

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|----------------|-------------------|--|--|--|-------------------------|
| 1 1433B_HUMAN | YWHAB | P31946 | 14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1) (KCIP-1) (Protein 1054) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed] | Ras protein signal transduction; activation of pro-apoptotic gene products; centrosome; cytosol; enzyme binding; melanosome; negative regulation of protein amino acid dephosphorylation; nucleus; perinuclear region of cytoplasm; positive regulation of catalytic activity; protein domain specific binding | Cytoplasm. Melanosome. | 14-3-3 family |
| 2 1433E_HUMAN | YWHAE | P62258 | 14-3-3 protein epsilon (14-3-3E) | enzyme binding; interspecies interaction between organisms; intracellular signaling cascade; melanosome | Cytoplasm. Melanosome. | 14-3-3 family |
| 3 1433G_HUMAN | YWHAG | P61981 | 14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed] | cytoplasm; insulin-like growth factor receptor binding; negative regulation of protein kinase activity; protein kinase C binding; protein kinase C inhibitor activity; regulation of neuron differentiation; regulation of signal transduction; regulation of synaptic plasticity | Cytoplasm. | 14-3-3 family |
| 4 1433Z_HUMAN | YWHAZ | P63104 | 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) | anti-apoptosis; melanosome; signal transduction; transcription factor binding | Cytoplasm. Melanosome. | 14-3-3 family |
| 5 1A03_HUMAN | HLA-A (HLAA) | P04439 | HLA class I histocompatibility antigen, A-3 alpha chain (MHC class I antigen A*3) | MHC class I protein complex; MHC class I receptor activity; antigen processing and presentation of peptide antigen via MHC class I; immune response; integral to plasma membrane; interspecies interaction between organisms; protein binding | Membrane; Single-pass type I membrane protein. | MHC class I family |
| 6 1C07_HUMAN | HLA-C (HLAC) | P10321 | HLA class I histocompatibility antigen, Cw-7 alpha chain (MHC class I antigen Cw*7) | MHC class I protein complex; antigen processing and presentation of peptide antigen via MHC class I; immune response; integral to membrane; interspecies interaction between organisms | Membrane; Single-pass type I membrane protein. | MHC class I family |
| 7 A4_HUMAN | APP (A4) (AD1) | P05067 | Amyloid beta A4 protein (Alzheimer disease amyloid protein) (ABPP) (APP1) (APP) (PreA4) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) [Cleaved into: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-secretase C-terminal fragment 59 (Gamma-CTF(59)) (Amyloid intracellular domain 59) (AICD-59) (AID(59)); Gamma-secretase C-terminal fragment 57 (Gamma-CTF(57)) (Amyloid intracellular domain 57) (AICD-57) (AID(57)); Gamma-secretase C-terminal fragment 50 (Gamma-CTF(50)) (Amyloid intracellular domain 50) (AICD-50) (AID(50)); C31] | Golgi apparatus; Notch signaling pathway; acetylcholine receptor binding; apoptosis; cell adhesion; cell surface; cellular copper ion homeostasis; coated pit; copper ion binding; endocytosis; extracellular region; heparin binding; identical protein binding; integral to plasma membrane; iron ion binding; neuromuscular process; platelet alpha granule lumen; serine-type endopeptidase inhibitor activity; zinc ion binding | Membrane; Single-pass type I membrane protein. Membrane , clathrin-coated pit. | APP family |
| 8 ABI1_HUMAN | ABI1 (SSH3BP1) | Q8IZP0 | Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain-binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AbiBP4) | cell junction; cytoskeletal protein binding; cytoskeleton; cytosol; endoplasmic reticulum; filopodium; growth cone; lamellipodium; negative regulation of cell proliferation; nucleus; peptidyl-tyrosine phosphorylation; soluble fraction; synapse; synaptosome; transmembrane receptor protein tyrosine kinase signaling pathway | Cytoplasm. Nucleus. Cell projection , lamellipodium. Cell projection , filopodium. Cell projection , growth cone. Cell junction , synapse , synaptosome. Cytoplasm , cytoskeleton. | ABI family |
| 9 ACOX1_HUMAN | ACOX1 (ACOX) | Q15067 | Peroxisomal acyl-coenzyme A oxidase 1 (AOX) (EC 1.3.3.6) (Palmitoyl-CoA oxidase) (Straight-chain acyl-CoA oxidase) (SCOX) | FAD binding; acyl-CoA dehydrogenase activity; acyl-CoA oxidase activity; electron carrier activity; fatty acid beta-oxidation; generation of precursor metabolites and energy; oxidation reduction; prostaglandin metabolic process; protein N-terminus binding | Peroxisome. | Acyl-CoA oxidase family |
| 10 ACTB_HUMAN | ACTB | P60709 | Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed] | ATP binding; NuA4 histone acetyltransferase complex; cell motion; histone methyltransferase complex; nitric-oxide synthase binding; sensory perception of sound; structural constituent of cytoskeleton | Cytoplasm , cytoskeleton. | Actin family |
| 11 ACTN1_HUMAN | ACTN1 | P12814 | Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle alpha-actinin-1) (F-actin cross-linking protein) | Z disc; actin binding; calcium ion binding; cytoskeleton; focal adhesion; focal adhesion formation; integrin binding; negative regulation of cell motion; nucleolus; pseudopodium; regulation of apoptosis; vinculin binding | Cytoplasm , cytoskeleton. Cytoplasm , myofibril , sarcomere , Z-disk. | Alpha-actinin family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|---------------------------|-------------------|--|---|---|---|
| 12 ACTN2_HUMAN | ACTN2 | P35609 | Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein) | FATZ 1 binding; Z disc; ZASP binding; actin binding; actin filament; calcium ion binding; dendritic spine; filopodium; focal adhesion; focal adhesion formation; identical protein binding; integrin binding; microspike assembly; nucleolus; protein dimerization activity; protein homotetramerization; pseudopodium; regulation of apoptosis; structural constituent of muscle; titin Z domain binding; titin binding | Cytoplasm , myofibril , sarcomere , Z-disk. | Alpha-actinin family |
| 13 ACTN4_HUMAN | ACTN4 | O43707 | Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) | actin filament binding; calcium ion binding; integrin binding; nucleolus; nucleoside binding; perinuclear region of cytoplasm; positive regulation of cell motion; positive regulation of sodium:hydrogen antiporter activity; protein complex; protein homodimerization activity; pseudopodium; regulation of apoptosis | Nucleus. Cytoplasm. | Alpha-actinin family |
| 14 ACTS_HUMAN | ACTA1 (ACTA) | P68133 | Actin, alpha skeletal muscle (Alpha-actin-1) | ADP binding; ATP binding; actin filament; muscle contraction; muscle thin filament assembly; myosin binding; skeletal muscle fiber development; stress fiber; striated muscle thin filament; structural constituent of cytoskeleton | Cytoplasm , cytoskeleton. | Actin family |
| 15 ACTZ_HUMAN | ACTR1A (CTRNI) | P61163 | Alpha-centractin (Centractin) (Centrosome-associated actin homolog) (Actin-RPV) (ARP1) | ATP binding; centrosome; dynactin complex; protein binding; vesicle-mediated transport | Cytoplasm , cytoskeleton. Centrosome. | Actin family, ARP1 subfamily |
| 16 ADA10_HUMAN | ADAM10 (KUZ) (MADM) | O14672 | Disintegrin and metalloproteinase domain-containing protein 10 (ADAM 10) (EC 3.4.24.81) (Mammalian disintegrin-metalloprotease) (Kuzbanian protein homolog) (CDw156) (CD antigen CD156c) | Golgi-associated vesicle; Notch signaling pathway; PMA-inducible membrane protein ectodomain proteolysis; SH3 domain binding; cell surface; cell-cell signaling; constitutive protein ectodomain proteolysis; endomembrane system; in utero embryonic development; integral to membrane; integrin binding; integrin-mediated signaling pathway; metalloendopeptidase activity; monocyte activation; negative regulation of cell adhesion; nucleus; plasma membrane; positive regulation of T cell chemotaxis; positive regulation of cell growth; positive regulation of cell proliferation; protein amino acid phosphorylation; protein homodimerization activity; protein kinase binding; response to tumor necrosis factor; zinc ion binding | Cell membrane; Single-pass type I membrane protein. Endomembrane system; Single-pass type I membrane protein. | |
| 17 ADT1_HUMAN | SLC25A4 (ANT1) | P12235 | ADP/ATP translocase 1 (Adenine nucleotide translocator 1) (ANT 1) (ADP,ATP carrier protein 1) (Solute carrier family 25 member 4) (ADP,ATP carrier protein, heart/skeletal muscle isoform T1) | adenine transmembrane transporter activity; generation of precursor metabolites and energy; integral to plasma membrane; interspecies interaction between organisms; mitochondrial genome maintenance; mitochondrial inner membrane; protein binding | Mitochondrion inner membrane; Multi-pass membrane protein. | Mitochondrial carrier family |
| 18 ALDOA_HUMAN | ALDOA (ALDA) | P04075 | Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) | ATP biosynthetic process; I band; actin binding; actin cytoskeleton; actin filament organization; extracellular vesicular exosome; fructose 1,6-bisphosphate metabolic process; fructose binding; fructose-bisphosphate aldolase activity; glycolysis; identical protein binding; muscle maintenance; nucleus; regulation of cell shape; striated muscle contraction; tubulin binding | | Class I fructose-bisphosphate aldolase family |
| 19 ANXA5_HUMAN | ANXA5 (ANX5) (ENX2) (PP4) | P08758 | Annexin A5 (Annexin-5) (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (Placental anticoagulant protein 4) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchorin CII) | anti-apoptosis; blood coagulation; calcium ion binding; calcium-dependent phospholipid binding; cytoplasm; negative regulation of coagulation; phospholipase inhibitor activity; protein binding; signal transduction | | Annexin family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|------------|---|-------------------|--|---|---|---|
| 20 | APIG1_HUMAN APIG1 (ADTG) (CLAPG1) | O43747 | AP-1 complex subunit gamma-1 (Adapter-related protein complex 1 subunit gamma-1) (Adaptor protein complex AP-1 subunit gamma-1) (Golgi adaptor HA1/AP1 adaptin subunit gamma-1) (Gamma1-adaptin) (Clathrin assembly protein complex 1 gamma-1 large chain) | Golgi apparatus part; clathrin adaptor complex; clathrin coated vesicle membrane; cytosol; endocytosis; intracellular protein transport; protein binding; protein transporter activity | Golgi apparatus. Cytoplasmic vesicle, clathrin-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. | Adaptor complexes large subunit family |
| 21 | ARF1_HUMAN ARF1 | P84077 | ADP-ribosylation factor 1 | COPI coating of Golgi vesicle; GTP binding; GTPase activity; Golgi membrane; cytosol; plasma membrane; protein binding; protein transport; receptor signaling protein activity; retrograde vesicle-mediated transport, Golgi to ER; small GTPase mediated signal transduction | Golgi apparatus. | Small GTPase superfamily, Arf family |
| 22 | ARMET_HUMAN ARMET (ARP) | P55145 | Protein ARMET (Mesencephalic astrocyte-derived neurotrophic factor) (MANF) (Arginine-rich protein) | extracellular region; growth factor activity | Secreted. | ARMET family |
| 23 | ARP2_HUMAN ACTR2 (ARP2) | P61160 | Actin-related protein 2 (Actin-like protein 2) | ATP binding; Arp2/3 protein complex; actin binding; cell motion; cell projection; cytoplasm | Cytoplasm, cytoskeleton. Cell projection. | Actin family, ARP2 subfamily |
| 24 | ARP3_HUMAN ACTR3 (ARP3) | P61158 | Actin-related protein 3 (Actin-like protein 3) | ATP binding; Arp2/3 protein complex; actin binding; cell motion; cytoplasm; regulation of actin filament polymerization | Cytoplasm, cytoskeleton. Cell projection. | Actin family, ARP3 subfamily |
| 25 | ARPC2_HUMAN ARPC2 (ARC34) (PRO2446) | O15144 | Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC) | Arp2/3 protein complex; actin binding; cell motion; cell projection; cytoplasm; structural constituent of cytoskeleton | Cytoplasm, cytoskeleton. Cell projection. | ARPC2 family |
| 26 | ARPC5_HUMAN ARPC5 (ARC16) | O15511 | Actin-related protein 2/3 complex subunit 5 (Arp2/3 complex 16 kDa subunit) (p16-ARC) | Arp2/3 protein complex; actin binding; actin cytoskeleton organization; cell motion; cell projection; cytoplasm; regulation of actin filament polymerization; structural constituent of cytoskeleton | Cytoplasm, cytoskeleton. Cell projection. | ARPC5 family |
| 27 | AT2A1_HUMAN ATP2A1 | O14983 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (SERCA1) (EC 3.6.3.8) (Calcium pump 1) (Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform) (SR Ca(2+)-ATPase 1) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase) | ATP binding; ATP biosynthetic process; calcium ion binding; calcium ion transport; calcium-transporting ATPase activity; integral to membrane; magnesium ion binding; positive regulation of fast-twitch skeletal muscle fiber contraction; protein binding; sarcoplasmic reticulum membrane | Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein. | Cation transport ATPase (P-type) family, Type IIA subfamily |
| 28 | AT2A2_HUMAN ATP2A2 (ATP2B) | P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SERCA2) (EC 3.6.3.8) (Calcium pump 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (SR Ca(2+)-ATPase 2) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase) | ATP binding; ATP biosynthetic process; S100 alpha binding; calcium ion binding; calcium-transporting ATPase activity; cell adhesion; epidermis development; integral to plasma membrane; magnesium ion binding; microsome; sarcoplasmic reticulum calcium ion transport; sarcoplasmic reticulum membrane | Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein. | Cation transport ATPase (P-type) family, Type IIA subfamily |
| 29 | AT2A3_HUMAN ATP2A3 | Q93084 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 (SERCA3) (EC 3.6.3.8) (Calcium pump 3) (SR Ca(2+)-ATPase 3) | ATP binding; ATP biosynthetic process; calcium ion binding; calcium ion transport; calcium-transporting ATPase activity; integral to membrane; magnesium ion binding; nuclear membrane; protein binding; sarcoplasmic reticulum membrane | Nucleus membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein. | Cation transport ATPase (P-type) family, Type IIA subfamily |
| 30 | ATD3A_HUMAN ATAD3A | Q9NVI7 | ATPase family AAA domain-containing protein 3A | ATP binding; nucleoside-triphosphatase activity; protein binding | | AAA ATPase family |
| 31 | ATP5H_HUMAN ATP5H (My032) | O75947 | ATP synthase subunit d, mitochondrial | ATP synthesis coupled proton transport; hydrogen ion transmembrane transporter activity; mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) | Mitochondrion. Mitochondrion inner membrane. | ATPase d subunit family |
| 32 | ATPB_HUMAN ATP5B (ATPMB) (ATPSB) | P06576 | ATP synthase subunit beta, mitochondrial (EC 3.6.3.14) | ATP binding; ATP synthesis coupled proton transport; MHC class I protein binding; angiogenesis; cell surface; eukaryotic cell surface binding; hydrogen ion transporting ATP synthase activity, rotational mechanism; hydrogen-exporting ATPase activity, phosphorylative mechanism; mitochondrial nucleoid; mitochondrial proton-transporting ATP synthase, catalytic core; plasma membrane; proton-transporting ATPase activity, rotational mechanism; regulation of intracellular pH | Mitochondrion. Mitochondrion inner membrane. | ATPase alpha/beta chains family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|---|-------------------|--|--|---|--|
| 33 ATPK_HUMAN | ATP5J2 (ATP5JL) | P56134 | ATP synthase subunit f, mitochondrial | ATP biosynthetic process; hydrogen ion transmembrane transporter activity; mitochondrial proton-transporting ATP synthase complex; proton transport; proton-transporting ATP synthase complex, coupling factor F(o) | Mitochondrion. Mitochondrion inner membrane. | ATPase F chain family |
| 34 ATPO_HUMAN | ATP5O (ATPO) | P48047 | ATP synthase subunit O, mitochondrial (Oligomycin sensitivity conferral protein) (OSCP) | ATP catabolic process; drug binding; hydrogen ion transporting ATP synthase activity, rotational mechanism; mitochondrial ATP synthesis coupled proton transport; mitochondrial proton-transporting ATP synthase complex; plasma membrane; proton-transporting ATP synthase complex, catalytic core F(1); proton-transporting ATPase activity, rotational mechanism | Mitochondrion. Mitochondrion inner membrane. | ATPase delta chain family |
| 35 B2MG_HUMAN | B2M (CDABP0092) (HDCMA22P) | P61769 | Beta-2-microglobulin [Cleaved into: Beta-2-microglobulin form pI 5.3] | Golgi membrane; MHC class I protein complex; antigen processing and presentation of peptide antigen via MHC class I; early endosome membrane; extracellular region; immune response; protein binding | Secreted. | Beta-2-microglobulin family |
| 36 BET1_HUMAN | BET1 | O15155 | BET1 homolog (hBET1) (Golgi vesicular membrane-trafficking protein p18) | ER to Golgi vesicle-mediated transport; Golgi membrane; endoplasmic reticulum membrane; integral to membrane; protein binding; protein transport | Golgi apparatus membrane; Single-pass type IV membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. | BET1 family |
| 37 C109A_HUMAN | CCDC109A (C10orf42) | Q8NE86 | Coiled-coil domain-containing protein 109A | integral to membrane | Membrane; Multi-pass membrane protein. | CCDC109 family |
| 38 CALM_HUMAN | CALM1 (CALM) (CAM) (CAM1); CALM2 (CAM2) (CAMB); CALM3 (CALML2) (CAM3) (CAMC) (CAMIII) | P62158 | Calmodulin (CaM) | G-protein coupled receptor protein signaling pathway; N-terminal myristoylation domain binding; calcium ion binding; centrosome; cytosol; negative regulation of ryanodine-sensitive calcium-release channel activity; plasma membrane; positive regulation of ryanodine-sensitive calcium-release channel activity; protein domain specific binding; regulation of cytokinesis; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum; response to calcium ion; spindle microtubule; spindle pole; titin binding | Spindle. | Calmodulin family |
| 39 CALX_HUMAN | CANX | P27824 | Calnexin (Major histocompatibility complex class I antigen-binding protein p88) (p90) (IP90) | calcium ion binding; endoplasmic reticulum membrane; integral to membrane; melanosome; protein folding; protein secretion; sugar binding; unfolded protein binding | Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome. | Calreticulin family |
| 40 CAN1_HUMAN | CAPN1 (CANPL1) (PIG30) | P07384 | Calpain-1 catalytic subunit (EC 3.4.22.52) (Calpain-1 large subunit) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (muCANP) (Micromolar-calpain) (Cell proliferation-inducing gene 30 protein) | calcium ion binding; calcium-dependent cysteine-type endopeptidase activity; cytoplasm; plasma membrane; positive regulation of cell proliferation; protein binding; proteolysis | Cytoplasm. Cell membrane. | Peptidase C2 family |
| 41 CAZA1_HUMAN | CAPZA1 | P52907 | F-actin-capping protein subunit alpha-1 (CapZ alpha-1) | F-actin capping protein complex; actin binding; actin cytoskeleton organization; barbed-end actin filament capping; cell motion; protein complex assembly | | F-actin-capping protein alpha subunit family |
| 42 CD36_HUMAN | CD36 (GP3B) (GP4) | P16671 | Platelet glycoprotein 4 (Platelet glycoprotein IV) (GPIV) (Glycoprotein IIIb) (GPIIIB) (Leukocyte differentiation antigen CD36) (PAS IV) (PAS-4) (Platelet collagen receptor) (Fatty acid translocase) (FAT) (Thrombospondin receptor) (CD antigen CD36) | Golgi apparatus; blood coagulation; cGMP-mediated signaling; cell adhesion; cell surface; cholesterol transport; integral to plasma membrane; lipid binding; lipid metabolic process; lipid storage; lipoprotein catabolic process; lipoprotein particle clearance; lipoprotein transport; low-density lipoprotein receptor activity; membrane fraction; nitric oxide mediated signal transduction; plasma membrane long-chain fatty acid transport; platelet alpha granule membrane; positive regulation of cell-matrix adhesion; positive regulation of foam cell differentiation; thrombospondin receptor activity; transforming growth factor beta binding | Membrane; Multi-pass membrane protein. | CD36 family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|--|-------------------|--|---|--|--|
| 43 CD68_HUMAN | CD68 | P34810 | Macrosialin (Gp110) (CD antigen CD68) | endosome; integral to membrane; lysosomal membrane; membrane fraction; plasma membrane | Cell membrane; Single-pass type I membrane protein. Endosome membrane; Single-pass type I membrane protein. Lysosome membrane; Single-pass type I membrane protein. | LAMP family |
| 44 CD9_HUMAN | CD9 (MIC3) (TSPAN29) (GIG2) | P21926 | CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetraspanin-29) (Tspan-29) (5H9 antigen) (Cell growth-inhibiting gene 2 protein) (CD antigen CD9) | cell adhesion; cell motion; fusion of sperm to egg plasma membrane; integral to plasma membrane; paranodal junction assembly; platelet activation; platelet alpha granule membrane; protein binding | Membrane; Multi-pass membrane protein. | Tetraspanin (TM4SF) family |
| 45 CK059_HUMAN | C11orf59 (PP7157) | Q6IAA8 | UPF0404 protein C11orf59 | | | UPF0404 family |
| 46 CLH1_HUMAN | CLTC (CLH17) (CLTCL2) (KIAA0034) | Q00610 | Clathrin heavy chain 1 (CLH-17) | clathrin coat of coated pit; clathrin coat of trans-Golgi network vesicle; intracellular protein transport; melanosome; protein binding; structural molecule activity; vesicle-mediated transport | Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane , coated pit; Peripheral membrane protein; Cytoplasmic side. Melanosome. Secreted. | Clathrin heavy chain family |
| 47 CLUS_HUMAN | CLU (APOJ) (CLI) (KUB1) (AAG4) | P10909 | Clusterin (Complement-associated protein SP-40,40) (Complement cytolytic inhibitor) (CLI) (NA1/NA2) (Apolipoprotein J) (Apo-J) (Testosterone-repressed prostate message 2) (TRPM-2) (Ku70-binding protein 1) (Aging-associated gene 4 protein) [Cleaved into: Clusterin beta chain (ApoJalpha) (Complement cytolytic inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytolytic inhibitor b chain)] | apoptosis; complement activation, classical pathway; innate immune response; lipid metabolic process; protein binding; reverse cholesterol transport; spherical high-density lipoprotein particle | | Clusterin family |
| 48 CMC2_HUMAN | SLC25A13 (ARALAR2) | Q9UJS0 | Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin) | ATP biosynthetic process; L-aspartate transmembrane transporter activity; L-glutamate transmembrane transporter activity; L-glutamate transport; aspartate transport; calcium ion binding; integral to plasma membrane; malate-aspartate shuttle; mitochondrial inner membrane; response to calcium ion | Mitochondrion inner membrane; Multi-pass membrane protein. | Mitochondrial carrier family |
| 49 COF1_HUMAN | CFL1 (CFL) | P23528 | Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) | Rho protein signal transduction; actin binding; anti-apoptosis; nuclear matrix | Nucleus matrix. Cytoplasm , cytoskeleton. | Actin-binding proteins ADF family |
| 50 COR1B_HUMAN | CORO1B | Q9BR76 | Coronin-1B (Coronin-2) | actin binding; cytoplasm; cytoskeleton | Cytoplasm , cytoskeleton. | WD repeat coronin family |
| 51 CPNS1_HUMAN | CAPNS1 (CAPN4) (CAPNS) | P04632 | Calpain small subunit 1 (CSS1) (Calcium-dependent protease small subunit 1) (Calcium-dependent protease small subunit) (CDPS) (Calpain regulatory subunit) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) | calcium ion binding; calcium-dependent cysteine-type endopeptidase activity; cytoplasm; nucleus; plasma membrane; positive regulation of cell proliferation; protein binding | Cytoplasm. Cell membrane. | |
| 52 CSRP1_HUMAN | CSRP1 (CSRP) (CYRP) | P21291 | Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) | nucleus; zinc ion binding | Nucleus. | |
| 53 CX7A2_HUMAN | COX7A2 (COX7AL) | P14406 | Cytochrome c oxidase polypeptide 7A2, mitochondrial (Cytochrome c oxidase polypeptide VIIa-liver/heart) (Cytochrome c oxidase subunit VIIa-L) (VIIaL) | cytochrome-c oxidase activity; electron carrier activity; mitochondrial respiratory chain | Mitochondrion inner membrane. | Cytochrome c oxidase VIIa family |
| 54 CXCL7_HUMAN | PPBP (CTAP3) (CXCL7) (SCYB7) (TGB1) (THBGB1) | P02775 | Platelet basic protein (PBP) (C-X-C motif chemokine 7) (Small-inducible cytokine B7) (Leukocyte-derived growth factor) (LDGF) (Macrophage-derived growth factor) (MDGF) [Cleaved into: Connective tissue-activating peptide III (CTAP-III) (Low-affinity platelet factor IV) (LA-PF4); TC-2; Connective tissue-activating peptide III(1-81) (CTAP-III(1-81)); Beta-thromboglobulin (Beta-TG); Neutrophil-activating peptide 2(74) (NAP-2(74)); Neutrophil-activating peptide 2(73) (NAP-2(73)); Neutrophil-activating peptide 2 (NAP-2); TC-1; Neutrophil-activating peptide 2(1-66) (NAP-2(1-66)); Neutrophil-activating peptide 2(1-63) (NAP-2(1-63))] | cell proliferation; chemokine activity; chemotaxis; defense response to bacterium; extracellular space; glucose transmembrane transporter activity; glucose transport; growth factor activity; immune response; platelet alpha granule lumen | Secreted. | Intercrine alpha (chemokine Cx) family |
| 55 CYFP1_HUMAN | CYFIP1 (KIAA0068) | Q7L576 | Cytoplasmic FMR1-interacting protein 1 (Specifically Rac1-associated protein 1) (Sra-1) (p140sra-1) | Rac GTPase binding; actin filament binding; axon extension; cell junction; lamellipodium; lamellipodium assembly; perinuclear region of cytoplasm; regulation of cell shape; ruffle; ruffle organization; synapse; synaptosome | Cytoplasm , perinuclear region. Cell projection , lamellipodium. Cell projection , ruffle. Cell junction , synapse , synaptosome. | CYFIP family |
| 56 DCLK1_HUMAN | DCLK1 (DCAMKL1) (DCDC3A) (KIAA0369) | O15075 | Serine/threonine-protein kinase DCLK1 (EC 2.7.11.1) (Doublecortin-like and CAM kinase-like 1) (Doublecortin-like kinase 1) | ATP binding; cell differentiation; central nervous system development; endosome transport; integral to plasma membrane; intracellular signaling cascade; protein amino acid phosphorylation; protein binding; protein serine/threonine kinase activity; receptor signaling protein activity | | Protein kinase superfamily, CAMK Ser/Thr protein kinase family, CaMK subfamily |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|----------------------|-------------------|---|---|---|--|
| 57 DECR_HUMAN | DECR1 (DECR) | Q16698 | 2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) | 2,4-dienoyl-CoA reductase (NADPH) activity; NADPH binding; fatty acid beta-oxidation; mitochondrion; oxidation reduction; protein homotetramerization | Mitochondrion. | Short-chain dehydrogenase s/reductases (SDR) family, 2,4-dienoyl-CoA reductase subfamily |
| 58 DHB12_HUMAN | HSD17B12 | Q53GQ0 | Estradiol 17-beta-dehydrogenase 12 (EC 1.1.1.62) (17-beta-hydroxysteroid dehydrogenase 12) (17-beta-HSD 12) (3-ketoacyl-CoA reductase) (KAR) (EC 1.3.1.-) | endoplasmic reticulum membrane; estradiol 17-beta-dehydrogenase activity; integral to membrane; oxidation reduction; steroid biosynthetic process | Endoplasmic reticulum membrane; Multi-pass membrane protein. | Short-chain dehydrogenase s/reductases (SDR) family, 17-beta-HSD 3 subfamily |
| 59 DHSA_HUMAN | SDHA (SDH2) (SDHF) | P31040 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp) | FAD binding; electron carrier activity; mitochondrial respiratory chain complex II; nervous system development; protein binding; respiratory electron transport chain; succinate dehydrogenase (ubiquinone) activity; succinate metabolic process; transport; tricarboxylic acid cycle | Mitochondrion inner membrane; Peripheral membrane protein; Matrix side. | FAD-dependent oxidoreductase 2 family, FRD/SDH subfamily |
| 60 EHD3_HUMAN | EHD3 (EHD2) (PAST3) | Q9NZN3 | EH domain-containing protein 3 | ATP binding; GTP binding; GTPase activity; calcium ion binding; nucleic acid binding; nucleus; plasma membrane; recycling endosome membrane | Cell membrane; Peripheral membrane protein; Cytoplasmic side. Endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein. | |
| 61 ESAM_HUMAN | ESAM (UNQ220/PRO246) | Q96AP7 | Endothelial cell-selective adhesion molecule | adherens junction; integral to membrane; protein binding; tight junction | Cell junction , adherens junction. Cell junction , tight junction. Cell membrane; Single-pass type I membrane protein. Cytoplasm. Secreted. | Transglutaminase superfamily, Transglutaminase family |
| 62 F13A_HUMAN | F13A1 (F13A) | P00488 | Coagulation factor XIII A chain (Coagulation factor XIIIa) (EC 2.3.2.13) (Protein-glutamine gamma-glutamyltransferase A chain) (Transglutaminase A chain) | acyltransferase activity; blood coagulation; calcium ion binding; cytoplasm; extracellular region; protein-glutamine gamma-glutamyltransferase activity | Cytoplasm. Cytoplasm. Nucleus. Nucleus. Cytoplasm , cytosol. | |
| 63 FHL1_HUMAN | FHL1 (SLIM1) | Q13642 | Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM-protein 1) (SLIM 1) (SLIM) | cell differentiation; cell growth; cytosol; muscle organ development; nucleus; organ morphogenesis; zinc ion binding | Cytoplasm. Cytoplasm. Nucleus. Nucleus. Cytoplasm , cytosol. | |
| 64 FIBA_HUMAN | FGA | P02671 | Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A] | eukaryotic cell surface binding; external side of plasma membrane; fibrinogen complex; platelet activation; platelet alpha granule lumen; protein binding, bridging; protein polymerization; receptor binding; response to calcium ion; signal transduction | Secreted. | |
| 65 FIBB_HUMAN | FGB | P02675 | Fibrinogen beta chain [Cleaved into: Fibrinopeptide B] | eukaryotic cell surface binding; external side of plasma membrane; fibrinogen complex; nucleus; platelet activation; platelet alpha granule lumen; protein binding, bridging; protein polymerization; receptor binding; response to calcium ion; signal transduction | Secreted. | |
| 66 FIBG_HUMAN | FGG (PRO2061) | P02679 | Fibrinogen gamma chain | calcium ion binding; eukaryotic cell surface binding; external side of plasma membrane; fibrinogen complex; platelet activation; platelet alpha granule lumen; protein binding, bridging; protein polymerization; receptor binding; response to calcium ion; signal transduction | Secreted. | |
| 67 FINC_HUMAN | FN1 (FN) | P02751 | Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Ugl-Y1; Ugl-Y2; Ugl-Y3] | ER-Golgi intermediate compartment; acute-phase response; cell migration; collagen binding; extracellular matrix structural constituent; fibrinogen complex; heparin binding; peptide cross-linking; platelet alpha granule lumen; proteinaceous extracellular matrix; regulation of cell shape; substrate adhesion-dependent cell spreading; transmembrane receptor protein tyrosine kinase signaling pathway | Secreted , extracellular space , extracellular matrix. | |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|----------------|--|-------------------|--|--|---|--|
| 68 FLNA_HUMAN | FLNA (FLN) (FLN1) | P21333 | Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Non-muscle filamin) | Fc-gamma receptor I complex binding; GTP-Ral binding; Rac GTPase binding; actin crosslink formation; actin cytoskeleton; actin cytoskeleton reorganization; actin filament binding; cell cortex; cytoplasmic sequestering of protein; establishment of protein localization; glycoprotein binding; inhibition of adenylate cyclase activity by dopamine receptor signaling pathway; negative regulation of protein catabolic process; negative regulation of transcription factor activity; nucleus; plasma membrane; positive regulation of I-kappaB kinase/NF-kappaB cascade; positive regulation of transcription factor import into nucleus; protein homodimerization activity; protein localization at cell surface; protein stabilization; receptor clustering; signal transducer activity; transcription factor binding | Cytoplasm , cell cortex. Cytoplasm , cytoskeleton. | Filamin family |
| 69 FYN_HUMAN | FYN | P06241 | Proto-oncogene tyrosine-protein kinase Fyn (EC 2.7.10.2) (p59-Fyn) (Protooncogene Syn) (SLK) | ATP binding; T cell receptor signaling pathway; calcium ion transport; cytosol; endosome; feeding behavior; glycoprotein binding; identical protein binding; interspecies interaction between organisms; learning; manganese ion binding; multicellular organismal development; non-membrane spanning protein tyrosine kinase activity; plasma membrane; protein amino acid phosphorylation; protein kinase cascade | Cell membrane. | Protein kinase superfamily, Tyr protein kinase family, SRC subfamily |
| 70 G3P_HUMAN | GAPDH (GAPD) (CDABP0047) (OK/SW-cl.12) | P04406 | Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) | NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity; glycolysis; membrane; oxidation reduction; perinuclear region of cytoplasm; protein binding | Cytoplasm. Cytoplasm , perinuclear region. Membrane. | Glyceraldehyde-3-phosphate dehydrogenase family |
| 71 G6B_HUMAN | G6B (C6orf25) | O95866 | Protein G6b | Golgi apparatus; endoplasmic reticulum; heparin binding; integral to membrane; plasma membrane; receptor activity | Endoplasmic reticulum. Golgi apparatus. Endoplasmic reticulum. Golgi apparatus. Cell membrane; Single-pass type I membrane protein. Cell membrane; Single-pass type I membrane protein. | |
| 72 G6PD_HUMAN | G6PD | P11413 | Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49) | NADP or NADPH binding; cellular response to oxidative stress; centrosome; cholesterol biosynthetic process; cytokine production; cytosol; erythrocyte maturation; glucose 6-phosphate utilization; glucose binding; glucose-6-phosphate dehydrogenase activity; glutathione metabolic process; internal side of plasma membrane; intracellular membrane-bounded organelle; negative regulation of protein amino acid glutathionylation; oxidation reduction; pentose-phosphate shunt, oxidative branch; protein homodimerization activity; ribose phosphate biosynthetic process | | Glucose-6-phosphate dehydrogenase family |
| 73 GBB1_HUMAN | GNB1 | P62873 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Transducin beta chain 1) | GTPase activity; Ras protein signal transduction; hormone-mediated signaling; muscarinic acetylcholine receptor signaling pathway; signal transducer activity | | WD repeat G protein beta family |
| 74 GELS_HUMAN | GSN | P06396 | Gelsolin (Actin-depolymerizing factor) (ADF) (Brevin) (AGEL) | actin binding; actin cytoskeleton; actin filament polymerization; actin filament severing; barbed-end actin filament capping; calcium ion binding; cytosol; extracellular region | Cytoplasm , cytoskeleton. Secreted. | Villin/gelsolin family |
| 75 GNA12_HUMAN | GNA12 | Q03113 | Guanine nucleotide-binding protein subunit alpha-12 (G-protein subunit alpha-12) (G alpha-12) | G-protein coupled receptor protein signaling pathway; GTP binding; GTPase activity; blood coagulation; plasma membrane; protein binding; signal transducer activity | Membrane; Lipid-anchor. | G-alpha family, G(12) subfamily |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family | |
|------------|-------------|--------------------------------|---------------|--|--|--|---|
| 76 | GNAI2_HUMAN | GNAI2 (GNAI2B) | P04899 | Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate cyclase-inhibiting G alpha protein) | GTP binding; GTPase activity; protein binding; response to nutrient; signal transducer activity | | G-alpha family, G(i/o/t/z) subfamily |
| 77 | GP1BB_HUMAN | GP1BB | P13224 | Platelet glycoprotein Ib beta chain (GP-Ib beta) (GPIb-beta) (GPIbB) (Antigen CD42b-beta) (CD antigen CD42c) | cell adhesion; cell surface receptor linked signal transduction; integral to plasma membrane; platelet activation; platelet alpha granule membrane; protein binding; transmembrane receptor activity | Membrane; Single-pass type I membrane protein. | |
| 78 | GPDM_HUMAN | GPD2 | P43304 | Glycerol-3-phosphate dehydrogenase, mitochondrial (GPDH-M) (GPD-M) (EC 1.1.5.3) (mtGPD) | calcium ion binding; glycerol-3-phosphate dehydrogenase activity; glycerol-3-phosphate dehydrogenase complex; oxidation reduction | Mitochondrion. | FAD-dependent glycerol-3-phosphate dehydrogenase family |
| 79 | GPV_HUMAN | GP5 | P40197 | Platelet glycoprotein V (GPV) (CD antigen CD42D) | blood coagulation; cell adhesion; integral to plasma membrane; platelet alpha granule membrane; protein binding | Membrane; Single-pass type I membrane protein. | |
| 80 | GSH0_HUMAN | GCLM (GLCLR) | P48507 | Glutamate--cysteine ligase regulatory subunit (Gamma-glutamylcysteine synthetase regulatory subunit) (Gamma-ECS regulatory subunit) (GCS light chain) (Glutamate--cysteine ligase modifier subunit) | cytosol; glutamate metabolic process; glutamate-cysteine ligase catalytic subunit binding; glutathione biosynthetic process; oxidation reduction; oxidoreductase activity; regulation of blood vessel size; response to drug; response to oxidative stress; soluble fraction | | Aldo/keto reductase family, Glutamate--cysteine ligase light chain subfamily |
| 81 | GTR3_HUMAN | SLC2A3 (GLUT3) | P11169 | Solute carrier family 2, facilitated glucose transporter member 3 (Glucose transporter type 3, brain) (GLUT-3) | carbohydrate metabolic process; cytoplasm; glucose transmembrane transporter activity; glucose transport; integral to membrane; plasma membrane; sugar:hydrogen symporter activity; transmembrane transport | Membrane; Multi-pass membrane protein. | Major facilitator superfamily, Sugar transporter (TC 2.A.1.1) family, Glucose transporter subfamily |
| 82 | HPCA_HUMAN | HPCA (BDR2) | P84074 | Neuron-specific calcium-binding protein hippocalcin (Calcium-binding protein BDR-2) | actin binding; calcium ion binding | | Recoverin family |
| 83 | HSP7C_HUMAN | HSPA8 (HSC70) (HSP73) (HSPA10) | P11142 | Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) | ATP binding; ATPase activity, coupled; cell surface; melanosome; protein binding; protein folding; response to unfolded protein | Cytoplasm. Melanosome. | Heat shock protein 70 family |
| 84 | HSPB1_HUMAN | HSPB1 (HSP27) (HSP28) | P04792 | Heat shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27) (Estrogen-regulated 24 kDa protein) (28 kDa heat shock protein) | anti-apoptosis; cell death; cell motion; cell surface; cytoplasm; identical protein binding; nucleus; regulation of translational initiation; response to heat; response to unfolded protein; spindle | Cytoplasm. Nucleus. Spindle. | Small heat shock protein (HSP20) family |
| 85 | HXK1_HUMAN | HK1 | P19367 | Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK I) (Brain form hexokinase) | ATP binding; cytosol; glycolysis; hexokinase activity; | Mitochondrion outer membrane. | Hexokinase family |
| 86 | HXK2_HUMAN | HK2 | P52789 | Hexokinase-2 (EC 2.7.1.1) (Hexokinase type II) (HK II) (Muscle form hexokinase) | ATP binding; cytosol; glycolysis; hexokinase activity; | Mitochondrion outer membrane. | Hexokinase family |
| 87 | IF5A1_HUMAN | EIF5A | P63241 | Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (eIF-4D) (Rev-binding factor) | U6 snRNA binding; annulate lamellae; cell proliferation; cytosol; induction of apoptosis; mRNA export from nucleus; nuclear pore; peptidyl-lysine modification to hypusine; positive regulation of translational initiation; protein N-terminus binding; protein export from nucleus; translation initiation factor activity; translational initiation; viral genome replication | Nucleus. | EIF-5A family |
| 88 | ILVBL_HUMAN | ILVBL (AHAS) | A1L0T0 | Acetolactate synthase-like protein (EC 2.2.1.-) (IlvB-like protein) | integral to membrane; magnesium ion binding; thiamin pyrophosphate binding; transferase activity | Membrane; Single-pass membrane protein. | TPP enzyme family |
| 89 | IQGA2_HUMAN | IQGAP2 | Q13576 | Ras GTPase-activating-like protein IQGAP2 | GTPase inhibitor activity; Ras GTPase activator activity; actin binding; actin cytoskeleton; calmodulin binding; regulation of small GTPase mediated signal transduction; small GTPase mediated signal transduction | | |
| 90 | ITA2_HUMAN | ITGA2 (CD49B) | P17301 | Integrin alpha-2 (Platelet membrane glycoprotein Ia) (GPIa) (Collagen receptor) (VLA-2 alpha chain) (CD49 antigen-like family member B) (CD antigen CD49b) | blood coagulation; calcium ion binding; cell-matrix adhesion; collagen binding; identical protein binding; integrin complex; integrin-mediated signaling pathway; interspecies interaction between organisms; magnesium ion binding; organ morphogenesis; receptor activity | Membrane; Single-pass type I membrane protein. | Integrin alpha chain family |
| 91 | ITA2B_HUMAN | ITGA2B (GP2B) (ITGAB) | P08514 | Integrin alpha-IIb (Platelet membrane glycoprotein IIb) (GPIIb) (GPIIb) (CD antigen CD41) [Cleaved into: Integrin alpha-IIb heavy chain; Integrin alpha-IIb light chain, form 1; Integrin alpha-IIb light chain, form 2] | calcium ion binding; cell adhesion; identical protein binding; integrin complex; integrin-mediated signaling pathway; platelet alpha granule membrane; receptor activity | Membrane; Single-pass type I membrane protein. | Integrin alpha chain family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|------------------------------------|-------------------|---|---|---|---|
| 92 ITB1_HUMAN | ITGB1 (FNRRB) (MDF2) (MSK12) | P05556 | Integrin beta-1 (Fibronectin receptor subunit beta) (Integrin VLA-4 subunit beta) (CD antigen CD29) | B cell differentiation; cell surface; cell-cell adhesion mediated by integrin; cell-matrix adhesion; cellular defense response; homophilic cell adhesion; identical protein binding; integrin complex; integrin-mediated signaling pathway; interspecies interaction between organisms; leukocyte adhesion; melanosome; neuromuscular junction; protein heterodimerization activity; receptor activity; ruffle; sarcolemma | Cell membrane; Single-pass type I membrane protein. Melanosome. | Integrin beta chain family |
| 93 ITB3_HUMAN | ITGB3 (GP3A) | P05106 | Integrin beta-3 (Platelet membrane glycoprotein IIIa) (GPIIIa) (CD antigen CD61) | blood coagulation; cell-matrix adhesion; identical protein binding; integrin complex; integrin-mediated signaling pathway; interspecies interaction between organisms; negative regulation of foam cell differentiation; negative regulation of lipid storage; negative regulation of lipid transport; negative regulation of lipoprotein metabolic process; negative regulation of low-density lipoprotein receptor biosynthetic process; platelet alpha granule membrane; receptor activity | Membrane; Single-pass type I membrane protein. | Integrin beta chain family |
| 94 JAM1_HUMAN | F11R (JAM1) (JCAM) (UNQ264/PRO301) | Q9Y624 | Junctional adhesion molecule A (JAM-A) (Junctional adhesion molecule 1) (JAM-1) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11 receptor) (CD antigen CD321) | inflammatory response; integral to membrane; interspecies interaction between organisms; tight junction | Cell junction , tight junction. Cell membrane; Single-pass type I membrane protein. | Immunoglobulin superfamily |
| 95 JAM3_HUMAN | JAM3 (UNQ859/PRO1868) | Q9BX67 | Junctional adhesion molecule C (JAM-C) (Junctional adhesion molecule 3) (JAM-3) (JAM-2) | integral to membrane; plasma membrane | Cell membrane; Single-pass type I membrane protein. | Immunoglobulin superfamily |
| 96 K6PL_HUMAN | PFKL | P17858 | 6-phosphofructokinase, liver type (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme B) (PFK-B) | 6-phosphofructokinase activity; 6-phosphofructokinase complex; ATP binding; fructose 6-phosphate metabolic process; fructose-6-phosphate binding; glycolysis; identical protein binding; kinase binding; magnesium ion binding; protein oligomerization | | Phosphofructokinase family, Two domains subfamily |
| 97 K6PP_HUMAN | PFKP (PFKF) | Q01813 | 6-phosphofructokinase type C (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme C) (PFK-C) (6-phosphofructokinase, platelet type) | 6-phosphofructokinase activity; 6-phosphofructokinase complex; ATP binding; glycolysis; magnesium ion binding; protein binding | | Phosphofructokinase family, Two domains subfamily |
| 98 LIMS1_HUMAN | LIMS1 (PINCH) (PINCH1) | P48059 | LIM and senescent cell antigen-like-containing domain protein 1 (Particularly interesting new Cys-His protein 1) (PINCH-1) (Renal carcinoma antigen NY-REN-48) | cell aging; focal adhesion; protein binding; zinc ion binding | Cell junction , focal adhesion. Cell membrane; Peripheral membrane protein; Cytoplasmic side. | |
| 99 LOX12_HUMAN | ALOX12 (LOG12) | P18054 | Arachidonate 12-lipoxygenase, 12S-type (12-LOX) (EC 1.13.11.31) (Platelet-type lipoxygenase 12) | anti-apoptosis; arachidonate 12-lipoxygenase activity; cell motion; cytosol; fatty acid oxidation; hepxilin-epoxide hydrolase activity; iron ion binding; leukotriene biosynthetic process; lipoxygenase activity; oxidation reduction; positive regulation of cell adhesion; positive regulation of cell growth; positive regulation of cell proliferation; protein binding; sarcolemma; superoxide release | Cytoplasm. | Lipoxygenase family |
| 100 LRBA_HUMAN | LRBA (BGL) (CDC4L) (LBA) | P50851 | Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like protein) (Beige-like protein) | protein binding | | |
| 101 LYAM3_HUMAN | SELP (GMRP) (GRMP) | P16109 | P-selectin (Granule membrane protein 140) (GMP-140) (PADGEM) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3) (CD62 antigen-like family member P) (CD antigen CD62P) | defense response to Gram-negative bacterium; external side of plasma membrane; extracellular space; fucose binding; glycosphingolipid binding; heparin binding; integral to plasma membrane; leukocyte adhesion; lipopolysaccharide binding; membrane fraction; oligosaccharide binding; platelet alpha granule membrane; positive regulation of platelet activation; protein binding; response to lipopolysaccharide; sialic acid binding; soluble fraction | Membrane; Single-pass type I membrane protein. | Selectin/LECAM family |
| 102 MARE2_HUMAN | MAPRE2 (RP1) | Q15555 | Microtubule-associated protein RP/EB family member 2 (APC-binding protein EB2) (End-binding protein 2) (EB2) | cell division; cell proliferation; cytoplasm; microtubule; microtubule binding; mitosis; signal transduction | Cytoplasm. | MAPRE family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|------------------|--------------------------------------|-------------------|---|--|--|--|
| 103 MDHM_HUMAN | MDH2 | P40926 | Malate dehydrogenase, mitochondrial (EC 1.1.1.37) | L-malate dehydrogenase activity; binding; glycolysis; malate metabolic process; mitochondrial matrix; oxidation reduction; tricarboxylic acid cycle | Mitochondrion matrix. | LDH/MDH superfamily, MDH type 1 family |
| 104 MGLL_HUMAN | MGLL | Q99685 | Monoglyceride lipase (MGL) (EC 3.1.1.23) (Lysophospholipase homolog) (Lysophospholipase-like) (HU-K5) | acylglycerol lipase activity; inflammatory response; lipid metabolic process; | | AB hydrolase superfamily, Monoacylglycerol lipase family |
| 105 ML12A_HUMAN | MYL12A (MLCB) (MRLC3) (RLC) | P19105 | Myosin regulatory light chain 12A (Myosin regulatory light chain MRLC3) (Myosin regulatory light chain 2, nonsarcomeric) (Myosin RLC) (MLC-2B) | lysophospholipase activity calcium ion binding; motor activity; myosin complex; protein binding | | |
| 106 MLE1_HUMAN | MYL1 | P05976 | Myosin light chain 1, skeletal muscle isoform (MLC1F) (A1 catalytic) (Alkali myosin light chain 1) | calcium ion binding; motor activity; muscle filament sliding; muscle myosin complex; muscle organ development; sarcomere; structural constituent of muscle | | |
| 107 MMRN1_HUMAN | MMRN1 (ECM) (EMILIN4) (GP1A*) (MMRN) | Q13201 | Multimerin-1 (Endothelial cell multimerin) (EMILIN-4) (Elastin microfibril interface located protein 4) (Elastin microfibril interface 4) [Cleaved into: Platelet glycoprotein Ia*; 155 kDa platelet multimerin (p-155) (p155)] | blood coagulation; cell adhesion; extracellular region; platelet alpha granule lumen | Secreted. | |
| 108 MPKS1_HUMAN | MAPKSP1 (MAP2K1IP1) (PRO2783) | Q9UHA4 | Mitogen-activated protein kinase scaffold protein 1 (Mitogen-activated protein kinase kinase 1-interacting protein 1) (MEK-binding partner 1) (Mp1) | late endosome membrane; protein binding | Late endosome membrane; Peripheral membrane protein; Cytoplasmic side. | MAPKSP1 family |
| 109 MYH11_HUMAN | MYH11 (KIAA0866) | P35749 | Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth muscle isoform) (SMMHC) | ATP binding; actin binding; calmodulin binding; cardiac muscle fiber development; elastic fiber assembly; melanosome; motor activity; muscle thick filament assembly; smooth muscle contraction; striated muscle contraction; striated muscle thick filament; structural constituent of muscle | Melanosome. | |
| 110 MYH9_HUMAN | MYH9 | P35579 | Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA) (Cellular myosin heavy chain, type A) (Non-muscle myosin heavy chain A) (NMMHC-A) | ADP binding; ATP binding; actin cytoskeleton reorganization; actin filament binding; actin filament-based movement; actin-dependent ATPase activity; angiogenesis; blood vessel endothelial cell migration; calmodulin binding; cleavage furrow; contractile ring; cytokinesis; cytosol; integrin-mediated signaling pathway; leukocyte migration; membrane protein ectodomain proteolysis; microfilament motor activity; monocyte differentiation; myosin complex; nucleus; platelet formation; protein anchor; protein homodimerization activity; protein transport; regulation of cell shape; ruffle; sensory perception of sound; stress fiber; uropod | | |
| 111 MYL6_HUMAN | MYL6 | P60660 | Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17) | actin-dependent ATPase activity; calcium ion binding; motor activity; muscle filament sliding; skeletal muscle tissue development; structural constituent of muscle; | | |
| 112 MYL6B_HUMAN | MYL6B (MLC1SA) | P14649 | Myosin light chain 6B (Smooth muscle and nonmuscle myosin light chain alkali 6B) (Myosin light chain 1 slow-twitch muscle A isoform) (MLC1sa) | unconventional myosin complex calcium ion binding; motor activity; muscle filament sliding; muscle myosin complex; protein binding; skeletal muscle tissue development; structural constituent of muscle; | | |
| 113 MYL9_HUMAN | MYL9 (MLC2) (MRLC1) (MYRL2) | P24844 | Myosin regulatory light polypeptide 9 (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin RLC) (MLC-2C) (LC20) | unconventional myosin complex calcium ion binding; motor activity; muscle myosin complex; regulation of muscle contraction; structural constituent of muscle | | |
| 114 NB5R3_HUMAN | CYB5R3 (DIA1) | P00387 | NADH-cytochrome b5 reductase 3 (Cytochrome b5 reductase) (B5R) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form] | blood circulation; cholesterol biosynthetic process; cytochrome-b5 reductase activity; electron carrier activity; endoplasmic reticulum membrane; hemoglobin complex; mitochondrial outer membrane; oxidation reduction | Endoplasmic reticulum membrane; Lipid-anchor; Cytoplasmic side. Mitochondrion outer membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm. | Flavoprotein pyridine nucleotide cytochrome reductase family |
| 115 NDUFB8_HUMAN | NDUFB8 | O95169 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial (NADH-ubiquinone oxidoreductase ASH1 subunit) (Complex I-ASH1) (CI-ASH1) | NADH dehydrogenase (ubiquinone) activity; endoplasmic reticulum; integral to membrane; mitochondrial electron transport, NADH to ubiquinone; mitochondrial respiratory chain complex I; transport | Mitochondrion inner membrane; Single-pass membrane protein; Matrix side. | Complex I NDUFB8 subunit family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|-------------------------------|-------------------|--|---|---|--|
| 116 NNTM_HUMAN | NNT | Q13423 | NAD(P) transhydrogenase, mitochondrial (EC 1.6.1.2) (Nicotinamide nucleotide transhydrogenase) (Pyridine nucleotide transhydrogenase) | NAD or NADH binding; NAD(P)+ transhydrogenase (AB-specific) activity; NAD(P)+ transhydrogenase (B-specific) activity; NADP or NADPH binding; electron carrier activity; integral to membrane; mitochondrial respiratory chain; oxidation reduction; proton transport; tricarboxylic acid cycle | Mitochondrion inner membrane; Multi-pass membrane protein; Matrix side. | AlaDH/PNT family; PNT beta subunit family |
| 117 PARVA_HUMAN | PARVA (MXRA2) | Q9NVD7 | Alpha-parvin (Calponin-like integrin-linked kinase-binding protein) (CH-ILKBP) (Matrix-remodeling-associated protein 2) (Actopaxin) | actin binding; cell adhesion; cytoplasm; cytoskeleton; focal adhesion | Cell junction , focal adhesion. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm , cytoskeleton. | Parvin family |
| 118 PARVB_HUMAN | PARVB (CGI-56) | Q9HB11 | Beta-parvin (Affixin) | actin binding; cell adhesion; cytoplasm; cytoskeleton; focal adhesion | Cell junction , focal adhesion. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm , cytoskeleton. | Parvin family |
| 119 PCF11_HUMAN | PCF11 (KIAA0824) | O94913 | Pre-mRNA cleavage complex 2 protein Pcf11 (Pre-mRNA cleavage complex II protein Pcf11) | mRNA cleavage; mRNA cleavage factor complex; nuclear mRNA splicing, via spliceosome | Nucleus. | |
| 120 PCYXL_HUMAN | PCYXL (PSEC0105) | Q8NBM8 | Prenylcysteine oxidase-like (EC 1.8.3.-) | extracellular region; oxidation reduction; oxidoreductase activity, acting on sulfur group of donors, oxygen as acceptor; prenylcysteine catabolic process | Secreted. | Prenylcysteine oxidase family |
| 121 PDIA3_HUMAN | PDIA3 (ERP57) (ERP60) (GRP58) | P30101 | Protein disulfide-isomerase A3 (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58 kDa glucose-regulated protein) | cell redox homeostasis; cysteine-type endopeptidase activity; endoplasmic reticulum; endoplasmic reticulum lumen; melanosome; phospholipase C activity; protein binding; protein disulfide isomerase activity; protein import into nucleus; protein retention in ER lumen; signal transduction | Endoplasmic reticulum lumen. Melanosome. | Protein disulfide isomerase family |
| 122 PDIA6_HUMAN | PDIA6 (TXNDC7) | Q15084 | Protein disulfide-isomerase A6 (EC 5.3.4.1) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7) | ER-Golgi intermediate compartment; cell redox homeostasis; endoplasmic reticulum; endoplasmic reticulum lumen; melanosome; protein binding; protein disulfide isomerase activity; protein folding | Endoplasmic reticulum lumen. Melanosome. | Protein disulfide isomerase family |
| 123 PECA1_HUMAN | PECAM1 | P16284 | Platelet endothelial cell adhesion molecule (PECAM-1) (EndoCAM) (GPIIA') (CD antigen CD31) | cell adhesion; cell recognition; extracellular space; integral to membrane; plasma membrane; platelet alpha granule membrane; protein binding; signal transduction | Membrane; Single-pass type I membrane protein. | |
| 124 PGH1_HUMAN | PTGS1 (COX1) | P23219 | Prostaglandin G/H synthase 1 (EC 1.14.99.1) (Cyclooxygenase-1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1) | Golgi apparatus; endoplasmic reticulum membrane; heme binding; microsome; nucleus; oxidation reduction; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; peroxidase activity; plasma membrane; prostaglandin biosynthetic process; prostaglandin-endoperoxide synthase activity; regulation of blood pressure; response to oxidative stress | Microsome membrane; Peripheral membrane protein. Endoplasmic reticulum membrane; Peripheral membrane protein. | Prostaglandin G/H synthase family |
| 125 PHF2_HUMAN | PHF2 (KIAA0662) | O75151 | PHD finger protein 2 (GRC5) | nucleus; protein binding; zinc ion binding | Nucleus. | |
| 126 PI4KA_HUMAN | PI4KA (PIK4) (PIK4CA) | P42356 | Phosphatidylinositol 4-kinase alpha (PI4-kinase alpha) (PtdIns-4-kinase alpha) (PI4K-alpha) (EC 2.7.1.67) | 1-phosphatidylinositol 4-kinase activity; ATP binding; Golgi-associated vesicle; phosphatidylinositol biosynthetic process; phosphoinositide phosphorylation; phosphoinositide-mediated signaling; protein binding; synaptic transmission | | PI3/PI4-kinase family, Type III PI4K subfamily |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|---|-------------------|--|---|---|--|
| 127 PLEK_HUMAN | PLEK (P47) | P08567 | Pleckstrin (Platelet p47 protein) | actin cytoskeleton reorganization; cortical actin cytoskeleton organization; cytoplasm; hemopoietic progenitor cell differentiation; inhibition of phospholipase C activity involved in G-protein coupled receptor signaling pathway; integrin-mediated signaling pathway; membrane fraction; negative regulation of calcium-mediated signaling; negative regulation of inositol phosphate biosynthetic process; phosphate binding; phosphatidylinositol-3,4-bisphosphate binding; phosphoinositide metabolic process; platelet aggregation; positive regulation of actin filament bundle formation; positive regulation of actin filament depolymerization; positive regulation of inositol-polyphosphate 5-phosphatase activity; positive regulation of integrin activation; positive regulation of platelet activation; protein homodimerization activity; protein kinase C binding; protein kinase C signaling cascade; protein secretion by cell | | |
| 128 PLF4_HUMAN | PF4 (CXCL4) (SCYB4) | P02776 | Platelet factor 4 (PF-4) (C-X-C motif chemokine 4) (Oncostatin-A) (Iroplact) [Cleaved into: Platelet factor 4, short form] | chemokine activity; cytokine-mediated signaling pathway; extracellular space; heparin binding; immune response; leukocyte chemotaxis; negative regulation of MHC class II biosynthetic process; negative regulation of angiogenesis; negative regulation of apoptosis; negative regulation of cytolysis; negative regulation of megakaryocyte differentiation; platelet activation; platelet alpha granule lumen; positive regulation of foam cell differentiation; positive regulation of gene expression; positive regulation of tumor necrosis factor production | Secreted. | Intercrine alpha (chemokine CxC) family |
| 129 PP1B_HUMAN | PPP1CB | P62140 | Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (EC 3.1.3.16) | cell cycle; cell division; cytoplasm; glycogen metabolic process; histone methyltransferase complex; iron ion binding; manganese ion binding; protein binding | Cytoplasm. | PPP phosphatase family, PP-1 subfamily |
| 130 PPIA_HUMAN | PPIA (CYPA) | P62937 | Peptidyl-prolyl cis-trans isomerase A (PPIase A) (Rotamase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) | cytosol; extracellular region; initiation of viral infection; interspecies interaction between organisms; nucleus; peptide binding; peptidyl-prolyl cis-trans isomerase activity; protein folding; provirus integration; regulation of viral genome replication; unfolded protein binding; virion binding | Cytoplasm. | Cyclophilin-type PPIase family, PPIase A subfamily |
| 131 PPIB_HUMAN | PPIB (CYPB) | P23284 | Peptidyl-prolyl cis-trans isomerase B (PPIase) (Rotamase) (EC 5.2.1.8) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1) | endoplasmic reticulum; endoplasmic reticulum lumen; melanosome; peptide binding; peptidyl-prolyl cis-trans isomerase activity; protein folding; unfolded protein binding | Endoplasmic reticulum lumen. Melanosome. | Cyclophilin-type PPIase family, PPIase B subfamily |
| 132 PPIF_HUMAN | PPIF (CYP3) | P30405 | Peptidyl-prolyl cis-trans isomerase, mitochondrial (PPIase) (Rotamase) (EC 5.2.1.8) (Cyclophilin F) | membrane fraction; mitochondrial matrix; peptide binding; peptidyl-prolyl cis-trans isomerase activity; protein folding | Mitochondrion matrix. | Cyclophilin-type PPIase family |
| 133 PRAF3_HUMAN | ARL6IP5 (DERP11) (JWA) (PRA2) (PRAF3) (HSPC127) | O75915 | PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Glutamate transporter EAAC1-interacting protein) (GTRAP3-18) (Prenylated Rab acceptor protein 2) (Protein JWa) (Dermal papilla-derived protein 11) (JM5) (Putative MAPK-activating protein PM27) (Cytoskeleton-related vitamin A-responsive protein) | L-glutamate transport; endoplasmic reticulum membrane; integral to membrane; protein binding | Endoplasmic reticulum membrane; Multi-pass membrane protein. Cytoplasm. | PRA1 family |
| 134 PROF1_HUMAN | PFN1 | P07737 | Profilin-1 (Profilin I) | actin binding; actin cytoskeleton; actin cytoskeleton organization; cytoplasm | Cytoplasm , cytoskeleton. | Profilin family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|-----------------------------|-------------------|--|--|---|---|
| 135 PURA_HUMAN | PURA (PUR1) | Q00577 | Transcriptional activator protein Pur-alpha (Purine-rich single-stranded DNA-binding protein alpha) | DNA replication factor A complex; DNA replication initiation; DNA unwinding during replication; RNA polymerase II transcription factor activity, enhancer binding; double-stranded telomeric DNA binding; nuclear chromosome, telomeric region; single-stranded DNA binding; transcription; transcription factor binding | Nucleus. | PUR DNA-binding protein family |
| 136 QCR1_HUMAN | UQCRC1 | P31930 | Cytochrome b-c1 complex subunit 1, mitochondrial (Ubiquinol-cytochrome-c reductase complex core protein 1) (Core protein I) (Complex III subunit 1) | aerobic respiration; metalloendopeptidase activity; mitochondrial respiratory chain; protein binding; proteolysis; transport; ubiquinol-cytochrome-c reductase activity; zinc ion binding | Mitochondrion inner membrane. | Peptidase M16 family, UQCRC1/QCR1 subfamily |
| 137 QCR2_HUMAN | UQCRC2 | P22695 | Cytochrome b-c1 complex subunit 2, mitochondrial (Ubiquinol-cytochrome-c reductase complex core protein 2) (Core protein II) (Complex III subunit 2) | aerobic respiration; electron transport chain; metalloendopeptidase activity; mitochondrial inner membrane; nucleus; oxidative phosphorylation; protein binding; proteolysis; respiratory chain; transport; zinc ion binding | Mitochondrion inner membrane; Peripheral membrane protein; Matrix side. | Peptidase M16 family, UQCRC2/QCR2 subfamily |
| 138 RAP1A_HUMAN | RAP1A (KREV1) | P62834 | Ras-related protein Rap-1A (GTP-binding protein smg-p21A) (Ras-related protein Krev-1) (C21KG) (G-22K) | GTP binding; GTPase activity; cell cycle; cytosol; negative regulation of cell cycle; plasma membrane | Cell membrane; Lipid-anchor. | Small GTPase superfamily, Ras family |
| 139 RASA3_HUMAN | RASA3 | Q14644 | Ras GTPase-activating protein 3 (GAP1(IP4BP)) (Ins P4-binding protein) | GTPase activator activity; calcium-release channel activity; intracellular; intracellular signaling cascade; intrinsic to internal side of plasma membrane; regulation of small GTPase mediated signal transduction; zinc ion binding | Cell membrane. | |
| 140 RB11A_HUMAN | RAB11A (RAB11) | P62491 | Ras-related protein Rab-11A (Rab-11) (YL8) | GTP binding; GTPase activity; plasma membrane; plasma membrane to endosome transport; recycling endosome membrane; small GTPase mediated signal transduction; syntaxin binding; trans-Golgi network; transporter activity | Cell membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein. | Small GTPase superfamily, Rab family |
| 141 RB27B_HUMAN | RAB27B | O00194 | Ras-related protein Rab-27B (C25KG) | GTP binding; GTPase activity; membrane; protein transport; small GTPase mediated signal transduction | Membrane; Lipid-anchor. | Small GTPase superfamily, Rab family |
| 142 RGS18_HUMAN | RGS18 (RGS13) | Q9NS28 | Regulator of G-protein signaling 18 (RGS18) | cytoplasm; negative regulation of signal transduction; signal transducer activity | Cytoplasm. | |
| 143 RHOA_HUMAN | RHOA (ARH12) (ARHA) (RHO12) | P61586 | Transforming protein RhoA (H12) | GTP binding; GTPase activity; Rho protein signal transduction; cytoplasm; cytoskeleton; magnesium ion binding; myosin binding; plasma membrane; positive regulation of I-kappaB kinase/NF-kappaB cascade; positive regulation of NF-kappaB import into nucleus; positive regulation of neuron differentiation; positive regulation of stress fiber formation | Cell membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm, cytoskeleton. | Small GTPase superfamily, Rho family |
| 144 RHOC_HUMAN | RHOC (ARH9) (ARHC) | P08134 | Rho-related GTP-binding protein RhoC (H9) | GTP binding; GTPase activity; intracellular; plasma membrane; positive regulation of I-kappaB kinase/NF-kappaB cascade; protein binding; signal transducer activity; small GTPase mediated signal transduction | Cell membrane; Lipid-anchor; Cytoplasmic side. | Small GTPase superfamily, Rho family |
| 145 RLA2_HUMAN | RPLP2 (D11S2243E) (RPP2) | P05387 | 60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44) | RNA binding; cytosolic large ribosomal subunit; structural constituent of ribosome; translational elongation | | Ribosomal protein L12P family |
| 146 RPN1_HUMAN | RPN1 | P04843 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (EC 2.4.1.119) (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit) (Ribophorin-1) (Ribophorin I) (RPN-I) | dolichyl-diphosphooligosaccharide-protein glycotransferase activity; integral to membrane; melanosome; oligosaccharyltransferase complex; protein amino acid N-linked glycosylation via asparagine; protein binding; rough endoplasmic reticulum membrane | Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome. | OST1 family |
| 147 RPN2_HUMAN | RPN2 | P04844 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (EC 2.4.1.119) (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (Ribophorin-2) (Ribophorin II) (RPN-II) (RIBIIR) | dolichyl-diphosphooligosaccharide-protein glycotransferase activity; integral to membrane; oligosaccharyltransferase complex; protein amino acid N-linked glycosylation via asparagine; protein binding | Endoplasmic reticulum membrane; Multi-pass membrane protein. | SWP1 family |
| 148 RSU1_HUMAN | RSU1 (RSP1) | Q15404 | Ras suppressor protein 1 (Rsu-1) (RSP-1) | protein binding; signal transduction | | |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|---|-------------------|---|--|--|-----------------------------------|
| 149 RTN4_HUMAN | RTN4 (KIAA0886) (NOGO) (My043) (SP1507) | Q9NQC3 | Reticulon-4 (Neurite outgrowth inhibitor) (Nogo protein) (Focnen) (Neuroendocrine-specific protein) (NSP) (Neuroendocrine-specific protein C homolog) (RTN-x) (Reticulon-5) | apoptosis; integral to endoplasmic reticulum membrane; negative regulation of anti-apoptosis; negative regulation of axon extension; nuclear envelope; protein binding; regulation of apoptosis; regulation of cell migration | Endoplasmic reticulum membrane; Multi-pass membrane protein. | |
| 150 SC22B_HUMAN | SEC22B (SEC22L1) | O75396 | Vesicle-trafficking protein SEC22b (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1) (ERS24) (ERS24) | ER to Golgi vesicle-mediated transport; ER-Golgi intermediate compartment membrane; Golgi membrane; endoplasmic reticulum membrane; integral to membrane; melanosome; protein binding; protein transport | Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type IV membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Melanosome. | Synaptobrevin family |
| 151 SCAM2_HUMAN | SCAMP2 | O15127 | Secretory carrier-associated membrane protein 2 (Secretory carrier membrane protein 2) | integral to membrane; post-Golgi vesicle-mediated transport; protein binding; protein transport; recycling endosome membrane; trans-Golgi network membrane | Golgi apparatus, trans-Golgi network membrane; Multi-pass membrane protein. Recycling endosome membrane; Multi-pass membrane protein. | SCAMP family |
| 152 SCPDH_HUMAN | SCCPDH (CGI-49) | Q8NBX0 | Probable saccharopine dehydrogenase (EC 1.5.1.9) | binding; oxidation reduction; saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity | | Saccharopine dehydrogenase family |
| 153 SDPR_HUMAN | SDPR | O95810 | Serum deprivation-response protein (Phosphatidylserine-binding protein) (PS-p68) | caveola; cytosol; phosphatidylserine binding; protein binding | Cytoplasm, cytosol. Membrane, caveola. | PTRF/SDPR family |
| 154 SEP11_HUMAN | 11-Sep | Q9NVA2 | Septin-11 | GTP binding; cell cycle; cell division; nucleus; protein binding; protein heterooligomerization; septin complex; stress fiber | | Septin family |
| 155 SEPT6_HUMAN | SEPT6 (KIAA0128) (SEP2) | Q14141 | Septin-6 | GTP binding; cell cycle; cytokinesis; nucleus; protein binding; septin complex | | Septin family |
| 156 SND1_HUMAN | SND1 (TDRD11) | Q7KZF4 | Staphylococcal nuclease domain-containing protein 1 (p100 co-activator) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) | Golgi apparatus; RNA interference; RNA-induced silencing complex; interspecies interaction between organisms; melanosome; nuclease activity; nucleic acid binding; nucleus; regulation of transcription, DNA-dependent; transcription; transcription cofactor activity | Cytoplasm. Nucleus. Melanosome. | |
| 157 SNP29_HUMAN | SNAP29 | O95721 | Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane fusion protein SNAP-29) (Soluble 29 kDa NSF attachment protein) | SNAP receptor activity; cell junction; cytoplasm; exocytosis; membrane fusion; protein transport; synapse; synaptosome; vesicle targeting | Cytoplasm. Membrane; Peripheral membrane protein. Cell junction, synapse, synaptosome. | SNAP-25 family |
| 158 SPCS1_HUMAN | SPCS1 (SPC12) (HSPC033) | Q9Y6A9 | Signal peptidase complex subunit 1 (EC 3.4.-.-) (Microsomal signal peptidase 12 kDa subunit) (SPase 12 kDa subunit) | integral to endoplasmic reticulum membrane; microsome; peptidase activity; proteolysis; signal peptidase complex; signal peptide processing | Microsome membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein. | SPCS1 family |
| 159 SSBP_HUMAN | SSBP1 (SSBP) | Q04837 | Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17) | DNA replication; mitochondrial nucleoid; single-stranded DNA binding | Mitochondrion. | |
| 160 STOM_HUMAN | STOM (BND7) (EPB72) | P27105 | Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b) | cytoskeleton; integral to plasma membrane; melanosome; membrane raft; protein binding; protein homooligomerization | Cell membrane; Single-pass membrane protein; Cytoplasmic side. Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome. | Band 7/mec-2 family |
| 161 STXB2_HUMAN | STXBP2 (UNC18B) | Q15833 | Syntaxin-binding protein 2 (Unc-18 homolog 2) (Unc18-2) (Unc-18B) | intracellular protein transport; syntaxin-2 binding; syntaxin-3 binding; vesicle docking during exocytosis | | STXBP/unc-18/SEC1 family |
| 162 TAGL2_HUMAN | TAGLN2 (KIAA0120) (CDABP0035) | P37802 | Transgelin-2 (SM22-alpha homolog) | cytoskeleton; muscle organ development; nuclear membrane; plasma membrane; protein binding | | Calponin family |
| 163 TBA4A_HUMAN | TUBA4A (TUBA1) | P68366 | Tubulin alpha-4A chain (Tubulin alpha-1 chain) (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) | GTP binding; GTPase activity; microtubule; microtubule-based movement; protein binding; protein complex; protein polymerization; structural molecule activity | | Tubulin family |
| 164 TBB1_HUMAN | TUBB1 | Q9H4B7 | Tubulin beta-1 chain | GTP binding; GTPase activity; microtubule; microtubule-based movement; protein complex; protein polymerization | | Tubulin family |
| 165 TBB2A_HUMAN | TUBB2A (TUBB2) | Q13885 | Tubulin beta-2A chain | GTP binding; GTPase activity; microtubule; microtubule-based movement; protein binding; protein complex; protein polymerization; structural molecule activity | | Tubulin family |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family | |
|------------|-------------|------------------------|---------------|--|--|---|--|
| 166 | TCPG_HUMAN | CCT3 (CCTG) (TRICS) | P49368 | T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRIC5) | ATP binding; cytoplasm; cytoskeleton; nucleus; plasma membrane; protein folding; unfolded protein binding | Cytoplasm. | TCP-1 chaperonin family |
| 167 | TLN1_HUMAN | TLN1 (KIAA1027) (TLN) | Q9Y490 | Talin-1 | LIM domain binding; actin binding; cell motion; cell-cell junction; cell-cell junction assembly; cytoplasm; cytoskeletal anchoring at plasma membrane; cytoskeleton; focal adhesion; intracellular membrane-bounded organelle; ruffle membrane; structural constituent of cytoskeleton; vinculin binding | Cell projection , ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm , cytoskeleton. | |
| 168 | TMEDA_HUMAN | TMED10 (TMP21) | P49755 | Transmembrane emp24 domain-containing protein 10 (21 kDa transmembrane-trafficking protein) (Transmembrane protein Tmp21) (Tmp-21-1) (p24delta) (S31III125) (S31II125) | ER-Golgi intermediate compartment; Golgi membrane; cis-Golgi network; integral to membrane; melanosome; microsome; protein binding; protein transport; regulated secretory pathway; vesicle targeting, to, from or within Golgi; zymogen granule membrane | Golgi apparatus membrane; Single-pass type I membrane protein; Luminal side. Melanosome. | EMP24/GP25L family |
| 169 | TPM1_HUMAN | TPM1 (C15orf13) (TMSA) | P09493 | Tropomyosin alpha-1 chain (Tropomyosin-1) (Alpha-tropomyosin) | actin binding; bleb; cardiac muscle contraction; cell motion; cellular response to reactive oxygen species; muscle filament sliding; muscle thin filament tropomyosin; negative regulation of cell migration; positive regulation of ATPase activity; positive regulation of cell adhesion; positive regulation of heart rate by epinephrine; positive regulation of stress fiber formation; regulation of muscle contraction; ruffle membrane; ruffle organization; sarcomere organization; stress fiber; structural constituent of cytoskeleton; structural constituent of muscle; ventricular cardiac muscle morphogenesis; wound healing | Cytoplasm , cytoskeleton. | Tropomyosin family |
| 170 | TPM3_HUMAN | TPM3 | P06753 | Tropomyosin alpha-3 chain (Tropomyosin-3) (Gamma-tropomyosin) (Tropomyosin-5) (hTM5) | actin binding; cell motion; muscle thin filament tropomyosin; regulation of muscle contraction | Cytoplasm , cytoskeleton. | Tropomyosin family |
| 171 | TPM4_HUMAN | TPM4 | P67936 | Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1) | actin binding; calcium ion binding; cell motion; muscle thin filament tropomyosin; structural constituent of muscle | Cytoplasm , cytoskeleton. | Tropomyosin family |
| 172 | TSP1_HUMAN | THBS1 (TSP) (TSP1) | P07996 | Thrombospondin-1 | activation of MAPK activity; anti-apoptosis; calcium ion binding; cell adhesion; cell cycle arrest; cell migration; cellular response to heat; chronic inflammatory response; collagen V binding; engulfment of apoptotic cell; eukaryotic cell surface binding; external side of plasma membrane; extracellular matrix; fibrinogen binding; fibrinogen complex; fibroblast growth factor 2 binding; fibronectin binding; heparin binding; identical protein binding; immune response; integrin binding; laminin binding; low-density lipoprotein binding; negative regulation of angiogenesis; negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II; negative regulation of blood vessel endothelial cell migration; negative regulation of cGMP-mediated signaling; negative regulation of dendritic cell antigen processing and presentation; negative regulation of endothelial cell proliferation; negative regulation of fibrinolysis; | | Thrombospondin family |
| 173 | TSP3_HUMAN | THBS3 (TSP3) | P49746 | Thrombospondin-3 | calcium ion binding; cell-matrix adhesion; extracellular region; platelet alpha granule lumen; protein binding; structural molecule activity | | Thrombospondin family |
| 174 | TWF2_HUMAN | TWF2 (PTK9L) (MSTP011) | Q6IBS0 | Twinfilin-2 (Twinfilin-1-like protein) (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) | ATP binding; actin binding; cytoskeleton; perinuclear region of cytoplasm | Cytoplasm , cytoskeleton. Cytoplasm , perinuclear region. | Actin-binding proteins ADF family, Twinfilin subfamily |

| Entry name | Gene names | Uniprot Accession | Protein names | Gene Ontology | Subcellular Localization | Protein family |
|-----------------|-------------------------------|-------------------|--|--|--|---------------------------------------|
| 175 UBP7_HUMAN | USP7 (HAUSP) | Q93009 | Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease) | cysteine-type endopeptidase activity; interspecies interaction between organisms; nucleus; protein C-terminus binding; protein deubiquitination; ubiquitin thioesterase activity; ubiquitin-dependent protein catabolic process; ubiquitin-specific protease activity | Nucleus. | Peptidase C19 family |
| 176 UBS3B_HUMAN | UBASH3B (KIAA1959) (STS1) | Q8TF42 | Ubiquitin-associated and SH3 domain-containing protein B (Suppressor of T-cell receptor signaling 1) (STS-1) (Cbl-interacting protein p70) | cytoplasm; nucleus | Cytoplasm. Nucleus. | |
| 177 URP2_HUMAN | FERMT3 (KIND3) (MIG2B) (URP2) | Q86UX7 | Fermitin family homolog 3 (Unc-112-related protein 2) (Kindlin-3) (MIG2-like protein) | cell adhesion; cytoplasm; plasma membrane; protein binding | Cytoplasm. Cell membrane; Peripheral membrane protein; Cytoplasmic side. | Kindlin family |
| 178 VDAC1_HUMAN | VDAC1 (VDAC) | P21796 | Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM) | anion transport; apoptosis; interspecies interaction between organisms; mitochondrial nucleoid; mitochondrial outer membrane; plasma membrane; pore complex; protein binding; voltage-gated anion channel activity | Mitochondrion outer membrane. Cell membrane. | Eukaryotic mitochondrial porin family |
| 179 VDAC3_HUMAN | VDAC3 | Q9Y277 | Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial membrane protein porin 3) | adenine transport; anion transport; integral to membrane; mitochondrial outer membrane; nucleotide binding; protein binding; voltage-gated anion channel activity | Mitochondrion outer membrane. | Eukaryotic mitochondrial porin family |
| 180 VINC_HUMAN | VCL | P18206 | Vinculin (Metavinculin) | actin binding; actin cytoskeleton; alpha-catenin binding; apical junction assembly; cell adhesion; cell motion; cell-cell junction; costamere; focal adhesion; lamellipodium assembly; negative regulation of cell migration; oxidoreductase activity; protein complex; structural molecule activity | Cytoplasm , cytoskeleton. Cell junction , adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. | Vinculin/alpha-catenin family |
| 181 VWF_HUMAN | VWF (F8VWF) | P04275 | von Willebrand factor (vWF) [Cleaved into: von Willebrand antigen 2 (von Willebrand antigen II)] | Weibel-Palade body; cell-substrate adhesion; chaperone binding; collagen binding; endoplasmic reticulum; extracellular space; glycoprotein binding; immunoglobulin binding; integrin binding; nucleolus; platelet activation; platelet alpha granule; protease binding; protein N-terminus binding; protein homodimerization activity; protein homooligomerization; proteinaceous extracellular matrix | Secreted. Secreted , extracellular space , extracellular matrix. | |
| 182 WASF2_HUMAN | WASF2 (WAVE2) | Q9Y6W5 | Wiskott-Aldrich syndrome protein family member 2 (WASP family protein member 2) (Protein WAVE-2) (Verprolin homology domain-containing protein 2) | G-protein signaling, coupled to cAMP nucleotide second messenger; actin binding; actin cytoskeleton; actin cytoskeleton organization; cytoplasm; lamellipodium | Cytoplasm , cytoskeleton. Cell projection , lamellipodium. | SCAR/WAVE family |