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| **Supplementary table 1.** List of proteins Identiﬁed in TES from *Toxocara canis* by LC-MS/MS.  |
| **Description** | **Accession** | **Coverage (%)** | **Peptides** | **MW (kda)** | **Molecular function** | **Biological Process** | **Cellular component** |
| Actin-4 | A0A0B2UPE7 | 2 | 1 | 50 | ATP binding | Unknown function | Unknown function |
| Ancylostoma secreted protein  | A0A0B2UP29 | 8 | 3 | 46 | Unknown function | Unknown function | Extracellular region |
| Ancylostoma secreted protein  | A0A0B2VNW7 | 7 | 2 | 27 | Unknown function | Unknown function | Extracellular region |
| Apolipophorin  | A0A0B2VHM0 | 3 | 7 | 349 | Lipid transporter activity | Unknown function | Unknown function |
| Aspartyl protease inhibitor  | A0A0B2V7F9 | 48 | 9 | 16 | Peptidase activity | Unknown function | Unknown function |
| Collectin-12  | A0A0B2VVS4 | 8 | 3 | 35 | Unknown function | Unknown function | Unknown function |
| Collectin-12 (Fragment)  | A0A0B2VX95 | 6 | 2 | 27 | Unknown function | Unknown function | Unknown function |
| Collectin-12 (Fragment)  | A0A0B2VMP2 | 19 | 4 | 27 | Unknown function | Unknown function | Unknown function |
| Cytochrome b-c1 complex subunit 1, mitochondrial  | A0A0B2VW76 | 4 | 2 | 52 | Catalytic activity and metal ion binding | Unknown function | Unknown function |
| Cytochrome b-c1 complex subunit 2, mitochondrial  | A0A0B2VRU7 | 12 | 5 | 54 | Unknown function | Unknown function | Unknown function |
| Elongation factor 1-alpha  | A0A0B2W5Q7 | 3 | 2 | 50 | Gtpase activity, GTP binding and translation elongation factor activity | Unknown function | Cytoplasm |
| Enolase  | A0A0B2VEA6 | 5 | 2 | 47 | Magnesium ion binding and phosphopyruvate hydratase activity | Glycolytic process | Phosphopyruvate hydratase complex |
| Excretory/secretory C-type lectin TES-32 | O44927 | 24 | 4 | 23 | Carbohydrate binding | Unknown function | Unknown function |
| Filamin-A  | A0A0B2VIW2 | 1 | 2 | 238 | ATP binding and transmembrane receptor protein serine/threonine kinase activity | Unknown function | Integral component of membrane |
| Supplementary table 1. (Continued). |
| Galectin  | A0A0B2V054 | 8 | 2 | 30 | Carbohydrate binding | Unknown function | Unknown function |
| Galectin  | A0A0B2V9X0 | 20 | 6 | 31 | Carbohydrate binding | Unknown function | Unknown function |
| Glucose-6-phosphate isomerase  | A0A0B2W5Z0 | 4 | 3 | 67 | Glucose-6-phosphate isomerase activity | Gluconeogenesis and glycolytic process | Unknown function |
| Heat shock 70 kda protein A | A0A0B2V5Y2 | 6 | 5 | 101 | ATP binding | Unknown function | Unknown function |
| Heat shock protein 70 B2  | A0A0B2VM41 | 4 | 2 | 70 | ATP binding | Response to stress | Unknown function |
| Histone H2A  | A0A0B2VPY8 | 41 | 5 | 13 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Histone H2A  | A0A0B2UQD6 | 35 | 5 | 13 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H2A  | A0A0B2V2B0 | 41 | 5 | 13 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H2A  | A0A0B2V2B5 | 41 | 5 | 13 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H2B | A0A0B2UXB4 | 60 | 11 | 13 | DNA binding | Unknown function | Chromosome and nucleus |
| Histone H2B  | A0A0B2UPH8 | 52 | 9 | 13 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H3 | A0A0B2V2I9 | 60 | 10 | 15 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H4 | A0A0B2V2I6 | 63 | 13 | 11 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Histone H4  | A0A0B2VBF2 | 37 | 13 | 19 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Histone H4 O | A0A0B2VU23 | 44 | 13 | 16 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Intermediate filament protein B | A0A0B2UZV0 | 3 | 2 | 64 | Structural molecule activity | Unknown function | Intermediate filament |
| Supplementary table 1. (Continued). |
| Supplementary table 1. (Continued). |
| Laminin subunit beta-1 | A0A0B2UNP1 | 1 | 2 | 195 | Unknown function | Unknown function | Unknown function |
| Laminin-like protein lam-2  | A0A0B2W1F7 | 4 | 2 | 71 | Basement membrane assembly and system development | Unknown function | Basement membrane |
| Macrophage migration inhibitory factor-like protein | A0A0B2V815 | 21 | 3 | 20 | Unknown function | Unknown function | Unknown function |
| Major antigen | A0A0B2VV61 | 1 | 3 | 24 | Unknown function | Unknown function | Unknown function |
| Myosin- | A0A0B2W3E0 | 20 | 37 | 23 | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin heavy chain (Fragment)  | Q9BLM9 | 20 | 33 | 208 | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin, essential light chain  | A0A0B2USP9 | 26 | 3 | 21 | Calcium ion binding | Unknown function | Unknown function |
| Myosin-3  | A0A0B2VG79 | 24 | 43 | 226 | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin-4 | A0A0B2VDE1 | 19 | 33 | 225 | ATP binding and motor activity | Unknown function | Myosin complex |
| OV-17 antigen | A0A0B2VR34 | 13 | 3 | 23 | Unknown function | Unknown function | Unknown function |
| Paramyosin  | A0A0B2V6Q8 | 2 | 2 | 101 | Motor activity | Unknown function | Unknown function |
| Phosphoenolpyruvate carboxykinase [GTP]  | A0A0B2V286 | 4 | 3 | 72 | GTP binding, kinase activity and phosphoenolpyruvate carboxykinase (GTP) activity | Gluconeogenesis | Unknown function |
| Phosphoethanolamine N-methyltransferase 1 | A0A0B2VTW9 | 12 | 3 | 30 | Methyltransferase activity | Unknown function | Unknown function |
| Phosphoglycerate kinase  | A0A0B2V4Q8 | 3 | 2 | 66 | Phosphoglycerate kinase activity | Glycolytic process | Unknown function |
| Protein disulfide-isomerase  | A0A0B2UJM4 | 12 | 7 | 55 | Protein disulfide isomerase activity | Cell redox homeostasis | Endoplasmic reticulum |
| Proteoglycan core protein (Fragment)  | O76131 | 23 | 4 | 24 | Unknown function | Unknown function | Unknown function |
| Supplementary table 1. (Continued). |
| Putative aconitate hydratase, mitochondrial  | A0A0B2UYK4 | 2 | 2 | 92 | 4 iron, 4 sulfur cluster binding, aconitate hydratase activity and metal ion binding | Tricarboxylic acid cycle | Mitochondrion |
| Putative methylmalonyl-coa mutase, mitochondrial  | A0A0B2UT85 | 5 | 6 | 124 | Cobalamin binding, metal ion binding and methylmalonyl-coa mutase activity | Metabolic process | Unknown function |
| Spindle-and centromere-associated protein | A0A0B2VVR8 | 8 | 16 | 24 | Unknown function | Unknown function | Unknown function |
| Spindle-and centromere-associated protein (Fragment)  | A0A0B2V586 | 13 | 26 | 23 | Unknown function | Unknown function | Unknown function |
| Superoxide dismutase [Cu-Zn]  | A0A0B2VI69 | 9 | 3 | 21 | Metal ion binding and superoxide dismutase activity | Unknown function | Unknown function |
| Superoxide dismutase [Cu-Zn]  | A0A0B2VPI6 | 53 | 5 | 16 | Metal ion binding and superoxide dismutase activity | Unknown function | Unknown function |
| Superoxide dismutase [Cu-Zn]  | A0A0B2UPS1 | 19 | 8 | 51 | Metalloendopeptidase activity, superoxide dismutase activity and zinc ion binding | Unknown function | Unknown function |
| Transthyretin-like protein 46 | A0A0B2W0X7 | 34 | 3 | 19 | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46  | A0A0B2W0V7 | 46 | 6 | 13 | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46  | A0A0B2W1X6 | 15 | 2 | 25 | Unknown function | Unknown function | Extracellular space |
| Tropomyosin | A0A0B2VD59 | 17 | 2 | 12 | Unknown function | Unknown function | Unknown function |
| Tropomyosin | A0A0B2VDB8 | 29 | 11 | 31 | Unknown function | Unknown function | Unknown function |
| Uncharacterized protein | A0A0B2UUN4 | 10 | 2 | 23 | Unknown function | Unknown function | Unknown function |
| Uncharacterized protein  | A0A0B2VUW2 | 2 | 2 | 43 | Unknown function | Unknown function | Unknown function |
| Supplementary table 1. (Continued). |  |  |  |  |  |  |  |
| Uncharacterized protein F32A5.4  | A0A0B2V2R3 | 38 | 10 | 21 | Unknown function | Unknown function | Unknown function |
| Versican core protein (Fragment)  | A0A0B2UQQ9 | 11 | 2 | 11 | Unknown function | Unknown function | Unknown function |
| 26 kda secreted antigen  | A0A0B2UQZ7 | 17 | 2 | 16 | Unknown function | Unknown function | Unknown function |
| 26 kda secreted antigen  | A0A0B2UWT5 | 10 | 3 | 28 | Unknown function | Unknown function | Unknown function |

The proteins identified were categorized by their molecular function, biological process and cellular component according to information obtained from the Gene Ontology database (UNIPROT).

\* Signal peptide.

| **Supplementary table 2.** List of proteins Identiﬁed in larval extract from *Toxocara canis* by LC-MS/MS |
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| **Description** | **Accession** | **Coverage (%)** | **Peptides** |  **MW (kda)** | **Molecular function** | **Biological Process** | **Cellular component** |
| 1,4-alpha-glucan-branching enzyme | A0A0B2UT58 | 28 | 10 | 84  | Catalytic activity, binding | Carbohydrate metabolic process | Unknown function |
| 10 kda heat shock protein, mitochondrial  | A0A0B2VXR2 | 23 | 2 | 12  | ATP binding | Protein folding | Cytoplasm |
| 10-formyltetrahydrofolate dehydrogenase | A0A0B2VES1 | 10 | 6 | 92  | Catalytic activity | Catabolic process | Unknown function |
| 14-3-3-like protein 2 | A0A0B2V712 | 18 | 4 | 30  | Unknown function | Unknown function | Unknown function |
| Proteasome subunit alpha type | A0A0B2VT82 | 41 | 6 |  27  | Catalytic activity | Catabolic process | Unknown function |
| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | A0A0B2VUR0 | 4 | 2 | 64  |  Phosphoglycerate mutase activity | Glucose catabolic process | Unknown function |
| 26S protease regulatory subunit 4 | A0A0B2W750 | 6 | 2 | 64  | ATP binding and peptidase activity | Catabolic process | Unknown function |
| 26S protease regulatory subunit 7  | A0A0B2V336 | 4 | 2 | 66  | ATP binding, peptidase activity and structural constituent of ribosome | Catabolic process and translation | Unknown function |
| 26S proteasome non-atpase regulatory subunit 1 | A0A0B2VFX2 | 3 | 2 | 78  | Enzyme regulator activity | Regulation of protein catabolic process | Unknown function |
| 26S proteasome non-atpase regulatory subunit 10 -  | A0A0B2W3T5 | 18 | 2 | 32  | Unknown function | Unknown function | Proteasome complex |
| 2-amino-3-ketobutyrate coenzyme A ligase, mitochondria | A0A0B2VIJ5 | 45 | 11 | 38  | Ligase activity and pyridoxal phosphate binding | Biosynthetic process | Unknown function |
| 2-oxoglutarate dehydrogenase, mitochondrial | A0A0B2VE95 | 6 | 6 | 123  | Oxoglutarate dehydrogenase and thiamine pyrophosphate binding | Tricarboxylic acid cycle | Unknown function |
| 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial | A0A0B2URD4 | 9 | 2 | 64  | Catalytic activity, sequence-specific DNA binding, transcription factor activity, sequence-specific DNA binding | Metabolic process | Unknown function |
| 3-oxoacyl-[acyl-carrier-protein] reductase fabg | A0A0B2V5U1 | 23 | 5 | 30  | Oxidoreductase activity | Unknown function | Unknown function |
| 40S ribosomal protein S14  | A0A0B2UT45 | 17 | 2 | 16  | Structural constituent of ribosome | Translation | Unknown function |
| 40S ribosomal protein s3a | A0A0B2UYS6 | 3 | 2 | 82  | Structural constituent of ribosome | Translation | Ribosome |
| 40S ribosomal protein S4 | A0A0B2VML1 | 4 | 4 | 134  | Structural, RNA binding | Translation | Integral component of membrane and ribosome |
| 40S ribosomal protein S5 | A0A0B2W326 | 11 | 2 | 24  | RNA binding and structural constituent of ribosome | Translation | Small ribosomal subunit |
| 40S ribosomal protein S8  | A0A0B2V6N2 | 19 | 3 | 24  | Structural constituent of ribosome | Translation | Ribosome |
| 4-hydroxybutyrate coenzyme A transferase | A0A0B2VKT7 | 35 | 9 | 51  | Transferase activity | Acetyl-coa metabolic process | Unknown function |
| 5-methylcytosine rrna methyltransferase NSUN4 | A0A0B2V8B6 | 5 | 3 | 110  | Methyltransferase activity | Unknown function | Unknown function |
| 60S acidic ribosomal protein  | A0A0B2V4S9 | 7 | 2 | 34  | Ribosome biogenesis | Unknown function | Ribosome |
| 60S acidic ribosomal protein P2  | A0A0B2V1V8 | 4 | 2 | 99  | Metal ion binding, Rho guanyl-nucleotide exchange factor activity and structural constituent of ribosome | Regulation of Rho protein signal transduction and translational elongation | Ribosome |
| 60S ribosomal protein L10  | A0A0B2UVJ8 | 19 | 5 | 25  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L17 | A0A0B2VZY5 | 14 | 2 | 22  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L18  | A0A0B2V8V3 | 16 | 3 | 25  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L23a  | A0A0B2VH97 | 34 | 4 | 18  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L4  | A0A0B2V6T8 | 12 | 3 | 42  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L5 | A0A0B2VGJ3 | 10 | 2 | 37  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L6  | A0A0B2V697 | 16 | 3 | 28  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L7  | A0A0B2VEX2 | 14 | 4 | 29  | Structural constituent of ribosome | Translation | Ribosome |
| 60S ribosomal protein L8  | A0A0B2VDX4 | 15 | 3 | 28  | Structural constituent of ribosome | Translation | Ribosome |
| 6-phosphogluconate dehydrogenase, decarboxylating | A0A0B2VGY3 | 26 | 8 | 53  | Phosphogluconate dehydrogenase (decarboxylating) activity | Pentose-phosphate shunt | Unknown function |
| 6-phosphogluconolactonase  | A0A0B2W1F3 | 32 | 5 | 26  | 6-phosphogluconolactonase activity | Carbohydrate metabolic process and pentose-phosphate shunt | Unknown function |
| Acetyl-coa acetyltransferase A, mitochondrial  | A0A0B2USF6 | 17 | 3 | 31  | Transferase activity | Metabolic process | Unknown function |
| Acetyl-coenzyme A synthetase | A0A0B2ULI6 | 28 | 2 | 29  | Catalytic activity | Metabolic process | Unknown function |
| Acetyltransferase component of pyruvate dehydrogenase complex  | A0A0B2V1E3 | 5 | 2 | 63  | Catalytic activity | Pyruvate metabolic process | Unknown function |
| Acid sphingomyelinase-like phosphodiesterase 3b | A0A0B2VEJ3 | 5 | 2 | 65  | Hydrolase activity | Unknown function | Unknown function |
| Actin-1 | A0A0B2W152 | 38 | 10 | 42  | ATP binding | Cytoskeleton organization | Unknown function |
| Actin-2 | A0A0B2URX3 | 19 | 4 | 31  | ATP binding | Cytoskeleton organization | Unknown function |
| Actin-4  | A0A0B2UPE7 | 30 | 10 | 51  | ATP binding | Unknown function | Unknown function |
| Actin-depolymerizing factor 2, isoform c  | A0A0B2VJL7 | 47 | 6 | 18  | Unknown function | Actin filament depolymerization | Unknown function |
| Actin-interacting protein 1 | A0A0B2USU3 | 5 | 2 | 62  | Unknown function | Unknown function | Unknown function |
| Actin-like protein | A0A0B2UY34 | 16 | 3 | 37  | ATP binding | Unknown function | Unknown function |
| Actin-like protein  | A0A0B2VA52 | 43 | 13 | 41 | ATP binding | Unknown function | Unknown function |
| Acyl-coa synthetase family member 2, mitochondrial | A0A0B2V7U9 | 12 | 4 | 57  | Catalytic activity | Metabolic process | Unknown function |
| Acyl-coa-binding protein  | A0A0B2UXI8 | 38 | 4 | 10  | Fatty-acyl-coa binding | Unknown function | Unknown function |
| Acyl-protein thioesterase 2 | A0A0B2V566 | 26 | 2 | 15  | Hydrolase activity | Unknown function | Unknown function |
| Adenosylhomocysteinas | A0A0B2URV3 | 8 | 2 | 50  | Adenosylhomocysteinase activity and NAD binding | Metabolic process and S-adenosylhomocysteine catabolic process | Unknown function |
| Adenylate kinase  | A0A0B2VKE4 | 10 | 3 | 34  | Catalytic activity | Biosynthetic process | Unknown function |
| Adenylate kinase isoenzyme 1 | A0A0B2V5R1 | 6 | 2 | 57  | Adenylate kinase activity, ATP binding and nucleoside diphosphate kinase activity | ATP metabolic process and nucleoside triphosphate biosynthetic process | Unknown function |
| Adenylosuccinate lyase | A0A0B2VZY2 | 16 | 4 | 37  | Lyase activity | Unknown function | Unknown function |
| Adenylyl cyclase-associated protein | A0A0B2UNH4 | 2 | 2 | 118  | Unknown function | Actin filament organization and cell morphogenesis | Unknown function |
| ADP,ATP carrier protein | A0A0B2V880 | 21 | 7 | 34  | Transporter activity | Transmembrane transport | Integral component of membrane and mitochondrial inner membrane |
| ADP-ribosylation factor 1-like 2 | A0A0B2VH36 | 10 | 2 | 28  | GTP binding | Small gtpase mediated signal transduction | Integral component of membrane and intracellular |
| Aggrecan core protein | A0A0B2VPN5 | 7 | 2 | 37  | Unknown function | Unknown function | Unknown function |
| Alanine aminotransferase 1 | A0A0B2V9Y4 | 6 | 2 | 61  | Pyridoxal phosphate binding and transaminase activity | Biosynthetic process | Unknown function |
| Alanine aminotransferase 2 | A0A0B2UUH6 | 27 | 9 | 52  | Transaminase activity | Biosynthetic process | Unknown function |
| Alanine--trna ligase, cytoplasmic | A0A0B2UK24 | 30 | 2 | 13  | Alanine-trna ligase activity and ATP binding | Alanyl-trna aminoacylation | Unknown function |
| Alcohol dehydrogenase [NADP(+)] | A0A0B2UMW1 | 28 | 7 | 37  | Oxidoreductase activity | Unknown function | Unknown function |
| Alcohol dehydrogenase class-3 | A0A0B2UZB3 | 8 | 2 | 46  | S-(hydroxymethyl)glutathione dehydrogenase activity and zinc ion binding | Ethanol oxidation | Unknown function |
| Aldehyde dehydrogenase | A0A0B2US81 | 6 | 2 | 57  | Aldehyde dehydrogenase [NAD(P)+] activity | Cellular aldehyde metabolic process | Integral component of membrane |
| Aldehyde dehydrogenase family 9 member A1 | A0A0B2VCZ3 | 5 | 2 | 86  | Oxidoreductase activity | Unknown function | Unknown function |
| Aldehyde dehydrogenase, mitochondrial | A0A0B2W0G2 | 6 | 2 | 57  | Oxidoreductase activity | Unknown function | Unknown function |
| Aldose reductase B | A0A0B2VWR6 | 10 | 2 | 33  | Oxidoreductase activity | Unknown function | Unknown function |
| Alpha-1,4 glucan phosphorylas | A0A0B2VP28 | 45 | 25 | 138  | Glycogen phosphorylase activity and pyridoxal phosphate binding | Carbohydrate metabolic process | Unknown function |
| Alpha-actinin | A0A0B2VKR6 | 28 | 16 | 80  | Calcium ion binding | Carbohydrate metabolic process | Unknown function |
| Alpha-actinin-2 | A0A0B2VEK6 | 38 | 8 | 31  | Unknown function | Unknown function | Unknown function |
| Alpha-mannosidase  | A0A0B2W2Q3 | 11 | 7 | 114  | Alpha-mannosidase activity, carbohydrate binding and zinc ion binding | Mannose metabolic process | Unknown function |
| Alpha-N-acetylgalactosaminidase | A0A0B2VLR7 | 11 | 3 | 47  | Hydrolase activity | Metabolic process | Unknown function |
| Aminopeptidase N | A0A0B2V4Q4 | 2 | 2 | 213  | Aminopeptidase activity, metallopeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Anion exchange protein | A0A0B2VA46 | 3 | 2 | 117  | Inorganic anion exchanger activity | Unknown function | Integral component of membrane |
| Annexin | A0A0B2UXN0 | 12 | 3 | 36  | Calcium-dependent phospholipid binding and calcium ion binding | Unknown function | Unknown function |
| ANT-3.1 | B5A257 | 24 | 4 | 31  | Unknown function | Unknown function | Unknown function |
| Antigen-like protein | A0A0B2UVL3 | 7 | 3 | 86  | Endopeptidase inhibitor activity | Unknown function | Unknown function |
| Antigen-like protein  | A0A0B2UV01 | 4 | 3 | 124  | Endopeptidase inhibitor activity | Unknown function | Unknown function |
| Apolipophorin | A0A0B2VHM0 | 42 | 102 | 350  | Lipid transporter activity | Unknown function | Unknown function |
| Apolipoprotein(A) | A0A0B2UXW0 | 20 | 4 | 35  | Serine-type endopeptidase activity | Unknown function | Unknown function |
| Arginase | A0A0B2V9N2 | 11 | 3 | 34  | Metal ion binding | Unknown function | Unknown function |
| Arginine kinase | A7YVI5 | 9 | 3 | 45  | ATP binding and kinase activity | Unknown function | Unknown function |
| Asparagine--trna ligase, cytoplasmic  | A0A0B2UY35 | 5 | 2 | 67  | Asparagine-trna ligase activity, ATP binding and nucleic acid binding | Asparaginyl-trna aminoacylation | Cytoplasm |
| Aspartate aminotransferase | A0A0B2UU86 | 7 | 2 | 47  | L-aspartate:2-oxoglutarate aminotransferase activity, L-phenylalanine:2-oxoglutarate aminotransferase activity, pyridoxal phosphate binding | Biosynthetic process and cellular amino acid metabolic process | Unknown function |
| Aspartate--trna ligase, cytoplasmic | A0A0B2VZV2 | 10 | 3 | 60  | Aspartate-trna ligase activity, ATP binding, nucleic acid binding | Aspartyl-trna aminoacylation | Cytoplasm |
| ATP synthase subunit alpha, mitochondrial | A0A0B2VVN2 | 9 | 3 | 85  | ATP binding and proton-transporting ATP synthase activity, rotational mechanism | ATP synthesis coupled proton transport | Proton-transporting ATP synthase complex, catalytic core F |
| ATP synthase subunit beta | A0A0B2URI6 | 5 | 2 | 59  | ATP binding and proton-transporting ATP synthase activity, rotational mechanism | ATP synthesis coupled proton transport | Unknown function |
| ATP-dependent (S)-NAD(P)H-hydrate dehydratase | A0A0B2VL41 | 14 | 3 | 33  | ADP-dependent NAD(P)H-hydrate dehydratase activity, ATP binding and ATP-dependent NAD(P)H-hydrate dehydratase activity | Nicotinamide nucleotide metabolic process | Unknown function |
| ATP-dependent 6-phosphofructokinase | A0A0B2VIU1 | 19 | 13 | 91  | 6-phosphofructokinase activity, ATP binding and metal ion binding | Fructose 6-phosphate metabolic process | Cytoplasm |
| ATP-dependent RNA helicase DDX1 | A0A0B2VM70 | 6 | 3 | 81  | ATP binding, helicase activity and nucleic acid binding | Unknown function | Unknown function |
| ATP-dependent RNA helicase DDX3Y | A0A0B2VS49 | 4 | 2 | 72  | ATP binding, helicase activity and nucleic acid binding | Unknown function | Unknown function |
| ATP-dependent RNA helicase DDX3Y | A0A0B2VTN7 | 26 | 12 | 72  | ATP binding, helicase activity and nucleic acid binding | Unknown function | Unknown function |
| BAG family molecular chaperone regulator 2 | A0A0B2VXF2 | 11 | 2 | 25  | Unknown function | Unknown function | Unknown function |
| Basement membrane proteoglycan | A0A0B2V9L0 | 6 | 15 | 621  | Unknown function | Unknown function | Unknown function |
| Beta-galactosidase | A0A0B2VH70 | 14 | 6 | 73  | Beta-galactosidase activity | Carbohydrate metabolic process | Unknown function |
| Beta-glucosidase 6 | A0A0B2VNT0 | 28 | 9 | 61  | Hydrolase activity and hydrolyzing O-glycosyl compounds | Carbohydrate metabolic process | Integral component of membrane |
| Beta-hexosaminidase | A0A0B2V160 | 13 | 5 | 62  | Beta-N-acetylhexosaminidase activity | Carbohydrate metabolic process | Unknown function |
| Bifunctional nitrilase/nitrile hydratase NIT4B (Fragment) | A0A0B2V2Q9 | 2 | 1 | 69.510  | Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | Nitrogen compound metabolic process | Unknown function |
| Branched-chain-amino-acid aminotransferase, cytosolic | A0A0B2UYH1 | 4 | 2 | 49  | Transaminase activity | Metabolic process | Integral component of membrane |
| Branched-chain-amino-acid aminotransferase, cytosolic  | A0A0B2UXS8 | 15 | 4 | 47  | Transaminase activity | Metabolic process | Unknown function |
| C-1-tetrahydrofolate synthase, cytoplasmic | A0A0B2VQD6 | 9 | 5 | 101  | ATP binding, formate-tetrahydrofolate ligase activity and methylenetetrahydrofolate dehydrogenase (NADP+) activity | Folic acid-containing compound biosynthetic process | Unknown function |
| Caffeoyl-coa O-methyltransferase 2  | A0A0B2W171 | 7 | 2 | 47  | O-methyltransferase activity | Unknown function | Unknown function |
| Calcium-binding protein 39  | A0A0B2UNY6 | 4 | 2 | 39  | Unknown function | Unknown function | Unknown function |
| Calcium-transporting atpase | A0A0B2V399 | 7 | 4 | 116  | ATP binding, calcium-transporting atpase activity and metal ion binding | Unknown function | Membrane |
| Calmodulin  | A0A0B2UVU2 | 20 | 2 | 16 | Calcium ion binding | Unknown function | Unknown function |
| Calnexin | A0A0B2VNA3 | 4 | 2 | 61  | Calcium ion binding | Protein folding | Endoplasmic reticulum and integral component of membrane |
| Calpain clp-1  | A0A0B2VN55 | 4 | 2 | 61  | Calcium-dependent cysteine-type endopeptidase activity | Unknown function | Intracellular |
| Calponin-like protein OV9M  | A0A0B2UJM8 | 17 | 4 | 37 | Unknown function | Unknown function | Unknown function |
| Calreticulin | A0A0B2V659 | 11 | 3 | 43  | Calcium ion binding | Protein folding | Endoplasmic reticulum |
| Calsequestrin | A0A0B2VMM7 | 16 | 3 | 49  | Calcium ion binding | Unknown function | Unknown function |
| Calumenin-A | A0A0B2VQG1 | 22 | 6 | 36  | Calcium ion binding | Unknown function | Unknown function |
| Carbonyl reductase [NADPH] 3 | A0A0B2VUM0 | 19 | 5 | 36  | Oxidoreductase activity | Unknown function | Unknown function |
| Carboxylic ester hydrolase  | A0A0B2UXV6 | 6 | 3 | 64  | Hydrolase activity | Unknown function | Unknown function |
| Carboxypeptidase | A0A0B2UYY2 | 2 | 4 | 260  | Serine-type carboxypeptidase activity | Unknown function | Unknown function |
| Carboxypeptidase D | A0A0B2UZT0 | 6 | 2 | 52  | Metallocarboxypeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Carboxypeptidase Q | A0A0B2VUQ6 | 19 | 2 | 25  | Carboxypeptidase activity | Unknown function | Unknown function |
| Carnitine O-acetyltransferase | A0A0B2UYP5 | 7 | 2 | 39  | Transferase activity and transferring acyl groups | Unknown function | Unknown function |
| Cathepsin B-like cysteine proteinase 6 | A0A0B2VTL1 | 10 | 2 | 45  | Cysteine-type peptidase activity | Unknown function | Unknown function |
| Cathepsin L  | A0A0B2VC96 | 6 | 2 | 74  | Cysteine-type peptidase activity and serine-type endopeptidase activity | Unknown function | Unknown function |
| Cathepsin Z | A0A0B2UNS7 | 4 | 2 | 35  | Cysteine-type peptidase activity | Unknown function | Unknown function |
| Cell surface glycoprotein 1 | A0A0B2VRS6 | 4 | 3 | 156  | Unknown function | Unknown function | Unknown function |
| Cgmp-dependent protein kinase egl-4 (Fragment) | A0A0B2VBB7 | 13 | 6 | 82  | ATP binding and cgmp-dependent protein kinase activity | Unknown function | Unknown function |
| Chaperonin-like protein Hsp-60, mitochondrial | A0A0B2W434 | 5 | 2 | 86  | ATP binding | Protein refolding | Cytoplasm |
| Chloride intracellular channel exc-4  | A0A0B2V9R6 | 7 | 2 | 46  | Unknown function | Unknown function | Unknown function |
| Chymotrypsin/elastase isoinhibitors 2 to 5  | A0A0B2W5D7 | 29 | 3 | 18  | Unknown function | Unknown function | Unknown function |
| Citrate lyase subunit beta-like protein, mitochondrial | A0A0B2V485 | 11 | 3 | 39  | Unknown function | Unknown function | Unknown function |
| Citrate synthase | A0A0B2W1Q6 | 5 | 2 | 51  | Citrate (Si)-synthase activity | Citrate metabolic process and tricarboxylic acid cycle | Unknown function |
| Clathrin interactor 1  | A0A0B2VQ91 | 4 | 2 | 61  | Unknown function | Unknown function | Unknown function |
| Coatomer subunit alpha | A0A0B2V512 | 11 | 11 | 148  | Structural molecule activity | Intracellular protein transport and vesicle-mediated transport | COPI vesicle coat |
| Coatomer subunit beta | A0A0B2W0H1 | 17 | 10 | 107  | Structural molecule activity | Intracellular protein transport and vesicle-mediated transport | COPI vesicle coat and Golgi membrane |
| Coatomer subunit epsilon  | A0A0B2UP71 | 36 | 4 | 21  | Structural molecule activity | Retrograde vesicle-mediated transport and Golgi to ER | Unknown function |
| Collagen alpha-2(IV) chain | A0A0B2V0L0 | 3 | 4 | 166  | Extracellular matrix structural constituent | Unknown function | Collagen trimer and proteinaceous extracellular matrix |
| Collectin-12  | A0A0B2UY45 | 2 | 2 | 125 | Nucleic acid binding | DNA integration | Unknown function |
| Conserved regulator of innate immunity protein 3 | A0A0B2W008 | 24 | 4 | 27  | Unknown function | Unknown function | Mitochondrial matrix |
| Contactin-associated protein-like 5 | A0A0B2VQT0 | 3 | 2 | 123  | Unknown function | Unknown function | Integral component of membrane |
| COP9 signalosome complex subunit 7  | A0A0B2UVU8 | 9 | 3 | 52  | Unknown function | Unknown function | Unknown function |
| Coronin | A0A0B2VDX3 | 12 | 4 | 68  | Unknown function | Unknown function | Unknown function |
| C-type lectin protein  | A0A0B2USF5 | 15 | 4 | 43  | Carbohydrate binding | Unknown function | Unknown function |
| Cullin-1 | A0A0B2V4M5 | 3 | 2 | 104  | Unknown function | Ubiquitin-dependent protein catabolic process | Cullin-RING ubiquitin ligase complex |
| Cullin-associated Nedd8-dissociated protein 1 | A0A0B2UR62 | 25 | 2 | 12  | Unknown function | Unknown function | Unknown function |
| Cysteine--trna ligase, cytoplasmic | A0A0B2VQE6 | 5 | 2 | 54  | ATP binding and cysteine-trna ligase activity | Cysteinyl-trna aminoacylation | Unknown function |
| Cytochrome b-c1 complex subunit 1, mitochondrial  | A0A0B2VW76 | 6 | 2 | 53  | Catalytic activity and metal ion binding | Unknown function | Unknown function |
| Cytochrome c type-1  | A0A0B2VRN9 | 14 | 2 | 18 | Electron carrier activity, heme binding and metal ion binding | Oxidation-reduction process | Mitochondrion and respiratory chain |
| Cytoplasmic dynein 1 light intermediate chain 2 | A0A0B2UYD7 | 3 | 2 | 76  | Microtubule motor activity | Microtubule-based movement | Cytoplasmic dynein complex |
| Cytosolic non-specific dipeptidase | A0A0B2V7K8 | 11 | 3 | 75  | Dipeptidase activity and metallopeptidase activity | Unknown function | Unknown function |
| D-aspartate oxidase 1 | A0A0B2UNV1 | 9 | 2 | 40  | D-amino-acid oxidase activity and FAD binding | D-amino acid metabolic process | Unknown function |
| Decapping nuclease dom-3  | A0A0B2UTA2 | 29 | 6 | 39  | Unknown function | Unknown function | Unknown function |
| Dehydrogenase/reductase SDR family member 1 | A0A0B2VSK7 | 13 | 3 | 45  | Unknown function | Unknown function | Integral component of membrane |
| Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondria | A0A0B2VA03 | 6 | 2 | 65  | 1-pyrroline-5-carboxylate dehydrogenase activity and oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | Glutamate biosynthetic process and proline biosynthetic process | Unknown function |
| Developmentally-regulated GTP-binding protein 1  | A0A0B2VDT2 | 20 | 4 | 35  | GTP binding | Unknown function | Unknown function |
| Dihydrolipoyl dehydrogenase, mitochondrial | A0A0B2V3B2 | 10 | 3 | 57  | Flavin adenine dinucleotide binding and oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor | Cell redox homeostasis | Cell |
| Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondria | A0A0B2VKD2 | 24 | 10 | 52  | Dihydrolipoyllysine-residue succinyltransferase activity | Tricarboxylic acid cycle | Unknown function |
| Dihydropteridine reductase | A0A0B2VM35 | 14 | 2 | 31  | Oxidoreductase activity | Unknown function | Unknown function |
| Dimethylglycine dehydrogenase, mitochondrial  | A0A0B2V8H3 | 7 | 3 | 93  | Oxidoreductase activity | Unknown function | Unknown function |
| Disorganized muscle protein 1 | A0A0B2W617 | 34 | 10 | 36  | Unknown function | Unknown function | Unknown function |
| DNA damage-binding protein 1 | A0A0B2VTC0 | 3 | 3 | 135  | Nucleic acid binding | Unknown function | Nucleus |
| Dnaj-like protein subfamily A member 2 | A0A0B2VLU4 | 4 | 2 | 74  | Protein folding | Unknown function | Unknown function |
| Dnaj-like protein subfamily C member 3 | A0A0B2W3W9 | 11 | 4 | 58  | Unknown function | Unknown function | Unknown function |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kda subuni | A0A0B2UT11 | 12 | 4 | 49  | Transferase activity, transferring glycosyl groups | Protein N-linked glycosylation via asparagine | Endoplasmic reticulum membrane and integral component of membrane |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kda subunit | A0A0B2VAT7 | 6 | 2 | 48  | Transferase activity, transferring glycosyl groups | Protein N-linked glycosylation via asparagine | Endoplasmic reticulum membrane and integral component of membrane |
| DVA-1 polyprotein  | A0A0B2VW26 | 4 | 2 | 70  | Unknown function | Unknown function | Unknown function |
| Dynein heavy chain, cytoplasmic | A0A0B2UYS0 | 7 | 23 | 535  | Atpase activity, ATP binding and microtubule motor activity | Microtubule-based movement | Dynein complex |
| E3 ubiquitin-protein ligase HUWE1  | A0A0B2VXD0 | 3 | 5 | 323  | Ligase activity | Unknown function | Integral component of membrane |
| EF-hand domain-containing protein D1 | A0A0B2VVQ9 | 9 | 2 | 27  | Calcium ion binding | Unknown function | Unknown function |
| EH domain-containing protein 3 | A0A0B2V7G7 | 5 | 2 | 43  | Calcium ion binding | Unknown function | Unknown function |
| Elongation factor 1-alpha | A0A0B2W5Q7 | 19 | 7 | 51  | Gtpase activity, GTP binding and translation elongation factor activity | Unknown function | Cytoplasm |
| Elongation factor 1-beta | A0A0B2W4V4 | 7 | 2 | 58  | Translation elongation factor activity | Unknown function | Unknown function |
| Elongation factor 2 | A0A0B2VI65 | 7 | 3 | 97  | Gtpase activity, GTP binding and translation elongation factor activity | Unknown function | Unknown function |
| Endophilin-B1  | A0A0B2UVR7 | 5 | 2 | 46  | Unknown function | Unknown function | Cytoplasm |
| Endoplasmin  | A0A0B2URQ0 | 6 | 3 | 90  | ATP binding | Protein folding and response to stress | Unknown function |
| Enolase | A0A0B2UQW4 | 53 | 18 | 38  | Magnesium ion binding and phosphopyruvate hydratase activity | Glycolytic process | Phosphopyruvate hydratase complex |
| Enolase  | A0A0B2VEA6 | 29 | 8 | 47  | Magnesium ion binding and phosphopyruvate hydratase activity | Glycolytic process | Phosphopyruvate hydratase complex |
| Enoyl-coa hydratase domain-containing protein 3, mitochondrial  | A0A0B2V3N4 | 20 | 5 | 32  | Catalytic activity | Metabolic process | Unknown function |
| Epidermal retinol dehydrogenase 2 | A0A0B2VVC8 | 8 | 2 | 33  | Oxidoreductase activity | Unknown function | Integral component of membrane |
| Epidermal retinol dehydrogenase 2  | A0A0B2VCJ7 | 11 | 2 | 38  | Oxidoreductase activity | Unknown function | Integral component of membrane |
| Epoxide hydrolase 1 | A0A0B2VCM0 | 8 | 2 | 52  | Cis-stilbene-oxide hydrolase activity | Unknown function | Integral component of membrane |
| Estradiol 17-beta-dehydrogenase 8 | A0A0B2VZ70 | 22 | 4 | 26  | Oxidoreductase activity | Unknown function | Unknown function |
| Eukaryotic initiation factor 4A | A0A0B2W320 | 11 | 3 | 47  | ATP binding, helicase activity and translation initiation factor activity | Unknown function | Unknown function |
| Eukaryotic translation initiation factor 2A | A0A0B2VUB3 | 16 | 6 | 62  | Translation initiation factor activity | Unknown function | Unknown function |
| Eukaryotic translation initiation factor 4 gamma 3 (Fragment) | A0A0B2VBC9 | 3 | 2 | 78  | Translation initiation factor activity | Unknown function | Unknown function |
| Eukaryotic translation initiation factor 5A-2 | A0A0B2W095 | 15 | 2 | 21  | Ribosome binding, translation elongation factor activity and translation initiation factor activity | Positive regulation of translational elongation, positive regulation of translational termination and translational frameshifting | Unknown function |
| Excretory/secretory C-type lectin TES-32  | O44927 | 11 | 2 | 23 | Carbohydrate binding | Unknown function | Unknown function |
| Exportin-1 | A0A0B2UQZ9 | 9 | 7 | 124  | Unknown function | Intracellular protein transport | Unknown function |
| Exportin-2  | A0A0B2V5T3 | 4 | 2 | 108  | Unknown function | Intracellular protein transport | Unknown function |
| Extracellular globin  | Q6KG54 | 17 | 2 | 20  | Heme binding, iron ion binding, oxygen binding and oxygen transporter activity | Unknown function | Unknown function |
| F-actin-capping protein subunit beta isoforms 1 and 2 | A0A0B2VQP9 | 13 | 4 | 40  | Unknown function | Actin cytoskeleton organization and barbed-end actin filament capping | Cytoplasm and F-actin capping protein complex |
| Ferritin  | A0A0B2VBR4 | 13 | 2 | 20  | Ferric iron binding and ferroxidase activity | Cellular iron ion homeostasis and iron ion transport | Cell |
| Fragile X mental retardation protein 1-like protein | A0A0B2UXJ5 | 8 | 2 | 53  | RNA binding | Unknown function | Unknown function |
| Fructose-1,6-bisphosphatase isozyme 2 | A0A0B2UNG9 | 9 | 2 | 37  | Fructose 1,6-bisphosphate 1-phosphatase activity | Fructose catabolic process | Unknown function |
| Fructose-bisphosphate aldolase | A0A0B2V6I9 | 8 | 3 | 50  | Fructose-bisphosphate aldolase activity | Glycolytic process | Unknown function |
| Fumarate reductase | A0A0B2W139 | 18 | 6 | 52  | Oxidoreductase activity | Unknown function | Unknown function |
| Galactokinase | A0A0B2VTC2 | 6 | 2 | 46  | ATP binding and galactokinase activity | Galactose metabolic process | Cytoplasm |
| Galactose-1-phosphate uridylyltransferase | A0A0B2V4N3 | 6 | 2 | 41  | UDP-glucose:hexose-1-phosphate uridylyltransferase activity and zinc ion binding | Galactose metabolic process | Unknown function |
| Galectin  | A0A0B2W2G3 | 20 | 2 | 16  | Carbohydrate binding | Unknown function | Unknown function |
| Gamma-glutamyltranspeptidase 1 | A0A0B2VJ19 | 5 | 2 | 60  | Gamma-glutamyltransferase activity | Glutathione metabolic process | Unknown function |
| GDP-L-fucose synthase | A0A0B2V3V7 | 6 | 2 | 45  | Coenzyme binding and oxidoreductase activity | Nucleotide-sugar biosynthetic process | Unknown function |
| GDP-mannose 4,6 dehydratase 1 | A0A0B2W3A8 | 25 | 3 | 18  | Unknown function | Unknown function | Unknown function |
| Gelsolin-like protein 1 | A0A0B2V0C5 | 27 | 8 | 53  | Glucose-6-phosphate dehydrogenase activity and NADP binding | Glucose metabolic process and pentose-phosphate shunt | Unknown function |
| Glucose-6-phosphate 1-dehydrogenase | A0A0B2UZ30 | 13 | 5 | 66  | Glucose-6-phosphate dehydrogenase activity and NADP binding | Glucose metabolic process and pentose-phosphate shunt | Unknown function |
| Glucose-6-phosphate isomerase | A0A0B2W5Z0 | 25 | 10 | 68  | Glucose-6-phosphate isomerase activity | Gluconeogenesis and glycolytic process | Unknown function |
| Glutamate dehydrogenase | A0A0B2UXI4 | 10 | 4 | 59  | Glutamate dehydrogenase (NAD+) activity | Cellular amino acid metabolic process | Unknown function |
| Glutamate dehydrogenase, mitochondrial OS | A0A0B2VUX1 | 12 | 6 | 76  | Glutamate dehydrogenase (NAD+) activity | Cellular amino acid metabolic process | Unknown function |
| Glutamate--cysteine ligase regulatory subunit (Fragment) SV=1  | A0A0B2UJ05 | 14 | 2 | 20  | Glutamate dehydrogenase (NAD+) activity | Cellular amino acid metabolic process | Unknown function |
| Glutathione peroxidase  | A0A0B2VSL8 | 6 | 2 | 42  | Glutathione peroxidase activity | Response to oxidative stress | Unknown function |
| Glutathione reductase, mitochondrial  | A0A0B2VS44 | 6 | 2 | 66  | Flavin adenine dinucleotide binding and oxidoreductase activity | Cell redox homeostasis and vesicle-mediated transport | Cell and integral component of membrane |
| Glutathione S-transferase  | A0A0B2VSH0 | 10 | 2 | 25  | Glutathione transferase activity | Metabolic process | Unknown function |
| Glutathione S-transferase 1  | A0A0B2UUN3 | 12 | 2 | 30  | Transferase activity | Unknown function | Unknown function |
| Glutathione S-transferase 2  | A0A0B2VSM5 | 64 | 16 | 24  | Glutathione transferase activity | Metabolic process | Unknown function |
| Glutathione synthetase | A0A0B2W072 | 28 | 9 | 57  | ATP binding, glutathione binding, glutathione synthase activity and magnesium ion binding | Unknown function | Unknown function |
| Glyceraldehyde-3-phosphate dehydrogenase | A0A0B2UTM8 | 26 | 10 | 44  | Glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity, NAD binding and NADP binding | Glucose metabolic process and glycolytic process | Unknown function |
| Glycerol-3-phosphate dehydrogenase | A0A0B2VLV4 | 6 | 3 | 86  | Calcium ion binding and sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity | Glycerol-3-phosphate metabolic process | Glycerol-3-phosphate dehydrogenase complex and integral component of membrane |
| Glycine cleavage system H protein, mitochondrial  | A0A0B2UZU2 | 19 | 2 | 18  | Unknown function | Glycine decarboxylation via glycine cleavage system | Glycine cleavage complex |
| Glycine dehydrogenase [decarboxylating], mitochondrial | A0A0B2VPG6 | 2 | 2 | 105  | Glycine dehydrogenase (decarboxylating) activity | Glycine catabolic process | Unknown function |
| Glycogen debranching enzyme | A0A0B2V6Z8 | 9 | 6 | 123  | 4-alpha-glucanotransferase activity and amylo-alpha-1,6-glucosidase activity | Glycogen catabolic process | Unknown function |
| Glycogenin-1 | A0A0B2VHB6 | 14 | 5 | 58  | Transferase activity, transferring glycosyl groups | Unknown function | Unknown function |
| Glycolipid transfer protein | A0A0B2ULK4 | 10 | 2 | 33  | Glycolipid binding and glycolipid transporter activity | Unknown function | Cytoplasm |
| Glyoxalase domain-containing protein 4  | A0A0B2VIQ1 | 18 | 6 | 36  | Unknown function | Unknown function | Unknown function |
| Glyoxylate reductase/hydroxypyruvate reductase | A0A0B2V8R3 | 12 | 2 | 36  | NAD binding Source: interprooxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | Unknown function | Unknown function |
| Golgin subfamily A member 4 | A0A0B2VFY7 | 2 | 2 | 196  | Unknown function | Protein targeting to Golgi | Intracellular |
| GPN-loop gtpase 3  | A0A0B2W503 | 10 | 2 | 31  | Unknown function | Unknown function | Unknown function |
| Group XV phospholipase A2  | A0A0B2VRZ9 | 6 | 2 | 53  | O-acyltransferase activity | Lipid metabolic process | Unknown function |
| Grpe protein homolog  | A0A0B2VF99 | 35 | 9 | 30  | Adenyl-nucleotide exchange factor activity Source: interproGO - Biological process | Protein folding | Mitochondrial matrix Source: uniprotkb-subcellComplete GO annotation... |
| GTP-binding protein SAR1 | A0A0B2VVE5 | 17 | 2 | 20  | GTP binding | Intracellular protein transport and vesicle-mediated transport | Endoplasmic reticulum and Golgi apparatus |
| Guanine nucleotide-binding proteinsubunit beta-2-like 1  | A0A0B2VWB8 | 22 | 5 | 35  | Unknown function | Unknown function | Unknown function |
| Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase MESH1 | A0A0B2V5E8 | 11 | 2 | 29  | Hydrolase activity | Unknown function | Unknown function |
| Haloacid dehalogenase-like hydrolase domain-containing protein 3  | A0A0B2VYV7 | 14 | 4 | 44  | Hydrolase activity | Metabolic process | Unknown function |
| HEAT repeat-containing protein 5B | A0A0B2VJY3 | 3 | 3 | 254  | Unknown function | Unknown function | Unknown function |
| Heat shock 70 kda protein  | A0A0B2W0B9 | 9 | 4 | 75  | ATP binding | Unknown function | Unknown function |
| Heat shock 70 kda protein A | A0A0B2V5Y2 | 52 | 36 | 102  | ATP binding | Unknown function | Unknown function |
| Heat shock 70 kda protein F, mitochondrial  | A0A0B2VD11 | 5 | 2 | 71  | ATP binding | Protein folding | Unknown function |
| Heat shock cognate protein HSP 90-beta | A0A0B2VT58 | 28 | 4 | 22  | ATP binding | Protein folding and response to stress | Unknown function |
| Heat shock protein 70 1A/1B | A0A0B2V5X6 | 41 | 26 | 83  | ATP binding | Unknown function | Unknown function |
| Heat shock protein 70 B2 | A0A0B2VM41 | 29 | 15 | 70  | ATP binding | Response to stress | Unknown function |
| Heat shock protein 75 kda, mitochondrial | A0A0B2V537 | 3 | 2 | 77  | ATP binding | Protein folding and response to stress | Unknown function |
| Heat shock protein beta-1  | A0A0B2VSQ1 | 27 | 3 | 23 | Unknown function | Unknown function | Unknown function |
| Heat shock protein HSP 90-alpha | A0A0B2V484 | 26 | 13 | 75  | ATP binding | Protein folding and response to stress | Unknown function |
| Heat shock protein Hsp-12.2 | A0A0B2W2C0 | 17 | 2 | 14  | Unknown function | Unknown function | Unknown function |
| Hemicentin-1 | A0A0B2UNR1 | 6 | 3 | 131  | Unknown function | Unknown function | Unknown function |
| Heterogeneous nuclear ribonucleoprotein F  | A0A0B2VXK4 | 5 | 2 | 68  | Nucleic acid binding and nucleotide binding | Unknown function | Intracellular ribonucleoprotein complex and viral nucleocapsid |
| Hexokinase | A0A0B2USB4 | 16 | 5 | 52  | ATP binding, glucose binding and hexokinase activity | Cellular glucose homeostasis and glycolytic process | Cell |
| Histidine--trna ligase  | A0A0B2VWW2 | 6 | 2 | 59  | ATP binding and histidine-trna ligase activity | Histidyl-trna aminoacylation | Cytoplasm |
| Histone H2A  | A0A0B2UQD6 | 33 | 5 | 13 | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H2B  | A0A0B2UPQ0 | 45 | 9 | 13 | DNA binding | Unknown function | Unknown function |
| Histone H2B O | A0A0B2UXB4 | 45 | 9 | 13 | DNA binding | Unknown function | Chromosome and nucleus |
| Histone H3  | A0A0B2V2I9 | 45 | 6 | 15  | DNA binding | Unknown function | Nucleosome and nucleus |
| Histone H4  | A0A0B2VBF2 | 36 | 14 | 19 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Histone H4 O | A0A0B2VU23 | 44 | 14 | 16 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Histone H4 OS | A0A0B2V2I6 | 62 | 14 | 11 | DNA bindin | Nucleosome assembly | Chromosome and nucleus |
| Hsc70-interacting protein | A0A0B2UTM4 | 18 | 3 |  26  | Unknown function | Unknown function | Unknown function |
| Hypoxanthine-guanine phosphoribosyltransferase  | A0A0B2VVB2 | 10 | 4 |  56  | Hypoxanthine phosphoribosyltransferase activity | Purine ribonucleoside salvage | Cytoplasm |
| Hypoxia up-regulated protein 1 | A0A0B2VJA4 | 11 | 7 |  121  | ATP binding | Unknown function | Integral component of membrane |
| Immunoglobulin-binding protein 1 | A0A0B2VJL5 | 18 | 4 |  39  | Regulation of signal transduction | Unknown function | Unknown function |
| Importin subunit alpha | A0A0B2UYQ7 | 15 | 7 |  57  | Protein transporter activity | Protein import into nucleus | Cytoplasm and nucleus |
| Importin-5 | A0A0B2VLS9 | 12 | 10 |  126  | Unknown function | Intracellular protein transport | Intracellular |
| Importin-7 | A0A0B2UYR7 | 5 | 4 |  114  | Unknown function | Intracellular protein transport | Intracellular |
| Inositol monophosphatase ttx-7 | A0A0B2USQ4 | 7 | 2 |  37  | Inositol monophosphate 1-phosphatase activity | Inositol phosphate dephosphorylation Source: interprophosphatidylinositol phosphorylation | Unknown function |
| Intermediate filament protein | A0A0B2UZV0 | 11 | 5 |  65  | Structural molecule activity | Unknown function | Intermediate filament |
| Intermediate filament protein ifa-1  | A0A0B2W4R1 | 8 | 4 |  80  | Structural molecule activity | Unknown function | Unknown function |
| Intracellular globin  | Q8WPB1 | 6 | 2 | 17  | Heme binding, iron ion binding, oxygen binding and oxygen transporter activity | Unknown function | Unknown function |
| Isochorismatase domain-containing protein 2, mitochondrial  | A0A0B2V5M9 | 18 | 2 | 22  | Catalytic activity | Metabolic process | Unknown function |
| Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial | A0A0B2VSC5 | 2 | 2 | 121  | Isocitrate dehydrogenase (NAD+) activity, magnesium ion binding, NAD binding and serine-type endopeptidase activity | Lipid metabolic process and tricarboxylic acid cycle | Unknown function |
| Isocitrate dehydrogenase [NADP] | A0A0B2VRT6 | 23 | 8 | 51  | Isocitrate dehydrogenase (NADP+) activity, magnesium ion binding and NAD binding | Isocitrate metabolic process and tricarboxylic acid cycle | Unknown function |
| Isocitrate dehydrogenase [NADP] cytoplasmic  | A0A0B2VTC3 | 16 | 4 | 62  | Isocitrate dehydrogenase (NADP+) activity, magnesium ion binding and NAD binding | Isocitrate metabolic process  | Unknown function |
| Kelch domain-containing protein 10 | A0A0B2URI4 | 6 | 2 | 46  | Unknown function | Unknown function | Unknown function |
| L-2-hydroxyglutarate dehydrogenase, mitochondrial | A0A0B2VYL1 | 9 | 2 | 48  | Oxidoreductase activity | Unknown function | Unknown function |
| Lactoylglutathione lyase  | A0A0B2V816 | 19 | 3 | 29  | Lactoylglutathione lyase activity and metal ion binding | Unknown function | Unknown function |
| Ladder protein (Fragment) | Q9U011 | 32 | 4 | 15  | Unknown function | Unknown function | Unknown function |
| Laminin-like protein epi-1 | A0A0B2UTI6 | 1 | 3 | 426  | Unknown function | Cell adhesion | Unknown function |
| Laminin-like protein lam-2 | A0A0B2W1F7 | 5 | 2 | 71  | Basement membrane assembly and system development | Unknown function | Basement membrane |
| Leukotriene A-4 hydrolase | A0A0B2VFU8 | 10 | 4 | 71  | Metallopeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Linear gramicidin synthase subunit B | A0A0B2VT50 | 1 | 2 | 666  | Hydrolase activity, acting on ester bonds, phosphopantetheine binding and transferase activity | Biosynthetic process | Unknown function |
| Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial | A0A0B2W4Z0 | 8 | 2 | 54  | Transferase activity, transferring acyl groups | Metabolic process | Unknown function |
| L-lactate dehydrogenase | A0A0B2V8Z4 | 12 | 3 | 40  | L-lactate dehydrogenase activity | Carbohydrate metabolic process and carboxylic acid metabolic process | Unknown function |
| Lon protease homolog, mitochondrial  | A0A0B2VG53 | 4 | 3 | 113  | ATP binding, ATP-dependent peptidase activity, sequence-specific DNA binding and serine-type endopeptidase activity | Cellular response to oxidative stress, chaperone-mediated protein complex assembly, misfolded or incompletely synthesized protein catabolic process, oxidation-dependent protein catabolic process and regulation of mitochondrial DNA replication | Mitochondrion matrix  |
| Long-chain-fatty-acid--coa ligase 5 7  | A0A0B2V681 | 4 | 2 | 147  | Ligase activity | Metabolic process | Unknown function |
| Low affinity immunoglobulin epsilon Fc receptor  | A0A0B2VS78 | 8 | 2 | 33  | Unknown function | Unknown function | Unknown function |
| L-sulfolactate dehydrogenase | A0A0B2VPF1 | 13 | 3 | 45  | Oxidoreductase activity | Unknown function | Unknown function |
| Lupus La protein | A0A0B2UQH1 | 6 | 2 | 51  | Nucleotide binding and RNA binding | RNA processing | Intracellular ribonucleoprotein complex and nucleus |
| M7gpppx diphosphatase | A0A0B2W1S2 | 4 | 2 | 41  | Hydrolase activity | Deadenylation-dependent decapping of nuclear-transcribed mrna and transcription, DNA-templated | Unknown function |
| Macrophage migration inhibitory factor-like protein | A0A0B2V815 | 34 | 4 | 21  | Unknown function | Unknown function | Unknown function |
| Major allergen Ani s 1  | A0A0B2V5M2 | 13 | 2 | 21  | Serine-type endopeptidase inhibitor activity | Unknown function | Unknown function |
| Major pepsin inhibitor 3  | A0A0B2VB99 | 16 | 2 | 17  | Unknown function | Unknown function | Unknown function |
| Major sperm protein  | A0A0B2VCS9 | 9 | 2 | 25  | Unknown function | Unknown function | Cytoskeleton |
| Malate dehydrogenase | A0A0B2V0K0 | 7 | 2 | 39  | L-malate dehydrogenase activity | Carbohydrate metabolic process, malate metabolic process and tricarboxylic acid cycle | Unknown function |
| Malate dehydrogenase  | A0A0B2VWV9 | 32 | 8 | 40  | L-malate dehydrogenase activity | Carbohydrate metabolic process, malate metabolic process and tricarboxylic acid cycle | Unknown function |
| Malic enzyme | A0A0B2W419 | 6 | 2 | 49  | Malate dehydrogenase (decarboxylating) (NAD+) activity, metal ion binding and NAD binding | Malate metabolic process | Unknown function |
| Malonate--coa ligase | A0A0B2V0E7 | 7 | 3 | 97  | Ligase activity | Protein N-linked glycosylation | Integral component of membrane and oligosaccharyltransferase complex |
| Maltase-glucoamylase, intestinal | A0A0B2UTW7 | 5 | 5 | 226  | Carbohydrate binding and hydrolase activity, hydrolyzing O-glycosyl compounds | Carbohydrate metabolic process | Unknown function |
| Maltase-glucoamylase, intestinal  | A0A0B2VX12 | 6 | 3 | 106  | Carbohydrate binding and hydrolase activity, hydrolyzing O-glycosyl compounds | Carbohydrate metabolic process | Unknown function |
| Mannose-6-phosphate isomerase  | A0A0B2UXP0 | 4 | 3 | 84  | Mannose-6-phosphate isomerase activity and zinc ion binding | Carbohydrate metabolic process and GDP-mannose biosynthetic process | Unknown function |
| Mesocentin | A0A0B2VWQ7 | 3 | 4 | 233  | Unknown function | Unknown function | Unknown function |
| Methylmalonic aciduria and homocystinuria type D-like protein, mitochondrial (Fragment) | A0A0B2VNJ6 | 14 | 2 | 28  | Unknown function | Cobalamin metabolic process | Unknown function |
| Methylmalonic aciduria type A-like protein, mitochondrial | A0A0B2UWH7 | 9 | 2 | 45  | Gtpase activity and GTP binding | Unknown function | Unknown function |
| Methylmalonyl-coa epimerase, mitochondria | A0A0B2V2S8 | 19 | 2 | 18  | Unknown function | Unknown function | Unknown function |
| Methyltransferase-like protein 13 | A0A0B2VXM1 | 7 | 2 | 41  | Methyltransferase activity | Unknown function | Integral component of membrane |
| Microsomal triglyceride transfer protein large subunitsv=1 | A0A0B2VPL4 | 3 | 2 | 113  | Lipid transporter activity | Unknown function | Unknown function |
| Microtubule-associated protein futsch | A0A0B2VQP3 | 3 | 4 | 189  | Microtubule cytoskeleton organization | Unknown function | Unknown function |
| MIF-like protein mif-2 | A0A0B2UST4 | 21 | 3 | 16  | Unknown function | Unknown function | Unknown function |
| Mitochondrial carrier-like protein 2 | A0A0B2VJ58 | 9 | 2 | 32  | Unknown function | Transport | Unknown function |
| Mitochondrial dicarboxylate carrier (Fragment) | A0A0B2UQ71 | 9 | 2 | 23  | Unknown function | Transport | Integral component of membrane |
| Moesin/ezrin/radixin-like protein 1 | A0A0B2V508 | 39 | 26 | 71  | Unknown function | Unknown function | Cytoplasm, cytoskeleton and extrinsic component of membrane |
| Muscle M-line assembly protein unc-89 | A0A0B2VB51 | 14 | 58 | 755  | Unknown function | Unknown function | Unknown function |
| Myoglobin | A0A0B2VPY5 | 12 | 2 | 17  | Heme binding, iron ion binding, oxygen binding and oxygen transporter activity | Unknown function | Unknown function |
| Myophilin | A0A0B2W3C5 | 25 | 2 | 17  | Unknown function | Unknown function | Unknown function |
| Myosin heavy chain, non-muscle | A0A0B2VRY5 | 5 | 4 | 137  | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin regulatory light chain 1  | A0A0B2VMN8 | 58 | 7 | 19  | Calcium ion binding | Unknown function | Unknown function |
| Myosin, essential light chain  | A0A0B2USP9 | 52 | 11 | 21  | Calcium ion binding | Unknown function | Unknown function |
| Myosin-3 | A0A0B2VG79 | 34 | 67 | 226  | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin-4 | A0A0B2VDE1 | 44 | 87 | 225  | ATP binding and motor activity | Unknown function | Myosin complex |
| Myosin-4  | A0A0B2VVW7 | 48 | 98 | 225  | ATP binding and motor activity | Unknown function | Myosin complex |
| N-acetyl-D-glucosamine kinase | A0A0B2V266 | 14 | 5 | 72  | Kinase activity | Unknown function | Unknown function |
| NAD-dependent malic enzyme, mitochondrial | A0A0B2VWM2 | 17 | 3 | 36  | Malate dehydrogenase (decarboxylating) (NAD+) activity and zinc ion binding | Malate metabolic process | Unknown function |
| NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 | A0A0B2V5M6 | 9 | 2 | 32  | Unknown function | Unknown function | Unknown function |
| NADH oxidase | A0A0B2V920 | 5 | 2 | 56  | FMN binding and oxidoreductase activity | Unknown function | Unknown function |
| NADH oxidase  | A0A0B2VL93 | 4 | 2 | 73  | FMN binding and oxidoreductase activity | Unknown function | Unknown function |
| NADH-dependent flavin oxidoreductase | A0A0B2VPR5 | 5 | 5 | 178  | FMN binding and oxidoreductase activity | Unknown function | Unknown function |
| N-alpha-acetyltransferase 15, nata auxiliary subunit  | A0A0B2VZ79 | 8 | 4 | 138  | Transferase activity | Unknown function | Unknown function |
| Nascent polypeptide-associated complex subunit alpha | A0A0B2VTP5 | 11 | 2 | 27  | Unknown function | Unknown function | Unknown function |
| Neprilysin-1 | A0A0B2VJQ9 | 7 | 19 | 424  | Metalloendopeptidase activity | Unknown function | Unknown function |
| Neprilysin-2 | A0A0B2VHN9 | 4 | 2 | 87  | Metalloendopeptidase activity | Unknown function | Integral component of membrane |
| Neprilysin-2  | A0A0B2VJ90 | 4 | 4 | 175  | Calcium ion binding | Unknown function | Unknown function |
| Neuronal calcium sensor 2 | A0A0B2VRW5 | 13 | 2 | 22  | Calcium ion binding | Unknown function | Unknown function |
| Neuroserpin | A0A0B2V666 | 3 | 2 | 120  | Unknown function | Unknown function | Extracellular space |
| Neutral alpha-glucosidase AB | A0A0B2VWJ3 | 3 | 2 | 116  | Carbohydrate binding and hydrolase activity, hydrolyzing O-glycosyl compounds | Carbohydrate metabolic process | Unknown function |
| NSFL1 cofactor  | A0A0B2V258 | 6 | 2 | 38  | Unknown function | Unknown function | Unknown function |
| Nuclear anchorage protein 1 | A0A0B2URS9 | 33 | 7 | 31  | Unknown function | Unknown function | Unknown function |
| Nuclear anchorage protein 1 (Fragment)  | A0A0B2UR53 | 28 | 3 | 23  | Unknown function | Unknown function | Unknown function |
| Nuclease domain-containing protein | A0A0B2VIN8 | 6 | 4 | 98  | Transcription cofactor activity | Posttranscriptional gene silencing by RNA | RISC complex |
| Nucleoredoxin-like protein 2  | A0A0B2VFB2 | 30 | 5 | 16  | Unknown function | Cell redox homeostasis | Cell |
| Nucleoside diphosphate kinase  | A0A0B2W3P6 | 14 | 2 | 23  | ATP binding and nucleoside diphosphate kinase activity | CTP biosynthetic process, GTP biosynthetic process and UTP biosynthetic process | Unknown function |
| Nucleosome assembly protein 1-like 1 | A0A0B2W0R2 | 10 | 3 | 39  | Unknown function | Nucleosome assembly | Nucleus |
| O-acetyl-ADP-ribose deacetylase  | A0A0B2UXD4 | 38 | 6 | 29  | Unknown function | Unknown function | Unknown function |
| Obg-like atpase 1 | A0A0B2VSB4 | 6 | 2 | 50  | Atpase activity, ATP binding, GTP binding, ribosomal large subunit binding and ribosome binding | Unknown function | Cytoplasm |
| Onchocystatin  | A0A0B2V581 | 36 | 4 | 22  | Cysteine-type endopeptidase inhibitor activity | Unknown function | Unknown function |
| OV-16 antigen O | A0A0B2V438 | 55 | 6 | 19 | Unknown function | Unknown function | Unknown function |
| OV-17 antigen  | A0A0B2VKQ1 | 54 | 10 | 15 | Unknown function | Unknown function | Unknown function |
| Palmitoyl-protein thioesterase 1 | A0A0B2US10 | 13 | 2 | 35  | Palmitoyl-(protein) hydrolase activity | Protein depalmitoylation | Unknown function |
| Paramyosin | A0A0B2UZA1 | 16 | 3 | 33  | Motor activity  | Unknown function | Myosin complex |
| Paternally-expressed protein | A0A0B2VKX7 | 23 | 32 | 358  | Unknown function | Unknown function | Unknown function |
| Peptide methionine sulfoxide reductase  | A0A0B2VN48 | 14 | 2 | 24  | Peptide-methionine (S)-S-oxide reductase activity | Protein repair and response to oxidative stress | Unknown function |
| Peptidyl-prolyl cis-trans isomerase  | A0A0B2UVT1 | 45 | 8 | 26  | Peptidyl-prolyl cis-trans isomerase activity | Protein folding | Unknown function |
| Peroxidasin-like protein  | A0A0B2W3R6 | 3 | 2 | 137  | Heme binding and peroxidase activity | Response to oxidative stress | Unknown function |
| Peroxiredoxin  | A0A0B2UW02 | 18 | 2 | 22  | Peroxiredoxin activity | Cell redox homeostasis | Cell |
| Peroxisomal multifunctional enzyme type 2 | A0A0B2VM54 | 9 | 2 | 47  | Unknown function | Unknown function | Unknown function |
| Persulfide dioxygenase ETHE1, mitochondrial (Fragment)SV=1 | A0A0B2UU32 | 8 | 2 | 34  | Dioxygenase activity | Unknown function | Unknown function |
| Phenylalanine--trna ligase beta subunit | A0A0B2UR17 | 3 | 2 | 87  | ATP binding, magnesium ion binding, phenylalanine-trna ligase activity and RNA binding | Phenylalanyl-trna aminoacylation | Cytoplasm and integral component of membrane |
| Phosphate carrier protein, mitochondrial | A0A0B2UNW3 | 6 | 2 | 53  | Transport | Unknown function | Integral component of membrane |
| Phosphatidylethanolamine-binding-like protein F40A3.3  | A0A0B2VUI6 | 39 | 4 | 20  | Unknown function | Unknown function | Unknown function |
| Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha | A0A0B2VF93 | 8 | 2 | 50  | Phosphatidylinositol phosphate kinase activity | Unknown function | Unknown function |
| Phosphatidylinositol phosphatase | A0A0B2VJK9 | 1 | 2 | 449  | Unknown function | Unknown function | Integral component of membrane |
| Phosphatidylinositol transfer protein beta isoform-  | A0A0B2VNE3 | 5 | 3 | 94  | Transport | Unknown function | Intracellular |
| Phosphatidylinositol transfer protein beta isoform-  | A0A0B2VTI2 | 22 | 4 | 24  | Transport | Unknown function | Intracellular |
| Phosphoenolpyruvate carboxykinase | A0A0B2UWV2 | 12 | 5 | 76  | Transport | Unknown function | Intracellular |
| Phosphoenolpyruvate carboxykinase [GTP] | A0A0B2V286 | 29 | 13 | 72  | GTP binding, kinase activity and phosphoenolpyruvate carboxykinase (GTP) activity | Gluconeogenesis | Unknown function |
| Phosphoglucomutase-1 | A0A0B2V7Y9 | 36 | 14 | 62  | Intramolecular transferase activity, phosphotransferases and magnesium ion binding | Carbohydrate metabolic process | Unknown function |
| Phosphoglucomutase-2 | A0A0B2USN0 | 14 | 4 | 67  | Intramolecular transferase activity, phosphotransferases and magnesium ion binding | Carbohydrate metabolic process | Unknown function |
| Phosphoglycerate kinase | A0A0B2V4Q8 | 15 | 6 | 67  | Phosphoglycerate kinase activity | Glycolytic process | Unknown function |
| PI-PLC X domain-containing protein 3  | A0A0B2UWU4 | 18 | 4 | 36  | Phosphoric diester hydrolase activity | Lipid metabolic process | Unknown function |
| PITH domain-containing protein | A0A0B2VU00 | 18 | 2 | 24  | Unknown function | Unknown function | Unknown function |
| Plasminogen | A0A0B2V8X7 | 14 | 3 | 32  | Serine-type endopeptidase activity | Unknown function | Unknown function |
| Plastin-2 | A0A0B2V3A5 | 8 | 4 | 89  | Unknown function | Unknown function | Integral component of membrane |
| Polyadenylate-binding protein | A0A0B2VUQ8 | 7 | 4 | 73  | Nucleotide binding and RNA binding | Unknown function | Cytoplasm |
| Polyprotein ABA-1 (Fragment)  | A0A0B2UPJ7 | 33 | 9 | 21  | Unknown function | Unknown function | Unknown function |
| Polyubiquitin-A  | A0A0B2V0G7 | 8 | 3 | 45  | Unknown function | Unknown function | Cytoplasm |
| Pre-mrna-splicing factor 8-like protein | A0A0B2VSU6 | 1 | 2 | 331  | U5 snrna binding and U6 snrna binding | Mrna splicing, via spliceosome | Spliceosomal complex |
| Probable-ribose 5-phosphate isomerase  | A0A0B2VT55 | 23 | 9 | 49  | Ribose-5-phosphate isomerase activity | Pentose-phosphate shunt, non-oxidative branch | Integral component of membrane |
| Profilin  | A0A0B2V1M0 | 71 | 7 | 14  | Unknown function | Unknown function | Unknown function |
| Prohibitin-like molecule TC-PRO-1 | O01720 | 9 | 2 | 30  | Unknown function | Unknown function | Membrane |
| Proliferation-associated protein 2G4 | A0A0B2VH06 | 11 | 4 | 60  | Unknown function | Unknown function | Unknown function |
| Proline synthase co-transcribed bacterial-like protein | A0A0B2UZ51 | 7 | 3 | 53  | Unknown function | Unknown function | Unknown function |
| Propionyl-coa carboxylase alpha chain, mitochondrial | A0A0B2UYS3 | 42 | 24 | 82  | ATP binding, biotin carboxylase activity and metal ion binding | Unknown function | Unknown function |
| Propionyl-coa carboxylase beta chain, mitochondria | A0A0B2V2B7 | 15 | 5 | 58  | Ligase activity | Unknown function | Unknown function |
| Proteasome activator complex subunit 4 | A0A0B2V1U0 | 3 | 4 | 220  | Ligase activity | Unknown function | Proteasome complex |
| Proteasome subunit alpha type | A0A0B2VCY4 | 20 | 4 | 28  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process |  Cytoplasm, nucleus and proteasome core complex, alpha-subunit complex |
| Proteasome subunit alpha type  | A0A0B2UY88 | 11 | 2 | 27  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process |  Cytoplasm, nucleus and proteasome core complex, alpha-subunit complex |
| Proteasome subunit alpha type-2  | A0A0B2VV07 | 16 | 5 | 42  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process | Proteasome core complex |
| Proteasome subunit alpha type-3 | A0A0B2V3S5 | 28 | 7 | 28  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process |  Nucleus and proteasome core complex, alpha-subunit complex |
| Proteasome subunit alpha type-7 | A0A0B2VGK4 | 35 | 5 | 36  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process |  Nucleus and proteasome core complex, alpha-subunit complex |
| Proteasome subunit beta type  | A0A0B2VKZ8 | 11 | 2 | 30  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process |  Cytoplasm, nucleus and proteasome core complex, alpha-subunit complex |
| Proteasome subunit beta  | A0A0B2V9V2 | 6 | 2 | 32  | Threonine-type endopeptidase activity | Ubiquitin-dependent protein catabolic process | Proteasome core complex |
| Protein bicaudal D-like protein 1 | A0A0B2USZ6 | 4 | 2 | 95  | Unknown function | Transport | Golgi apparatus |
| Protein cuta-like protein  | A0A0B2V141 | 27 | 2 | 19  | Unknown function | Response to metal ion | Unknown function |
| Protein disulfide-isomerase | A0A0B2UJM4 | 8 | 2 | 56  | Protein disulfide isomerase activity | Cell redox homeostasis | Endoplasmic reticulum |
| Protein disulfide-isomerase 2 | A0A0B2VF53 | 8 | 2 | 30  | Isomerase activity | Cell redox homeostasis | Cell |
| Protein disulfide-isomerase A5 | A0A0B2VSW0 | 6 | 2 | 69  | Isomerase activity | Cell redox homeostasis | Cell |
| Protein DJ-1 | A0A0B2VMK9 | 8 | 2 | 31  | Protein deglycase activity  | Unknown function | Unknown function |
| Protein phosphatase 1 regulator subunit 7 (Fragment)  | A0A0D4CDQ4 | 18 | 2 | 28  | Unknown function | Unknown function | Unknown function |
| Protein phosphatase 1 regulatory subunit | A0A0B2UYT0 | 23 | 4 | 33  | Unknown function | Unknown function | Unknown function |
| Protein SET | A0A0B2VDM1 | 13 | 2 | 30  | Unknown function | Nucleosome assembly | Unknown function |
| Protein transport protein Sec23A | A0A0B2VKH6 | 26 | 7 | 62  | ER to Golgi vesicle-mediated transport and intracellular protein transport | Unknown function | COPII vesicle coat |
| Protein UBASH3A-like protein (Fragment)  | A0A0B2VJS1 | 10 | 2 | 36  | Unknown function | Unknown function | Unknown function |
| Protein-L-isoaspartate O-methyltransferase  | A0A0B2UUJ5 | 7 | 2 | 30  | Protein-L-isoaspartate (D-aspartate) O-methyltransferase activity | Unknown function | Unknown function |
| Protein-L-isoaspartate(D-aspartate) O-methyltransferase  | A0A0B2VPA3 | 28 | 5 | 37  | Protein-L-isoaspartate (D-aspartate) O-methyltransferase activity | Unknown function | Unknown function |
| Proteoglycan core protein (Fragment)  | O76131 | 10 | 2 | 24 | Unknown function | Unknown function | Unknown function |
| Pseudouridine-5'-monophosphatase | A0A0B2UV91 | 11 | 3 | 31  | Hydrolase activity | Metabolic process | Unknown function |
| Pseudouridine-5'-monophosphatase  | A0A0B2W352 | 13 | 2 | 26  | Hydrolase activity | Metabolic process | Unknown function |
| Purine nucleoside phosphorylase | A0A0B2UMT2 | 13 | 2 | 35  | Purine-nucleoside phosphorylase activity | Nucleoside metabolic process | Unknown function |
| Puromycin-sensitive aminopeptidase | A0A0B2UWZ6 | 7 | 4 | 116  | Aminopeptidase activity, metallopeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Putative 26S protease regulatory subunit 10B | A0A0B2VH61 | 20 | 5 | 45  | ATP binding and peptidase activity | Protein catabolic process | Cytoplasm |
| Putative 26S protease regulatory subunit 6B  | A0A0B2VCM4 | 11 | 3 | 51  | ATP binding and peptidase activity | Protein catabolic process | Cytoplasm |
| Putative 3-hydroxyacyl-coa dehydrogenase  | A0A0B2VZX9 | 38 | 8 | 36  | 3-hydroxyacyl-coa dehydrogenase activity and NAD+ binding | Fatty acid metabolic process | Unknown function |
| Putative actin-related protein 2/3 complex subunit 2  | A0A0B2V1L8 | 20 | 4 | 43  | Unknown function | Arp2/3 complex-mediated actin nucleation | Unknown function |
| Putative acyl-coa-binding protein  | A0A0B2VLK6 | 58 | 3 | 9  | Unknown function | Unknown function | Unknown function |
| Putative aspartyl aminopeptidase | A0A0B2UMQ9 | 10 | 3 | 57  | Fatty-acyl-coa binding | Unknown function | Unknown function |
| Putative ATP-citrate synthase | A0A0B2VDT7 | 6 | 5 | 130  | ATP binding, cofactor binding and transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer | Metabolic process | Unknown function |
| Putative ATP-dependent RNA helicase DDX17  | A0A0B2VV15 | 4 | 2 | 84  | ATP binding, helicase activity and nucleic acid binding | Unknown function | Unknown function |
| Putative carbonic anhydrase 3 | A0A0B2VML9 | 31 | 6 | 31  | Carbonate dehydratase activity and zinc ion binding | One-carbon metabolic process | Unknown function |
| Putative clathrin heavy chain 1 | A0A0B2UZS0 | 19 | 19 | 178  | Structural molecule activity | Intracellular protein transport and vesicle-mediated transport | Clathrin coat of coated pit and clathrin coat of trans-Golgi network vesicle |
| Putative coatomer subunit beta  | A0A0B2VLJ2 | 4 | 3 | 130  | Structural molecule activity | Intracellular protein transport and vesicle-mediated transport | Membrane coat |
| Putative coatomer subunit delta | A0A0B2W2J6 | 14 | 5 | 60  | Unknown function | Protein transport and retrograde vesicle-mediated transport, Golgi to ER | COPI vesicle coat |
| Putative coatomer subunit gamma  | A0A0B2V1P0 | 11 | 6 | 104  | Structural molecule activity | Intracellular protein transport and vesicle-mediated transport | Cytoplasm |
| Putative deoxyribose-phosphate aldolase | A0A0B2VNZ9 | 23 | 5 | 38  | Deoxyribose-phosphate aldolase activity | Deoxyribonucleotide catabolic process | Cytoplasm |
| Putative elongation factor 1-gamma | A0A0B2VB97 | 16 | 7 | 79  | Translation elongation factor activity | Unknown function | Unknown function |
| Putative enoyl-coa hydratase, mitochondrial | A0A0B2VBE0 | 32 | 6 | 47  | Catalytic activity | Metabolic process | Unknown function |
| Putative fumarate hydratase, mitochondria | A0A0B2W747 | 6 | 2 | 54  | Fumarate hydratase activity | Fumarate metabolic process and tricarboxylic acid cycle | Unknown function |
| Putative glutamine synthetase | A0A0B2VTB9 | 11 | 3 | 44  | Glutamate-ammonia ligase activity | Glutamine biosynthetic process | Unknown function |
| Putative glycerol kinase | A0A0B2V873 | 5 | 2 | 61  | Kinase activity and phosphotransferase activity, alcohol group as acceptor | Carbohydrate metabolic process | Unknown function |
| Putative glycogen [starch] synthase | A0A0B2V2X8 | 10 | 5 | 76  | Glycogen (starch) synthase activity | Glycogen biosynthetic process | Unknown function |
| Putative glycogen [starch] synthase  | A0A0B2W530 | 7 | 2 | 43  | Glycogen (starch) synthase activity | Glycogen biosynthetic process | Unknown function |
| Putative helicase C28H8.3 | A0A0B2W6A1 | 4 | 4 | 205  | ATP binding Source: interprohelicase activity Source: uniprotkb-KWnucleic acid binding | Unknown function | Unknown function |
| Putative hydroxyacid-oxoacid transhydrogenase, mitochondrial  | A0A0B2US39 | 14 | 4 | 51  | Metal ion binding and oxidoreductase activity | Unknown function | Unknown function |
| Putative imidazolonepropionase | A0A0B2VLH7 | 20 | 7 | 47  | Histidine catabolic process to glutamate and formamide | Unknown function | Cytoplasm |
| Putative inorganic pyrophosphatase 1 | A0A0B2UUS3 | 10 | 3 | 55  | Inorganic diphosphatase activity and magnesium ion binding | Phosphate-containing compound metabolic process | Cytoplasm |
| Putative leucine-rich repeat-containing protein SV=1  | A0A0B2V722 | 2 | 6 | 714  | Unknown function | Unknown function | Unknown function |
| Putative malate dehydrogenase, mitochondrial | A0A0B2UWI4 | 23 | 10 | 77  | L-malate dehydrogenase activity and structural constituent of ribosome | Carbohydrate metabolic process and malate metabolic process | Unknown function |
| Putative medium-chain specific acyl-coa dehydrogenase, mitochondrial | A0A0B2UNJ7 | 10 | 3 | 46  | Acyl-coa dehydrogenase activity and flavin adenine dinucleotide binding | Unknown function | Unknown function |
| Putative methylmalonyl-coa mutase, mitochondrial | A0A0B2UT85 | 13 | 7 | 125  | Cobalamin binding, metal ion binding and methylmalonyl-coa mutase activity | Metabolic process | Unknown function |
| Putative methylmalonyl-coa mutase, mitochondrial  | A0A0B2V0T5 | 9 | 4 | 73  | Cobalamin binding, metal ion binding and methylmalonyl-coa mutase activity | Metabolic process | Unknown function |
| Putative neurobeachin-like protein  | A0A0B2URZ8 | 2 | 3 | 262  | Unknown function | Unknown function | Unknown function |
| Putative nipsnap protein K02D10.1 | A0A0B2VRD3 | 9 | 3 | 54  | Unknown function | Unknown function | Unknown function |
| Putative nuclear transport factor 2  | A0A0B2UUX2 | 55 | 5 | 15  | Unknown function | Transport | Intracellular |
| Putative oxidoreductase dhs-27 | A0A0B2VGN1 | 8 | 2 | 55  | Unknown function | Unknown function | Unknown function |
| Putative oxidoreductase dhs-27  | A0A0B2V8G8 | 6 | 2 | 48  | Unknown function | Unknown function | Unknown function |
| Putative peptidyl-trna hydrolase 2 | A0A0B2UXR2 | 7 | 2 | 49  | Aminoacyl-trna hydrolase activity | Unknown function | Mitochondrial membrane |
| Putative peroxiredoxin  | A0A0B2V2L3 | 12 | 2 | 25  | Peroxiredoxin activity | Cell redox homeostasis | Cell |
| Putative prefoldin subunit 3 O | A0A0B2VLE7 | 20 | 2 | 21  | Unknown function | Protein folding | Prefoldin complex |
| Putative proteasome subunit beta type-7  | A0A0B2VE91 | 16 | 4 | 35  | Threonine-type endopeptidase activity | Proteolysis involved in cellular protein catabolic process | Proteasome core complex |
| Putative quinone oxidoreductase | A0A0B2VBG4 | 9 | 2 | 37  | Oxidoreductase activity and zinc ion binding | Unknown function | Unknown function |
| Putative serine carboxypeptidase F32A5.3 (Fragment) | A0A0B2UYK2 | 20 | 2 | 15  | Serine-type carboxypeptidase activity | Unknown function | Unknown function |
| Putative serine/threonine-protein phosphatase PP2A regulatory subunit | A0A0B2V5G2 | 11 | 6 | 78  | Protein phosphatase type 2A regulator activity | Protein complex assembly | Unknown function |
| Putative serine--trna ligase, cytoplasmic | A0A0B2V8Y3 | 26 | 9 | 54  | ATP binding and serine-trna ligase activity | Seryl-trna aminoacylation | Cytoplasm |
| Putative serpin-like protein | A0A0B2VFZ3 | 5 | 2 | 50  | Unknown function | Unknown function | Extracellular space |
| Putative succinyl-coa ligase [ADP/GDP-forming] subunit alpha, mitochondrial  | A0A0B2V8B7 | 10 | 2 | 49  | Cofactor binding and ligase activity | Unknown function | Metabolic process |
| Putative thioredoxin-2  | A0A0B2W1E2 | 11 | 2 | 24  | Protein disulfide oxidoreductase activity | Cell redox homeostasis and glycerol ether metabolic process | Cell |
| Putative thiosulfate sulfurtransferase  | A0A0B2VVX9 | 14 | 10 | 89  | Transferase activity | Unknown function | Unknown function |
| Putative trans-2-enoyl-coa reductase 2, mitochondrial | A0A0B2VYM7 | 49 | 12 | 43  | Oxidoreductase activity and zinc ion binding | Unknown function | Unknown function |
| Putative trans-2-enoyl-coa reductase 2, mitochondrial  | A0A0B2W0R7 | 7 | 2 | 45  | Oxidoreductase activity and zinc ion binding | Unknown function | Unknown function |
| Putative trna pseudouridine synthase | A0A0B2V167 | 5 | 3 | 115  | Adenylate kinase activity, ATP binding, protein prenyltransferase activity, pseudouridine synthase activity and RNA binding | Protein prenylation, pseudouridine synthesis | Unknown function |
| Putative UDP-glucuronosyltransferase ugt-47 (Fragment) | A0A0B2URX2 | 6 | 3 | 61  | Pyridoxal phosphate binding and transferase activity, transferring hexosyl groups | Biosynthetic process | Integral component of membrane |
| Putative UDP-N-acetylglucosamine pyrophosphorylase | A0A0B2UNI1 | 4 | 2 | 74  | Uridylyltransferase activity | Metabolic process | Unknown function |
| Putative urocanate hydratase | A0A0B2UYJ3 | 24 | 11 | 75  | Urocanate hydratase activity | Unknown function | Unknown function |
| Putative voltage-dependent anion-selective channel  | A0A0B2V317 | 22 | 4 | 31  | Voltage-gated anion channel activity | Unknown function | Mitochondrial outer membrane |
| Putative V-type proton atpase subunit H 2 | A0A0B2UVK7 | 10 | 3 | 54  | Proton-transporting atpase activity, rotational mechanism | ATP hydrolysis coupled proton transport | Vacuolar proton-transporting V-type atpase, V1 domain |
| Pyridoxal-dependent decarboxylase domain-containing protein 1 | A0A0B2UNL1 | 9 | 4 | 97  | Catalytic activity | Unknown function | Unknown function |
| Pyruvate carboxylase 1 | A0A0B2W0H0 | 8 | 4 | 106  | ATP binding, biotin binding, biotin carboxylase activity, metal ion binding and pyruvate carboxylase activity | Gluconeogenesis and pyruvate metabolic process | Unknown function |
| Pyruvate dehydrogenase | A0A0B2V2E9 | 7 | 2 | 39  | Pyruvate dehydrogenase (acetyl-transferring) activity | Acetyl-coa biosynthetic process from pyruvate | Unknown function |
| Pyruvate dehydrogenase E1 component subunit beta, mitochondrial | A0A0B2URY6 | 7 | 2 | 39  | Pyruvate dehydrogenase (acetyl-transferring) activity | Acetyl-coa biosynthetic process from pyruvate | Unknown function |
| Pyruvate dehydrogenase | A0A0B2VNJ4 | 9 | 2 | 39  | Pyruvate dehydrogenase (acetyl-transferring) activity | Acetyl-coa biosynthetic process from pyruvate | Unknown function |
| Pyruvate kinase | A0A0B2URT1 | 13 | 7 | 74  | Kinase activity, magnesium ion binding, potassium ion binding and pyruvate kinase activity | Unknown function | Unknown function |
| Quinone oxidoreductase-like protein 2-like protein | A0A0B2VLU5 | 23 | 4 | 37  | Oxidoreductase activity and zinc ion binding | Unknown function | Unknown function |
| Rab GDP dissociation inhibitor alpha | A0A0B2VGL4 | 16 | 7 | 83  | 2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity, oxidoreductase activity and Rab GDP-dissociation inhibitor activity | Protein transport, small gtpase mediated signal transduction and ubiquinone biosynthetic process | Intracellular |
| Ran gtpase-activating protein 2 | A0A0B2UZX7 | 4 | 2 | 117  | Gtpase activator activity | Unknown function | Unknown function |
| Ran-binding protein 16 | A0A0B2W1T3 | 4 | 2 | 107  | Unknown function | Unknown function | Unknown function |
| Ras gtpase-activating-like protein IQGAP1 | A0A0B2VTV9 | 5 | 3 | 113  | Unknown function | Regulation of gtpase activity and signal transduction | Unknown function |
| Ras-related protein Rab-10  | A0A0B2W1C0 | 30 | 6 | 27  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-11A  | A0A0B2W5G8 | 16 | 3 | 21  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-1A | A0A0B2VKF4 | 17 | 5 | 53  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-2  | A0A0B2W5R0 | 26 | 4 | 24  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-5B  | A0A0B2V6A1 | 12 | 2 | 29  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-6A | A0A0B2UPN5 | 22 | 3 | 24  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Ras-related protein Rab-7a  | A0A0B2UVL4 | 14 | 2 | 24  | GTP binding | Small gtpase mediated signal transduction | Intracellular |
| Receptor expression-enhancing protein | A0A0B2VHK1 | 13 | 2 | 23  | Unknown function | Unknown function | Membrane |
| Recombination repair protein 1 | A0A0B2UVE6 | 5 | 2 | 57  | DNA-(apurinic or apyrimidinic site) lyase activity, DNA binding and metal ion binding | DNA repair | Intracellular |
| Regulator of microtubule dynamics protein 1 (Fragment) | A0A0B2VK45 | 28 | 5 | 27  | Unknown function | Unknown function | Unknown function |
| Regulator of microtubule dynamics protein 1 | A0A0B2VIE8 | 11 | 2 | 33  | Unknown function | Unknown function | Unknown function |
| Reticulocyte-binding protein 2-like protein a | A0A0B2VVR5 | 6 | 2 | 74 | Unknown function | Unknown function | Unknown function |
| Reticulon-like protein  | A0A0B2VR17 | 12 | 2 | 29  | Unknown function | Unknown function | Endoplasmic reticulum membrane  |
| Ribokinase  | A0A0B2VUH0 | 7 | 2 | 39  | ATP binding, metal ion binding and ribokinase activity | D-ribose catabolic process | Cytoplasm and nucleus |
| Ribonuclease  | A0A0B2V9E1 | 30 | 3 | 19  | Unknown function | Unknown function | Unknown function |
| Ribose-phosphate pyrophosphokinase 2 | A0A0B2VDU9 | 13 | 3 | 35  | Kinase activity, magnesium ion binding and ribose phosphate diphosphokinase activity | Nucleoside metabolic process, nucleotide biosynthetic process and ribonucleoside monophosphate biosynthetic process | Unknown function |
| Ribosomal protein L15 | A0A0B2VSD9 | 13 | 2 | 24  | Structural constituent of ribosome | Translation | Ribosome |
| Ribosomal protein  | A0A0B2VN18 | 8 | 2 | 24  | RNA binding and structural constituent of ribosome | Translation | Large ribosomal subunit |
| Ribosome maturation protein SBDS  | A0A0B2VZK2 | 20 | 4 | 29  | Mature ribosome assembly | Unknown function | Unknown function |
| Sedoheptulokinase | A0A0B2VKN8 | 9 | 2 | 42  | Kinase activity and phosphotransferase activity, alcohol group as accepto | Carbohydrate metabolic process | Unknown function |
| Serine hydroxymethyltransferase | A0A0B2W560 | 11 | 4 | 55  | Glycine hydroxymethyltransferase activity, methyltransferase activity and pyridoxal phosphate binding | Glycine metabolic process Source: interproL-serine metabolic process Source: interprotetrahydrofolate interconversion | Unknown function |
| Serpin B6 | A0A0B2VH56 | 8 | 2 | 44  | Unknown function | Unknown function | Extracellular space |
| Sex muscle abnormal protein 5  | A0A0B2VF66 | 15 | 2 | 25  | Unknown function | Unknown function | Unknown function |
| Sex-regulated protein janus-A  | A0A0B2W351 | 23 | 2 | 20  | Unknown function | Unknown function | Integral component of membrane |
| S-formylglutathione hydrolase | A0A0B2V099 | 18 | 4 | 40  | Carboxylic ester hydrolase activity and S-formylglutathione hydrolase activity | Formaldehyde catabolic process | Cytoplasm |
| Sideroflexin | A0A0B2VLR6 | 7 | 2 | 36  | Ion transmembrane transporter activity | Unknown function | Integral component of membrane and mitochondrial membrane |
| Signal peptidase complex catalytic subunit SEC11 (Fragment)  | A0A0B2UTR8 | 12 | 2 | 25  | Serine-type peptidase activity | Signal peptide processing | Endoplasmic reticulum membrane Source: uniprotkb-subcellintegral component of membrane |
| Single-stranded DNA-binding protein, mitochondrial  | A0A0B2UZX5 | 15 | 2 | 21  | Single-stranded DNA binding | DNA replication | Unknown function |
| Sister chromatid cohesion protein PDS5-like protein B  | A0A0B2VFB9 | 2 | 2 | 192  | Unknown function | Unknown function | Unknown function |
| Small glutamine-rich tetratricopeptide repeat-containing protein beta | A0A0B2UTD7 | 5 | 2 | 35  | Unknown function | Unknown function | Unknown function |
| Small heat shock protein OV25-1 | A0A0B2V0M9 | 25 | 2 | 12  | Unknown function | Unknown function | Unknown function |
| S-methyl-5'-thioadenosine phosphorylase  | A0A0B2VZB1 | 10 | 2 | 35  | S-methyl-5-thioadenosine phosphorylase activity | L-methionine biosynthetic process from methylthioadenosine and purine ribonucleoside salvage | Cytoplasm and Nucleus |
| Sodium/potassium-transporting atpase subunit alpha  | A0A0B2VLL4 | 3 | 2 | 111  | ATP binding, metal ion binding and sodium:potassium-exchanging atpase activity | Unknown function | Membrane |
| Soluble calcium-activated nucleotidase 1 | A0A0B2UZJ5 | 9 | 2 | 48  | Calcium ion binding and pyrophosphatase activity | Unknown function | Integral component of membrane |
| Sorbitol dehydrogenase  | A0A0B2VJ07 | 10 | 2 | 39  | Oxidoreductase activity and zinc ion binding | Unknown function | Unknown function |
| Spectrin alpha chain | A0A0B2W457 | 10 | 15 | 277  | Calcium ion binding | Unknown function | Unknown function |
| Spectrin beta chain, non-erythrocytic | A0A0B2UNZ4 | 1 | 2 | 412  | Unknown function | Unknown function | Unknown function |
| Spermidine synthase | A0A0B2V470 | 11 | 4 | 40  | Transferase activity | Polyamine metabolic process | Unknown function |
| Sperm-specific class P protein 34 | A0A0B2VM80 | 31 | 2 | 12  | Unknown function | Unknown function | Unknown function |
| Spindle-and centromere-associated protein | A0A0B2VMU3 | 3 | 2 | 159  | Unknown function | Unknown function | Unknown function |
| Spindle-and centromere-associated protein  | A0A0B2VVR8 | 3 | 5 | 241  | Unknown function | Unknown function | Unknown function |
| Spondin-1 | A0A0B2V6W4 | 8 | 5 | 97  | Serine-type endopeptidase inhibitor activity | Unknown function | Unknown function |
| Sprotein F37C4.5  | A0A0B2VYI9 | 11 | 5 | 66  | Unknown function | Unknown function | Unknown function |
| Steroidogenic acute regulatory-like protein 1  | A0A0B2VDN3 | 8 | 2 | 27  | Lipid binding | Unknown function | Unknown function |
| Stress-induced-phosphoprotein 1 | A0A0B2W396 | 18 | 4 | 37  | Unknown function | Unknown function | Unknown function |
| Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrialcanis | A0A0B2VZN8 | 23 | 10 | 72  | Flavin adenine dinucleotide binding and succinate dehydrogenase (ubiquinone) activity | Electron transport chain and tricarboxylic acid cycle | Mitochondrial inner membrane |
| Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial  | A0A0B2W2B1 | *8* | *2* | *34*  | 2 iron, 2 sulfur cluster binding, 3 iron, 4 sulfur cluster binding, 4 iron, 4 sulfur cluster binding, electron carrier activity, metal ion binding and succinate dehydrogenase (ubiquinone) activity | Tricarboxylic acid cycle | Mitochondrial inner membrane |
| Succinate-semialdehyde dehydrogenase, mitochondrial | A0A0B2UT14 | 9 | 4 | 84  | Oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | Unknown function | Unknown function |
| Succinyl-coa ligase subunit beta | A0A0B2VMI1 | 10 | 2 | 50  | ATP binding and ligase activity | Metabolic process | Unknown function |
| Sucrase-isomaltase, intestinal | A0A0B2USA9 | 3 | 2 | 109  | Carbohydrate binding and hydrolase activity, hydrolyzing O-glycosyl compounds | Carbohydrate metabolic process | Integral component of membrane |
| Sulfhydryl oxidase  | A0A0B2VSJ1 | 8 | 4 | 119  | Thiol oxidase activity | Cell redox homeostasis | Cell Source: GOCintegral component of membrane |
| Superoxide dismutase [Cu-Zn]  | A0A0B2UYA2 | 18 | 2 | 19  | Metal ion binding and superoxide dismutase activity | Unknown function | Unknown function |
| Syntaxin-12 | A0A0B2UNN7 | 10 | 2 | 28  | Unknown function | Intracellular protein transport, membrane fusion and vesicle-mediated transport | Integral component of membrane and intracellular |
| Syntrophin-1  | A0A0B2UU58 | 6 | 5 | 141  | Ribosome binding, structural molecule activity and UDP-glucose 4-epimerase activity | Galactose metabolic process, mature ribosome assembly, peroxisome fission and synapse organization | Dystrophin-associated glycoprotein and integral component of peroxisomal membrane |
| TAR DNA-binding protein 43  | A0A0B2W0H4 | 7 | 2 | 49  | DNA binding and nucleotide binding | Unknown function | Unknown function |
| Tau-tubulin kinase 2 | A0A0B2W586 | 12 | 3 | 30  | ATP binding and protein serine/threonine kinase activity | Unknown function | Unknown function |
| TBA-1 (Fragment)  | P91811 | 80 | 27 | 16  | Unknown function | Unknown function | Unknown function |
| T-complex protein 1 subunit beta | A0A0B2V9X9 | 10 | 2 | 48  | ATP binding | Protein folding | Cytoplasm |
| T-complex protein 1 subunit delta | A0A0B2VB47 | 9 | 3 | 59  | ATP binding | Protein folding | Cytoplasm |
| T-complex protein 1 subunit epsilon (Fragment) | A0A0B2W6N6 | 10 | 2 | 37  | ATP binding | Protein folding | Cytoplasm |
| T-complex protein 1 subunit eta | A0A0B2UT03 | 13 | 5 | 73  | ATP binding | Protein folding | Cytoplasm |
| T-complex protein 1 subunit theta | A0A0B2V231 | 6 | 3 | 85  | ATP binding | Protein folding | Cytoplasm |
| Thioredoxin domain-containing protein C06A6.5 | A0A0B2URC6 | 5 | 2 | 47  | Unknown function | Cell redox homeostasis | Cell |
| Thioredoxin-like protein 1  | A0A0B2V1D8 | 13 | 3 | 34  | Protein disulfide oxidoreductase activity | Cell redox homeostasis and glycerol ether metabolic process | Cell |
| Threonine--trna ligase, cytoplasmic | A0A0B2VUA0 | 10 | 2 | 25  | ATP binding and threonine-trna ligase activity | Threonyl-trna aminoacylation | Cytoplasm |
| Threonine--trna ligase, cytoplasmic5b | A0A0B2VH09 | 7 | 2 | 47  | ATP binding and ligase activity, forming aminoacyl-trna and related compounds | Trna aminoacylation | Integral component of membrane |
| Thyrotropin-releasing hormone-degrading ectoenzyme | A0A0B2UZP1 | 5 | 7 | 215  | Metallopeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Thyrotropin-releasing hormone-degrading ectoenzyme | A0A0B2V4Y5 | 2 | 3 | 216  | Metallopeptidase activity and zinc ion binding | Unknown function | Unknown function |
| Titin | A0A0B2VJV3 | 3 | 3 | 166  | Unknown function | Unknown function | Unknown function |
| Transaldolase | A0A0B2UIN7 | 28 | 8 | 43  | Sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity | Carbohydrate metabolic process and pentose-phosphate shunt | Cytoplasm |
| Transcription elongation factor B polypeptide 2  | A0A0B2UUH4 | 20 | 2 | 13  | Translation elongation factor activity | Unknown function | Unknown function |
| Transcriptional activator protein Pur-alpha | A0A0B2VN98 | 12 | 3 | 29  | Unknown function | Unknown function | Unknown function |
| Transitional endoplasmic reticulum atpase-like protein 2 | A0A0B2VWN1 | 6 | 5 | 90  | ATP binding and hydrolase activity | Unknown function | Unknown function |
| Transketolase | A0A0B2USJ9 | 4 | 3 | 115  | Catalytic activity | Metabolic process | Integral component of membrane |
| Translational activator GCN1 | A0A0B2VIH7 | 7 | 12 | 296  | Protein kinase regulator activity and ribosome binding | Cellular response to stress, positive regulation of kinase activity and regulation of translation | Unknown function |
| Transportin-3 | A0A0B2VBU8 | 5 | 3 | 103  | Unknown function | Unknown function | Unknown function |
| Transthyretin-like protein 15  | A0A0B2VU78 | 84 | 12 | 14  | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46 | A0A0B2W0V7 | 53 | 5 | 14  | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46  | A0A0B2VAW6 | 19 | 2 | 17 | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46  | A0A0B2VLT1 | 32 | 4 | 17  | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 4 | A0A0B2W1X6 | 17 | 4 | 26  | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 46 O | A0A0B2W0X7 | 18 | 2 | 19 | Unknown function | Unknown function | Extracellular space |
| Transthyretin-like protein 5 O | A0A0B2UZ68 | 33 | 3 | 15 | Unknown function | Unknown function | Extracellular space |
| Trehalase  | A0A0B2W287 | 4 | 2 | 84  | Alpha,alpha-trehalase activity | Trehalose metabolic process | Integral component of membrane |
| Trifunctional enzyme subunit alpha, mitochondrial  | A0A0B2V6D4 | 7 | 3 | 102  | 3-hydroxyacyl-coa dehydrogenase activity and enoyl-coa hydratase activity | Fatty acid beta-oxidation | Mitochondrial fatty acid beta-oxidation multienzyme complex |
| Triosephosphate isomerase  | A0A0B2VFZ0 | 14 | 2 | 27  | Triose-phosphate isomerase activity | Gluconeogenesis, glycolytic process and pentose-phosphate shunt | Unknown function |
| Tropomyosin | A0A0B2VDB8 | 27 | 7 | 31  | Unknown function | Unknown function | Unknown function |
| Troponin I 2  | A0A0B2VTU0 | 9 | 2 | 31  | Unknown function | Unknown function | Troponin complex |
| Troponin T | A0A0B2USX2 | 7 | 3 | 44  | Unknown function | Regulation of muscle contraction | Troponin complex |
| Troponin T  | A0A0B2UWG3 | 8 | 2 | 46  | Unknown function | Regulation of muscle contraction | Troponin complex |
| Tubulin alpha chain | A0A0B2VPL2 | 25 | 7 | 50  | Gtpase activity, GTP binding and structural constituent of cytoskeleton | Microtubule-based process | Cytoplasm and microtubule |
| Tubulin alpha-3 chain | A0A0B2VB05 | 24 | 7 | 50  | Gtpase activity, GTP binding and structural constituent of cytoskeleton | Microtubule-based process | Cytoplasm and microtubule |
| Tubulin beta-1 chain | A0A0B2VUK1 | 18 | 8 | 50  | Gtpase activity, GTP binding and structural constituent of cytoskeleton | Microtubule-based process | Cytoplasm and microtubule |
| Tubulin--tyrosine ligase-like protein 12 | A0A0B2UUX0 | 15 | 6 | 67  | Gtpase activity, GTP binding and structural constituent of cytoskeleton | Microtubule-based process | Cytoplasm and microtubule |
| Twitchin | A0A0B2UWL8 | 19 | 15 | 140  | ATP binding and protein kinase activity | Unknown function | Unknown function |
| Type I inositol 1,4,5-trisphosphate 5-phosphatase | A0A0B2VMC0 | 4 | 2 | 57  | Unknown function | Unknown function | Unknown function |
| Ubiquitin carboxyl-terminal hydrolase | A0A0B2V0M3 | 31 | 5 | 26  | Thiol-dependent ubiquitin-specific protease activity | Ubiquitin-dependent protein catabolic proces | Intracellular |
| Ubiquitin carboxyl-terminal hydrolase | A0A0B2W064 | 5 | 3 | 96  | Thiol-dependent ubiquitin-specific protease activity | Protein deubiquitination and ubiquitin-dependent protein catabolic process | Unknown function |
| Ubiquitin conjugation factor E4 B | A0A0B2W2B2 | 3 | 2 | 156  | Oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor and ubiquitin-ubiquitin ligase activity | Ubiquitin-dependent protein catabolic process | Ubiquitin ligase complex |
| Ubiquitin-60S ribosomal protein L40 | A0A0B2VKW1 | 26 | 3 | 14  | Structural constituent of ribosome | Translation | Ribosome |
| Ubiquitin-conjugating enzyme E2 variant 2 | A0A0B2VYL2 | 45 | 6 | 16  | Unknown function | Unknown function | Unknown function |
| Ubiquitin-like modifier-activating enzyme 1  | A0A0B2VLR1 | 16 | 12 | 135  | ATP binding and small protein activating enzyme activity | Cellular protein modification process | Unknown function |
| UDP-glucose:glycoprotein glucosyltransferase | A0A0B2V1L1 | 2 | 2 | 180  | UDP-glucose:glycoprotein glucosyltransferase activity | Protein glycosylation | Unknown function |
| Unconventional myosin- | A0A0B2VKU9 | 2 | 3 | 205  | ATP binding and motor activity | Unknown function | Integral component of membrane and myosin complex |
| Uridine kinase-like protein 5  | A0A0B2VM06 | 17 | 2 | 21  | ATP binding and kinase activity | Unknown function | Unknown function |
| Uridine nucleosidase 1 | A0A0B2V7F0 | 8 | 2 | 37  | Unknown function | Unknown function | Unknown function |
| Uridine phosphorylase 1 | A0A0B2VJE9 | 18 | 4 | 33  | Uridine phosphorylase activity | Nucleoside metabolic process and nucleotide catabolic process | Cytoplasm |
| UTP--glucose-1-phosphate uridylyltransferase | A0A0B2UVR3 | 13 | 3 | 56  | UTP:glucose-1-phosphate uridylyltransferase activity | UDP-glucose metabolic process | Unknown function |
| UV excision repair protein RAD23-like protein B | A0A0B2VIK3 | 14 | 3 | 37  | Damaged DNA binding | Nucleotide-excision repair and proteasome-mediated ubiquitin-dependent protein catabolic process | Nucleus |
| Vacuolar protein sorting-associated protein 13C  | A0A0B2VQY0 | 4 | 7 | 339  | Unknown function | Unknown function | Unknown function |
| Vacuolar protein sorting-associated protein 35 | A0A0B2VCY0 | 3 | 2 | 85  | Protein transporter activity | Retrograde transport, endosome to Golgi | Cytosol Source: GOCretromer complex |
| Valine--trna ligase | A0A0B2UQ06 | 15 | 2 | 28  | Aminoacyl-trna ligase activity and ATP binding | Trna aminoacylation for protein translation | Unknown function |
| Vesicle-fusing atpase | A0A0B2VYN1 | 3 | 2 | 87  | ATP binding | Unknown function | Unknown function |
| Vinculin | A0A0B2V444 | 4 | 2 | 114  | Structural molecule activity | Cell adhesion | Actin cytoskeleton |
| Vitellogenin-6 | A0A0B2V8F3 | 54 | 86 | 198  | Lipid transporter activity | Unknown function | Unknown function |
| V-type proton atpase catalytic subunit A | A0A0B2UT46 | 13 | 5 | 68  | ATP binding and proton-transporting atpase activity, rotational mechanism | ATP hydrolysis coupled proton transport and ATP metabolic process | Proton-transporting V-type atpase, V1 domain |
| V-type proton atpase subunit E | A0A0B2VBC3 | 22 | 4 | 26  | Proton-transporting atpase activity, rotational mechanism | ATP hydrolysis coupled proton transport | Proton-transporting two-sector atpase complex, catalytic domain |
| Xaa-Pro dipeptidase  | A0A0B2VTX0 | 19 | 6 | 48  | Aminopeptidase activity and manganese ion binding | Unknown function | Unknown function |
| Xaa-Pro dipeptidase  | A0A0B2VW06 | 8 | 3 | 56  | Aminopeptidase activity and manganese ion binding | Unknown function | Unknown function |
| Zinc finger RNA-binding protein 2 | A0A0B2VHS0 | 3 | 2 | 102  | Nucleic acid binding and zinc ion binding | Unknown function | Unknown function |