	furin, modulates its rate of internalization and directs its intracellular trafficking (By similarity). Involved in ciliogenesis. Plays a role in cell-cell contacts and adherens junctions during the development of blood vessels, heart and brain organs. Plays a role in platelets morphology

		[GO:0050821]; receptor clustering [GO:0043113]; regulation of cell migration [GO:0030334]; semaphorin-plexin signaling pathway [GO:0071526]; wound healing, spreading of cells [GO:0044319]			
ARPC1B	cytoskeleton organization	Arp2/3 complex-mediated actin nucleation [GO:0034314]; ephrin receptor signaling pathway [GO:0048013]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; movement of cell or subcellular component [GO:0006928]	structural constituent of cytoskeleton [GO:0005200]	actin cytoskeleton [GO:0015629]; Arp2/3 protein complex [GO:0005885]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]	Functions as component of the Arp2/3 complex which is involved in regulation of actin polymerization and together with an activating nucleation-promoting factor (NPF) mediates the formation of branched actin networks.
LASP1	cytoskeleton organization	ion transport [GO:0006811]	ion transmembrane transporter activity [GO:0015075]; SH3/SH2 adaptor activity [GO:0005070]; zinc ion binding [GO:0008270]	cortical actin cytoskeleton [GO:0030864]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]	Plays an important role in the regulation of dynamic actin-based, cytoskeletal activities. Agonist-dependent changes in LASP1 phosphorylation may also serve to regulate actin-associated ion transport activities, not only in the parietal cell but also in certain other F-actin-rich secretory epithelial cell types (By similarity). {ECO:0000250}.
ROCK1	cytoskeleton organization	actin cytoskeleton organization [GO:0030036]; apical constriction [GO:0003383]; bleb assembly [GO:0032060]; cellular component disassembly involved in execution phase of apoptosis [GO:0006921]; cortical actin cytoskeleton organization [GO:0030866]; ephrin receptor	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; protein kinase activity [GO:0004672]; protein serine/threonine kinase activity [GO:0004674]	bleb [GO:0032059]; centriole [GO:0005814]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; Golgi membrane [GO:0000139]; lamellipodium [GO:0030027]; plasma membrane [GO:0005886];	Protein kinase which is a key regulator of actin cytoskeleton and cell polarity. Involved in regulation of smooth muscle contraction, actin cytoskeleton organization, stress fiber and focal adhesion formation, neurite retraction, cell adhesion and motility via phosphorylation of DAPK3, GFAP, LIMK1, LIMK2, MYL9/MLC2, PFN1 and PPP1R12A. Phosphorylates FHOD1 and acts synergistically

		signaling pathway [GO:0048013]; establishment of protein localization to plasma membrane [GO:0090002]; I-kappaB kinase/NF-kappaB signaling [GO:0007249]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; leukocyte tethering or rolling [GO:0050901]; membrane to membrane docking [GO:0022614]; myoblast migration [GO:0051451]; negative regulation of angiogenesis [GO:0016525]; negative regulation of bicellular tight junction assembly [GO:1903347]; negative regulation of myosin-light-chain-phosphatase activity [GO:0035509]; negative regulation of neuron apoptotic process [GO:0043524]; negative regulation of protein binding [GO:0032091]; positive regulation of focal adhesion assembly [GO:0051894]; protein phosphorylation [GO:0006468]; regulation of actin cytoskeleton organization [GO:0032956]; regulation of cell adhesion [GO:0030155]; regulation of cell motility [GO:2000145]; regulation of establishment of cell		ruffle [GO:0001726]	with it to promote SRC-dependent non-apoptotic plasma membrane blebbing. Phosphorylates JIP3 and regulates the recruitment of JNK to JIP3 upon UVB-induced stress. Acts as a suppressor of inflammatory cell migration by regulating PTEN phosphorylation and stability. Acts as a negative r

		polarity [GO:2000114]; regulation of establishment of endothelial barrier [GO:1903140]; regulation of focal adhesion assembly [GO:0051893]; regulation of keratinocyte differentiation [GO:0045616]; regulation of stress fiber assembly [GO:0051492]; Rho protein signal transduction [GO:0007266]; signal transduction [GO:0007165]; smooth muscle contraction [GO:0006939]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]			
TAGLN	cytoskeleton organization	epithelial cell differentiation [GO:0030855]; muscle organ development [GO:0007517]		cytoplasm [GO:0005737]	Actin cross-linking/gelling protein (By similarity). Involved in calcium interactions and contractile properties of the cell that may contribute to replicative senescence. {ECO:0000250}.
MYH10	cytoskeleton organization	actin filament-based movement [GO:0030048]; actomyosin structure organization [GO:0031032]; adult heart development [GO:0007512]; aorta development [GO:0035904]; axon guidance [GO:0007411]; cardiac myofibril assembly [GO:0055003]; cardiac septum development [GO:0003279]; cell adhesion [GO:0007155]; cell proliferation [GO:0008283];	actin binding [GO:0003779]; actin-dependent ATPase activity [GO:0030898]; actin filament binding [GO:0051015]; ADP binding [GO:0043531]; ATP binding [GO:0005524]; microfilament motor activity [GO:0000146]	actin cytoskeleton [GO:0015629]; actomyosin [GO:0042641]; axon [GO:0030424]; brush border [GO:0005903]; cell cortex [GO:0005938]; cleavage furrow [GO:0032154]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendritic spine [GO:0043197]; extracellular exosome	Cellular myosin that appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Involved with LARP6 in the stabilization of type I collagen mRNAs for CO1A1 and CO1A2. During cell spreading, plays an important role in cytoskeleton reorganization, focal contacts formation (in the central part but not the margins of spreading cells), and lamellipodial extension; this function is mechanically antagonized by MYH9. {ECO:0000269|PubMed:20052411,

		cerebellar Purkinje cell layer development [GO:0021680]; coronary vasculature development [GO:0060976]; exocytosis [GO:0006887]; fourth ventricle development [GO:0021592]; in utero embryonic development [GO:0001701]; lateral ventricle development [GO:0021670]; mitotic cytokinesis [GO:0000281]; neuromuscular process controlling balance [GO:0050885]; neuron migration [GO:0001764]; nuclear migration [GO:0007097]; plasma membrane repair [GO:0001778]; regulation of cell shape [GO:0008360]; retina development in camera-type eye [GO:0060041]; substrate-dependent cell migration, cell extension [GO:0006930]; third ventricle development [GO:0021678]; ventricular cardiac muscle cell development [GO:0055015]		[GO:0070062]; growth cone [GO:0030426]; lamellipodium [GO:0030027]; midbody [GO:0030496]; mitochondrion [GO:0005739]; myosin complex [GO:0016459]; myosin II complex [GO:0016460]; myosin II filament [GO:0097513]; neuromuscular junction [GO:0031594]; neuronal cell body [GO:0043025]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; spindle [GO:0005819]; stress fiber [GO:0001725]	ECO:0000269|PubMed:20603131}.
SUN2	cytoskeleton organization	centrosome localization [GO:0051642]; cytoskeletal anchoring at nuclear membrane [GO:0090286]; mitotic spindle organization [GO:0007052]; nuclear envelope organization	identical protein binding [GO:0042802]; lamin binding [GO:0005521]; microtubule binding [GO:0008017]	condensed nuclear chromosome [GO:0000794]; endosome membrane [GO:0010008]; integral component of nuclear inner membrane [GO:0005639];	Component of SUN-protein-containing multivariate complexes also called LINC complexes which link the nucleoskeleton and cytoskeleton by providing versatile outer nuclear membrane attachment sites for cytoskeletal filaments. Specifically, SYNE2 and SUN2

		[GO:0006998]; nuclear matrix anchoring at nuclear membrane [GO:0090292]; nuclear migration [GO:0007097]; nuclear migration along microfilament [GO:0031022]; positive regulation of cell migration [GO:0030335]		LINC complex [GO:0034993]; nuclear chromosome, telomeric region [GO:0000784]; nuclear envelope [GO:0005635]; nuclear membrane [GO:0031965]	assemble in arrays of transmembrane actin-associated nuclear (TAN) lines which are bound to F-actin cables and couple the nucleus to retrograde actin flow during actin-dependent nuclear movement. Required for interkinetic nuclear migration (INM) and essential for nucleokinesis and centrosome-nucleus coupling during radial neuronal migration in the cerebral cortex and during glial migration. Anchors chromosome mo
CNN2	cytoskeleton organization	actomyosin structure organization [GO:0031032]; cellular response to mechanical stimulus [GO:0071260]; cytoskeleton organization [GO:0007010]; regulation of actin filament-based process [GO:0032970]	actin binding [GO:0003779]	cell-cell junction [GO:0005911]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; membrane [GO:0016020]; stress fiber [GO:0001725]	Thin filament-associated protein that is implicated in the regulation and modulation of smooth muscle contraction. It is capable of binding to actin, calmodulin, troponin C and tropomyosin. The interaction of calponin with actin inhibits the actomyosin Mg-ATPase activity.
VIM	cytoskeleton organization	astrocyte development [GO:0014002]; Bergmann glial cell differentiation [GO:0060020]; intermediate filament organization [GO:0045109]; lens fiber cell development [GO:0070307]; movement of cell or subcellular component [GO:0006928]; muscle filament sliding [GO:0030049]; negative regulation of neuron projection development [GO:0010977]; positive regulation of gene expression [GO:0010628]; SMAD protein signal transduction	double-stranded RNA binding [GO:0003725]; glycoprotein binding [GO:0001948]; identical protein binding [GO:0042802]; keratin filament binding [GO:1990254]; protein C-terminus binding [GO:0008022]; scaffold protein binding [GO:0097110]; structural constituent of cytoskeleton [GO:0005200	cell leading edge [GO:0031252]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; intermediate filament [GO:0005882]; intermediate filament cytoskeleton [GO:0045111]; neuron projection [GO:0043005]; peroxisome [GO:0005777]; plasma	Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells. Vimentin is attached to the nucleus, endoplasmic reticulum, and mitochondria, either laterally or terminally. {ECO:0000269|PubMed:21746880}.; FUNCTION: Involved with LARP6 in the stabilization of type I collagen mRNAs for CO1A1 and CO1A2. {ECO:0000269|PubMed:21746880}.

		[GO:0060395]; viral process [GO:0016032]	]; structural constituent of eye lens [GO:0005212]	membrane [GO:0005886]	
LMCD1	extracellular matrix	cellular protein metabolic process [GO:0044267]; mitophagy in response to mitochondrial depolarization [GO:0098779]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; positive regulation of calcineurin-NFAT signaling cascade [GO:0070886]; positive regulation of defense response to virus by host [GO:0002230]; regulation of cardiac muscle hypertrophy [GO:0010611]; transcription, DNA-templated [GO:0006351]; xenophagy [GO:0098792]	transcription corepressor activity [GO:0003714]; zinc ion binding [GO:0008270]	cytoplasm [GO:0005737]; extracellular space [GO:0005615]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	Transcriptional cofactor that restricts GATA6 function by inhibiting DNA-binding, resulting in repression of GATA6 transcriptional activation of downstream target genes. Represses GATA6-mediated trans activation of lung- and cardiac tissue-specific promoters. Inhibits DNA-binding by GATA4 and GATA1 to the cTNC promoter (By similarity). Plays a critical role in the development of cardiac hypertrophy via activation of calcineurin/nuclear factor of activated T-cells signaling pathway. {ECO:0000250, ECO:0000269|PubMed:20026769}.
SPARCL1	extracellular matrix	signal transduction [GO:0007165]	calcium ion binding [GO:0005509]	extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	
FBLN1	extracellular matrix	blood coagulation, fibrin clot formation [GO:0072378]; embryo implantation [GO:0007566]; extracellular matrix organization [GO:0030198]; negative regulation of cell adhesion [GO:0007162]; negative regulation of cell motility [GO:2000146]; negative regulation of ERK1 and ERK2	calcium ion binding [GO:0005509]; extracellular matrix structural constituent [GO:0005201]; fibrinogen binding [GO:0070051]; fibronectin binding [GO:0001968]; identical	basement membrane [GO:0005604]; elastic fiber [GO:0071953]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular	Incorporated into fibronectin-containing matrix fibers. May play a role in cell adhesion and migration along protein fibers within the extracellular matrix (ECM). Could be important for certain developmental processes and contribute to the supramolecular organization of ECM architecture, in particular to those of basement membranes. Has been

		cascade [GO:0070373]; negative regulation of protein phosphorylation [GO:0001933]; negative regulation of stem cell proliferation [GO:2000647]; negative regulation of substrate adhesion-dependent cell spreading [GO:1900025]; negative regulation of transformation of host cell by virus [GO:1904188]; negative regulation of transforming growth factor-beta secretion [GO:2001202]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of gene expression [GO:0010628]; positive regulation of substrate-dependent cell migration, cell attachment to substrate [GO:1904237]; viral process [GO:0016032]	protein binding [GO:0042802]; integrin binding [GO:0005178]; peptidase activator activity [GO:0016504]; protein complex binding [GO:0032403]; protein C-terminus binding [GO:0008022]	matrix [GO:0005578]	implicated in a role in cellular transformation and tumor invasion, it appears to be a tumor suppressor. May play a role in haemostasis and thrombosis owing to its ability to bind fibrinogen and incorporate into clots. Could play a significant role in modulating the neurotrophic activities of APP, particularly soluble APP.
TPSAB1	extracellular matrix	defense response [GO:0006952]; extracellular matrix disassembly [GO:0022617]	serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	extracellular region [GO:0005576]; extracellular space [GO:0005615]	Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type. May play a role in innate immunity. Isoform 2 cleaves large substrates, such as fibronectin, more efficiently than isoform 1, but seems less efficient toward small substrates (PubMed:18854315). {ECO:0000250, ECO:0000250|UniProtKB:P21845, ECO:0000269|PubMed:18854315}.

F2	extracellular matrix	acute-phase response [GO:0006953]; blood coagulation [GO:0007596]; blood coagulation, intrinsic pathway [GO:0007597]; cell surface receptor signaling pathway [GO:0007166]; cellular protein metabolic process [GO:0044267]; cellular response to mechanical stimulus [GO:0071260]; ER to Golgi vesicle-mediated transport [GO:0006888]; fibrinolysis [GO:0042730]; leukocyte migration [GO:0050900]; multicellular organism development [GO:0007275]; negative regulation of astrocyte differentiation [GO:0048712]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of platelet activation [GO:0010544]; negative regulation of proteolysis [GO:0045861]; peptidyl-glutamic acid carboxylation [GO:0017187]; platelet activation [GO:0030168]; positive regulation of blood coagulation [GO:0030194]; positive regulation of cell growth [GO:0030307]; positive regulation of cell proliferation [GO:0008284]; positive regulation of collagen biosynthetic process [GO:0032967]; positive regulation of phosphatidylinositol	calcium ion binding [GO:0005509]; growth factor activity [GO:0008083]; receptor binding [GO:0005102]; serine-type endopeptidase activity [GO:0004252]; thrombospondin receptor activity [GO:0070053]	blood microparticle [GO:0072562]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi lumen [GO:0005796]; plasma membrane [GO:0005886]	Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombomodulin, protein C. Functions in blood homeostasis, inflammation and wound healing. {ECO:0000269|PubMed:2856554}.

		3-kinase signaling [GO:0014068]; positive regulation of phospholipase C-activating G-protein coupled receptor signaling pathway [GO:1900738]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of reactive oxygen species metabolic process [GO:2000379]; positive regulation of release of sequestered calcium ion into cytosol [GO:0051281]; proteolysis [GO:0006508]; regulation of blood coagulation [GO:0030193]; regulation of cell shape [GO:0008360]; regulation of cytosolic calcium ion concentration [GO:0051480]; regulation of gene expression [GO:0010468]; response to inactivity [GO:0014854]; response to wounding [GO:0009611]; signal peptide processing [GO:0006465]			
SERPIND1	extracellular matrix	bioluminescence [GO:0008218]; blood coagulation [GO:0007596]; chemotaxis [GO:0006935]	endopeptidase inhibitor activity [GO:0004866]; heparin binding [GO:0008201]; serine-type endopeptidase inhibitor activity [GO:0004867]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	Thrombin inhibitor activated by the glycosaminoglycans, heparin or dermatan sulfate. In the presence of the latter, HC-II becomes the predominant thrombin inhibitor in place of antithrombin III (AT-III). Also inhibits chymotrypsin, but in a glycosaminoglycan-independent manner. {ECO:0000269|PubMed:1939083}.; FUNCTION:

					Peptides at the N-terminal of HC-II have chemotactic activity for both monocytes and neutrophils. {ECO:0000269|PubMed:1939083}.
MFGE8	extracellular matrix	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cellular protein metabolic process [GO:0044267]; phagocytosis, engulfment [GO:0006911]; phagocytosis, recognition [GO:0006910]; positive regulation of apoptotic cell clearance [GO:2000427]; positive regulation of cell proliferation [GO:0008284]; response to estrogen [GO:0043627]; single fertilization [GO:0007338]; viral process [GO:0016032]	phosphatidylethanolamine binding [GO:0008429]; phosphatidylserine binding [GO:0001786]	external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; extrinsic component of plasma membrane [GO:0019897]; membrane [GO:0016020]	Plays an important role in the maintenance of intestinal epithelial homeostasis and the promotion of mucosal healing. Promotes VEGF-dependent neovascularization (By similarity). Contributes to phagocytic removal of apoptotic cells in many tissues. Specific ligand for the alpha-v/beta-3 and alpha-v/beta-5 receptors. Also binds to phosphatidylserine-enriched cell surfaces in a receptor-independent manner. Zona pellucida-binding protein which may play a role in gamete interaction. Binds specifically to rotavirus and inhibits its replication. {ECO:0000250, ECO:0000269|PubMed:19204935}.; FUNCTION: Medin is the main constituent of aortic medial amyloid. {ECO:0000269
COL6A3	extracellular matrix	cell adhesion [GO:0007155]; collagen catabolic process [GO:0030574]; extracellular matrix organization [GO:0030198]; muscle organ development [GO:0007517]	serine-type endopeptidase inhibitor activity [GO:0004867]	collagen type VI trimer [GO:0005589]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561];	Collagen VI acts as a cell-binding protein.

				proteinaceous extracellular matrix [GO:0005578]; sarcolemma [GO:0042383]	
VTN	extracellular matrix	cell adhesion [GO:0007155]; cell adhesion mediated by integrin [GO:0033627]; cell-matrix adhesion [GO:0007160]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; immune response [GO:0006955]; negative regulation of blood coagulation [GO:0030195]; negative regulation of endopeptidase activity [GO:0010951]; oligodendrocyte differentiation [GO:0048709]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of protein binding [GO:0032092]; positive regulation of receptor-mediated endocytosis [GO:0048260]; positive regulation of smooth muscle cell migration [GO:0014911]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; positive regulation of wound healing [GO:0090303]; regulation of	extracellular matrix binding [GO:0050840]; heparin binding [GO:0008201]; integrin binding [GO:0005178]; polysaccharide binding [GO:0030247]; scavenger receptor activity [GO:0005044]	alphav-beta3 integrin-vitronectin complex [GO:0071062]; blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	Vitronectin is a cell adhesion and spreading factor found in serum and tissues. Vitronectin interact with glycosaminoglycans and proteoglycans. Is recognized by certain members of the integrin family and serves as a cell-to-substrate adhesion molecule. Inhibitor of the membrane-damaging effect of the terminal cytolytic complement pathway.; FUNCTION: Somatomedin-B is a growth hormone-dependent serum factor with protease-inhibiting activity.

		complement activation [GO:0030449]; smooth muscle cell-matrix adhesion [GO:0061302]			
COL6A1	extracellular matrix	cell adhesion [GO:0007155]; cellular response to amino acid stimulus [GO:0071230]; collagen catabolic process [GO:0030574]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; osteoblast differentiation [GO:0001649]; protein heterotrimerization [GO:0070208]	platelet-derived growth factor binding [GO:0048407]	collagen type VI trimer [GO:0005589]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; lysosomal membrane [GO:0005765]; membrane [GO:0016020]; protein complex [GO:0043234]; sarcolemma [GO:0042383]	Collagen VI acts as a cell-binding protein.
ABI3BP	extracellular matrix	extracellular matrix organization [GO:0030198]; positive regulation of cell-substrate adhesion [GO:0010811]	heparin binding [GO:0008201]	extracellular space [GO:0005615]; interstitial matrix [GO:0005614]	
COL14A1	extracellular matrix	collagen fibril organization [GO:0030199]; extracellular matrix organization [GO:0030198]; single organismal cell-cell adhesion [GO:0016337]	collagen binding [GO:0005518]; extracellular matrix structural constituent [GO:0005201]; poly(A) RNA binding [GO:0044822]; protein binding, bridging [GO:0030674]	collagen trimer [GO:0005581]; collagen type XIV trimer [GO:0005596]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular	Plays an adhesive role by integrating collagen bundles. It is probably associated with the surface of interstitial collagen fibrils via COL1. The COL2 domain may then serve as a rigid arm which sticks out from the fibril and protrudes the large N-terminal globular domain into the extracellular space, where it might interact with other matrix molecules or cell surface receptors (By similarity). {ECO:0000250, ECO:0000269|PubMed:2187872}.

				matrix [GO:0005578]	
FN1	extracellular matrix	acute-phase response [GO:0006953]; angiogenesis [GO:0001525]; calcium-independent cell-matrix adhesion [GO:0007161]; cell activation [GO:0001775]; cell adhesion [GO:0007155]; cell-substrate junction assembly [GO:0007044]; cellular response to BMP stimulus [GO:0071773]; cellular response to glucose stimulus [GO:0071333]; cellular response to interleukin-1 [GO:0071347]; cellular response to lipopolysaccharide [GO:0071222]; cellular response to mercury ion [GO:0071288]; cellular response to platelet-derived growth factor stimulus [GO:0036120]; cellular response to prostaglandin E stimulus [GO:0071380]; cellular response to transforming growth factor beta stimulus [GO:0071560]; cellular response to vascular endothelial growth factor stimulus [GO:0035924]; endodermal cell differentiation [GO:0035987]; extracellular matrix disassembly [GO:0022617]; extracellular matrix organization [GO:0030198]; glial cell migration [GO:0008347];	collagen binding [GO:0005518]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; mercury ion binding [GO:0045340]; peptidase activator activity [GO:0016504]; protease binding [GO:0002020]	apical plasma membrane [GO:0016324]; basal lamina [GO:0005605]; blood microparticle [GO:0072562]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex [GO:0005577]; platelet alpha granule lumen [GO:0031093]	Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape. Involved in osteoblast compaction through the fibronectin fibrillogenesis cell-mediated matrix assembly process, essential for osteoblast mineralization. Participates in the regulation of type I collagen deposition by osteoblasts.; FUNCTION: Anastellin binds fibronectin and induces fibril formation. This fibronectin polymer, named superfibronectin, exhibits enhanced adhesive properties. Both anastellin and superfibronectin inhibit tumor g

		integrin activation [GO:0033622]; leukocyte migration [GO:0050900]; negative regulation of apoptotic process [GO:0043066]; negative regulation of transforming growth factor-beta secretion [GO:2001202]; peptide cross-linking [GO:0018149]; platelet degranulation [GO:0002576]; positive regulation of axon extension [GO:0045773]; positive regulation of cell proliferation [GO:0008284]; positive regulation of chemotaxis [GO:0050921]; positive regulation of fibroblast proliferation [GO:0048146]; positive regulation of gene expression [GO:0010628]; positive regulation of substrate-dependent cell migration, cell attachment to substrate [GO:1904237]; regulation of cell shape [GO:0008360]; regulation of ERK1 and ERK2 cascade [GO:0070372]; regulation of protein phosphorylation [GO:0001932]; response to glucocorticoid [GO:0051384]; response to ischemia [GO:0002931]; response to ozone [GO:0010193]; response to wounding [GO:0009611]; substrate adhesion-dependent cell			

		spreading [GO:0034446]; wound healing [GO:0042060]			
COL6A2	extracellular matrix	cell adhesion [GO:0007155]; collagen catabolic process [GO:0030574]; extracellular matrix organization [GO:0030198]; protein heterotrimerization [GO:0070208]; response to glucose [GO:0009749]		collagen trimer [GO:0005581]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; proteinaceous extracellular matrix [GO:0005578]; protein complex [GO:0043234]; sarcolemma [GO:0042383]	Collagen VI acts as a cell-binding protein.
APOE	extracellular matrix	AMPA glutamate receptor clustering [GO:0097113]; artery morphogenesis [GO:0048844]; cellular calcium ion homeostasis [GO:0006874]; cGMP-mediated signaling [GO:0019934]; cholesterol catabolic process [GO:0006707]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; chylomicron remnant clearance [GO:0034382]; cytoskeleton	antioxidant activity [GO:0016209]; beta-amyloid binding [GO:0001540]; cholesterol binding [GO:0015485]; cholesterol transporter activity [GO:0017127]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; lipid binding [GO:0008289]; lipid transporter	blood microparticle [GO:0072562]; chylomicron [GO:0042627]; cytoplasm [GO:0005737]; dendrite [GO:0030425]; early endosome [GO:0005769]; endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region	Mediates the binding, internalization, and catabolism of lipoprotein particles. It can serve as a ligand for the LDL (apo B/E) receptor and for the specific apo-E receptor (chylomicron remnant) of hepatic tissues. {ECO:0000303|PubMed:3283935}.

		organization [GO:0007010]; fatty acid homeostasis [GO:0055089]; G-protein coupled receptor signaling pathway [GO:0007186]; high-density lipoprotein particle assembly [GO:0034380]; high-density lipoprotein particle clearance [GO:0034384]; high-density lipoprotein particle remodeling [GO:0034375]; intracellular transport [GO:0046907]; lipoprotein biosynthetic process [GO:0042158]; lipoprotein catabolic process [GO:0042159]; lipoprotein metabolic process [GO:0042157]; long-chain fatty acid transport [GO:0015909]; low-density lipoprotein particle remodeling [GO:0034374]; maintenance of location in cell [GO:0051651]; negative regulation of beta-amyloid formation [GO:1902430]; negative regulation of blood coagulation [GO:0030195]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of cholesterol biosynthetic process [GO:0045541]; negative regulation of cholesterol efflux [GO:0090370];	activity [GO:0005319]; lipoprotein particle binding [GO:0071813]; low-density lipoprotein particle receptor binding [GO:0050750]; metal chelating activity [GO:0046911]; phosphatidylcholine-sterol O-acyltransferase activator activity [GO:0060228]; phospholipid binding [GO:0005543]; protein homodimerization activity [GO:0042803]; tau protein binding [GO:0048156]; very-low-density lipoprotein particle receptor binding [GO:0070326]	[GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; Golgi apparatus [GO:0005794]; high-density lipoprotein particle [GO:0034364]; intermediate-density lipoprotein particle [GO:0034363]; low-density lipoprotein particle [GO:0034362]; membrane [GO:0016020]; neuronal cell body [GO:0043025]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	

		negative regulation of dendritic spine development [GO:0061000]; negative regulation of dendritic spine maintenance [GO:1902951]; negative regulation of endothelial cell proliferation [GO:0001937]; negative regulation of inflammatory response [GO:0050728]; negative regulation of lipid biosynthetic process [GO:0051055]; negative regulation of lipid transport across blood brain barrier [GO:1903001]; negative regulation of MAP kinase activity [GO:0043407]; negative regulation of neuron apoptotic process [GO:0043524]; negative regulation of neuron death [GO:1901215]; negative regulation of phospholipid efflux [GO:1902999]; negative regulation of platelet activation [GO:0010544]; negative regulation of postsynaptic membrane organization [GO:1901627]; negative regulation of presynaptic membrane organization [GO:1901630]; neuron projection regeneration [GO:0031102]; nitric oxide mediated signal transduction [GO:0007263]; NMDA glutamate			

		receptor clustering [GO:0097114]; phospholipid efflux [GO:0033700]; positive regulation by host of viral process [GO:0044794]; positive regulation of beta-amyloid formation [GO:1902004]; positive regulation of cGMP biosynthetic process [GO:0030828]; positive regulation of cholesterol efflux [GO:0010875]; positive regulation of cholesterol esterification [GO:0010873]; positive regulation of dendritic spine development [GO:0060999]; positive regulation of dendritic spine maintenance [GO:1902952]; positive regulation of lipid biosynthetic process [GO:0046889]; positive regulation of lipid transport across blood brain barrier [GO:1903002]; positive regulation of low-density lipoprotein particle receptor catabolic process [GO:0032805]; positive regulation of membrane protein ectodomain proteolysis [GO:0051044]; positive regulation of neurofibrillary tangle assembly [GO:1902998]; positive regulation of neuron death [GO:1901216]; positive regulation of nitric-oxide synthase activity			

		[GO:0051000]; positive regulation of phospholipid efflux [GO:1902995]; positive regulation of postsynaptic membrane organization [GO:1901628]; positive regulation of presynaptic membrane organization [GO:1901631]; protein import [GO:0017038]; receptor-mediated endocytosis [GO:0006898]; regulation of axon extension [GO:0030516]; regulation of beta-amyloid clearance [GO:1900221]; regulation of Cdc42 protein signal transduction [GO:0032489]; regulation of gene expression [GO:0010468]; regulation of neuronal synaptic plasticity [GO:0048168]; regulation of neuron death [GO:1901214]; regulation of tau-protein kinase activity [GO:1902947]; response to dietary excess [GO:0002021]; response to reactive oxygen species [GO:0000302]; retinoid metabolic process [GO:0001523]; reverse cholesterol transport [GO:0043691]; synaptic transmission, cholinergic [GO:0007271]; triglyceride catabolic process			

		[GO:0019433]; triglyceride metabolic process [GO:0006641]; vasodilation [GO:0042311]; very-low-density lipoprotein particle clearance [GO:0034447]; very-low-density lipoprotein particle remodeling [GO:0034372]; virion assembly [GO:0019068]			
AEBP1	extracellular matrix	muscle organ development [GO:0007517]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; peptide metabolic process [GO:0006518]; protein processing [GO:0016485]; skeletal system development [GO:0001501]; transcription, DNA-templated [GO:0006351]	carboxypeptidase activity [GO:0004180]; metallocarboxypeptidase activity [GO:0004181]; RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977]; serine-type carboxypeptidase activity [GO:0004185]; transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding [GO:0001227]; transcription corepressor activity [GO:0003714]; transcription factor activity, sequence-specific DNA binding	cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; nucleus [GO:0005634]	May positively regulate MAP-kinase activity in adipocytes, leading to enhanced adipocyte proliferation and reduced adipocyte differentiation. May also positively regulate NF-kappa-B activity in macrophages by promoting the phosphorylation and subsequent degradation of I-kappa-B-alpha (NFKBIA), leading to enhanced macrophage inflammatory responsiveness. Can act as a transcriptional repressor. {ECO:0000250}.

			[GO:0003700]; zinc ion binding [GO:0008270]		
TGFBI	extracellular matrix	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cell proliferation [GO:0008283]; cellular protein metabolic process [GO:0044267]; chondrocyte differentiation [GO:0002062]; extracellular matrix organization [GO:0030198]; negative regulation of cell adhesion [GO:0007162]; response to stimulus [GO:0050896]; visual perception [GO:0007601]	collagen binding [GO:0005518]; extracellular matrix binding [GO:0050840]; integrin binding [GO:0005178]	basement membrane [GO:0005604]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]; proteinaceous extracellular matrix [GO:0005578]; trans-Golgi network [GO:0005802]	Plays a role in cell adhesion (PubMed:8024701). May play a role in cell-collagen interactions (By similarity). {ECO:0000250|UniProtKB:O11780, ECO:0000269|PubMed:8024701}.
AHSG	extracellular matrix	acute-phase response [GO:0006953]; negative regulation of biomineral tissue development [GO:0070168]; negative regulation of bone mineralization [GO:0030502]; negative regulation of insulin receptor signaling pathway [GO:0046627]; ossification [GO:0001503]; pinocytosis [GO:0006907]; platelet degranulation [GO:0002576]; positive regulation of phagocytosis [GO:0050766]; regulation of bone mineralization [GO:0030500]; regulation of inflammatory response [GO:0050727]; skeletal system	cysteine-type endopeptidase inhibitor activity [GO:0004869]; endopeptidase inhibitor activity [GO:0004866]; kinase inhibitor activity [GO:0019210]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	Promotes endocytosis, possesses opsonic properties and influences the mineral phase of bone. Shows affinity for calcium and barium ions.

		development [GO:0001501]			
THBS1	extracellular matrix	activation of MAPK activity [GO:0000187]; behavioral response to pain [GO:0048266]; cell adhesion [GO:0007155]; cell cycle arrest [GO:0007050]; cell migration [GO:0016477]; cellular response to heat [GO:0034605]; chronic inflammatory response [GO:0002544]; engulfment of apoptotic cell [GO:0043652]; extracellular matrix organization [GO:0030198]; immune response [GO:0006955]; inflammatory response [GO:0006954]; negative regulation of angiogenesis [GO:0016525]; negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II [GO:0002581]; negative regulation of apoptotic process [GO:0043066]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of cell-matrix adhesion [GO:0001953]; negative regulation of cGMP-mediated signaling [GO:0010754]; negative regulation of cysteine-type	calcium ion binding [GO:0005509]; collagen V binding [GO:0070052]; fibrinogen binding [GO:0070051]; fibroblast growth factor binding [GO:0017134]; fibronectin binding [GO:0001968]; glycoprotein binding [GO:0001948]; heparin binding [GO:0008201]; identical protein binding [GO:0042802]; integrin binding [GO:0005178]; laminin binding [GO:0043236]; low-density lipoprotein particle binding [GO:0030169]; phosphatidylserine binding [GO:0001786]; proteoglycan binding [GO:0043394]; transforming growth factor beta binding [GO:0050431]	cell surface [GO:0009986]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex [GO:0005577]; platelet alpha granule [GO:0031091]; platelet alpha granule lumen [GO:0031093]; sarcoplasmic reticulum [GO:0016529]; secretory granule [GO:0030141]	Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Binds heparin. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp (By similarity). Ligand for CD36 mediating antiangiogenic properties. Plays a role in ER stress response, via its interaction with the activating transcription factor 6 alpha (ATF6) which produces adaptive ER stress response factors (By similarity). {ECO:0000250, ECO:0000269|PubMed:11134179, ECO:0000269|PubMed:15014436}.

		endopeptidase activity involved in apoptotic process [GO:0043154]; negative regulation of dendritic cell antigen processing and presentation [GO:0002605]; negative regulation of endothelial cell chemotaxis [GO:2001027]; negative regulation of endothelial cell migration [GO:0010596]; negative regulation of endothelial cell proliferation [GO:0001937]; negative regulation of extrinsic apoptotic signaling pathway [GO:2001237]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of fibroblast growth factor receptor signaling pathway [GO:0040037]; negative regulation of focal adhesion assembly [GO:0051895]; negative regulation of interleukin-12 production [GO:0032695]; negative regulation of nitric oxide mediated signal transduction [GO:0010751]; negative regulation of plasma membrane long-chain fatty acid transport [GO:0010748]; negative regulation of plasminogen activation [GO:0010757]; peptide cross-linking [GO:0018149]; platelet degranulation [GO:0002576];			

		positive regulation of angiogenesis [GO:0045766]; positive regulation of blood coagulation [GO:0030194]; positive regulation of blood vessel endothelial cell migration [GO:0043536]; positive regulation of cell migration [GO:0030335]; positive regulation of chemotaxis [GO:0050921]; positive regulation of endothelial cell apoptotic process [GO:2000353]; positive regulation of endothelial cell migration [GO:0010595]; positive regulation of extrinsic apoptotic signaling pathway via death domain receptors [GO:1902043]; positive regulation of fibroblast migration [GO:0010763]; positive regulation of macrophage activation [GO:0043032]; positive regulation of macrophage chemotaxis [GO:0010759]; positive regulation of phosphorylation [GO:0042327]; positive regulation of protein kinase B signaling [GO:0051897]; positive regulation of reactive oxygen species metabolic process [GO:2000379]; positive regulation of transforming growth factor beta1 production [GO:0032914]; positive regulation of			

		transforming growth factor beta receptor signaling pathway [GO:0030511]; positive regulation of translation [GO:0045727]; positive regulation of tumor necrosis factor biosynthetic process [GO:0042535]; protein O-linked fucosylation [GO:0036066]; regulation of cGMP metabolic process [GO:0030823]; response to calcium ion [GO:0051592]; response to drug [GO:0042493]; response to endoplasmic reticulum stress [GO:0034976]; response to glucose [GO:0009749]; response to hypoxia [GO:0001666]; response to magnesium ion [GO:0032026]; response to progesterone [GO:0032570]; response to unfolded protein [GO:0006986]; sprouting angiogenesis [GO:0002040]			
CTSG	extracellular matrix	angiotensin maturation [GO:0002003]; cellular protein metabolic process [GO:0044267]; defense response to fungus [GO:0050832]; extracellular matrix disassembly [GO:0022617]; immune response [GO:0006955]; negative regulation of growth of symbiont in host [GO:0044130]; neutrophil mediated	heparin binding [GO:0008201]; peptidase activity [GO:0008233]; serine-type endopeptidase activity [GO:0004252]	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; secretory granule [GO:0030141]	Serine protease with trypsin- and chymotrypsin-like specificity. Cleaves complement C3. Has antibacterial activity against the Gram-negative bacterium P.aeruginosa, antibacterial activity is inhibited by LPS from P.aeruginosa, Z-Gly-Leu-Phe-CH2Cl and phenylmethylsulfonyl fluoride. {ECO:0000269|PubMed:1861080, ECO:0000269|PubMed:1937776,

		killing of gram-positive bacterium [GO:0070946]; positive regulation of immune response [GO:0050778]; protein phosphorylation [GO:0006468]; protein processing [GO:0016485]; proteolysis [GO:0006508]; response to lipopolysaccharide [GO:0032496]			ECO:0000269|PubMed:8194606}.
LUM	extracellular matrix	cartilage development [GO:0051216]; collagen fibril organization [GO:0030199]; extracellular matrix organization [GO:0030198]; keratan sulfate biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of transforming growth factor beta1 production [GO:0032914]; response to growth factor [GO:0070848]; response to organic cyclic compound [GO:0014070]; visual perception [GO:0007601]	collagen binding [GO:0005518]; extracellular matrix structural constituent [GO:0005201]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; fibrillar collagen trimer [GO:0005583]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix [GO:0005578]	
LPL	extracellular matrix	cholesterol homeostasis [GO:0042632]; chylomicron remodeling [GO:0034371]; fatty acid biosynthetic process [GO:0006633]; lipoprotein metabolic process	apolipoprotein binding [GO:0034185]; heparin binding [GO:0008201]; lipoprotein lipase activity [GO:0004465]; phospholipase	anchored component of membrane [GO:0031225]; cell surface [GO:0009986]; chylomicron [GO:0042627]; extracellular exosome [GO:0070062];	The primary function of this lipase is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (VLDL). Binding to heparin sulfate proteogylcans at the cell surface is vital to the function. The

		[GO:0042157]; phospholipid metabolic process [GO:0006644]; positive regulation of chemokine secretion [GO:0090197]; positive regulation of cholesterol storage [GO:0010886]; positive regulation of inflammatory response [GO:0050729]; positive regulation of macrophage derived foam cell differentiation [GO:0010744]; positive regulation of sequestering of triglyceride [GO:0010890]; response to cold [GO:0009409]; response to drug [GO:0042493]; response to glucose [GO:0009749]; retinoid metabolic process [GO:0001523]; triglyceride biosynthetic process [GO:0019432]; triglyceride catabolic process [GO:0019433]; triglyceride homeostasis [GO:0070328]; triglyceride metabolic process [GO:0006641]; very-low-density lipoprotein particle remodeling [GO:0034372]	activity [GO:0004620]; receptor binding [GO:0005102]; triglyceride binding [GO:0017129]; triglyceride lipase activity [GO:0004806]	extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	apolipoprotein, APOC2, acts as a coactivator of LPL activity in the presence of lipids on the luminal surface of vascular endothelium (By similarity). {ECO:0000250}.
VCAN	extracellular matrix	cell adhesion [GO:0007155]; cell recognition [GO:0008037]; central nervous system development [GO:0007417]; chondroitin sulfate biosynthetic process [GO:0030206]; chondroitin sulfate catabolic process	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; extracellular matrix structural constituent	extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi lumen [GO:0005796]; intracellular	May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.

		[GO:0030207]; dermatan sulfate biosynthetic process [GO:0030208]; extracellular matrix organization [GO:0030198]; glial cell migration [GO:0008347]; glycosaminoglycan metabolic process [GO:0030203]; multicellular organism development [GO:0007275]; osteoblast differentiation [GO:0001649]; skeletal system development [GO:0001501]	[GO:0005201]; glycosaminoglycan binding [GO:0005539]; hyaluronic acid binding [GO:0005540]	membrane-bounded organelle [GO:0043231]; lysosomal lumen [GO:0043202]; membrane [GO:0016020]; proteinaceous extracellular matrix [GO:0005578]	
PRELP	extracellular matrix	cell aging [GO:0007569]; keratan sulfate biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; skeletal system development [GO:0001501]	extracellular matrix structural constituent [GO:0005201]; heparin binding [GO:0008201]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix [GO:0005578]	May anchor basement membranes to the underlying connective tissue. {ECO:0000250}.
LTBP2	extracellular matrix	extracellular fibril organization [GO:0043206]; protein secretion [GO:0009306]; protein targeting [GO:0006605]; transforming growth factor beta receptor signaling pathway [GO:0007179]	calcium ion binding [GO:0005509]; heparin binding [GO:0008201]	extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; intracellular [GO:0005622]; proteinaceous extracellular matrix [GO:0005578]	May play an integral structural role in elastic-fiber architectural organization and/or assembly.
APOH	extracellular matrix	aging [GO:0007568]; blood coagulation, intrinsic pathway [GO:0007597]; negative regulation	glycoprotein binding [GO:0001948]; heparin binding	cell surface [GO:0009986]; chylomicron [GO:0042627]; extracellular	Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May

		of angiogenesis [GO:0016525]; negative regulation of blood coagulation [GO:0030195]; negative regulation of endothelial cell migration [GO:0010596]; negative regulation of endothelial cell proliferation [GO:0001937]; negative regulation of fibrinolysis [GO:0051918]; negative regulation of myeloid cell apoptotic process [GO:0033033]; negative regulation of respiratory burst [GO:0060268]; negative regulation of smooth muscle cell apoptotic process [GO:0034392]; organ regeneration [GO:0031100]; plasminogen activation [GO:0031639]; platelet degranulation [GO:0002576]; positive regulation of blood coagulation [GO:0030194]; positive regulation of lipoprotein lipase activity [GO:0051006]; positive regulation of triglyceride catabolic process [GO:0010898]; regulation of fibrinolysis [GO:0051917]; response to triglyceride [GO:0034014]; triglyceride metabolic process [GO:0006641]; triglyceride transport [GO:0034197]	[GO:0008201]; identical protein binding [GO:0042802]; lipid binding [GO:0008289]; lipoprotein lipase activator activity [GO:0060230]; phospholipid binding [GO:0005543]	exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; plasma membrane [GO:0005886]; platelet dense granule lumen [GO:0031089]; very-low-density lipoprotein particle [GO:0034361]	prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.
OGN	extracellular matrix	axonogenesis [GO:0007409]; keratan sulfate	heparin binding	extracellular exosome [GO:0070062];	Induces bone formation in conjunction with TGF-beta-1 or TGF-beta-2.

		biosynthetic process [GO:0018146]; keratan sulfate catabolic process [GO:0042340]; negative regulation of smooth muscle cell proliferation [GO:0048662]	[GO:0008201]	extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; Golgi lumen [GO:0005796]; lysosomal lumen [GO:0043202]; proteinaceous extracellular matrix [GO:0005578]	
HMGB1	immune response	activation of innate immune response [GO:0002218]; apoptotic cell clearance [GO:0043277]; apoptotic DNA fragmentation [GO:0006309]; autophagy [GO:0006914]; base-excision repair [GO:0006284]; chromatin assembly [GO:0031497]; dendritic cell chemotaxis [GO:0002407]; DNA geometric change [GO:0032392]; DNA ligation involved in DNA repair [GO:0051103]; DNA recombination [GO:0006310]; DNA topological change [GO:0006265]; endothelial cell chemotaxis [GO:0035767]; endothelial cell proliferation [GO:0001935]; eye development [GO:0001654]; inflammatory response [GO:0006954]; inflammatory response to antigenic stimulus [GO:0002437];	bubble DNA binding [GO:0000405]; calcium-dependent protein kinase regulator activity [GO:0010858]; chemoattractant activity [GO:0042056]; C-X-C chemokine binding [GO:0019958]; cytokine activity [GO:0005125]; damaged DNA binding [GO:0003684]; DNA binding, bending [GO:0008301]; DNA polymerase binding [GO:0070182]; double-stranded DNA binding [GO:0003690]; double-stranded RNA binding [GO:0003725]; four-way junction DNA binding	cell surface [GO:0009986]; condensed chromosome [GO:0000793]; early endosome [GO:0005769]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	Multifunctional redox sensitive protein with various roles in different cellular compartments. In the nucleus is one of the major chromatin-associated non-histone proteins and acts as a DNA chaperone involved in replication, transcription, chromatin remodeling, V(D)J recombination, DNA repair and genome stability. Proposed to be an universal biosensor for nucleic acids. Promotes host inflammatory response to sterile and infectious signals and is involved in the coordination and integration of innate and adaptive immune responses. In the cytoplasm functions as sensor and/or chaperone for immunogenic nucleic acids implicating the activation of TLR9-mediated immu

		innate immune response [GO:0045087]; lung development [GO:0030324]; macrophage activation involved in immune response [GO:0002281]; myeloid dendritic cell activation [GO:0001773]; negative regulation of apoptotic cell clearance [GO:2000426]; negative regulation of blood vessel endothelial cell migration [GO:0043537]; negative regulation of CD4-positive, alpha-beta T cell differentiation [GO:0043371]; negative regulation of interferon-gamma production [GO:0032689]; negative regulation of RNA polymerase II transcriptional preinitiation complex assembly [GO:0017055]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; neuron projection development [GO:0031175]; neutrophil clearance [GO:0097350]; plasmacytoid dendritic cell activation [GO:0002270]; positive regulation of activated T cell proliferation [GO:0042104]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cysteine-type endopeptidase	[GO:0000400]; lipopolysaccharide binding [GO:0001530]; lyase activity [GO:0016829]; phosphatidylserine binding [GO:0001786]; poly(A) RNA binding [GO:0044822]; protein kinase activator activity [GO:0030295]; RAGE receptor binding [GO:0050786]; repressing transcription factor binding [GO:0070491]; single-stranded DNA binding [GO:0003697]; single-stranded RNA binding [GO:0003727]; supercoiled DNA binding [GO:0097100]; transcription factor activity, sequence-specific DNA binding [GO:0003700]; transcription factor binding [GO:0008134]		

		activity involved in apoptotic process [GO:0043280]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; positive regulation of dendritic cell differentiation [GO:2001200]; positive regulation of DNA binding [GO:0043388]; positive regulation of DNA ligation [GO:0051106]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of glycogen catabolic process [GO:0045819]; positive regulation of interferon-alpha production [GO:0032727]; positive regulation of interferon-beta production [GO:0032728]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-12 production [GO:0032735]; positive regulation of interleukin-1 beta secretion [GO:0050718]; positive regulation of interleukin-1 secretion [GO:0050716]; positive regulation of interleukin-6 secretion [GO:2000778]; positive regulation of JNK cascade [GO:0046330]; positive regulation of MAPK cascade [GO:0043410]; positive regulation of			

		mismatch repair [GO:0032425]; positive regulation of monocyte chemotaxis [GO:0090026]; positive regulation of myeloid cell differentiation [GO:0045639]; positive regulation of NIK/NF-kappaB signaling [GO:1901224]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of toll-like receptor 2 signaling pathway [GO:0034137]; positive regulation of toll-like receptor 4 signaling pathway [GO:0034145]; positive regulation of toll-like receptor 9 signaling pathway [GO:0034165]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of tumor necrosis factor production [GO:0032760]; positive regulation of wound healing [GO:0090303]; regulation of autophagy [GO:0010506]; regulation of nucleotide-excision repair [GO:2000819]; regulation of restriction endodeoxyribonuclease activity [GO:0032072]; regulation of T cell mediated immune response to tumor cell [GO:0002840]; regulation of tolerance induction			

		[GO:0002643]; regulation of transcription from RNA polymerase II promoter [GO:0006357]; response to glucocorticoid [GO:0051384]; T-helper 1 cell activation [GO:0035711]; T-helper 1 cell differentiation [GO:0045063]; tumor necrosis factor secretion [GO:1990774]; V(D)J recombination [GO:0033151]			
ANXA7	immune response	autophagy [GO:0006914]; cell proliferation [GO:0008283]; cellular calcium ion homeostasis [GO:0006874]; cellular water homeostasis [GO:0009992]; epithelial cell differentiation [GO:0030855]; hemostasis [GO:0007599]; membrane fusion [GO:0061025]; negative regulation of gene expression [GO:0010629]; regulation of cell shape [GO:0008360]; response to calcium ion [GO:0051592]; response to organic cyclic compound [GO:0014070]; response to salt stress [GO:0009651]; social behavior [GO:0035176]	calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; integrin binding [GO:0005178]; poly(A) RNA binding [GO:0044822]	cytosol [GO:0005829]; endoplasmic reticulum membrane [GO:0005789]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; nuclear envelope [GO:0005635]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.
ANXA11	immune response	cell cycle [GO:0007049]; cell division [GO:0051301]; phagocytosis [GO:0006909]; response to calcium ion [GO:0051592]	calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein	azurophil granule [GO:0042582]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062];	Binds specifically to calcyclin in a calcium-dependent manner (By similarity). Required for midbody formation and completion of the terminal phase of cytokinesis. {ECO:0000250,

			binding [GO:0048306]; calcium ion binding [GO:0005509]; MHC class II protein complex binding [GO:0023026]; phosphatidylethanolamine binding [GO:0008429]; poly(A) RNA binding [GO:0044822]; S100 protein binding [GO:0044548]	melanosome [GO:0042470]; membrane [GO:0016020]; midbody [GO:0030496]; nuclear envelope [GO:0005635]; nucleoplasm [GO:0005654]; phagocytic vesicle [GO:0045335]; specific granule [GO:0042581]; spindle [GO:0005819]	ECO:0000269|PubMed:15197175}.
HSP90AA1	immune response	cardiac muscle cell apoptotic process [GO:0010659]; chaperone-mediated autophagy [GO:0061684]; chaperone-mediated protein complex assembly [GO:0051131]; ERBB2 signaling pathway [GO:0038128]; Fc-gamma receptor signaling pathway involved in phagocytosis [GO:0038096]; G2/M transition of mitotic cell cycle [GO:0000086]; mitochondrial transport [GO:0006839]; neuron migration [GO:0001764]; positive regulation of cardiac muscle contraction [GO:0060452]; positive regulation of cell size [GO:0045793]; positive regulation of lamellipodium assembly [GO:0010592];	ATPase activity [GO:0016887]; ATP binding [GO:0005524]; CTP binding [GO:0002135]; dATP binding [GO:0032564]; GTPase binding [GO:0051020]; GTP binding [GO:0005525]; histone deacetylase binding [GO:0042826]; identical protein binding [GO:0042802]; MHC class II protein complex binding [GO:0023026]; mRNA binding [GO:0003729]; nitric-oxide synthase regulator	apical plasma membrane [GO:0016324]; basolateral plasma membrane [GO:0016323]; brush border membrane [GO:0031526]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; endocytic vesicle lumen [GO:0071682]; extracellular exosome [GO:0070062]; extracellular matrix [GO:0031012]; extracellular region [GO:0005576]; lysosomal lumen [GO:0043202]; melanosome [GO:0042470]; membrane [GO:0016020]; myelin sheath [GO:0043209];	Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved for instance in cell cycle control and signal transduction. Undergoes a functional cycle that is linked to its ATPase activity. This cycle probably induces conformational changes in the client proteins, thereby causing their activation. Interacts dynamically with various co-chaperones that modulate its substrate recognition, ATPase cycle and chaperone function. Binds bacterial lipopolysaccharide (LPS) et mediates LPS-induced inflammatory response, including TNF secretion by monocytes. {ECO:0000269|PubMed:11274138, ECO:0000269|PubM

		positive regulation of nitric oxide biosynthetic process [GO:0045429]; positive regulation of protein import into nucleus, translocation [GO:0033160]; protein import into mitochondrial outer membrane [GO:0045040]; protein refolding [GO:0042026]; protein stabilization [GO:0050821]; protein unfolding [GO:0043335]; receptor-mediated endocytosis [GO:0006898]; regulation of cellular response to heat [GO:1900034]; regulation of nitric-oxide synthase activity [GO:0050999]; regulation of protein complex assembly [GO:0043254]; regulation of protein ubiquitination [GO:0031396]; response to antibiotic [GO:0046677]; response to cold [GO:0009409]; response to estrogen [GO:0043627]; response to heat [GO:0009408]; response to salt stress [GO:0009651]; response to unfolded protein [GO:0006986]; signal transduction [GO:0007165]; skeletal muscle contraction [GO:0003009]; vascular endothelial growth factor receptor signaling pathway [GO:0048010]	activity [GO:0030235]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; protein homodimerization activity [GO:0042803]; protein tyrosine kinase activity [GO:0004713]; TPR domain binding [GO:0030911]; UTP binding [GO:0002134]	neuronal cell body [GO:0043025]; neuron projection [GO:0043005]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; protein complex [GO:0043234]; ruffle membrane [GO:0032587]	

ANXA5	immune response	blood coagulation [GO:0007596]; cellular response to gonadotropin-releasing hormone [GO:0097211]; cellular response to lead ion [GO:0071284]; mitophagy in response to mitochondrial depolarization [GO:0098779]; negative regulation of apoptotic process [GO:0043066]; negative regulation of blood coagulation [GO:0030195]; negative regulation of prolactin secretion [GO:1902721]; positive regulation of apoptotic process [GO:0043065]; positive regulation of defense response to virus by host [GO:0002230]; protein homooligomerization [GO:0051260]; regulation of sperm motility [GO:1901317]; response to calcium ion [GO:0051592]; response to thyroid hormone [GO:0097066]; signal transduction [GO:0007165]; xenophagy [GO:0098792]	calcium-dependent phospholipid binding [GO:0005544]; calcium ion binding [GO:0005509]; calcium-transporting ATPase activity [GO:0005388]; peptide hormone binding [GO:0017046]; phospholipase inhibitor activity [GO:0004859]; phospholipid binding [GO:0005543]	axon terminus [GO:0043679]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; endothelial microparticle [GO:0072563]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925]; intercalated disc [GO:0014704]; intracellular [GO:0005622]; membrane [GO:0016020]; nucleus [GO:0005634]; perikaryon [GO:0043204]; sarcolemma [GO:0042383]; synaptic vesicle [GO:0008021]; Z disc [GO:0030018]	This protein is an anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade.
FGG	immune response	blood coagulation [GO:0007596]; blood coagulation, fibrin clot formation [GO:0072378]; cell-matrix adhesion [GO:0007160]; cellular protein complex assembly [GO:0043623]; extracellular matrix organization [GO:0030198]; fibrinolysis [GO:0042730];	cell adhesion molecule binding [GO:0050839]; metal ion binding [GO:0046872]; receptor binding [GO:0005102]; structural molecule activity [GO:0005198]	blood microparticle [GO:0072562]; cell cortex [GO:0005938]; cell surface [GO:0009986]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular	Together with fibrinogen alpha (FGA) and fibrinogen beta (FGB), polymerizes to form an insoluble fibrin matrix. Has a major function in hemostasis as one of the primary components of blood clots. In addition, functions during the early stages of wound repair to stabilize the lesion and guide cell migration during re-epithelialization. Was originally thought to

		negative regulation of endothelial cell apoptotic process [GO:2000352]; negative regulation of extrinsic apoptotic signaling pathway via death domain receptors [GO:1902042]; plasminogen activation [GO:0031639]; platelet aggregation [GO:0070527]; platelet degranulation [GO:0002576]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of exocytosis [GO:0045921]; positive regulation of heterotypic cell-cell adhesion [GO:0034116]; positive regulation of peptide hormone secretion [GO:0090277]; positive regulation of protein secretion [GO:0050714]; positive regulation of substrate adhesion-dependent cell spreading [GO:1900026]; positive regulation of vasoconstriction [GO:0045907]; protein polymerization [GO:0051258]; protein secretion [GO:0009306]; response to calcium ion [GO:0051592]; signal transduction [GO:0007165]		region [GO:0005576]; extracellular space [GO:0005615]; fibrinogen complex [GO:0005577]; plasma membrane [GO:0005886]; platelet alpha granule [GO:0031091]; platelet alpha granule lumen [GO:0031093]	be essential for platelet aggregation, based on in vitro studies using anticoagulated blood. However, subsequent studies have shown that it is not absolutely required for thrombus formation in vivo. Enhances expression of SELP in activated platelets via an ITGB3-dependent pathway. Maternal fibrinogen is
HYOU1	immune response	cellular response to hypoxia [GO:0071456]; ER to Golgi vesicle-mediated transport [GO:0006888]; IRE1-mediated	ATP binding [GO:0005524]; chaperone binding [GO:0051087]	endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum [GO:0005783]; endoplasmic	Has a pivotal role in cytoprotective cellular mechanisms triggered by oxygen deprivation. May play a role as a molecular chaperone and participate in protein folding.

		unfolded protein response [GO:0036498]; negative regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic signaling pathway [GO:1903382]; negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway [GO:1903298]; receptor-mediated endocytosis [GO:0006898]; response to endoplasmic reticulum stress [GO:0034976]; response to ischemia [GO:0002931]		reticulum chaperone complex [GO:0034663]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; focal adhesion [GO:0005925]; membrane [GO:0016020]; smooth endoplasmic reticulum [GO:0005790]	{ECO:0000269|PubMed:10037731}.
C3	immune response	blood coagulation [GO:0007596]; complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; fatty acid metabolic process [GO:0006631]; G-protein coupled receptor signaling pathway [GO:0007186]; immune response [GO:0006955]; inflammatory response [GO:0006954]; positive regulation of activation of membrane attack complex [GO:0001970]; positive regulation of angiogenesis [GO:0045766]; positive regulation of apoptotic cell clearance	C5L2 anaphylatoxin chemotactic receptor binding [GO:0031715]; cofactor binding [GO:0048037]; endopeptidase inhibitor activity [GO:0004866]; lipid binding [GO:0008289]; receptor binding [GO:0005102]; serine-type endopeptidase activity [GO:0004252]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	C3 plays a central role in the activation of the complement system. Its processing by C3 convertase is the central reaction in both classical and alternative complement pathways. After activation C3b can bind covalently, via its reactive thioester, to cell surface carbohydrates or immune aggregates.; FUNCTION: Derived from proteolytic degradation of complement C3, C3a anaphylatoxin is a mediator of local inflammatory process. In chronic inflammation, acts as a chemoattractant for neutrophils (By similarity). It induces the contraction of smooth muscle, increases vascular permeability and causes histamine release from mast cells and basophilic leukocytes. {ECO:

		[GO:2000427]; positive regulation of developmental growth [GO:0048639]; positive regulation of ERK1 and ERK2 cascade [GO:0070374]; positive regulation of glucose transport [GO:0010828]; positive regulation of G-protein coupled receptor protein signaling pathway [GO:0045745]; positive regulation of lipid storage [GO:0010884]; positive regulation of protein phosphorylation [GO:0001934]; positive regulation of type IIa hypersensitivity [GO:0001798]; positive regulation of vascular endothelial growth factor production [GO:0010575]; regulation of complement activation [GO:0030449]; regulation of immune response [GO:0050776]; regulation of triglyceride biosynthetic process [GO:0010866]; response to estradiol [GO:0032355]; response to glucocorticoid [GO:0051384]; response to magnesium ion [GO:0032026]; response to progesterone [GO:0032570]; signal transduction [GO:0007165]; tolerance induction [GO:0002507]			

C7	immune response	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; cytolysis [GO:0019835]; regulation of complement activation [GO:0030449]		extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; membrane attack complex [GO:0005579]	Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target cells. C7 serves as a membrane anchor.
C9	immune response	complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; hemolysis by symbiont of host erythrocytes [GO:0019836]; regulation of complement activation [GO:0030449]		blood microparticle [GO:0072562]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; integral component of plasma membrane [GO:0005887]; membrane attack complex [GO:0005579]; plasma membrane [GO:0005886]	Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target cells. C9 is the pore-forming subunit of the MAC.
G6PD	immune response	cellular response to oxidative stress [GO:0034599]; cholesterol biosynthetic process [GO:0006695]; erythrocyte maturation [GO:0043249]; glucose 6-phosphate metabolic process [GO:0051156]; glucose metabolic process [GO:0006006]; glutathione metabolic process [GO:0006749]; lipid metabolic process [GO:0006629]; NADPH	glucose-6-phosphate dehydrogenase activity [GO:0004345]; glucose binding [GO:0005536]; identical protein binding [GO:0042802]; NADP binding [GO:0050661]; protein homodimerization activity [GO:0042803]	centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; intracellular membrane-bounded organelle [GO:0043231]; membrane [GO:0016020]; microtubule	Catalyzes the rate-limiting step of the oxidative pentose-phosphate pathway, which represents a route for the dissimilation of carbohydrates besides glycolysis. The main function of this enzyme is to provide reducing power (NADPH) and pentose phosphates for fatty acid and nucleic acid synthesis. {ECO:0000269|PubMed:15858258, ECO:0000269|PubMed:24769394}.

		regeneration [GO:0006740]; NADP metabolic process [GO:0006739]; negative regulation of protein glutathionylation [GO:0010734]; oxidation-reduction process [GO:0055114]; pentose biosynthetic process [GO:0019322]; pentose-phosphate shunt [GO:0006098]; pentose-phosphate shunt, oxidative branch [GO:0009051]; regulation of neuron apoptotic process [GO:0043523]; response to ethanol [GO:0045471]; response to food [GO:0032094]; response to organic cyclic compound [GO:0014070]; ribose phosphate biosynthetic process [GO:0046390]; substantia nigra development [GO:0021762]		organizing center [GO:0005815]; nucleus [GO:0005634]	
SERPING1	immune response	aging [GO:0007568]; blood circulation [GO:0008015]; blood coagulation, intrinsic pathway [GO:0007597]; complement activation, classical pathway [GO:0006958]; fibrinolysis [GO:0042730]; innate immune response [GO:0045087]; negative regulation of complement activation, lectin pathway [GO:0001869]; platelet degranulation [GO:0002576]	serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	Activation of the C1 complex is under control of the C1-inhibitor. It forms a proteolytically inactive stoichiometric complex with the C1r or C1s proteases. May play a potentially crucial role in regulating important physiological pathways including complement activation, blood coagulation, fibrinolysis and the generation of kinins. Very efficient inhibitor of FXIIa. Inhibits chymotrypsin and kallikrein. {ECO:0000269|PubMed:8495195}.

ANXA1	immune response	actin cytoskeleton reorganization [GO:0031532]; adaptive immune response [GO:0002250]; alpha-beta T cell differentiation [GO:0046632]; arachidonic acid secretion [GO:0050482]; cell surface receptor signaling pathway [GO:0007166]; cellular response to glucocorticoid stimulus [GO:0071385]; cellular response to hydrogen peroxide [GO:0070301]; DNA duplex unwinding [GO:0032508]; DNA rewinding [GO:0036292]; endocrine pancreas development [GO:0031018]; estrous cycle [GO:0044849]; gliogenesis [GO:0042063]; G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger [GO:0007187]; granulocyte chemotaxis [GO:0071621]; hepatocyte differentiation [GO:0070365]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; insulin secretion [GO:0030073]; keratinocyte differentiation [GO:0030216]; monocyte chemotaxis [GO:0002548]; myoblast migration	annealing helicase activity [GO:0036310]; calcium-dependent phospholipid binding [GO:0005544]; calcium-dependent protein binding [GO:0048306]; calcium ion binding [GO:0005509]; double-stranded DNA-dependent ATPase activity [GO:0033676]; helicase activity [GO:0004386]; phospholipase A2 inhibitor activity [GO:0019834]; phospholipid binding [GO:0005543]; protein binding, bridging [GO:0030674]; receptor binding [GO:0005102]; single-stranded DNA binding [GO:0003697]; single-stranded RNA binding [GO:0003727]; structural molecule activity [GO:0005198]	apical plasma membrane [GO:0016324]; basolateral plasma membrane [GO:0016323]; cell surface [GO:0009986]; cornified envelope [GO:0001533]; cytoplasm [GO:0005737]; cytoplasmic vesicle membrane [GO:0030659]; early endosome membrane [GO:0031901]; endosome [GO:0005768]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of endosome membrane [GO:0031313]; extrinsic component of external side of plasma membrane [GO:0031232]; extrinsic component of membrane [GO:0019898]; focal adhesion [GO:0005925]; lateral plasma membrane [GO:0016328]; mast cell granule [GO:0042629]; mitochondrial membrane [GO:0031966]; motile cilium	Plays important roles in the innate immune response as effector of glucocorticoid-mediated responses and regulator of the inflammatory process. Has anti-inflammatory activity (PubMed:8425544). Plays a role in glucocorticoid-mediated down-regulation of the early phase of the inflammatory response (By similarity). Promotes resolution of inflammation and wound healing (PubMed:25664854). Functions at least in part by activating the formyl peptide receptors and downstream signaling cascades (PubMed:15187149, PubMed:25664854). Promotes chemotaxis of granulocytes and monocytes via activation of the formyl peptide receptors (PubMed:15187149). Contributes to the adapti

		involved in skeletal muscle regeneration [GO:0014839]; negative regulation of apoptotic process [GO:0043066]; negative regulation of exocytosis [GO:0045920]; negative regulation of interleukin-8 secretion [GO:2000483]; negative regulation of phospholipase A2 activity [GO:1900138]; negative regulation of T-helper 2 cell differentiation [GO:0045629]; neutrophil clearance [GO:0097350]; neutrophil homeostasis [GO:0001780]; peptide cross-linking [GO:0018149]; phagocytosis [GO:0006909]; positive regulation of G1/S transition of mitotic cell cycle [GO:1900087]; positive regulation of interleukin-2 production [GO:0032743]; positive regulation of neutrophil apoptotic process [GO:0033031]; positive regulation of prostaglandin biosynthetic process [GO:0031394]; positive regulation of T cell proliferation [GO:0042102]; positive regulation of T-helper 1 cell differentiation [GO:0045627]; positive regulation of vesicle fusion [GO:0031340]; positive regulation of wound healing [GO:0090303]; prolactin secretion		[GO:0031514]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; phagocytic cup [GO:0001891]; plasma membrane [GO:0005886]; protein complex [GO:0043234]; sarcolemma [GO:0042383]; vesicle [GO:0031982]	

		[GO:0070459]; prostate gland development [GO:0030850]; regulation of cell shape [GO:0008360]; regulation of hormone secretion [GO:0046883]; regulation of inflammatory response [GO:0050727]; regulation of interleukin-1 production [GO:0032652]; regulation of leukocyte migration [GO:0002685]; response to drug [GO:0042493]; response to estradiol [GO:0032355]; response to interleukin-1 [GO:0070555]; response to peptide hormone [GO:0043434]; response to X-ray [GO:0010165]; signal transduction [GO:0007165]			
CA2	immune response	angiotensin-activated signaling pathway [GO:0038166]; bicarbonate transport [GO:0015701]; carbon dioxide transport [GO:0015670]; cellular response to fluid shear stress [GO:0071498]; kidney development [GO:0001822]; morphogenesis of an epithelium [GO:0002009]; odontogenesis of dentin-containing tooth [GO:0042475]; one-carbon metabolic process [GO:0006730]; positive regulation of bone resorption [GO:0045780];	arylesterase activity [GO:0004064]; carbonate dehydratase activity [GO:0004089]; zinc ion binding [GO:0008270]	apical part of cell [GO:0045177]; axon [GO:0030424]; basolateral plasma membrane [GO:0016323]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; microvillus [GO:0005902]; myelin sheath [GO:0043209]; plasma	Essential for bone resorption and osteoclast differentiation (By similarity). Reversible hydration of carbon dioxide. Can hydrate cyanamide to urea. Involved in the regulation of fluid secretion into the anterior chamber of the eye. Contributes to intracellular pH regulation in the duodenal upper villous epithelium during proton-coupled peptide absorption. Stimulates the chloride-bicarbonate exchange activity of SLC26A6. {ECO:0000250, ECO:0000269|PubMed:10550681, ECO:0000269|PubMed:11831900,

		positive regulation of cellular pH reduction [GO:0032849]; positive regulation of dipeptide transmembrane transport [GO:2001150]; positive regulation of osteoclast differentiation [GO:0045672]; positive regulation of synaptic transmission, GABAergic [GO:0032230]; regulation of anion transport [GO:0044070]; regulation of chloride transport [GO:2001225]; regulation of intracellular pH [GO:0051453]; response to estrogen [GO:0043627]; response to pH [GO:0009268]; response to zinc ion [GO:0010043]; secretion [GO:0046903]		membrane [GO:0005886]	ECO:0000269|PubMed:15990874}.
ITIH2	immune response	hyaluronan metabolic process [GO:0030212]	endopeptidase inhibitor activity [GO:0004866]; serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	May act as a carrier of hyaluronan in serum or as a binding protein between hyaluronan and other matrix protein, including those on cell surfaces in tissues to regulate the localization, synthesis and degradation of hyaluronan which are essential to cells undergoing biological processes.
ITGB2	immune response	aging [GO:0007568]; apoptotic process [GO:0006915]; cell adhesion [GO:0007155]; cell-cell signaling [GO:0007267]; cell-matrix adhesion [GO:0007160]; cellular extravasation [GO:0045123]; cellular response to low-density lipoprotein particle	cell adhesion molecule binding [GO:0050839]; glycoprotein binding [GO:0001948]; ICAM-3 receptor activity [GO:0030369]; metal ion binding	cell surface [GO:0009986]; extracellular exosome [GO:0070062]; extracellular vesicle [GO:1903561]; integrin alphaL-beta2 complex [GO:0034687]; integrin complex	Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. Integrins alpha-M/beta-2 and alpha-X/beta-2 are receptors for the iC3b fragment of the third complement component and for fibrinogen. Integrin alpha-X/beta-2 recognizes the sequence G-P-R in fibrinogen alpha-chain. Integrin alpha-M/beta-2

		stimulus [GO:0071404]; endodermal cell differentiation [GO:0035987]; endothelial cell migration [GO:0043542]; extracellular matrix organization [GO:0030198]; heterotypic cell-cell adhesion [GO:0034113]; inflammatory response [GO:0006954]; integrin-mediated signaling pathway [GO:0007229]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; leukocyte migration involved in inflammatory response [GO:0002523]; natural killer cell activation [GO:0030101]; neutrophil chemotaxis [GO:0030593]; positive regulation of angiogenesis [GO:0045766]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of nitric oxide biosynthetic process [GO:0045429]; receptor clustering [GO:0043113]; receptor internalization [GO:0031623]; regulation of cell shape [GO:0008360]; regulation of immune response [GO:0050776]; regulation of	[GO:0046872]; protein kinase binding [GO:0019901]	[GO:0008305]; membrane [GO:0016020]; plasma membrane [GO:0005886]; receptor complex [GO:0043235]; secretory granule [GO:0030141]	recognizes P1 and P2 peptides of fibrinogen gamma chain. Integrin alpha-M/beta-2 is also a receptor for factor X. Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. Contributes to natural killer cell cytotoxicity (PubMed:15356110). Involved in leukocyte adhesion and transmigration of leukocytes including T-cells and neutrophils (PubMed:11812992).

		peptidyl-tyrosine phosphorylation [GO:0050730]; toll-like receptor 4 signaling pathway [GO:0034142]			
AOC3	immune response	amine metabolic process [GO:0009308]; cell adhesion [GO:0007155]; inflammatory response [GO:0006954]; response to antibiotic [GO:0046677]; xenobiotic metabolic process [GO:0006805]	aliphatic-amine oxidase activity [GO:0052595]; aminoacetone:oxygen oxidoreductase(deaminating) activity [GO:0052594]; calcium ion binding [GO:0005509]; copper ion binding [GO:0005507]; phenethylamine:oxygen oxidoreductase (deaminating) activity [GO:0052596]; primary amine oxidase activity [GO:0008131]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; quinone binding [GO:0048038]; tryptamine:oxygen oxidoreductase (deaminating) activity [GO:0052593]	cell surface [GO:0009986]; cytoplasm [GO:0005737]; early endosome [GO:0005769]; endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]; integral component of membrane [GO:0016021]; microvillus [GO:0005902]; plasma membrane [GO:0005886]	Cell adhesion protein that participates in lymphocyte extravasation and recirculation by mediating the binding of lymphocytes to peripheral lymph node vascular endothelial cells in an L-selectin-independent fashion. Has semicarbazide-sensitive (SSAO) monoamine oxidase activity. May play a role in adipogenesis. {ECO:0000269|PubMed:17400359, ECO:0000269|PubMed:19588076, ECO:0000269|PubMed:23349812, ECO:0000269|PubMed:9653080}.
ITIH1	immune response	hyaluronan metabolic process [GO:0030212]	calcium ion binding [GO:0005509	blood microparticle [GO:0072562];	May act as a carrier of hyaluronan in serum or as a binding protein between

			]; serine-type endopeptidase inhibitor activity [GO:0004867]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	hyaluronan and other matrix protein, including those on cell surfaces in tissues to regulate the localization, synthesis and degradation of hyaluronan which are essential to cells undergoing biological processes.; FUNCTION: Contains a potential peptide which could stimulate a broad spectrum of phagocytotic cells.
F12	immune response	blood coagulation, intrinsic pathway [GO:0007597]; Factor XII activation [GO:0002542]; fibrinolysis [GO:0042730]; innate immune response [GO:0045087]; plasma kallikrein-kinin cascade [GO:0002353]; positive regulation of blood coagulation [GO:0030194]; positive regulation of fibrinolysis [GO:0051919]; positive regulation of plasminogen activation [GO:0010756]; protein autoprocessing [GO:0016540]; protein processing [GO:0016485]; response to misfolded protein [GO:0051788]; zymogen activation [GO:0031638]	calcium ion binding [GO:0005509]; misfolded protein binding [GO:0051787]; serine-type endopeptidase activity [GO:0004252]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIa and then trypsin cleaves it to beta-factor XIIa. Alpha-factor XIIa activates factor XI to factor XIa. {ECO:0000269|PubMed:21304106}.
ALB	immune response	bile acid and bile salt transport [GO:0015721]; cellular response to starvation [GO:0009267]; hemolysis by symbiont of host erythrocytes [GO:0019836]; lipoprotein metabolic process [GO:0042157]; maintenance of	antioxidant activity [GO:0016209]; chaperone binding [GO:0051087]; copper ion binding [GO:0005507]; DNA binding [GO:0003677]; drug binding	basement membrane [GO:0005604]; blood microparticle [GO:0072562]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular region	Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood. Major zinc transporter in plasma, typically binds about 80% of all plasma zinc.

		mitochondrion location [GO:0051659]; negative regulation of apoptotic process [GO:0043066]; negative regulation of programmed cell death [GO:0043069]; platelet degranulation [GO:0002576]; positive regulation of circadian sleep/wake cycle, non-REM sleep [GO:0046010]; receptor-mediated endocytosis [GO:0006898]; response to mercury ion [GO:0046689]; response to nutrient [GO:0007584]; response to organic substance [GO:0010033]; response to platinum ion [GO:0070541]; retina homeostasis [GO:0001895]; sodium-independent organic anion transport [GO:0043252]; transport [GO:0006810]	[GO:0008144]; fatty acid binding [GO:0005504]; identical protein binding [GO:0042802]; pyridoxal phosphate binding [GO:0030170]; toxic substance binding [GO:0015643]; zinc ion binding [GO:0008270]	[GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; myelin sheath [GO:0043209]; nucleus [GO:0005634]; platelet alpha granule lumen [GO:0031093]; protein complex [GO:0043234]	{ECO:0000269|PubMed:19021548}.
S100A8	immune response	activation of cysteine-type endopeptidase activity involved in apoptotic process [GO:0006919]; acute inflammatory response [GO:0002526]; astrocyte development [GO:0014002]; autophagy [GO:0006914]; chemokine production [GO:0032602]; chronic inflammatory response [GO:0002544]; cytokine production [GO:0001816]; defense response to	arachidonic acid binding [GO:0050544]; calcium ion binding [GO:0005509]; microtubule binding [GO:0008017]; RAGE receptor binding [GO:0050786]; Toll-like receptor 4 binding [GO:0035662]; zinc ion binding [GO:0008270]	cytoskeleton [GO:0005856]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	S100A8 is a calcium- and zinc-binding protein which plays a prominent role in the regulation of inflammatory processes and immune response. It can induce neutrophil chemotaxis and adhesion. Predominantly found as calprotectin (S100A8/A9) which has a wide plethora of intra- and extracellular functions. The intracellular functions include: facilitating leukocyte arachidonic acid trafficking and metabolism, modulation of the tubulin-dependent cytoskeleton during migration of phagocytes and activation of the neutrophilic NADPH-oxidase. Activates

		bacterium [GO:0042742]; defense response to fungus [GO:0050832]; inflammatory response [GO:0006954]; innate immune response [GO:0045087]; leukocyte migration involved in inflammatory response [GO:0002523]; neutrophil aggregation [GO:0070488]; neutrophil chemotaxis [GO:0030593]; peptidyl-cysteine S-nitrosylation [GO:0018119]; positive regulation of cell growth [GO:0030307]; positive regulation of inflammatory response [GO:0050729]; positive regulation of intrinsic apoptotic signaling pathway [GO:2001244]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of peptide secretion [GO:0002793]; regulation of cytoskeleton organization [GO:0051493]; response to ethanol [GO:0045471]; response to lipopolysaccharide [GO:0032496]; response to zinc ion [GO:0010043]; sequestering of zinc ion [GO:0032119]; wound healing [GO:0042060]			NADPH-oxidase by facilitating the enzyme complex assembly at the cell membrane, transferring arachidonic acid, an essent

TF	immune response	cellular iron ion homeostasis [GO:0006879]; cellular response to iron ion [GO:0071281]; ferrous iron import into cell [GO:0097460]; iron ion homeostasis [GO:0055072]; platelet degranulation [GO:0002576]; positive regulation of receptor-mediated endocytosis [GO:0048260]; regulation of protein stability [GO:0031647]; retina homeostasis [GO:0001895]; transferrin transport [GO:0033572]	ferric iron binding [GO:0008199]; ferric iron transmembrane transporter activity [GO:0015091]; ferrous iron binding [GO:0008198]; transferrin receptor binding [GO:1990459]	apical plasma membrane [GO:0016324]; basal part of cell [GO:0045178]; basal plasma membrane [GO:0009925]; blood microparticle [GO:0072562]; cell surface [GO:0009986]; coated pit [GO:0005905]; cytoplasmic, membrane-bounded vesicle [GO:0016023]; early endosome [GO:0005769]; endocytic vesicle [GO:0030139]; endosome membrane [GO:0010008]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of external side of plasma membrane [GO:0031232]; HFE-transferrin receptor complex [GO:1990712]; late endosome [GO:0005770]; perinuclear region of cytoplasm [GO:0048471]; recycling endosome [GO:0055037]; secretory	Transferrins are iron binding transport proteins which can bind two Fe(3+) ions in association with the binding of an anion, usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation.

				granule lumen [GO:0034774]; vesicle [GO:0031982]	
IGHM	immune response	adaptive immune response [GO:0002250]; antibacterial humoral response [GO:0019731]; B cell receptor signaling pathway [GO:0050853]; complement activation, classical pathway [GO:0006958]; defense response to Gram-negative bacterium [GO:0050829]; innate immune response [GO:0045087]; phagocytosis, engulfment [GO:0006911]; phagocytosis, recognition [GO:0006910]; positive regulation of B cell activation [GO:0050871]	antigen binding [GO:0003823]	blood microparticle [GO:0072562]; cell surface [GO:0009986]; external side of plasma membrane [GO:0009897]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; hexameric IgM immunoglobulin complex [GO:0071757]; integral component of membrane [GO:0016021]; pentameric IgM immunoglobulin complex [GO:0071756]; plasma membrane [GO:0005886]	IgM antibodies play an important role in primary defense mechanisms. They have been shown to be involved in early recognition of external invaders like bacteria and viruses, cellular waste and modified self, as well as in recognition and elimination of precancerous and cancerous lesions. The membrane-bound form is found in the majority of normal B-cells alongside with IgD. Membrane-bound IgM induces the phosphorylation of CD79A and CD79B by the Src family of protein tyrosine kinases. It may cause death of cells by apoptosis. It is also found in soluble form, which represents about 30% of the total serum immunoglobulins where it is found almost exclusively as a
MPO	immune response	aging [GO:0007568]; defense response [GO:0006952]; defense response to fungus [GO:0050832]; hydrogen peroxide catabolic process [GO:0042744]; hypochlorous acid biosynthetic process [GO:0002149]; low-density lipoprotein particle remodeling [GO:0034374]; negative regulation of apoptotic process [GO:0043066]; negative regulation of growth of symbiont in host [GO:0044130]; oxidation-reduction process [GO:0055114];	chromatin binding [GO:0003682]; heme binding [GO:0020037]; heparin binding [GO:0008201]; metal ion binding [GO:0046872]; peroxidase activity [GO:0004601]	azurophil granule [GO:0042582]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; lysosome [GO:0005764]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; secretory granule [GO:0030141]	Part of the host defense system of polymorphonuclear leukocytes. It is responsible for microbicidal activity against a wide range of organisms. In the stimulated PMN, MPO catalyzes the production of hypohalous acids, primarily hypochlorous acid in physiologic situations, and other toxic intermediates that greatly enhance PMN microbicidal activity.

		removal of superoxide radicals [GO:0019430]; respiratory burst involved in defense response [GO:0002679]; response to food [GO:0032094]; response to gold nanoparticle [GO:1990268]; response to lipopolysaccharide [GO:0032496]; response to mechanical stimulus [GO:0009612]; response to oxidative stress [GO:0006979]; response to yeast [GO:0001878]			
CFHR1	immune response	complement activation [GO:0006956]		blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]	Involved in complement regulation. The dimerized forms have avidity for tissue-bound complement fragments and efficiently compete with the physiological complement inhibitor CFH. Can associate with lipoproteins and may play a role in lipid metabolism. {ECO:0000269|PubMed:23487775}.
ITGA5	immune response	angiogenesis [GO:0001525]; cell adhesion [GO:0007155]; cell-cell adhesion mediated by integrin [GO:0033631]; cell-substrate adhesion [GO:0031589]; cell-substrate junction assembly [GO:0007044]; endodermal cell differentiation [GO:0035987]; extracellular matrix organization [GO:0030198]; heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules [GO:0007157]; heterotypic cell-cell adhesion	metal ion binding [GO:0046872]; platelet-derived growth factor receptor binding [GO:0005161]; vascular endothelial growth factor receptor 2 binding [GO:0043184]; virus receptor activity [GO:0001618]	alphav-beta3 integrin-vitronectin complex [GO:0071062]; cell surface [GO:0009986]; cytoplasmic vesicle [GO:0031410]; endoplasmic reticulum [GO:0005783]; external side of plasma membrane [GO:0009897]; focal adhesion [GO:0005925]; Golgi apparatus [GO:0005794]; integrin complex [GO:0008305];	Integrin alpha-5/beta-1 is a receptor for fibronectin and fibrinogen. It recognizes the sequence R-G-D in its ligands. ITGA5:ITGB1 binds to PLA2G2A via a site (site 2) which is distinct from the classical ligand-binding site (site 1) and this induces integrin conformational changes and enhanced ligand binding to site 1 (PubMed:18635536, PubMed:25398877). {ECO:0000269|PubMed:18635536, ECO:0000269|PubMed:25398877}.; FUNCTION: (Microbial infection) Integrin ITGA5:ITGB1 acts as a receptor for human metapneumovirus (PubMed:12907437).

		[GO:0034113]; integrin-mediated signaling pathway [GO:0007229]; leukocyte cell-cell adhesion [GO:0007159]; leukocyte migration [GO:0050900]; memory [GO:0007613]; negative regulation of anoikis [GO:2000811]; positive regulation of cell migration [GO:0030335]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050731]; positive regulation of sprouting angiogenesis [GO:1903672]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0030949]; wound healing, spreading of epidermal cells [GO:0035313]		plasma membrane [GO:0005886]; ruffle [GO:0001726]; synapse [GO:0045202]	Integrin ITGA2:ITGB1 acts as a receptor for human parvovirus B19 (PubMed:24478423). In case of HIV-1 infection, the interaction with
HBA1	immune response	bicarbonate transport [GO:0015701]; cellular oxidant detoxification [GO:0098869]; hydrogen peroxide catabolic process [GO:0042744]; oxygen transport [GO:0015671]; positive regulation of cell death [GO:0010942]; protein heterooligomerization [GO:0051291]; receptor-mediated endocytosis [GO:0006898]; response to hydrogen	heme binding [GO:0020037]; iron ion binding [GO:0005506]; oxygen binding [GO:0019825]; oxygen transporter activity [GO:0005344]	blood microparticle [GO:0072562]; cytosol [GO:0005829]; cytosolic small ribosomal subunit [GO:0022627]; endocytic vesicle lumen [GO:0071682]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; haptoglobin-hemoglobin complex	Involved in oxygen transport from the lung to the various peripheral tissues.

		peroxide [GO:0042542]		[GO:0031838]; hemoglobin complex [GO:0005833]; membrane [GO:0016020]	
H3F3A	immune response	blood coagulation [GO:0007596]; brain development [GO:0007420]; cellular protein metabolic process [GO:0044267]; chromatin silencing at rDNA [GO:0000183]; DNA replication-independent nucleosome assembly [GO:0006336]; gene silencing by RNA [GO:0031047]; negative regulation of gene expression, epigenetic [GO:0045814]; nucleosome assembly [GO:0006334]; positive regulation of cell growth [GO:0030307]; positive regulation of gene expression, epigenetic [GO:0045815]; response to hormone [GO:0009725]; telomere organization [GO:0032200]	histone binding [GO:0042393]; nucleosomal DNA binding [GO:0031492]; RNA polymerase II core promoter sequence-specific DNA binding [GO:0000979]; RNA polymerase II distal enhancer sequence-specific DNA binding [GO:0000980]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; nuclear chromosome [GO:0000228]; nuclear chromosome, telomeric region [GO:0000784]; nuclear nucleosome [GO:0000788]; nucleoplasm [GO:0005654]; nucleosome [GO:0000786]; nucleus [GO:0005634]; protein complex [GO:0043234]	Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active genes. Constitutes the predominant form of histone H3 in non-dividing cells and is incorporated into chromatin independently of DNA synthesis. Deposited at sites of nucleosomal displacement throughout transcribed genes, suggesting that it represents an epigenetic imprint of transcriptionally active chromatin. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA acce
C1R	immune response	complement activation [GO:0006956]; complement activation, classical pathway [GO:0006958]; immune response [GO:0006955]; innate immune response [GO:0045087]	calcium ion binding [GO:0005509]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]	C1r B chain is a serine protease that combines with C1q and C1s to form C1, the first component of the classical pathway of the complement system.
ELANE	immune response	acute inflammatory response to antigenic stimulus [GO:0002438]; cellular calcium ion homeostasis	cytokine binding [GO:0019955]; endopeptidase activity	cell surface [GO:0009986]; cytoplasm [GO:0005737]; extracellular exosome	Modifies the functions of natural killer cells, monocytes and granulocytes. Inhibits C5a-dependent neutrophil enzyme release and

		[GO:0006874]; defense response to bacterium [GO:0042742]; extracellular matrix disassembly [GO:0022617]; leukocyte migration [GO:0050900]; negative regulation of chemokine biosynthetic process [GO:0045079]; negative regulation of chemotaxis [GO:0050922]; negative regulation of growth of symbiont in host [GO:0044130]; negative regulation of inflammatory response [GO:0050728]; negative regulation of interleukin-8 biosynthetic process [GO:0045415]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; neutrophil mediated killing of fungus [GO:0070947]; phagocytosis [GO:0006909]; positive regulation of immune response [GO:0050778]; positive regulation of interleukin-8 biosynthetic process [GO:0045416]; positive regulation of MAP kinase activity [GO:0043406]; positive regulation of smooth muscle cell proliferation [GO:0048661]; protein catabolic process [GO:0030163]; proteolysis [GO:0006508]; response to lipopolysaccharide [GO:0032496];	[GO:0004175]; heparin binding [GO:0008201]; peptidase activity [GO:0008233]; protease binding [GO:0002020]; RNA polymerase II transcription corepressor activity [GO:0001106]; serine-type endopeptidase activity [GO:0004252]	[GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; secretory granule [GO:0030141]; transcriptional repressor complex [GO:0017053]	chemotaxis. {ECO:0000269|PubMed:15140022}.

		response to UV [GO:0009411]; response to yeast [GO:0001878]			
C1QC	immune response	complement activation [GO:0006956]; complement activation, classical pathway [GO:0006958]; immune response [GO:0006955]; innate immune response [GO:0045087]; negative regulation of granulocyte differentiation [GO:0030853]; negative regulation of macrophage differentiation [GO:0045650]	serine-type endopeptidase activity [GO:0004252]	blood microparticle [GO:0072562]; collagen trimer [GO:0005581]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	C1q associates with the proenzymes C1r and C1s to yield C1, the first component of the serum complement system. The collagen-like regions of C1q interact with the Ca(2+)-dependent C1r(2)C1s(2) proenzyme complex, and efficient activation of C1 takes place on interaction of the globular heads of C1q with the Fc regions of IgG or IgM antibody present in immune complexes.
SERPINC1	immune response	blood coagulation [GO:0007596]; negative regulation of inflammatory response [GO:0050728]; regulation of blood coagulation, intrinsic pathway [GO:2000266]; response to nutrient [GO:0007584]	heparin binding [GO:0008201]; protease binding [GO:0002020]; serine-type endopeptidase inhibitor activity [GO:0004867]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; plasma membrane [GO:0005886]	Most important serine protease inhibitor in plasma that regulates the blood coagulation cascade. AT-III inhibits thrombin, matriptase-3/TMPRSS7, as well as factors IXa, Xa and XIa. Its inhibitory activity is greatly enhanced in the presence of heparin. {ECO:0000269|PubMed:15853774}.
CFD	immune response	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; platelet degranulation [GO:0002576]; proteolysis [GO:0006508]	serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]	extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; platelet alpha granule lumen [GO:0031093]	Factor D cleaves factor B when the latter is complexed with factor C3b, activating the C3bbb complex, which then becomes the C3 convertase of the alternate pathway. Its function is homologous to that of C1s in the classical pathway.
STAT6	immune response	cellular response to hydrogen peroxide [GO:0070301]; cellular response to reactive nitrogen species [GO:1902170]; interleukin-4-mediated signaling	identical protein binding [GO:0042802]; protein phosphatase binding [GO:0019903]; RNA	cytoplasm [GO:0005737]; cytosol [GO:0005829]; membrane raft [GO:0045121]; nuclear chromatin [GO:0000790];	Carries out a dual function: signal transduction and activation of transcription. Involved in IL4/interleukin-4- and IL3/interleukin-3-mediated signaling.

		pathway [GO:0035771]; mammary gland epithelial cell proliferation [GO:0033598]; mammary gland morphogenesis [GO:0060443]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; negative regulation of type 2 immune response [GO:0002829]; positive regulation of isotype switching to IgE isotypes [GO:0048295]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of type I interferon production [GO:0032481]; regulation of cell proliferation [GO:0042127]; regulation of transcription from RNA polymerase II promoter [GO:0006357]; signal transduction [GO:0007165]; T-helper 1 cell lineage commitment [GO:0002296]; transcription, DNA-templated [GO:0006351]	polymerase II core promoter sequence-specific DNA binding [GO:0000979]; signal transducer activity [GO:0004871]; transcription factor activity, sequence-specific DNA binding [GO:0003700]	nucleoplasm [GO:0005654]	{ECO:0000269|PubMed:17210636}.
C8B	immune response	complement activation [GO:0006956]; complement activation, alternative pathway [GO:0006957]; complement activation, classical pathway [GO:0006958]; cytolysis [GO:0019835];		extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extracellular vesicle [GO:1903561]; membrane	Constituent of the membrane attack complex (MAC) that plays a key role in the innate and adaptive immune response by forming pores in the plasma membrane of target cells.

		immune response [GO:0006955]; regulation of complement activation [GO:0030449]		[GO:0016020]; membrane attack complex [GO:0005579]	
AZU1	immune response	antimicrobial humoral response [GO:0019730]; calcium-mediated signaling using intracellular calcium source [GO:0035584]; cell chemotaxis [GO:0060326]; cellular extravasation [GO:0045123]; defense response to Gram-negative bacterium [GO:0050829]; defense response to virus [GO:0051607]; glial cell migration [GO:0008347]; induction of positive chemotaxis [GO:0050930]; inflammatory response [GO:0006954]; macrophage chemotaxis [GO:0048246]; microglial cell activation [GO:0001774]; monocyte activation [GO:0042117]; negative regulation of apoptotic process [GO:0043066]; neutrophil mediated killing of bacterium [GO:0070944]; positive regulation of cell adhesion [GO:0045785]; positive regulation of fractalkine biosynthetic process [GO:0050754]; positive regulation of gene expression [GO:0010628]; positive regulation of interleukin-1 beta biosynthetic process [GO:0050725];	heparan sulfate proteoglycan binding [GO:0043395]; heparin binding [GO:0008201]; peptidase activity [GO:0008233]; serine-type endopeptidase activity [GO:0004252]; toxic substance binding [GO:0015643]	azurophil granule [GO:0042582]; azurophil granule membrane [GO:0035577]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; extrinsic component of membrane [GO:0019898]	This is a neutrophil granule-derived antibacterial and monocyte- and fibroblast-specific chemotactic glycoprotein. Binds heparin. The cytotoxic action is limited to many species of Gram-negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope. It may play a role in mediating recruitment of monocytes in the second wave of inflammation. Has antibacterial activity against the Gram-nagative bacterium P.aeruginosa, this activity is inhibited by LPS from P.aeruginosa. Acting alone, it does not have antimicrob

		positive regulation of MHC class II biosynthetic process [GO:0045348]; positive regulation of peptidyl-threonine phosphorylation [GO:0010800]; positive regulation of phagocytosis [GO:0050766]; positive regulation of protein kinase activity [GO:0045860]; positive regulation of tumor necrosis factor biosynthetic process [GO:0042535]; protein kinase C-activating G-protein coupled receptor signaling pathway [GO:0007205]; protein kinase C signaling [GO:0070528]; protein processing [GO:0016485]; proteolysis [GO:0006508]; regulation of vascular permeability [GO:0043114]			
RAB12	intracellular signal transduction	autophagy [GO:0006914]; cellular protein catabolic process [GO:0044257]; endosome to lysosome transport [GO:0008333]; positive regulation of macroautophagy [GO:0016239]; protein transport [GO:0015031]; small GTPase mediated signal transduction [GO:0007264]	GDP binding [GO:0019003]; GTP binding [GO:0005525]	autophagosome [GO:0005776]; cytoplasmic vesicle [GO:0031410]; Golgi membrane [GO:0000139]; lysosomal membrane [GO:0005765]; lysosome [GO:0005764]; recycling endosome membrane [GO:0055038]	The small GTPases Rab are key regulators of intracellular membrane trafficking, from the formation of transport vesicles to their fusion with membranes. Rabs cycle between an inactive GDP-bound form and an active GTP-bound form that is able to recruit to membranes different set of downstream effectors directly responsible for vesicle formation, movement, tethering and fusion. That Rab may play a role in protein transport from recycling endosomes to lysosomes regulating, for instance, the degradation of the transferrin receptor. Involved in autophagy (By similarity). {ECO:0000250}.

VAT1	intracellular signal transduction	negative regulation of mitochondrial fusion [GO:0010637]	oxidoreductase activity [GO:0016491]; zinc ion binding [GO:0008270]	extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; mitochondrial outer membrane [GO:0005741]	Possesses ATPase activity (By similarity). Plays a part in calcium-regulated keratinocyte activation in epidermal repair mechanisms. Has no effect on cell proliferation. Negatively regulates mitochondrial fusion in cooperation with mitofusin proteins (MFN1-2). {ECO:0000250, ECO:0000269|PubMed:12898150, ECO:0000269|PubMed:17105775, ECO:0000269|PubMed:19508442}.
ARHGAP1	intracellular signal transduction	regulation of small GTPase mediated signal transduction [GO:0051056]; Rho protein signal transduction [GO:0007266]; small GTPase mediated signal transduction [GO:0007264]	GTPase activator activity [GO:0005096]; SH3/SH2 adaptor activity [GO:0005070]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; perinuclear region of cytoplasm [GO:0048471]	GTPase activator for the Rho, Rac and Cdc42 proteins, converting them to the putatively inactive GDP-bound state. Cdc42 seems to be the preferred substrate.
ARL2	intracellular signal transduction	bicellular tight junction assembly [GO:0070830]; cell cycle [GO:0007049]; centrosome organization [GO:0051297]; maintenance of protein location in nucleus [GO:0051457]; negative regulation of GTPase activity [GO:0034260]; positive regulation of cell-substrate adhesion [GO:0010811]; positive regulation of microtubule polymerization [GO:0031116]; regulation of insulin secretion [GO:0050796]; regulation of microtubule polymerization [GO:0031113]; small GTPase mediated	GTPase activity [GO:0003924]; GTPase inhibitor activity [GO:0005095]; GTP binding [GO:0005525]	centrosome [GO:0005813]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; lateral plasma membrane [GO:0016328]; mitochondrial intermembrane space [GO:0005758]; mitochondrial matrix [GO:0005759]; nucleus [GO:0005634]	Small GTP-binding protein which cycles between an inactive GDP-bound and an active GTP-bound form, and the rate of cycling is regulated by guanine nucleotide exchange factors (GEF) and GTPase-activating proteins (GAP). GTP-binding protein that does not act as an allosteric activator of the cholera toxin catalytic subunit. Regulates formation of new microtubules and centrosome integrity. Prevents the TBCD-induced microtubule destruction. Participates in association with TBCD, in the disassembly of the apical junction complexes. Antagonizes the effect of TBCD on epithelial cell detachment and tight and adherens junctions disassembly. Together with ARL2, plays a

		signal transduction [GO:0007264]; tubulin complex assembly [GO:0007021]			
ARF4	intracellular signal transduction	activation of phospholipase D activity [GO:0031584]; apical protein localization [GO:0045176]; brain development [GO:0007420]; cell migration [GO:0016477]; dendritic spine development [GO:0060996]; epidermal growth factor receptor signaling pathway [GO:0007173]; ER to Golgi vesicle-mediated transport [GO:0006888]; establishment or maintenance of epithelial cell apical/basal polarity [GO:0045197]; learning [GO:0007612]; negative regulation of apoptotic process [GO:0043066]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; protein ADP-ribosylation [GO:0006471]; protein localization to cilium [GO:0061512]; protein transport [GO:0015031]; regulation of reactive oxygen species metabolic process [GO:2000377]; response to axon injury [GO:0048678]; retrograde vesicle-mediated transport, Golgi to ER [GO:0006890]; small	ARF guanyl-nucleotide exchange factor activity [GO:0005086]; epidermal growth factor receptor binding [GO:0005154]; GTPase activity [GO:0003924]; GTP binding [GO:0005525]	cytosol [GO:0005829]; dendritic spine [GO:0043197]; extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; membrane [GO:0016020]; ruffle membrane [GO:0032587]	GTP-binding protein that functions as an allosteric activator of the cholera toxin catalytic subunit, an ADP-ribosyltransferase. Involved in protein trafficking; may modulate vesicle budding and uncoating within the Golgi apparatus.

		GTPase mediated signal transduction [GO:0007264]			
EFEMP1	intracellular signal transduction	camera-type eye development [GO:0043010]; embryonic eye morphogenesis [GO:0048048]; epidermal growth factor receptor signaling pathway [GO:0007173]; negative regulation of chondrocyte differentiation [GO:0032331]; negative regulation of neuron projection development [GO:0010977]; peptidyl-tyrosine phosphorylation [GO:0018108]; positive regulation of cell projection organization [GO:0031346]; positive regulation of cell proliferation [GO:0008284]; post-embryonic eye morphogenesis [GO:0048050]; regulation of glial cell migration [GO:1903975]; regulation of transcription, DNA-templated [GO:0006355]; visual perception [GO:0007601]	calcium ion binding [GO:0005509]; epidermal growth factor-activated receptor activity [GO:0005006]; epidermal growth factor receptor binding [GO:0005154]	basement membrane [GO:0005604]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; proteinaceous extracellular matrix [GO:0005578]	Binds EGFR, the EGF receptor, inducing EGFR autophosphorylation and the activation of downstream signaling pathways. May play a role in cell adhesion and migration. May function as a negative regulator of chondrocyte differentiation. In the olfactory epithelium, it may regulate glial cell migration, differentiation and the ability of glial cells to support neuronal neurite outgrowth. {ECO:0000269|PubMed:19804359, ECO:0000269|PubMed:19887559, ECO:0000269|PubMed:20005202}.
TBC1D4	intracellular signal transduction	activation of GTPase activity [GO:0090630]; cellular response to insulin stimulus [GO:0032869]; intracellular protein transport [GO:0006886]; membrane organization [GO:0061024]; negative regulation of vesicle fusion [GO:0031339]; regulation of vesicle fusion	GTPase activator activity [GO:0005096]; Rab GTPase binding [GO:0017137]	cytoplasm [GO:0005737]; cytoplasmic vesicle membrane [GO:0030659]; endomembrane system [GO:0012505]; extracellular exosome [GO:0070062]; intracellular [GO:0005622]	May act as a GTPase-activating protein for RAB2A, RAB8A, RAB10 and RAB14. Isoform 2 promotes insulin-induced glucose transporter SLC2A4/GLUT4 translocation at the plasma membrane, thus increasing glucose uptake. {ECO:0000269|PubMed:15971998, ECO:0000269|PubMed:18771725, ECO:0000269|PubMed:22908308}.

		[GO:0031338]; vesicle-mediated transport [GO:0016192]			
ADCY5	intracellular signal transduction	activation of adenylate cyclase activity [GO:0007190]; activation of protein kinase A activity [GO:0034199]; adenosine receptor signaling pathway [GO:0001973]; adenylate cyclase-activating dopamine receptor signaling pathway [GO:0007191]; adenylate cyclase-activating G-protein coupled receptor signaling pathway [GO:0007189]; adenylate cyclase-inhibiting dopamine receptor signaling pathway [GO:0007195]; adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway [GO:0007193]; cAMP biosynthetic process [GO:0006171]; cAMP-mediated signaling [GO:0019933]; cellular response to forskolin [GO:1904322]; cellular response to glucagon stimulus [GO:0071377]; locomotory behavior [GO:0007626]; neuromuscular process controlling balance [GO:0050885]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; regulation of insulin secretion involved in cellular response to glucose stimulus	adenylate cyclase activity [GO:0004016]; adenylate cyclase binding [GO:0008179]; ATP binding [GO:0005524]; metal ion binding [GO:0046872]; protein heterodimerization activity [GO:0046982]	integral component of membrane [GO:0016021]; intracellular [GO:0005622]; plasma membrane [GO:0005886]; primary cilium [GO:0072372]	Catalyzes the formation of the signaling molecule cAMP in response to G-protein signaling (PubMed:15385642, PubMed:26206488, PubMed:24700542). Mediates signaling downstream of ADRB1 (PubMed:24700542). Regulates the increase of free cytosolic Ca(2+) in response to increased blood glucose levels and contributes to the regulation of Ca(2+)-dependent insulin secretion (PubMed:24740569). {ECO:0000269|PubMed:15385642, ECO:0000269|PubMed:24700542, ECO:0000269|PubMed:24740569, ECO:0000269|PubMed:26206488}.

		[GO:0061178]; renal water homeostasis [GO:0003091]			
SLC3A2	metabolism	amino acid transport [GO:0006865]; calcium ion transport [GO:0006816]; carbohydrate metabolic process [GO:0005975]; cell growth [GO:0016049]; leucine import [GO:0060356]; leukocyte migration [GO:0050900]; response to exogenous dsRNA [GO:0043330]; tryptophan transport [GO:0015827]	calcium:sodium antiporter activity [GO:0005432]; catalytic activity [GO:0003824]; double-stranded RNA binding [GO:0003725]; neutral amino acid transmembrane transporter activity [GO:0015175]; poly(A) RNA binding [GO:0044822]	apical plasma membrane [GO:0016324]; cell surface [GO:0009986]; cytoplasm [GO:0005737]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; melanosome [GO:0042470]; membrane [GO:0016020]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	Required for the function of light chain amino-acid transporters. Involved in sodium-independent, high-affinity transport of large neutral amino acids such as phenylalanine, tyrosine, leucine, arginine and tryptophan. Involved in guiding and targeting of LAT1 and LAT2 to the plasma membrane. When associated with SLC7A6 or SLC7A7 acts as an arginine/glutamine exchanger, following an antiport mechanism for amino acid transport, influencing arginine release in exchange for extracellular amino acids. Plays a role in nitric oxide synthesis in human umbilical vein endothelial cells (HUVECs) via transport of L-arginine. Required for normal and neoplastic cell growth.
HDLBP	metabolism	cholesterol metabolic process [GO:0008203]; lipid transport [GO:0006869]	lipid binding [GO:0008289]; poly(A) RNA binding [GO:0044822]	cytoplasm [GO:0005737]; high-density lipoprotein particle [GO:0034364]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	Appears to play a role in cell sterol metabolism. It may function to protect cells from over-accumulation of cholesterol.
ABHD10	metabolism	cellular glucuronidation [GO:0052695]; glucuronoside catabolic process [GO:0019391]	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]	cytosol [GO:0005829]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	Catalyzes the deglucuronidation of mycophenolic acid acyl-glucuronide, a metabolite of the immunosuppressant drug mycophenolate. {ECO:0000269|PubMed:22294686}.
TGM2	metabolism	apoptotic cell clearance [GO:0043277]; branching involved in salivary gland morphogenesis [GO:0060445]; negative regulation of endoplasmic reticulum calcium	metal ion binding [GO:0046872]; protein-glutamine gamma-glutamyltransferase activity [GO:0003810]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; focal adhesion [GO:0005925];	Catalyzes the cross-linking of proteins and the conjugation of polyamines to proteins.

		ion concentration [GO:0032471]; peptide cross-linking [GO:0018149]; phospholipase C-activating G-protein coupled receptor signaling pathway [GO:0007200]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cell adhesion [GO:0045785]; positive regulation of mitochondrial calcium ion concentration [GO:0051561]; salivary gland cavitation [GO:0060662]		intrinsic component of plasma membrane [GO:0031226]; mitochondrion [GO:0005739]	
TSTA3	metabolism	'de novo' GDP-L-fucose biosynthetic process [GO:0042351]; cytolysis [GO:0019835]; GDP-mannose metabolic process [GO:0019673]; leukocyte cell-cell adhesion [GO:0007159]	coenzyme binding [GO:0050662]; electron carrier activity [GO:0009055]; GDP-4-dehydro-D-rhamnose reductase activity [GO:0042356]; GDP-L-fucose synthase activity [GO:0050577]; isomerase activity [GO:0016853]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]	Catalyzes the two-step NADP-dependent conversion of GDP-4-dehydro-6-deoxy-D-mannose to GDP-fucose, involving an epimerase and a reductase reaction. {ECO:0000269|PubMed:8910301}.
MECR	metabolism	fatty acid biosynthetic process [GO:0006633]; fatty acid metabolic process [GO:0006631]	trans-2-enoyl-CoA reductase (NADPH) activity [GO:0019166]; zinc ion binding [GO:0008270]	mitochondrion [GO:0005739]; nucleus [GO:0005634]	Oxidoreductase with a preference for short and medium chain substrates, including trans-2-hexenoyl-CoA (C6), trans-2-decenoyl-CoA (C10), and trans-2-hexadecenoyl-CoA (C16). May play a role in mitochondrial fatty acid synthesis. {ECO:0000269|PubMed:18479707}.
DPYD	metabolism	beta-alanine biosynthetic process [GO:0019483];	4 iron, 4 sulfur cluster binding	cytoplasm [GO:0005737];	Involved in pyrimidine base degradation. Catalyzes the reduction of

		purine nucleobase catabolic process [GO:0006145]; pyrimidine nucleobase catabolic process [GO:0006208]; pyrimidine nucleoside catabolic process [GO:0046135]; thymidine catabolic process [GO:0006214]; thymine catabolic process [GO:0006210]; uracil catabolic process [GO:0006212]	[GO:0051539]; dihydropyrimidine dehydrogenase (NADP+) activity [GO:0017113]; flavin adenine dinucleotide binding [GO:0050660]; metal ion binding [GO:0046872]; NADP binding [GO:0050661]; protein homodimerization activity [GO:0042803]	cytosol [GO:0005829]	uracil and thymine. Also involved the degradation of the chemotherapeutic drug 5-fluorouracil.
GCDH	metabolism	fatty acid beta-oxidation using acyl-CoA dehydrogenase [GO:0033539]; fatty-acyl-CoA biosynthetic process [GO:0046949]; lipid homeostasis [GO:0055088]; lysine catabolic process [GO:0006554]; tryptophan metabolic process [GO:0006568]	electron carrier activity [GO:0009055]; fatty-acyl-CoA binding [GO:0000062]; flavin adenine dinucleotide binding [GO:0050660]; glutaryl-CoA dehydrogenase activity [GO:0004361]; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor [GO:0052890]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	Catalyzes the oxidative decarboxylation of glutaryl-CoA to crotonyl-CoA and CO(2) in the degradative pathway of L-lysine, L-hydroxylysine, and L-tryptophan metabolism. It uses electron transfer flavoprotein as its electron acceptor. Isoform Short is inactive. {ECO:0000269|PubMed:17176108, ECO:0000269|PubMed:6423663, ECO:0000269|PubMed:8541831}.
ACAT1	metabolism	adipose tissue development [GO:0060612]; brain development [GO:0007420]; branched-chain amino acid catabolic process [GO:0009083];	acetyl-CoA C-acetyltransferase activity [GO:0003985]; coenzyme binding [GO:0050662]; metal ion	extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743]; mitochondrial matrix	Plays a major role in ketone body metabolism.

		ketone body biosynthetic process [GO:0046951]; ketone body catabolic process [GO:0046952]; liver development [GO:0001889]; metanephric proximal convoluted tubule development [GO:0072229]; protein homooligomerization [GO:0051260]; response to hormone [GO:0009725]; response to organic cyclic compound [GO:0014070]; response to starvation [GO:0042594]	binding [GO:0046872]	[GO:0005759]; mitochondrion [GO:0005739]	
GPT	metabolism	cellular amino acid biosynthetic process [GO:0008652]; L-alanine catabolic process [GO:0042853]	L-alanine:2-oxoglutarate aminotransferase activity [GO:0004021]; pyridoxal phosphate binding [GO:0030170]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]	Catalyzes the reversible transamination between alanine and 2-oxoglutarate to form pyruvate and glutamate. Participates in cellular nitrogen metabolism and also in liver gluconeogenesis starting with precursors transported from skeletal muscles (By similarity). {ECO:0000250}.
DBI	metabolism	phosphatidylcholine acyl-chain remodeling [GO:0036151]; transport [GO:0006810]	benzodiazepine receptor binding [GO:0030156]; lipid binding [GO:0008289]; long-chain fatty acyl-CoA binding [GO:0036042]; protein dimerization activity [GO:0046983]	endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; perinuclear endoplasmic reticulum [GO:0097038]	Binds medium- and long-chain acyl-CoA esters with very high affinity and may function as an intracellular carrier of acyl-CoA esters. It is also able to displace diazepam from the benzodiazepine (BZD) recognition site located on the GABA type A receptor. It is therefore possible that this protein also acts as a neuropeptide to modulate the action of the GABA receptor.
IDH2	metabolism	2-oxoglutarate metabolic process [GO:0006103]; carbohydrate metabolic process [GO:0005975]; glyoxylate cycle [GO:0006097]; isocitrate metabolic	isocitrate dehydrogenase (NADP+) activity [GO:0004450]; magnesium ion binding [GO:0000287]; NAD	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743];	carbohydrate metabolic process

		process [GO:0006102]; tricarboxylic acid cycle [GO:0006099]	binding [GO:0051287]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; peroxisome [GO:0005777]	
HADHA	metabolism	cardiolipin acyl-chain remodeling [GO:0035965]; fatty acid beta-oxidation [GO:0006635]; response to drug [GO:0042493]; response to insulin [GO:0032868]	3-hydroxyacyl-CoA dehydrogenase activity [GO:0003857]; acetyl-CoA C-acetyltransferase activity [GO:0003985]; enoyl-CoA hydratase activity [GO:0004300]; fatty-acyl-CoA binding [GO:0000062]; long-chain-3-hydroxyacyl-CoA dehydrogenase activity [GO:0016509]; long-chain-enoyl-CoA hydratase activity [GO:0016508]; NAD binding [GO:0051287]	mitochondrial fatty acid beta-oxidation multienzyme complex [GO:0016507]; mitochondrial inner membrane [GO:0005743]; mitochondrial nucleoid [GO:0042645]; mitochondrion [GO:0005739]	Bifunctional subunit.
IDH3B	metabolism	2-oxoglutarate metabolic process [GO:0006103]; isocitrate metabolic process [GO:0006102]; NADH metabolic process [GO:0006734]; tricarboxylic acid cycle [GO:0006099]	electron carrier activity [GO:0009055]; isocitrate dehydrogenase (NAD+) activity [GO:0004449]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	carbohydrate metabolic process
ACSL1	metabolism	adiponectin-activated signaling pathway [GO:0033211];	ATP binding [GO:0005524]; long-chain	endoplasmic reticulum membrane	Activation of long-chain fatty acids for both synthesis of cellular lipids,

		alpha-linolenic acid metabolic process [GO:0036109]; linoleic acid metabolic process [GO:0043651]; lipid biosynthetic process [GO:0008610]; long-chain fatty acid import [GO:0044539]; long-chain fatty acid metabolic process [GO:0001676]; long-chain fatty-acyl-CoA biosynthetic process [GO:0035338]; positive regulation of protein serine/threonine kinase activity [GO:0071902]; response to drug [GO:0042493]; response to nutrient [GO:0007584]; response to oleic acid [GO:0034201]; response to organic cyclic compound [GO:0014070]; triglyceride metabolic process [GO:0006641]; xenobiotic catabolic process [GO:0042178]	fatty acid-CoA ligase activity [GO:0004467]	[GO:0005789]; integral component of membrane [GO:0016021]; membrane [GO:0016020]; mitochondrial outer membrane [GO:0005741]; mitochondrion [GO:0005739]; peroxisomal membrane [GO:0005778]; plasma membrane [GO:0005886]	and degradation via beta-oxidation. Preferentially uses palmitoleate, oleate and linoleate.
ALDH6A1	metabolism	beta-alanine catabolic process [GO:0019484]; branched-chain amino acid catabolic process [GO:0009083]; brown fat cell differentiation [GO:0050873]; thymine catabolic process [GO:0006210]; thymine metabolic process [GO:0019859]; valine catabolic process [GO:0006574]; valine metabolic process [GO:0006573]	aldehyde dehydrogenase (NAD) activity [GO:0004029]; fatty-acyl-CoA binding [GO:0000062]; malonate-semialdehyde dehydrogenase (acetylating) activity [GO:0018478]; methylmalonate-semialdehyde dehydrogenase (acylating) activity [GO:0004491	extracellular exosome [GO:0070062]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleoplasm [GO:0005654]	Plays a role in valine and pyrimidine metabolism. Binds fatty acyl-CoA.

			]; poly(A) RNA binding [GO:0044822]; thiolester hydrolase activity [GO:0016790]		
PCCA	metabolism	biotin metabolic process [GO:0006768]; short-chain fatty acid catabolic process [GO:0019626]	ATP binding [GO:0005524]; biotin binding [GO:0009374]; biotin carboxylase activity [GO:0004075]; enzyme binding [GO:0019899]; metal ion binding [GO:0046872]; propionyl-CoA carboxylase activity [GO:0004658]	cytosol [GO:0005829]; mitochondrial matrix [GO:0005759]	
NDUFB4	metabolism	mitochondrial electron transport, NADH to ubiquinone [GO:0006120]; mitochondrial respiratory chain complex I assembly [GO:0032981]; response to oxidative stress [GO:0006979]	NADH dehydrogenase (ubiquinone) activity [GO:0008137]	extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; mitochondrial inner membrane [GO:0005743]; mitochondrial respiratory chain complex I [GO:0005747]; mitochondrion [GO:0005739]; nuclear membrane [GO:0031965]; nucleoplasm [GO:0005654]	Accessory subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I), that is believed not to be involved in catalysis. Complex I functions in the transfer of electrons from NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone.
NDUFA6	metabolism	mitochondrial electron transport, NADH to ubiquinone [GO:0006120]; mitochondrial respiratory chain complex I assembly [GO:0032981];	NADH dehydrogenase (ubiquinone) activity [GO:0008137]	mitochondrial inner membrane [GO:0005743]; mitochondrial membrane [GO:0031966]; mitochondrial	Accessory subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I), that is believed to be not involved in catalysis. Complex I functions in the transfer of electrons from

		response to oxidative stress [GO:0006979]		respiratory chain complex I [GO:0005747]	NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone.
ME2	metabolism	malate metabolic process [GO:0006108]; regulation of NADP metabolic process [GO:1902031]	electron carrier activity [GO:0009055]; malate dehydrogenase (decarboxylating) (NAD+) activity [GO:0004471]; malic enzyme activity [GO:0004470]; metal ion binding [GO:0046872]; NAD binding [GO:0051287]; oxaloacetate decarboxylase activity [GO:0008948]	intracellular membrane-bounded organelle [GO:0043231]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	
IDH3G	metabolism	2-oxoglutarate metabolic process [GO:0006103]; carbohydrate metabolic process [GO:0005975]; isocitrate metabolic process [GO:0006102]; NADH metabolic process [GO:0006734]; negative regulation of growth [GO:0045926]; tricarboxylic acid cycle [GO:0006099]	ATP binding [GO:0005524]; isocitrate dehydrogenase (NAD+) activity [GO:0004449]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	carbohydrate metabolic process
GBAS	metabolism	ATP biosynthetic process [GO:0006754]; negative regulation of ATP citrate synthase activity [GO:2000984]; oxidative phosphorylation [GO:0006119]		integral component of plasma membrane [GO:0005887]; membrane [GO:0016020]; mitochondrion [GO:0005739]	

COX 5B	metabolism	mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]; respiratory gaseous exchange [GO:0007585]	cytochrome-c oxidase activity [GO:0004129]; metal ion binding [GO:0046872]	extracellular exosome [GO:0070062]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
TPP 1	metabolism	bone resorption [GO:0045453]; central nervous system development [GO:0007417]; epithelial cell differentiation [GO:0030855]; IRE1-mediated unfolded protein response [GO:0036498]; lipid metabolic process [GO:0006629]; lysosome organization [GO:0007040]; nervous system development [GO:0007399]; neuromuscular process controlling balance [GO:0050885]; peptide catabolic process [GO:0043171]; protein catabolic process [GO:0030163]; proteolysis [GO:0006508]	endopeptidase activity [GO:0004175]; metal ion binding [GO:0046872]; peptidase activity [GO:0008233]; peptide binding [GO:0042277]; serine-type endopeptidase activity [GO:0004252]; serine-type peptidase activity [GO:0008236]; tripeptidyl-peptidase activity [GO:0008240]	extracellular exosome [GO:0070062]; lysosomal lumen [GO:0043202]; lysosome [GO:0005764]; melanosome [GO:0042470]; mitochondrion [GO:0005739]	Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity). {ECO:0000250}.
COX 6B1	metabolism	mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]; substantia nigra development [GO:0021762]	cytochrome-c oxidase activity [GO:0004129]	mitochondrial inner membrane [GO:0005743]; mitochondrial intermembrane space [GO:0005758]; mitochondrion [GO:0005739]	Connects the two COX monomers into the physiological dimeric form. {ECO:0000250}.
GGT 5	metabolism	cellular amino acid metabolic process [GO:0006520]; glutathione biosynthetic process [GO:0006750]; glutathione metabolic process [GO:0006749];	gamma-glutamyltransferase activity [GO:0003840]; glutathione hydrolase activity [GO:0036374]	anchored component of external side of plasma membrane [GO:0031362]; integral component of membrane	Cleaves the gamma-glutamyl peptide bond of glutathione conjugates, but maybe not glutathione itself. Converts leukotriene C4 (LTC4) to leukotriene D4 (LTD4).

		inflammatory response [GO:0006954]; leukotriene biosynthetic process [GO:0019370]; leukotriene metabolic process [GO:0006691]		[GO:0016021]; plasma membrane [GO:0005886]	
APOB	metabolism	artery morphogenesis [GO:0048844]; cellular protein catabolic process [GO:0044257]; cellular response to prostaglandin stimulus [GO:0071379]; cellular response to tumor necrosis factor [GO:0071356]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; cholesterol transport [GO:0030301]; fertilization [GO:0009566]; in utero embryonic development [GO:0001701]; leukocyte migration [GO:0050900]; lipoprotein biosynthetic process [GO:0042158]; lipoprotein catabolic process [GO:0042159]; lipoprotein metabolic process [GO:0042157]; lipoprotein transport [GO:0042953]; low-density lipoprotein particle clearance [GO:0034383]; low-density lipoprotein particle remodeling [GO:0034374]; nervous system development [GO:0007399]; positive regulation of cholesterol storage	cholesterol transporter activity [GO:0017127]; heparin binding [GO:0008201]; lipase binding [GO:0035473]; low-density lipoprotein particle receptor binding [GO:0050750]; phospholipid binding [GO:0005543]	actin cytoskeleton [GO:0015629]; chylomicron [GO:0042627]; chylomicron remnant [GO:0034360]; clathrin-coated endocytic vesicle membrane [GO:0030669]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; early endosome [GO:0005769]; endocytic vesicle lumen [GO:0071682]; endoplasmic reticulum lumen [GO:0005788]; endoplasmic reticulum membrane [GO:0005789]; endosome lumen [GO:0031904]; endosome membrane [GO:0010008]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; Golgi apparatus [GO:0005794]; intermediate-density	Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.

		[GO:0010886]; positive regulation of gene expression [GO:0010628]; positive regulation of lipid storage [GO:0010884]; positive regulation of macrophage derived foam cell differentiation [GO:0010744]; post-embryonic development [GO:0009791]; receptor-mediated endocytosis [GO:0006898]; regulation of cholesterol biosynthetic process [GO:0045540]; response to carbohydrate [GO:0009743]; response to lipopolysaccharide [GO:0032496]; response to selenium ion [GO:0010269]; response to virus [GO:0009615]; retinoid metabolic process [GO:0001523]; spermatogenesis [GO:0007283]; sperm motility [GO:0030317]; triglyceride catabolic process [GO:0019433]; triglyceride mobilization [GO:0006642]; very-low-density lipoprotein particle assembly [GO:0034379]		lipoprotein particle [GO:0034363]; intracellular membrane-bounded organelle [GO:0043231]; low-density lipoprotein particle [GO:0034362]; mature chylomicron [GO:0034359]; neuronal cell body [GO:0043025]; plasma membrane [GO:0005886]; very-low-density lipoprotein particle [GO:0034361]	
GUSB	metabolism	carbohydrate metabolic process [GO:0005975]; glycosaminoglycan catabolic process [GO:0006027]; hyaluronan catabolic process [GO:0030214]	beta-glucuronidase activity [GO:0004566]; protein domain specific binding [GO:0019904]; receptor binding	extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; intracellular membrane-bounded organelle [GO:0043231];	Plays an important role in the degradation of dermatan and keratan sulfates.

			[GO:0005102]	lysosomal lumen [GO:0043202]; membrane [GO:0016020]	
PLIN1	metabolism	lipid metabolic process [GO:0006629]	lipid binding [GO:0008289]	endoplasmic reticulum [GO:0005783]; lipid particle [GO:0005811]	Modulator of adipocyte lipid metabolism. Coats lipid storage droplets to protect them from breakdown by hormone-sensitive lipase (HSL). Its absence may result in leanness. Plays a role in unilocular lipid droplet formation by activating CIDEC. Their interaction promotes lipid droplet enlargement and directional net neutral lipid transfer. May modulate lipolysis and triglyceride levels. {ECO:0000269|PubMed:23399566}.
PON1	metabolism	aromatic compound catabolic process [GO:0019439]; carboxylic acid catabolic process [GO:0046395]; cholesterol metabolic process [GO:0008203]; organophosphate catabolic process [GO:0046434]; phosphatidylcholine metabolic process [GO:0046470]; positive regulation of binding [GO:0051099]; positive regulation of cholesterol efflux [GO:0010875]; positive regulation of transporter activity [GO:0032411]; response to external stimulus [GO:0009605]; response to fatty acid [GO:0070542]; response to fluoride [GO:1902617]; response to nutrient levels [GO:0031667]; response to toxic	acyl-L-homoserine-lactone lactonohydrolase activity [GO:0102007]; aryldialkylphosphatase activity [GO:0004063]; arylesterase activity [GO:0004064]; calcium ion binding [GO:0005509]; phospholipid binding [GO:0005543]; protein homodimerization activity [GO:0042803]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; intracellular membrane-bounded organelle [GO:0043231]; spherical high-density lipoprotein particle [GO:0034366]	Hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Capable of hydrolyzing a broad spectrum of organophosphate substrates and lactones, and a number of aromatic carboxylic acid esters. Mediates an enzymatic protection of low density lipoproteins against oxidative modification and the consequent series of events leading to atheroma formation. {ECO:0000269|PubMed:10479665, ECO:0000269|PubMed:15772423}.

		substance [GO:0009636]			
GSTM1	metabolism	cellular detoxification of nitrogen compound [GO:0070458]; glutathione derivative biosynthetic process [GO:1901687]; glutathione metabolic process [GO:0006749]; nitrobenzene metabolic process [GO:0018916]; xenobiotic catabolic process [GO:0042178]	enzyme binding [GO:0019899]; glutathione binding [GO:0043295]; glutathione transferase activity [GO:0004364]; protein homodimerization activity [GO:0042803]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. {ECO:0000269|PubMed:16548513}.
APOA4	metabolism	cellular protein metabolic process [GO:0044267]; cholesterol biosynthetic process [GO:0006695]; cholesterol efflux [GO:0033344]; cholesterol homeostasis [GO:0042632]; cholesterol metabolic process [GO:0008203]; chylomicron assembly [GO:0034378]; chylomicron remodeling [GO:0034371]; high-density lipoprotein particle assembly [GO:0034380]; high-density lipoprotein particle remodeling [GO:0034375]; hydrogen peroxide catabolic process [GO:0042744]; innate immune response in mucosa [GO:0002227]; leukocyte cell-cell adhesion [GO:0007159]; lipid homeostasis [GO:0055088]; lipid transport [GO:0006869]; lipoprotein biosynthetic process	antioxidant activity [GO:0016209]; cholesterol binding [GO:0015485]; cholesterol transporter activity [GO:0017127]; copper ion binding [GO:0005507]; lipid binding [GO:0008289]; lipid transporter activity [GO:0005319]; phosphatidylcholine binding [GO:0031210]; phosphatidylcholine-sterol O-acyltransferase activator activity [GO:0060228]; protein homodimerization activity [GO:0042803]	blood microparticle [GO:0072562]; chylomicron [GO:0042627]; cytosol [GO:0005829]; early endosome [GO:0005769]; endoplasmic reticulum lumen [GO:0005788]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; high-density lipoprotein particle [GO:0034364]; very-low-density lipoprotein particle [GO:0034361]	May have a role in chylomicrons and VLDL secretion and catabolism. Required for efficient activation of lipoprotein lipase by ApoC-II; potent activator of LCAT. Apoa-IV is a major component of HDL and chylomicrons.

		[GO:0042158]; lipoprotein metabolic process [GO:0042157]; multicellular organism lipid catabolic process [GO:0044240]; negative regulation of plasma lipoprotein particle oxidation [GO:0034445]; neuron projection regeneration [GO:0031102]; phosphatidylcholine metabolic process [GO:0046470]; phospholipid efflux [GO:0033700]; positive regulation of cholesterol esterification [GO:0010873]; positive regulation of fatty acid biosynthetic process [GO:0045723]; positive regulation of lipoprotein lipase activity [GO:0051006]; positive regulation of triglyceride catabolic process [GO:0010898]; protein-lipid complex assembly [GO:0065005]; regulation of cholesterol transport [GO:0032374]; regulation of intestinal cholesterol absorption [GO:0030300]; removal of superoxide radicals [GO:0019430]; response to lipid hydroperoxide [GO:0006982]; response to stilbenoid [GO:0035634]; retinoid metabolic process [GO:0001523]; reverse cholesterol transport			

		[GO:0043691]; triglyceride homeostasis [GO:0070328]; very-low-density lipoprotein particle remodeling [GO:0034372]			
APOD	metabolism	aging [GO:0007568]; angiogenesis [GO:0001525]; brain development [GO:0007420]; glucose metabolic process [GO:0006006]; lipid metabolic process [GO:0006629]; negative regulation of cytokine production involved in inflammatory response [GO:1900016]; negative regulation of focal adhesion assembly [GO:0051895]; negative regulation of lipoprotein lipid oxidation [GO:0060588]; negative regulation of monocyte chemotactic protein-1 production [GO:0071638]; negative regulation of platelet-derived growth factor receptor signaling pathway [GO:0010642]; negative regulation of protein import into nucleus [GO:0042308]; negative regulation of smooth muscle cell-matrix adhesion [GO:2000098]; negative regulation of smooth muscle cell proliferation [GO:0048662]; negative regulation of T cell migration [GO:2000405]; peripheral nervous system axon	cholesterol binding [GO:0015485]; lipid transporter activity [GO:0005319]	cytosolic ribosome [GO:0022626]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]; neuronal cell body [GO:0043025]; perinuclear region of cytoplasm [GO:0048471]	APOD occurs in the macromolecular complex with lecithin-cholesterol acyltransferase. It is probably involved in the transport and binding of bilin. Appears to be able to transport a variety of ligands in a number of different contexts.

		regeneration [GO:0014012]; response to axon injury [GO:0048678]; response to drug [GO:0042493]; response to reactive oxygen species [GO:0000302]; tissue regeneration [GO:0042246]			
ACSL4	metabolism	dendritic spine development [GO:0060996]; embryonic process involved in female pregnancy [GO:0060136]; fatty acid transport [GO:0015908]; lipid biosynthetic process [GO:0008610]; lipid metabolic process [GO:0006629]; long-chain fatty-acyl-CoA biosynthetic process [GO:0035338]; negative regulation of prostaglandin secretion [GO:0032307]; positive regulation of cell growth [GO:0030307]; response to interleukin-15 [GO:0070672]; response to nutrient [GO:0007584]; triglyceride metabolic process [GO:0006641]	arachidonate-CoA ligase activity [GO:0047676]; ATP binding [GO:0005524]; long-chain fatty acid-CoA ligase activity [GO:0004467]; very long-chain fatty acid-CoA ligase activity [GO:0031957]	cytoplasm [GO:0005737]; endoplasmic reticulum membrane [GO:0005789]; ER-mitochondrion membrane contact site [GO:0044233]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; lipid particle [GO:0005811]; membrane [GO:0016020]; mitochondrial outer membrane [GO:0005741]; neuronal cell body [GO:0043025]; peroxisomal membrane [GO:0005778]	Activation of long-chain fatty acids for both synthesis of cellular lipids, and degradation via beta-oxidation. Preferentially uses arachidonate and eicosapentaenoate as substrates.
APOC1	metabolism	cholesterol efflux [GO:0033344]; cholesterol metabolic process [GO:0008203]; chylomicron remnant clearance [GO:0034382]; high-density lipoprotein particle remodeling [GO:0034375]; lipid metabolic process [GO:0006629]; lipoprotein metabolic process [GO:0042157];	fatty acid binding [GO:0005504]; lipase inhibitor activity [GO:0055102]; phosphatidylcholine binding [GO:0031210]; phosphatidylcholine-sterol O-	chylomicron [GO:0042627]; endoplasmic reticulum [GO:0005783]; extracellular exosome [GO:0070062]; high-density lipoprotein particle [GO:0034364]; very-low-density lipoprotein	Inhibitor of lipoprotein binding to the low density lipoprotein (LDL) receptor, LDL receptor-related protein, and very low density lipoprotein (VLDL) receptor. Associates with high density lipoproteins (HDL) and the triacylglycerol-rich lipoproteins in the plasma and makes up about 10% of the protein of the VLDL and 2% of that of HDL. Appears to interfere

		negative regulation of cholesterol transport [GO:0032375]; negative regulation of fatty acid biosynthetic process [GO:0045717]; negative regulation of lipid catabolic process [GO:0050995]; negative regulation of lipid metabolic process [GO:0045833]; negative regulation of lipoprotein lipase activity [GO:0051005]; negative regulation of phosphatidylcholine catabolic process [GO:0010900]; negative regulation of receptor-mediated endocytosis [GO:0048261]; negative regulation of very-low-density lipoprotein particle clearance [GO:0010916]; phospholipid efflux [GO:0033700]; plasma lipoprotein particle remodeling [GO:0034369]; positive regulation of cholesterol esterification [GO:0010873]; regulation of cholesterol transport [GO:0032374]; triglyceride metabolic process [GO:0006641]; very-low-density lipoprotein particle assembly [GO:0034379]; very-low-density lipoprotein particle clearance [GO:0034447]	acyltransferase activator activity [GO:0060228]; phospholipase inhibitor activity [GO:0004859]	particle [GO:0034361]	directly with fatty acid uptake and is also the major plasma inhibitor of cholesteryl ester transfer protein (CETP). Binds free fatty acids and reduces their intracellular esterification. Modulates the interaction of APOE with beta-migrating VLDL and inhibits binding of beta-VLDL to the LDL receptor-related p
SLC2A1	metabolism	cellular response to glucose starvation [GO:0042149];	dehydroascorbic acid transporter	apical plasma membrane [GO:0016324];	Facilitative glucose transporter. This isoform may be responsible for

		glucose transport [GO:0015758]; lactose biosynthetic process [GO:0005989]; L-ascorbic acid metabolic process [GO:0019852]; protein complex assembly [GO:0006461]; regulation of insulin secretion [GO:0050796]; response to osmotic stress [GO:0006970]	activity [GO:0033300]; D-glucose transmembrane transporter activity [GO:0055056]; glucose transmembrane transporter activity [GO:0005355]; identical protein binding [GO:0042802]; protein self-association [GO:0043621]; xenobiotic transporter activity [GO:0042910]	basolateral plasma membrane [GO:0016323]; blood microparticle [GO:0072562]; caveola [GO:0005901]; cell-cell junction [GO:0005911]; cortical actin cytoskeleton [GO:0030864]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; female pronucleus [GO:0001939]; Golgi membrane [GO:0000139]; integral component of plasma membrane [GO:0005887]; melanosome [GO:0042470]; membrane [GO:0016020]; midbody [GO:0030496]; plasma membrane [GO:0005886]	constitutive or basal glucose uptake. Has a very broad substrate specificity; can transport a wide range of aldoses including both pentoses and hexoses. {ECO:0000269|PubMed:18245775, ECO:0000269|PubMed:19449892}.
SLC1A5	metabolism	amino acid transport [GO:0006865]; glutamine transport [GO:0006868]; neutral amino acid transport [GO:0015804]	amino acid transmembrane transporter activity [GO:0015171]; L-glutamine transmembrane transporter activity [GO:0015186]; neutral amino acid transmembrane transporter activity [GO:0015175]; receptor activity [GO:0004872	extracellular exosome [GO:0070062]; Golgi apparatus [GO:0005794]; integral component of plasma membrane [GO:0005887]; melanosome [GO:0042470]; membrane [GO:0016020]; plasma membrane [GO:0005886]	Sodium-dependent amino acids transporter that has a broad substrate specificity, with a preference for zwitterionic amino acids. It accepts as substrates all neutral amino acids, including glutamine, asparagine, and branched-chain and aromatic amino acids, and excludes methylated, anionic, and cationic amino acids. May also be activated by insulin. Through binding of the fusogenic protein syncytin-1/ERVW-1 may mediate trophoblasts syncytialization, the spontaneous fusion of

			]; symporter activity [GO:0015293]; virus receptor activity [GO:0001618]		their plasma membranes, an essential process in placental development (PubMed:10708449, PubMed:23492904). Acts as a cell surface receptor for feline endogenous virus RD114, baboon M7 endoge
ENO2	metabolism	canonical glycolysis [GO:0061621]; gluconeogenesis [GO:0006094]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0004634]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; extracellular space [GO:0005615]; myelin sheath [GO:0043209]; perikaryon [GO:0043204]; phosphopyruvate hydratase complex [GO:0000015]; photoreceptor inner segment [GO:0001917]; plasma membrane [GO:0005886]	Has neurotrophic and neuroprotective properties on a broad spectrum of central nervous system (CNS) neurons. Binds, in a calcium-dependent manner, to cultured neocortical neurons and promotes cell survival (By similarity). {ECO:0000250}.
TMX2	metabolism	cell redox homeostasis [GO:0045454]		cell [GO:0005623]; integral component of membrane [GO:0016021]	
DNAJA1	others	androgen receptor signaling pathway [GO:0030521]; DNA damage response, detection of DNA damage [GO:0042769]; negative regulation of apoptotic process [GO:0043066]; negative regulation of JUN kinase activity [GO:0043508]; negative regulation of protein ubiquitination [GO:0031397]; positive regulation of apoptotic process [GO:0043065]; protein folding [GO:0006457];	ATP binding [GO:0005524]; C3HC4-type RING finger domain binding [GO:0055131]; chaperone binding [GO:0051087]; G-protein coupled receptor binding [GO:0001664]; Hsp70 protein binding [GO:0030544]; low-density lipoprotein particle receptor	cytoplasmic side of endoplasmic reticulum membrane [GO:0098554]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]	Co-chaperone for HSPA8/Hsc70 (PubMed:10816573). Stimulates ATP hydrolysis, but not the folding of unfolded proteins mediated by HSPA1A (in vitro) (PubMed:24318877). Plays a role in protein transport into mitochondria via its role as co-chaperone. Functions as co-chaperone for HSPA1B and negatively regulates the translocation of BAX from the cytosol to mitochondria in response to cellular stress, thereby protecting cells against apoptosis (PubMed:14752510).

		protein localization to mitochondrion [GO:0070585]; regulation of protein transport [GO:0051223]; response to heat [GO:0009408]; response to unfolded protein [GO:0006986]; spermatogenesis [GO:0007283]; sperm motility [GO:0030317]; toxin transport [GO:1901998]	binding [GO:0050750]; metal ion binding [GO:0046872]; ubiquitin protein ligase binding [GO:0031625]		Promotes apoptosis in response to cellular stress mediated by exposure to anisomycin or UV (PubMed:24512202). {ECO:0000269|PubMed:10816573, ECO:0000269|PubMed:14752510, ECO:0000269|PubMed:24318877, ECO:00002
UFD1L	others	ER-associated misfolded protein catabolic process [GO:0071712]; error-free translesion synthesis [GO:0070987]; retrograde protein transport, ER to cytosol [GO:0030970]; skeletal system development [GO:0001501]; ubiquitin-dependent protein catabolic process [GO:0006511]	thiol-dependent ubiquitin-specific protease activity [GO:0004843]	cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; UFD1-NPL4 complex [GO:0036501]; VCP-NPL4-UFD1 AAA ATPase complex [GO:0034098]	Essential component of the ubiquitin-dependent proteolytic pathway which degrades ubiquitin fusion proteins. The ternary complex containing UFD1L, VCP and NPLOC4 binds ubiquitinated proteins and is necessary for the export of misfolded proteins from the ER to the cytoplasm, where they are degraded by the proteasome. The NPLOC4-UFD1L-VCP complex regulates spindle disassembly at the end of mitosis and is necessary for the formation of a closed nuclear envelope. It may be involved in the development of some ectoderm-derived structures.
XPNPEP3	others	glomerular filtration [GO:0003094]; protein processing [GO:0016485]	aminopeptidase activity [GO:0004177]; manganese ion binding [GO:0030145]; metallopeptidase activity [GO:0008237]	extracellular exosome [GO:0070062]; mitochondrion [GO:0005739]	
PSMF1	others	anaphase-promoting complex-dependent catabolic process [GO:0031145]; antigen processing and presentation of exogenous peptide antigen via MHC	endopeptidase inhibitor activity [GO:0004866]; proteasome binding [GO:0070628]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; membrane [GO:0016020]; nucleoplasm	Plays an important role in control of proteasome function. Inhibits the hydrolysis of protein and peptide substrates by the 20S proteasome. Also inhibits the activation of the proteasome by the

		class I, TAP-dependent [GO:0002479]; Fc-epsilon receptor signaling pathway [GO:0038095]; MAPK cascade [GO:0000165]; negative regulation of canonical Wnt signaling pathway [GO:0090090]; negative regulation of proteasomal protein catabolic process [GO:1901799]; negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle [GO:0051436]; NIK/NF-kappaB signaling [GO:0038061]; positive regulation of canonical Wnt signaling pathway [GO:0090263]; positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition [GO:0051437]; proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]; protein polyubiquitination [GO:0000209]; regulation of cellular amino acid metabolic process [GO:0006521]; regulation of mRNA stability [GO:0043488]; stimulatory C-type lectin receptor signaling pathway [GO:0002223]; T cell receptor signaling pathway [GO:0050852]; tumor necrosis		[GO:0005654]; proteasome core complex [GO:0005839]	proteasome regulatory proteins PA700 and PA28. {ECO:0000269|PubMed:10764772}.

		factor-mediated signaling pathway [GO:0033209]; ubiquitin-dependent protein catabolic process [GO:0006511]; Wnt signaling pathway, planar cell polarity pathway [GO:0060071]			
TIMM44	others	protein import into mitochondrial matrix [GO:0030150]; protein targeting to mitochondrion [GO:0006626]	ATP binding [GO:0005524]; chaperone binding [GO:0051087]	mitochondrial inner membrane [GO:0005743]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	Essential component of the PAM complex, a complex required for the translocation of transit peptide-containing proteins from the inner membrane into the mitochondrial matrix in an ATP-dependent manner. Recruits mitochondrial HSP70 to drive protein translocation into the matrix using ATP as an energy source.
GRPEL1	others	protein folding [GO:0006457]	adenyl-nucleotide exchange factor activity [GO:0000774]; unfolded protein binding [GO:0051082]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	Essential component of the PAM complex, a complex required for the translocation of transit peptide-containing proteins from the inner membrane into the mitochondrial matrix in an ATP-dependent manner. Seems to control the nucleotide-dependent binding of mitochondrial HSP70 to substrate proteins.
NUDC	others	cell division [GO:0051301]; cell proliferation [GO:0008283]; mitotic nuclear division [GO:0007067]; multicellular organism development [GO:0007275]; sister chromatid cohesion [GO:0007062]		cytoplasm [GO:0005737]; cytosol [GO:0005829]; microtubule [GO:0005874]; nucleoplasm [GO:0005654]	Plays a role in neurogenesis and neuronal migration (By similarity). Necessary for correct formation of mitotic spindles and chromosome separation during mitosis. Necessary for cytokinesis and cell proliferation. {ECO:0000250, ECO:0000269|PubMed:12679384, ECO:0000269|PubMed:12852857}.
ST13	others	chaperone cofactor-dependent protein refolding [GO:0070389]; negative regulation of protein refolding [GO:0061084];	dATP binding [GO:0032564]; protein binding, bridging [GO:0030674]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062];	One HIP oligomer binds the ATPase domains of at least two HSC70 molecules dependent on activation of the HSC70 ATPase by HSP40. Stabilizes the ADP state of

		protein folding [GO:0006457]; protein homooligomerization [GO:0051260]		protein complex [GO:0043234]	HSC70 that has a high affinity for substrate protein. Through its own chaperone activity, it may contribute to the interaction of HSC70 with various target proteins (By similarity). {ECO:0000250}.
TKT	others	glyceraldehyde-3-phosphate biosynthetic process [GO:0046166]; pentose-phosphate shunt [GO:0006098]; pentose-phosphate shunt, non-oxidative branch [GO:0009052]; regulation of growth [GO:0040008]; xylulose biosynthetic process [GO:0005999]	cofactor binding [GO:0048037]; metal ion binding [GO:0046872]; protein homodimerization activity [GO:0042803]; transketolase activity [GO:0004802]	cytosol [GO:0005829]; extracellular exosome [GO:0070062]; myelin sheath [GO:0043209]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; peroxisome [GO:0005777]; vesicle [GO:0031982]	Catalyzes the transfer of a two-carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate.
SLC 4A1	others	anion transport [GO:0006820]; bicarbonate transport [GO:0015701]; cellular ion homeostasis [GO:0006873]; chloride transmembrane transport [GO:1902476]; chloride transport [GO:0006821]; regulation of intracellular pH [GO:0051453]	anion:anion antiporter activity [GO:0015301]; anion transmembrane transporter activity [GO:0008509]; ankyrin binding [GO:0030506]; bicarbonate transmembrane transporter activity [GO:0015106]; chloride transmembrane transporter activity [GO:0015108]; inorganic anion exchanger activity [GO:0005452]; protein anchor [GO:0043495]; protein homodimerization activity [GO:0042803]	basolateral plasma membrane [GO:0016323]; blood microparticle [GO:0072562]; cortical cytoskeleton [GO:0030863]; extracellular exosome [GO:0070062]; integral component of membrane [GO:0016021]; integral component of plasma membrane [GO:0005887]; plasma membrane [GO:0005886]; Z disc [GO:0030018]	Functions both as a transporter that mediates electroneutral anion exchange across the cell membrane and as a structural protein. Major integral membrane glycoprotein of the erythrocyte membrane; required for normal flexibility and stability of the erythrocyte membrane and for normal erythrocyte shape via the interactions of its cytoplasmic domain with cytoskeletal proteins, glycolytic enzymes, and hemoglobin. Functions as a transporter that mediates the 1:1 exchange of inorganic anions across the erythrocyte membrane. Mediates chloride-bicarbonate exchange in the kidney, and is required for normal acidification of the urine. {ECO:0000269|PubMed:10926824, ECO:

AFM	others	vitamin transport [GO:0051180]	vitamin E binding [GO:0008431]	blood microparticle [GO:0072562]; extracellular exosome [GO:0070062]; extracellular region [GO:0005576]; extracellular space [GO:0005615]	Vitamin E binding protein. May transport vitamin E in body fluids under conditions where the lipoprotein system is not sufficient. May be involved in the regulation and transport of vitamin E at the blood-brain barrier. {ECO:0000269|PubMed:12463752, ECO:0000269|PubMed:15952736, ECO:0000269|PubMed:19046407}.
CHCHD2	transcription/translation	positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; regulation of cellular response to hypoxia [GO:1900037]; transcription, DNA-templated [GO:0006351]	sequence-specific DNA binding [GO:0043565]; transcription factor binding [GO:0008134]	mitochondrion [GO:0005739]; nucleus [GO:0005634]	Transcription factor. Binds to the oxygen responsive element of COX4I2 and activates its transcription under hypoxia conditions (4% oxygen), as well as normoxia conditions (20% oxygen) (PubMed:23303788). {ECO:0000269|PubMed:23303788}.
MRPS23	transcription/translation	mitochondrial translational elongation [GO:0070125]; mitochondrial translational termination [GO:0070126]	poly(A) RNA binding [GO:0044822]; structural constituent of ribosome [GO:0003735]	intermediate filament cytoskeleton [GO:0045111]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; nuclear membrane [GO:0031965]; ribosome [GO:0005840]	
NPM1	transcription/translation	cell aging [GO:0007569]; CENP-A containing nucleosome assembly [GO:0034080]; centrosome cycle [GO:0007098]; DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest [GO:0006977]; DNA repair [GO:0006281]; intracellular protein transport [GO:0006886];	histone binding [GO:0042393]; NF-kappaB binding [GO:0051059]; poly(A) RNA binding [GO:0044822]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; protein kinase	centrosome [GO:0005813]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; focal adhesion [GO:0005925]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus	Involved in diverse cellular processes such as ribosome biogenesis, centrosome duplication, protein chaperoning, histone assembly, cell proliferation, and regulation of tumor suppressors p53/TP53 and ARF. Binds ribosome presumably to drive ribosome nuclear export. Associated with nucleolar ribonucleoprotein structures and bind single-stranded nucleic acids. Acts as a chaperonin for the core histones H3, H2B and H4. Stimulates

		negative regulation of apoptotic process [GO:0043066]; negative regulation of cell proliferation [GO:0008285]; negative regulation of centrosome duplication [GO:0010826]; negative regulation of protein kinase activity by regulation of protein phosphorylation [GO:0044387]; nucleocytoplasmic transport [GO:0006913]; nucleosome assembly [GO:0006334]; positive regulation of cell cycle G2/M phase transition [GO:1902751]; positive regulation of cell proliferation [GO:0008284]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; positive regulation of transcription, DNA-templated [GO:0045893]; positive regulation of translation [GO:0045727]; protein localization [GO:0008104]; protein oligomerization [GO:0051259]; regulation of centriole replication [GO:0046599]; regulation of eIF2 alpha phosphorylation by dsRNA [GO:0060735]; regulation of endodeoxyribonuclease activity [GO:0032071]; regulation of endoribonuclease	binding [GO:0019901]; protein kinase inhibitor activity [GO:0004860]; ribosomal large subunit binding [GO:0043023]; ribosomal small subunit binding [GO:0043024]; RNA binding [GO:0003723]; Tat protein binding [GO:0030957]; transcription coactivator activity [GO:0003713]; unfolded protein binding [GO:0051082]	[GO:0005634]; spindle pole centrosome [GO:0031616]	APEX1 endonuclease activity on apurinic/apyrimidinic (AP) double-stranded DNA but inhibits APEX1 endonuclease activity on AP single-stranded RNA. May exert a control of APEX1 endonuclease activity within nucleoli devoted to repair AP on r

		activity [GO:0060699]; response to stress [GO:0006950]; ribosome assembly [GO:0042255]; signal transduction [GO:0007165]; viral process [GO:0016032]			
WARS	transcription/translation	angiogenesis [GO:0001525]; negative regulation of cell proliferation [GO:0008285]; regulation of angiogenesis [GO:0045765]; translation [GO:0006412]; tRNA aminoacylation for protein translation [GO:0006418]; tryptophanyl-tRNA aminoacylation [GO:0006436]	ATP binding [GO:0005524]; tryptophan-tRNA ligase activity [GO:0004830]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	Isoform 1, isoform 2 and T1-TrpRS have aminoacylation activity while T2-TrpRS lacks it. Isoform 2, T1-TrpRS and T2-TrpRS possess angiostatic activity whereas isoform 1 lacks it. T2-TrpRS inhibits fluid shear stress-activated responses of endothelial cells. Regulates ERK, Akt, and eNOS activation pathways that are associated with angiogenesis, cytoskeletal reorganization and shear stress-responsive gene expression. {ECO:0000269|PubMed:11773625, ECO:0000269|PubMed:11773626, ECO:0000269|PubMed:1373391, ECO:0000269|PubMed:14630953}.
NCL	transcription/translation	angiogenesis [GO:0001525]; cellular response to lipopolysaccharide [GO:0071222]; endocytosis [GO:0006897]; liver regeneration [GO:0097421]; negative regulation of apoptotic process [GO:0043066]; positive regulation of interleukin-6 secretion [GO:2000778]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; positive regulation of transcription of	calcium ion binding [GO:0005509]; identical protein binding [GO:0042802]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; protein C-terminus binding [GO:0008022]; RNA binding [GO:0003723]; rRNA primary transcript	cell cortex [GO:0005938]; cell surface [GO:0009986]; cytoplasmic ribonucleoprotein granule [GO:0036464]; dense fibrillar component [GO:0001651]; extracellular exosome [GO:0070062]; fibrillar center [GO:0001650]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleolus	Nucleolin is the major nucleolar protein of growing eukaryotic cells. It is found associated with intranucleolar chromatin and pre-ribosomal particles. It induces chromatin decondensation by binding to histone H1. It is thought to play a role in pre-rRNA transcription and ribosome assembly. May play a role in the process of transcriptional elongation. Binds RNA oligonucleotides with 5'-UUAGGG-3' repeats more tightly than the telomeric single-stranded DNA 5'-TTAGGG-3' repeats. {ECO:0000269|PubMed:10393184}.

		nuclear large rRNA transcript from RNA polymerase I promoter [GO:1901838]; positive regulation of tumor necrosis factor production [GO:0032760]; regulation of rRNA processing [GO:2000232]; spermatogenesis [GO:0007283]	binding [GO:0042134]; selenocysteine insertion sequence binding [GO:0035368]; single-stranded DNA binding [GO:0003697]; telomeric DNA binding [GO:0042162]	[GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	
STIP1	transcription/translation	response to stress [GO:0006950]	poly(A) RNA binding [GO:0044822]	Golgi apparatus [GO:0005794]; myelin sheath [GO:0043209]; nucleus [GO:0005634]; protein complex [GO:0043234]	Mediates the association of the molecular chaperones HSC70 and HSP90 (HSPCA and HSPCB).
DDX39B	transcription/translation	liver development [GO:0001889]; mRNA 3'-end processing [GO:0031124]; mRNA export from nucleus [GO:0006406]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation of DNA damage checkpoint [GO:2000002]; positive regulation of cell growth involved in cardiac muscle cell development [GO:0061051]; positive regulation of DNA biosynthetic process [GO:2000573]; positive regulation of DNA-templated transcription, elongation [GO:0032786]; positive regulation of translation [GO:0045727]; positive regulation of vascular smooth	ATPase activity [GO:0016887]; ATP binding [GO:0005524]; ATP-dependent protein binding [GO:0043008]; ATP-dependent RNA helicase activity [GO:0004004]; poly(A) RNA binding [GO:0044822]; RNA-dependent ATPase activity [GO:0008186]; U4 snRNA binding [GO:0030621]; U6 snRNA binding [GO:0017070]	cytoplasm [GO:0005737]; nuclear matrix [GO:0016363]; nuclear speck [GO:0016607]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; transcription export complex [GO:0000346]	Involved in nuclear export of spliced and unspliced mRNA. Assembling component of the TREX complex which is thought to couple mRNA transcription, processing and nuclear export, and specifically associates with spliced mRNA and not with unspliced pre-mRNA. TREX is recruited to spliced mRNAs by a transcription-independent mechanism, binds to mRNA upstream of the exon-junction complex (EJC) and is recruited in a splicing- and cap-dependent manner to a region near the 5' end of the mRNA where it functions in mRNA export to the cytoplasm via the TAP/NFX1 pathway. May undergo several rounds of ATP hydrolysis during assembly of TREX to drive subsequent loading of com

		muscle cell proliferation [GO:1904707]; RNA export from nucleus [GO:0006405]; RNA secondary structure unwinding [GO:0010501]; RNA splicing [GO:0008380]; spliceosomal complex assembly [GO:0000245]; termination of RNA polymerase II transcription [GO:0006369]; viral mRNA export from host cell nucleus [GO:0046784]			
HNRNPU	transcription/translation	cellular response to dexamethasone stimulus [GO:0071549]; circadian regulation of gene expression [GO:0032922]; CRD-mediated mRNA stabilization [GO:0070934]; gene expression [GO:0010467]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation of telomere maintenance via telomerase [GO:0032211]; osteoblast differentiation [GO:0001649]; positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity [GO:2000373]; positive regulation of gene expression [GO:0010628]; RNA processing [GO:0006396]	ATP binding [GO:0005524]; core promoter binding [GO:0001047]; DNA binding [GO:0003677]; enhancer binding [GO:0035326]; poly(A) RNA binding [GO:0044822]; poly(G) binding [GO:0034046]; ribonucleoprotein complex binding [GO:0043021]; RNA binding [GO:0003723]; telomerase RNA binding [GO:0070034]	catalytic step 2 spliceosome [GO:0071013]; cell surface [GO:0009986]; CRD-mediated mRNA stability complex [GO:0070937]; cytoplasmic ribonucleoprotein granule [GO:0036464]; intracellular ribonucleoprotein complex [GO:0030529]; membrane [GO:0016020]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	Component of the CRD-mediated complex that promotes MYC mRNA stabilization. Binds to pre-mRNA. Has high affinity for scaffold-attached region (SAR) DNA. Binds to double- and single-stranded DNA and RNA. Plays a role in the circadian regulation of the core clock component ARNTL/BMAL1 transcription (By similarity). {ECO:0000250|UniProtKB:Q8VEK3, ECO:0000269|PubMed:19029303}.
RCN1	transcription/translation	camera-type eye development [GO:0043010]; in utero embryonic development [GO:0001701]	calcium ion binding [GO:0005509]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]	May regulate calcium-dependent activities in the endoplasmic reticulum lumen or post-ER compartment.

RPL9	transcription/translation	cytoplasmic translation [GO:0002181]; nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]; SRP-dependent cotranslational protein targeting to membrane [GO:0006614]; translation [GO:0006412]; translational initiation [GO:0006413]; viral transcription [GO:0019083]	RNA binding [GO:0003723]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; cytosolic large ribosomal subunit [GO:0022625]; focal adhesion [GO:0005925]; membrane [GO:0016020]; nucleolus [GO:0005730]; nucleus [GO:0005634]; ribosome [GO:0005840]	
EARS2	transcription/translation	glutamyl-tRNA aminoacylation [GO:0006424]; tRNA aminoacylation for mitochondrial protein translation [GO:0070127]	ATP binding [GO:0005524]; glutamate-tRNA(Gln) ligase activity [GO:0050561]; glutamate-tRNA ligase activity [GO:0004818]; RNA binding [GO:0003723]; tRNA binding [GO:0000049]	mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]	Catalyzes the attachment of glutamate to tRNA(Glu) in a two-step reaction: glutamate is first activated by ATP to form Glu-AMP and then transferred to the acceptor end of tRNA(Glu). {ECO:0000250}.
XPO7	transcription/translation	mRNA transport [GO:0051028]; protein export from nucleus [GO:0006611]	nuclear export signal receptor activity [GO:0005049]; Ran GTPase binding [GO:0008536]	cytoplasm [GO:0005737]; nuclear pore [GO:0005643]; nucleus [GO:0005634]	Mediates the nuclear export of proteins (cargos) with broad substrate specificity. In the nucleus binds cooperatively to its cargo and to the GTPase Ran in its active GTP-bound form. Docking of this trimeric complex to the nuclear pore complex (NPC) is mediated through binding to nucleoporins. Upon transit of a nuclear export complex into the cytoplasm, disassembling of the complex and hydrolysis of Ran-GTP to Ran-GDP (induced by RANBP1 and RANGAP1, respectively) cause release of the cargo from the

					export receptor. XPO7 then return to the nuclear compartment and mediate another round of transport. The directionality of nuclear export is thought to be conferred
RPA1	transcription/translation	base-excision repair [GO:0006284]; DNA damage response, detection of DNA damage [GO:0042769]; DNA-dependent DNA replication [GO:0006261]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]; double-strand break repair via homologous recombination [GO:0000724]; error-free translesion synthesis [GO:0070987]; error-prone translesion synthesis [GO:0042276]; G1/S transition of mitotic cell cycle [GO:0000082]; interstrand cross-link repair [GO:0036297]; mismatch repair [GO:0006298]; nucleotide-excision repair [GO:0006289]; nucleotide-excision repair, DNA gap filling [GO:0006297]; nucleotide-excision repair, DNA incision [GO:0033683]; nucleotide-excision repair, DNA incision, 3'-to lesion [GO:0006295]; nucleotide-excision repair, DNA incision, 5'-to lesion [GO:0006296]; nucleotide-excision	damaged DNA binding [GO:0003684]; metal ion binding [GO:0046872]; single-stranded DNA binding [GO:0003697]	DNA replication factor A complex [GO:0005662]; nuclear chromosome, telomeric region [GO:0000784]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; PML body [GO:0016605]	As part of the heterotrimeric replication protein A complex (RPA/RP-A), binds and stabilizes single-stranded DNA intermediates, that form during DNA replication or upon DNA stress. It prevents their reannealing and in parallel, recruits and activates different proteins and complexes involved in DNA metabolism. Thereby, it plays an essential role both in DNA replication and the cellular response to DNA damage (PubMed:9430682). In the cellular response to DNA damage, the RPA complex controls DNA repair and DNA damage checkpoint activation. Through recruitment of ATRIP activates the ATR kinase a master regulator of the DNA damage response (PubMed:24332808). It is

		repair, preincision complex assembly [GO:0006294]; nucleotide-excision repair, preincision complex stabilization [GO:0006293]; protein sumoylation [GO:0016925]; regulation of cellular response to heat [GO:1900034]; regulation of signal transduction by p53 class mediator [GO:1901796]; telomere maintenance [GO:0000723]; telomere maintenance via recombination [GO:0000722]; transcription-coupled nucleotide-excision repair [GO:0006283]; translesion synthesis [GO:0019985]			
HNRNPR	transcription/translation	circadian rhythm [GO:0007623]; gene expression [GO:0010467]; mRNA destabilization [GO:0061157]; mRNA processing [GO:0006397]; mRNA splicing, via spliceosome [GO:0000398]; negative regulation of catalytic activity [GO:0043086]; positive regulation of mRNA catabolic process [GO:0061014]	mRNA 3'-UTR binding [GO:0003730]; nucleotide binding [GO:0000166]; poly(A) RNA binding [GO:0044822]; RNA binding [GO:0003723]	axon terminus [GO:0043679]; catalytic step 2 spliceosome [GO:0071013]; dendrite [GO:0030425]; endoplasmic reticulum [GO:0005783]; growth cone [GO:0030426]; intracellular ribonucleoprotein complex [GO:0030529]; nucleoplasm [GO:0005654]; spliceosomal complex [GO:0005681]	Component of ribonucleosomes, which are complexes of at least 20 other different heterogenious nuclear ribonucleoproteins (hnRNP). hnRNP play an important role in processing of precursor mRNA in the nucleus.
BASP1	transcription/translation	diaphragm development [GO:0060539]; glomerular visceral epithelial cell differentiation [GO:0072112]; gonad development [GO:0008406]; mesenchymal to	protein domain specific binding [GO:0019904]; transcription corepressor activity [GO:0003714	cell junction [GO:0030054]; cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; extracellular exosome [GO:0070062]; growth cone	

		epithelial transition [GO:0060231]; metanephric mesenchyme development [GO:0072075]; negative regulation of transcription, DNA-templated [GO:0045892]; positive regulation of heart growth [GO:0060421]; positive regulation of metanephric ureteric bud development [GO:2001076]; substantia nigra development [GO:0021762]; thorax and anterior abdomen determination [GO:0007356]	]; transcription regulatory region DNA binding [GO:0044212]	[GO:0030426]; nuclear speck [GO:0016607]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; vesicle [GO:0031982]	
EEF1E1	transcription/translation	glutathione metabolic process [GO:0006749]; negative regulation of cell proliferation [GO:0008285]; positive regulation of apoptotic process [GO:0043065]; positive regulation of cellular senescence [GO:2000774]; positive regulation of DNA damage response, signal transduction by p53 class mediator [GO:0043517]; tRNA aminoacylation for protein translation [GO:0006418]	glutathione transferase activity [GO:0004364]; translation elongation factor activity [GO:0003746]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; extracellular exosome [GO:0070062]; nucleus [GO:0005634]	Positive modulator of ATM response to DNA damage.
EIF3K	transcription/translation	formation of translation preinitiation complex [GO:0001731]; regulation of translational initiation [GO:0006446]; translational initiation [GO:0006413]	ribosome binding [GO:0043022]; translation initiation factor activity [GO:0003743]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; eukaryotic 43S preinitiation complex [GO:0016282]; eukaryotic 48S preinitiation complex [GO:0033290]; eukaryotic translation	Component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is required for several steps in the initiation of protein synthesis. The eIF-3 complex associates with the 40S ribosome and facilitates the recruitment of eIF-1, eIF-1A, eIF-2:GTP:methionyl-tRNAi and eIF-5 to form the 43S preinitiation complex (43S

				initiation factor 3 complex [GO:0005852]; extracellular exosome [GO:0070062]; membrane [GO:0016020]; nucleus [GO:0005634]	PIC). The eIF-3 complex stimulates mRNA recruitment to the 43S PIC and scanning of the mRNA for AUG recognition. The eIF-3 complex is also required for disassembly and recycling of post-termination ribosomal complexes and subsequently prevents premature joining of the 40S and 60S ribosomal subunits prior to initiation.

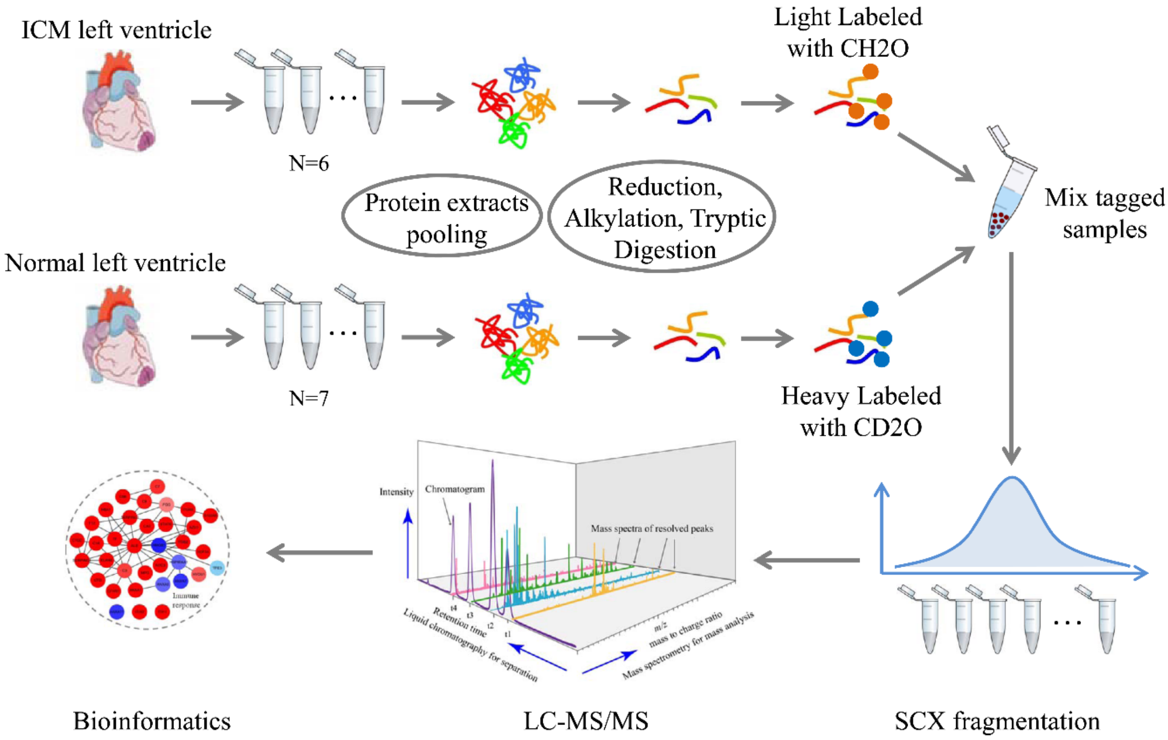

Figure S1. Schematic representation of the quantitative proteomics experiment. Proteins were extracted from the left ventricles of 7 normal heart donors and 6 ICM patients. After pooling the protein extracts, the normal and ICM samples were reduced, alkylated and tryptically digested. Then, by using a stable isotope dimethyl-labeling strategy, we performed comparative quantitative proteomic analysis of the left ventricles from normal heart donors (heavy-labeled with CD_2O) and ICM patients (light-labeled with CH_2O).

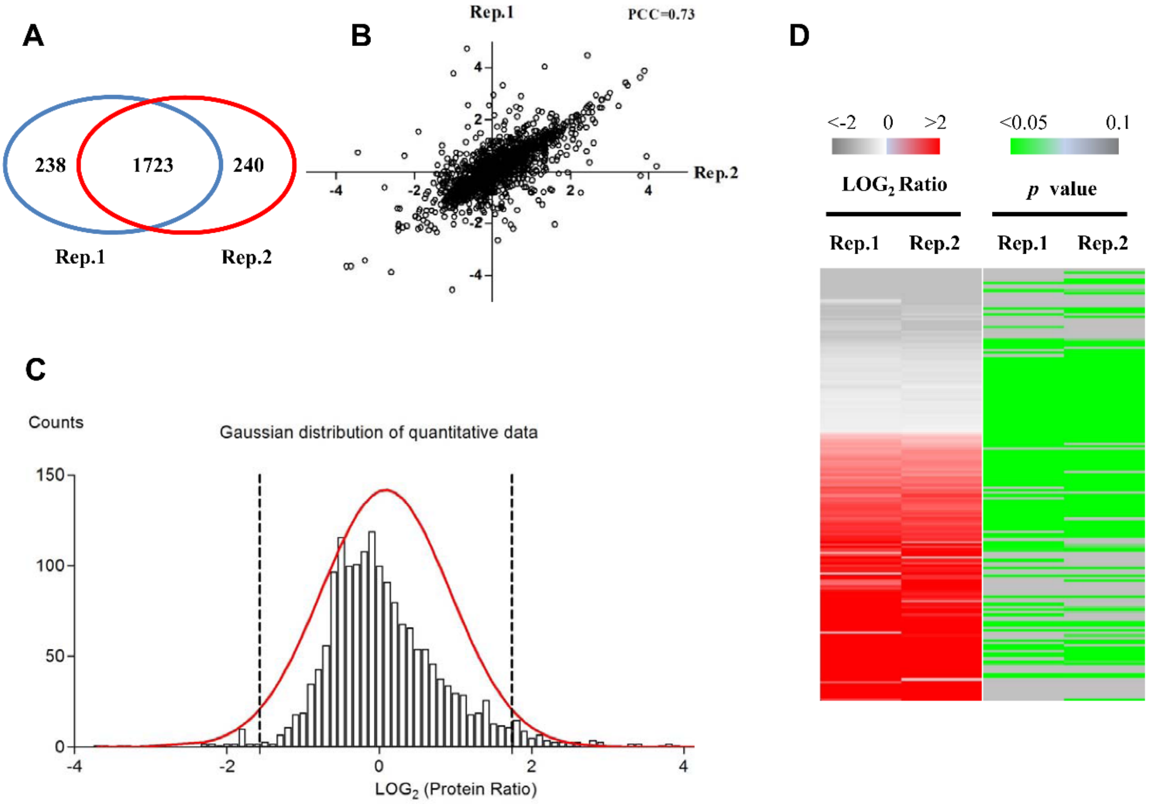

Figure S2. Quantitative proteomics data overview. A. A total of 2201 proteins were successfully quantified in the two experimental replicates, among which 1,723 proteins overlapped. **B.** Pearson correlation analysis of the overlapped proteins showed a good correlation (Pearson correlation coefficient (PCC) = 0.73) for the two replicates. **C.** Gaussian distribution of the average quantitative data (Log_2 (ratio)) shared by the two replicates. **D.** Heatmap of the 167 differentially expressed proteins (average ratio of <0.8 or >1.2 and $p<0.05$ in both repetitions or ratio of <0.67 or >1.5 in both repetitions) in the left ventricles of ICM patients.

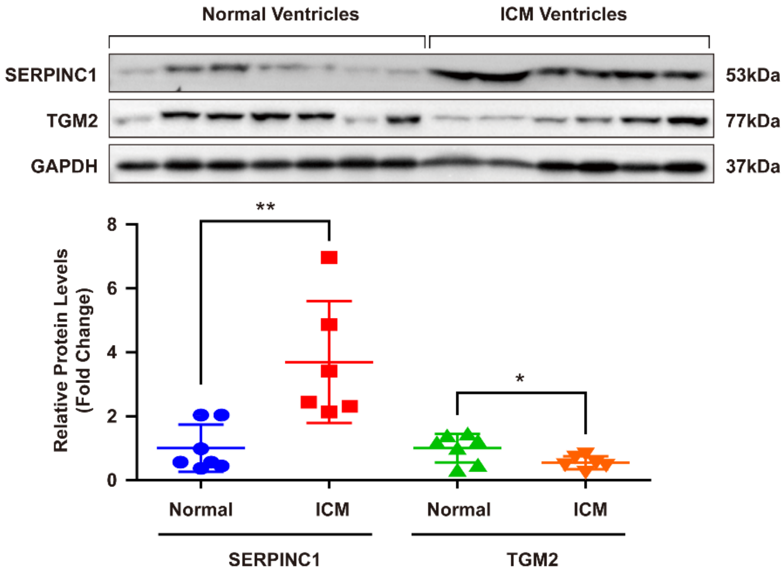

Figure S3. Western blot analysis of TGM2 and SERPINC1. The downregulation of the protein TGM2 and the upregulation of the protein SERPINC1 were confirmed by western blot analysis (ICM group: n=6; normal group: n=7). GAPDH served as a loading control.