



Functional Annotation Chart

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Current Gene List: condition_specific_genes_
Current Background: Homo sapiens
2052 DAVID IDs
Options
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1690 chart records
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| Sublist | Category | Term | RT | Genes | | Count | % 877 | P-Value 2.0E-131 | Benjamini 6.1E-130 |
|---------|--------------------------|--|----|-------|-------|-------|----------|---------------------|-----------------------|
| | | | | RT | Genes | | | | |
| | UP_KW_PTM | Acetylation | RT | | | 877 | 42.7 | 2.0E-131 | 6.1E-130 |
| | GOTERM_MF_DIRECT | protein binding | RT | | | 1773 | 86.4 | 1.6E-123 | 2.3E-120 |
| | GOTERM_CC_DIRECT | cytosol | RT | | | 991 | 48.3 | 7.3E-113 | 7.2E-110 |
| | GOTERM_MF_DIRECT | RNA binding | RT | | | 444 | 21.6 | 6.9E-105 | 5.0E-102 |
| | GOTERM_CC_DIRECT | nucleoplasm | RT | | | 764 | 37.2 | 7.0E-95 | 3.5E-92 |
| | GOTERM_CC_DIRECT | cytoplasm | RT | | | 900 | 43.9 | 2.0E-69 | 6.7E-67 |
| | UP_KW_PTM | Phosphoprotein | RT | | | 1366 | 66.6 | 1.5E-65 | 2.2E-64 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2) | RT | | | 325 | 15.8 | 4.9E-64 | 4.4E-60 |
| | UP_KW_CELLULAR_COMPONENT | Cytoplasm | RT | | | 938 | 45.7 | 3.5E-63 | 2.0E-61 |
| | GOTERM_BP_DIRECT | cytoplasmic translation | RT | | | 77 | 3.8 | 1.1E-61 | 5.9E-58 |
| | GOTERM_CC_DIRECT | nucleus | RT | | | 912 | 44.4 | 1.7E-58 | 4.3E-56 |
| | GOTERM_CC_DIRECT | extracellular exosome | RT | | | 443 | 21.6 | 8.9E-53 | 1.8E-50 |
| | UP_KW_PTM | Ubl conjugation | RT | | | 584 | 28.5 | 1.6E-52 | 1.6E-51 |
| | GOTERM_CC_DIRECT | cytosolic ribosome | RT | | | 71 | 3.5 | 2.6E-51 | 4.3E-49 |
| | UP_KW_CELLULAR_COMPONENT | Nucleus | RT | | | 909 | 44.3 | 1.2E-50 | 3.3E-49 |
| | UP_KW_PTM | Isopeptide bond | RT | | | 448 | 21.8 | 2.4E-50 | 1.8E-49 |
| | UP_KW_BIOLOGICAL_PROCESS | Host-virus interaction | RT | | | 213 | 10.4 | 1.7E-45 | 2.3E-43 |
| | GOTERM_BP_DIRECT | translation | RT | | | 97 | 4.7 | 1.3E-39 | 3.4E-36 |
| | GOTERM_CC_DIRECT | ribonucleoprotein complex | RT | | | 109 | 5.3 | 5.4E-38 | 7.7E-36 |
| | GOTERM_CC_DIRECT | cytosolic large ribosomal subunit | RT | | | 49 | 2.4 | 8.4E-38 | 1.0E-35 |
| | UP_KW_MOLECULAR_FUNCTION | Ribosomal protein | RT | | | 91 | 4.4 | 5.6E-37 | 3.2E-35 |
| | UP_KW_MOLECULAR_FUNCTION | Ribonucleoprotein | RT | | | 118 | 5.8 | 6.5E-37 | 3.2E-35 |
| | GOTERM_CC_DIRECT | ribosome | RT | | | 82 | 4.0 | 3.4E-36 | 3.8E-34 |
| | GOTERM_MF_DIRECT | structural constituent of ribosome | RT | | | 88 | 4.3 | 5.3E-36 | 2.6E-33 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2); alternate | RT | | | 118 | 5.8 | 4.4E-35 | 2.0E-31 |
| | KEGG_PATHWAY | Ribosome | RT | | | 82 | 4.0 | 8.2E-30 | 2.8E-27 |
| | GOTERM_CC_DIRECT | nuclear speck | RT | | | 124 | 6.0 | 3.8E-29 | 3.8E-27 |
| | UP_KW_MOLECULAR_FUNCTION | RNA-binding | RT | | | 183 | 8.9 | 1.5E-28 | 4.9E-27 |
| | KEGG_PATHWAY | Coronavirus disease - COVID-19 | RT | | | 96 | 4.7 | 3.2E-28 | 5.5E-26 |
| | GOTERM_CC_DIRECT | focal adhesion | RT | | | 122 | 5.9 | 4.4E-28 | 4.0E-26 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1); alternate | RT | | | 70 | 3.4 | 9.9E-25 | 2.9E-21 |
| | UP_KW_BIOLOGICAL_PROCESS | mRNA processing | RT | | | 118 | 5.8 | 4.7E-23 | 3.2E-21 |
| | GOTERM_MF_DIRECT | cadherin binding | RT | | | 97 | 4.7 | 3.2E-22 | 1.2E-19 |
| | GOTERM_CC_DIRECT | membrane | RT | | | 733 | 35.7 | 4.4E-22 | 3.7E-20 |
| | GOTERM_MF_DIRECT | mRNA binding | RT | | | 81 | 3.9 | 3.0E-21 | 8.7E-19 |
| | GOTERM_CC_DIRECT | endoplasmic reticulum | RT | | | 213 | 10.4 | 6.0E-21 | 4.6E-19 |
| | UP_KW_BIOLOGICAL_PROCESS | mRNA splicing | RT | | | 97 | 4.7 | 6.1E-21 | 2.8E-19 |
| | GOTERM_CC_DIRECT | polysomal ribosome | RT | | | 26 | 1.3 | 2.0E-20 | 1.4E-18 |
| | GOTERM_CC_DIRECT | cytosolic small ribosomal subunit | RT | | | 30 | 1.5 | 1.3E-18 | 8.9E-17 |
| | GOTERM_MF_DIRECT | ubiquitin protein ligase binding | RT | | | 89 | 4.3 | 1.4E-18 | 3.4E-16 |
| | UP_KW_DOMAIN | Coiled coil | RT | | | 361 | 17.6 | 8.5E-18 | 2.6E-16 |
| | INTERPRO | Nucleotide-bd_a/b_plait_sf | RT | | | 76 | 3.7 | 4.6E-17 | 2.0E-13 |
| | KEGG_PATHWAY | Protein processing in endoplasmic reticulum | RT | | | 64 | 3.1 | 1.3E-16 | 1.4E-14 |
| | GOTERM_CC_DIRECT | melanosome | RT | | | 42 | 2.0 | 4.4E-16 | 2.7E-14 |
| | INTERPRO | RBD_domain_sf | RT | | | 73 | 3.6 | 9.1E-16 | 2.0E-12 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|--|----|---|-------|------|---------|-----------|
| | GOTERM_MF_DIRECT | identical protein binding | RT |  | 287 | 14.0 | 1.2E-15 | 2.6E-13 |
| | GOTERM_CC_DIRECT | ficolin-1-rich granule lumen | RT |  | 46 | 2.2 | 1.9E-15 | 1.1E-13 |
| | UP_SEQ_FEATURE | DOMAIN:RRM | RT |  | 67 | 3.3 | 2.0E-15 | 4.5E-12 |
| | SMART | RRM | RT |  | 63 | 3.1 | 4.9E-15 | 2.4E-12 |
| | KEGG_PATHWAY | Th17 cell differentiation | RT |  | 47 | 2.3 | 4.9E-15 | 4.1E-13 |
| | KEGG_PATHWAY | Endocytosis | RT |  | 78 | 3.8 | 1.0E-14 | 7.0E-13 |
| | UP_SEQ_FEATURE | COMPBIAS:Basic residues | RT |  | 135 | 6.6 | 1.8E-14 | 3.3E-11 |
| | INTERPRO | RRM_dom | RT |  | 65 | 3.2 | 2.3E-14 | 3.3E-11 |
| | GOTERM_BP_DIRECT | apoptotic process | RT |  | 122 | 5.9 | 2.5E-14 | 4.2E-11 |
| | GOTERM_BP_DIRECT | RNA splicing | RT |  | 61 | 3.0 | 3.2E-14 | 4.2E-11 |
| | KEGG_PATHWAY | Epstein-Barr virus infection | RT |  | 67 | 3.3 | 3.9E-14 | 2.2E-12 |
| | GOTERM_BP_DIRECT | mRNA splicing, via spliceosome | RT |  | 59 | 2.9 | 4.1E-14 | 4.4E-11 |
| | KEGG_PATHWAY | Human T-cell leukemia virus 1 infection | RT |  | 71 | 3.5 | 4.8E-14 | 2.3E-12 |
| | UP_KW_MOLECULAR_FUNCTION | Chaperone | RT |  | 67 | 3.3 | 1.2E-13 | 2.8E-12 |
| | UP_KW_DISEASE | Diamond-Blackfan anemia | RT |  | 18 | 0.9 | 1.5E-13 | 1.5E-11 |
| | GOTERM_BP_DIRECT | protein stabilization | RT |  | 63 | 3.1 | 2.2E-13 | 1.9E-10 |
| | UP_SEQ_FEATURE | COMPBIAS:Acidic residues | RT |  | 167 | 8.1 | 9.9E-13 | 1.5E-9 |
| | UP_KW_BIOLOGICAL_PROCESS | Apoptosis | RT |  | 121 | 5.9 | 1.5E-12 | 5.1E-11 |
| | GOTERM_CC_DIRECT | mitochondrion | RT |  | 221 | 10.8 | 2.1E-12 | 1.1E-10 |
| | GOTERM_BP_DIRECT | translational initiation | RT |  | 27 | 1.3 | 2.1E-12 | 1.6E-9 |
| | UP_KW_CELLULAR_COMPONENT | Endoplasmic reticulum | RT |  | 225 | 11.0 | 3.0E-12 | 5.6E-11 |
| | GOTERM_BP_DIRECT | mRNA processing | RT |  | 61 | 3.0 | 3.0E-12 | 2.0E-9 |
| | GOTERM_CC_DIRECT | small ribosomal subunit | RT |  | 19 | 0.9 | 3.1E-12 | 1.6E-10 |
| | GOTERM_MF_DIRECT | protein domain specific binding | RT |  | 60 | 2.9 | 4.5E-12 | 8.3E-10 |
| | GOTERM_CC_DIRECT | immunological synapse | RT |  | 24 | 1.2 | 4.7E-12 | 2.3E-10 |
| | UP_KW_BIOLOGICAL_PROCESS | Protein transport | RT |  | 134 | 6.5 | 8.1E-12 | 2.2E-10 |
| | GOTERM_BP_DIRECT | protein folding | RT |  | 50 | 2.4 | 1.5E-11 | 9.0E-9 |
| | UP_SEQ_FEATURE | COMPBIAS:Basic and acidic residues | RT |  | 678 | 33.0 | 1.7E-11 | 2.2E-8 |
| | GOTERM_CC_DIRECT | endosome membrane | RT |  | 67 | 3.3 | 2.4E-11 | 1.1E-9 |
| | GOTERM_CC_DIRECT | lysosomal membrane | RT |  | 83 | 4.0 | 3.7E-11 | 1.7E-9 |
| | GOTERM_CC_DIRECT | nuclear envelope | RT |  | 54 | 2.6 | 4.5E-11 | 2.0E-9 |
| | GOTERM_BP_DIRECT | ribosomal small subunit biogenesis | RT |  | 30 | 1.5 | 5.3E-11 | 2.8E-8 |
| | GOTERM_CC_DIRECT | perinuclear region of cytoplasm | RT |  | 130 | 6.3 | 6.6E-11 | 2.7E-9 |
| | GOTERM_CC_DIRECT | macromolecular complex | RT |  | 123 | 6.0 | 6.8E-11 | 2.7E-9 |
| | UP_KW_CELLULAR_COMPONENT | Endosome | RT |  | 128 | 6.2 | 9.6E-11 | 1.3E-9 |
| | KEGG_PATHWAY | Influenza A | RT |  | 54 | 2.6 | 1.3E-10 | 5.4E-9 |
| | GOTERM_BP_DIRECT | multivesicular body assembly | RT |  | 19 | 0.9 | 1.3E-10 | 5.8E-8 |
| | GOTERM_BP_DIRECT | antigen processing and presentation | RT |  | 23 | 1.1 | 1.3E-10 | 5.8E-8 |
| | GOTERM_CC_DIRECT | nucleolus | RT |  | 209 | 10.2 | 1.5E-10 | 5.8E-9 |
| | GOTERM_BP_DIRECT | proteasome-mediated ubiquitin-dependent protein catabolic process | RT | | 57 | 2.8 | 1.7E-10 | 6.8E-8 |
| | UP_KW_MOLECULAR_FUNCTION | Repressor | RT | | 120 | 5.8 | 2.4E-10 | 4.7E-9 |
| | UP_KW_CELLULAR_COMPONENT | Spliceosome | RT | | 45 | 2.2 | 2.9E-10 | 3.2E-9 |
| | GOTERM_BP_DIRECT | positive regulation of I-kappaB kinase/NF-kappaB signaling | RT | | 54 | 2.6 | 4.4E-10 | 1.7E-7 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin) | RT | | 65 | 3.2 | 4.6E-10 | 5.1E-7 |
| | UP_KW_CELLULAR_COMPONENT | Lysosome | RT | | 87 | 4.2 | 5.2E-10 | 4.9E-9 |
| | KEGG_PATHWAY | PD-L1 expression and PD-1 checkpoint pathway in cancer | RT | | 35 | 1.7 | 6.4E-10 | 2.4E-8 |
| | UP_SEQ_FEATURE | MOTIF:Nuclear localization signal | RT | | 88 | 4.3 | 6.5E-10 | 6.4E-7 |
| | GOTERM_CC_DIRECT | secretory granule lumen | RT | | 36 | 1.8 | 7.0E-10 | 2.6E-8 |
| | GOTERM_CC_DIRECT | small-subunit processome | RT | | 28 | 1.4 | 7.9E-10 | 2.8E-8 |
| | KEGG_PATHWAY | Amyotrophic lateral sclerosis | RT | | 88 | 4.3 | 9.1E-10 | 3.1E-8 |
| | GOTERM_BP_DIRECT | chaperone-mediated protein folding | RT | | 21 | 1.0 | 1.1E-9 | 3.7E-7 |
| | KEGG_PATHWAY | Th1 and Th2 cell differentiation | RT | | 35 | 1.7 | 1.8E-9 | 5.1E-8 |
| | KEGG_PATHWAY | Measles | RT | | 45 | 2.2 | 1.8E-9 | 5.1E-8 |
| | GOTERM_BP_DIRECT | protein transport | RT | | 89 | 4.3 | 2.2E-9 | 7.2E-7 |
| | GOTERM_BP_DIRECT | positive regulation of transcription from RNA polymerase II promoter | RT | | 189 | 9.2 | 2.4E-9 | 7.2E-7 |
| | GOTERM_BP_DIRECT | positive regulation of transcription, DNA-templated | RT | | 124 | 6.0 | 2.5E-9 | 7.2E-7 |
| | GOTERM_MF_DIRECT | unfolded protein binding | RT | | 39 | 1.9 | 2.5E-9 | 4.0E-7 |
| | UP_KW_PTM | Methylation | RT | | 196 | 9.6 | 2.7E-9 | 1.6E-8 |
| | GOTERM_CC_DIRECT | eukaryotic translation initiation factor 3 complex | RT | | 13 | 0.6 | 2.9E-9 | 9.8E-8 |
| | GOTERM_BP_DIRECT | response to virus | RT | | 34 | 1.7 | 3.3E-9 | 8.2E-7 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----|-------|-------|------|---------|-----------|
| | GOTERM_BP_DIRECT | ubiquitin-dependent protein catabolic process | RT | | 55 | 2.7 | 3.4E-9 | 8.2E-7 |
| | GOTERM_BP_DIRECT | negative regulation of apoptotic process | RT | | 95 | 4.6 | 3.4E-9 | 8.2E-7 |
| | GOTERM_BP_DIRECT | cell cycle | RT | | 73 | 3.6 | 3.4E-9 | 8.2E-7 |
| | GOTERM_CC_DIRECT | centrosome | RT | | 112 | 5.5 | 3.6E-9 | 1.2E-7 |
| | KEGG_PATHWAY | Apoptosis | RT | | 44 | 2.1 | 3.7E-9 | 9.6E-8 |
| | GOTERM_CC_DIRECT | autophagosome membrane | RT | | 22 | 1.1 | 5.4E-9 | 1.7E-7 |
| | KEGG_PATHWAY | Antigen_processing_and_presentation | RT | | 31 | 1.5 | 5.4E-9 | 1.3E-7 |
| | GOTERM_CC_DIRECT | ER to Golgi transport vesicle membrane | RT | | 23 | 1.1 | 6.4E-9 | 2.0E-7 |
| | GOTERM_BP_DIRECT | intracellular protein transport | RT | | 62 | 3.0 | 6.8E-9 | 1.5E-6 |
| | KEGG_PATHWAY | Salmonella infection | RT | | 65 | 3.2 | 8.6E-9 | 1.9E-7 |
| | GOTERM_BP_DIRECT | ESCRT III complex disassembly | RT | | 10 | 0.5 | 9.7E-9 | 2.1E-6 |
| | KEGG_PATHWAY | Human immunodeficiency virus 1 infection | RT | | 58 | 2.8 | 1.0E-8 | 2.1E-7 |
| | KEGG_PATHWAY | T cell receptor signaling pathway | RT | | 40 | 1.9 | 1.1E-8 | 2.1E-7 |
| | GOTERM_CC_DIRECT | luminal side of endoplasmic reticulum membrane | RT | | 16 | 0.8 | 1.4E-8 | 4.2E-7 |
| | GOTERM_MF_DIRECT | protein binding_involved in protein folding | RT | | 22 | 1.1 | 1.4E-8 | 2.0E-6 |
| | GOTERM_BP_DIRECT | rRNA processing | RT | | 37 | 1.8 | 1.5E-8 | 3.2E-6 |
| | GOTERM_CC_DIRECT | endoplasmic reticulum membrane | RT | | 170 | 8.3 | 1.5E-8 | 4.4E-7 |
| | KEGG_PATHWAY | Viral carcinogenesis | RT | | 56 | 2.7 | 1.6E-8 | 3.1E-7 |
| | KEGG_PATHWAY | Kaposi sarcoma-associated herpesvirus infection | RT | | 54 | 2.6 | 1.8E-8 | 3.3E-7 |
| | UP_KW molecuLAR_FUNCTION | Chromatin regulator | RT | | 68 | 3.3 | 1.9E-8 | 3.1E-7 |
| | GOTERM_CC_DIRECT | spliceosomal complex | RT | | 37 | 1.8 | 1.9E-8 | 5.5E-7 |
| | UP_SEQ_FEATURE | DOMAIN:RRM 1 | RT | | 32 | 1.6 | 2.0E-8 | 1.6E-5 |
| | UP_SEQ_FEATURE | DOMAIN:RRM 2 | RT | | 32 | 1.6 | 2.0E-8 | 1.6E-5 |
| | GOTERM_BP_DIRECT | autophagosome maturation | RT | | 21 | 1.0 | 2.6E-8 | 5.1E-6 |
| | GOTERM_BP_DIRECT | positive regulation of translation | RT | | 28 | 1.4 | 2.6E-8 | 5.1E-6 |
| | KEGG_PATHWAY | Autophagy - animal | RT | | 48 | 2.3 | 2.9E-8 | 4.9E-7 |
| | GOTERM_BP_DIRECT | regulation of RNA splicing | RT | | 26 | 1.3 | 3.8E-8 | 7.1E-6 |
| | GOTERM_BP_DIRECT | autophagy | RT | | 41 | 2.0 | 4.5E-8 | 8.1E-6 |
| | GOTERM_BP_DIRECT | vesicle-mediated transport | RT | | 49 | 2.4 | 5.3E-8 | 9.3E-6 |
| | GOTERM_MF_DIRECT | enzyme binding | RT | | 75 | 3.7 | 6.8E-8 | 9.0E-6 |
| | GOTERM_BP_DIRECT | formation of cytoplasmic translation initiation complex | RT | | 12 | 0.6 | 7.5E-8 | 1.3E-5 |
| | GOTERM_CC_DIRECT | midbody | RT | | 44 | 2.1 | 7.7E-8 | 2.1E-6 |
| | UP_KW_BIological_PROCESS | Cell cycle | RT | | 126 | 6.1 | 8.4E-8 | 1.9E-6 |
| | UP_KW molecuLAR_FUNCTION | Activator | RT | | 123 | 6.0 | 1.0E-7 | 1.4E-6 |
| | GOTERM_MF_DIRECT | protein kinase binding | RT | | 90 | 4.4 | 1.0E-7 | 1.2E-5 |
| | GOTERM_CC_DIRECT | Golgi apparatus | RT | | 161 | 7.8 | 1.1E-7 | 2.9E-6 |
| | GOTERM_MF_DIRECT | MHC class II protein complex binding | RT | | 15 | 0.7 | 1.1E-7 | 1.2E-5 |
| | GOTERM_CC_DIRECT | catalytic step 2 spliceosome | RT | | 28 | 1.4 | 1.1E-7 | 3.0E-6 |
| | GOTERM_BP_DIRECT | chaperone mediated protein folding requiring cofactor | RT | | 16 | 0.8 | 1.2E-7 | 1.9E-5 |
| | KEGG_PATHWAY | Huntington disease | RT | | 72 | 3.5 | 1.2E-7 | 2.0E-6 |
| | KEGG_PATHWAY | Parkinson disease | RT | | 65 | 3.2 | 1.3E-7 | 2.0E-6 |
| | GOTERM_CC_DIRECT | cytoplasmic side of plasma membrane | RT | | 31 | 1.5 | 1.4E-7 | 3.6E-6 |
| | GOTERM_CC_DIRECT | Golgi membrane | RT | | 111 | 5.4 | 1.5E-7 | 3.8E-6 |
| | GOTERM_CC_DIRECT | intracellular membrane-bounded organelle | RT | | 138 | 6.7 | 1.9E-7 | 4.6E-6 |
| | GOTERM_BP_DIRECT | negative regulation of transcription, DNA-templated | RT | | 98 | 4.8 | 2.0E-7 | 3.2E-5 |
| | GOTERM_CC_DIRECT | chaperone complex | RT | | 15 | 0.7 | 2.2E-7 | 5.3E-6 |
| | KEGG_PATHWAY | Viral life cycle - HIV-1 | RT | | 25 | 1.2 | 2.3E-7 | 3.3E-6 |
| | GOTERM_CC_DIRECT | phagocytic vesicle membrane | RT | | 26 | 1.3 | 2.5E-7 | 5.7E-6 |
| | KEGG_PATHWAY | Pathways of neurodegeneration - multiple diseases | RT | | 99 | 4.8 | 2.7E-7 | 3.8E-6 |
| | GOTERM_CC_DIRECT | eukaryotic 43S preinitiation complex | RT | | 12 | 0.6 | 2.7E-7 | 6.1E-6 |
| | GOTERM_CC_DIRECT | polysome | RT | | 17 | 0.8 | 2.8E-7 | 6.1E-6 |
| | GOTERM_CC_DIRECT | recycling endosome membrane | RT | | 31 | 1.5 | 3.3E-7 | 7.1E-6 |
| | UP_SEQ_FEATURE | REGION:Disordered | RT | | 1431 | 69.7 | 3.3E-7 | 2.3E-4 |
| | UP_SEQ_FEATURE | REGION:Disordered | RT | | 11 | 0.5 | 3.3E-7 | 2.3E-4 |
| | KEGG_PATHWAY | Hepatitis B | RT | | 45 | 2.2 | 3.6E-7 | 4.9E-6 |
| | GOTERM_CC_DIRECT | nuclear body | RT | | 65 | 3.2 | 3.8E-7 | 8.1E-6 |
| | GOTERM_CC_DIRECT | lysosome | RT | | 58 | 2.8 | 4.1E-7 | 8.5E-6 |
| | GOTERM_CC_DIRECT | endosome | RT | | 60 | 2.9 | 4.4E-7 | 9.0E-6 |
| | GOTERM_BP_DIRECT | negative regulation of mRNA splicing, via spliceosome | RT | | 13 | 0.6 | 5.0E-7 | 7.8E-5 |
| | GOTERM_MF_DIRECT | heat shock protein binding | RT | | 22 | 1.1 | 5.2E-7 | 5.4E-5 |
| | GOTERM_BP_DIRECT | chromatin organization | RT | | 49 | 2.4 | 5.4E-7 | 8.2E-5 |
| | GOTERM_BP_DIRECT | T cell receptor signaling pathway | RT | | 32 | 1.6 | 6.6E-7 | 9.6E-5 |
| | KEGG_PATHWAY | Necroptosis | RT | | 44 | 2.1 | 6.7E-7 | 8.7E-6 |
| | GOTERM_MF_DIRECT | chaperone binding | RT | | 30 | 1.5 | 8.4E-7 | 8.1E-5 |
| | GOTERM_BP_DIRECT | cell division | RT | | 71 | 3.5 | 8.5E-7 | 1.2E-4 |
| | UP_KW_BIological_PROCESS | Ubl conjugation pathway | RT | | 131 | 6.4 | 8.9E-7 | 1.7E-5 |
| | GOTERM_MF_DIRECT | mRNA 5'-UTR binding | RT | | 14 | 0.7 | 9.3E-7 | 8.3E-5 |
| | GOTERM_MF_DIRECT | DNA binding | RT | | 198 | 9.6 | 9.7E-7 | 8.3E-5 |
| | GOTERM_CC_DIRECT | nuclear membrane | RT | | 52 | 2.5 | 1.2E-6 | 2.3E-5 |
| | KEGG_PATHWAY | NOD-like receptor signaling pathway | RT | | 48 | 2.3 | 1.4E-6 | 1.8E-5 |
| | GOTERM_BP_DIRECT | positive regulation of viral genome replication | RT | | 14 | 0.7 | 1.5E-6 | 2.0E-4 |
| | GOTERM_BP_DIRECT | innate immune response | RT | | 89 | 4.3 | 1.6E-6 | 2.0E-4 |
| | GOTERM_BP_DIRECT | response to endoplasmic reticulum stress | RT | | 27 | 1.3 | 1.6E-6 | 2.0E-4 |
| | GOTERM_BP_DIRECT | multivesicular body sorting pathway | RT | | 13 | 0.6 | 1.6E-6 | 2.0E-4 |
| | GOTERM_BP_DIRECT | response to unfolded protein | RT | | 20 | 1.0 | 1.6E-6 | 2.0E-4 |
| | GOTERM_CC_DIRECT | eukaryotic 48S preinitiation complex | RT | | 11 | 0.5 | 1.6E-6 | 3.2E-5 |
| | GOTERM_BP_DIRECT | macroautophagy | RT | | 23 | 1.1 | 1.7E-6 | 2.1E-4 |
| | UP_KW_CELLULAR_COMPONENT | Mitochondrion | RT | | 197 | 9.6 | 1.9E-6 | 1.5E-5 |
| | GOTERM_MF_DIRECT | chromatin binding | RT | | 86 | 4.2 | 2.1E-6 | 1.6E-4 |
| | GOTERM_MF_DIRECT | ubiquitin binding | RT | | 28 | 1.4 | 2.1E-6 | 1.6E-4 |
| | UP_SEQ_FEATURE | LIPID:S-geranylgeranyl cysteine | RT | | 29 | 1.4 | 2.1E-6 | 1.3E-3 |
| | GOTERM_MF_DIRECT | translation initiation factor activity | RT | | 21 | 1.0 | 2.3E-6 | 1.7E-4 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO); alternate | RT | | 18 | 0.9 | 2.4E-6 | 1.4E-3 |
| | GOTERM_BP_DIRECT | negative regulation of translation | RT | | 27 | 1.3 | 2.4E-6 | 2.9E-4 |
| | GOTERM_BP_DIRECT | alternative mRNA splicing, via spliceosome | RT | | 13 | 0.6 | 2.7E-6 | 3.2E-4 |
| | GOTERM_BP_DIRECT | T cell activation | RT | | 20 | 1.0 | 2.9E-6 | 3.2E-4 |
| | GOTERM_BP_DIRECT | regulation of alternative mRNA splicing, via spliceosome | RT | | 20 | 1.0 | 2.9E-6 | 3.2E-4 |
| | KEGG_PATHWAY | Phagosome | RT | | 41 | 2.0 | 2.9E-6 | 3.5E-5 |
| | KEGG_PATHWAY | Human cytomegalovirus infection | RT | | 54 | 2.6 | 3.1E-6 | 3.6E-5 |
| | GOTERM_MF_DIRECT | transcription factor binding | RT | | 20 | 1.0 | 3.1E-6 | 2.2E-4 |
| | KEGG_PATHWAY | Prion disease | RT | | 62 | 3.0 | 3.2E-6 | 3.6E-5 |
| | KEGG_PATHWAY | Viral myocarditis | RT | | 24 | 1.2 | 3.4E-6 | 3.7E-5 |
| | KEGG_PATHWAY | Toxoplasmosis | RT | | 33 | 1.6 | 3.6E-6 | 3.8E-5 |
| | | | | | | | | |

| Sublist | Category | Term | RT Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----------|-------|-----|---------|-----------|
| | GOTERM_BP_DIRECT | regulation_of_protein_stability | RT | 25 | 1.2 | 4.2E-6 | 4.5E-4 |
| | UP_KW_MOLECULAR_FUNCTION | Initiation_factor | RT | 20 | 1.0 | 4.6E-6 | 5.5E-5 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1) | RT | 23 | 1.1 | 4.8E-6 | 2.7E-3 |
| | UP_KW_BIOLOGICAL_PROCESS | Innate immunity | RT | 81 | 3.9 | 4.9E-6 | 7.4E-5 |
| | UP_KW_BIOLOGICAL_PROCESS | Biological_rhythms | RT | 38 | 1.9 | 4.9E-6 | 7.4E-5 |
| | GOTERM_MF_DIRECT | transcription_cofactor_activity | RT | 32 | 1.6 | 5.2E-6 | 3.4E-4 |
| | GOTERM_CC_DIRECT | PML_body | RT | 28 | 1.4 | 5.3E-6 | 1.0E-4 |
| | GOTERM_BP_DIRECT | membrane_fission | RT | 16 | 0.8 | 5.4E-6 | 5.7E-4 |
| | KEGG_PATHWAY | Oxidative_phosphorylation | RT | 37 | 1.8 | 5.4E-6 | 5.6E-5 |
| | GOTERM_CC_DIRECT | nuclear_pore | RT | 26 | 1.3 | 5.6E-6 | 1.0E-4 |
| | GOTERM_CC_DIRECT | ruffle | RT | 26 | 1.3 | 5.6E-6 | 1.0E-4 |
| | KEGG_PATHWAY | Shigellosis | RT | 57 | 2.8 | 5.7E-6 | 5.6E-5 |
| | KEGG_PATHWAY | Cellular_senescence | RT | 41 | 2.0 | 5.8E-6 | 5.6E-5 |
| | GOTERM_CC_DIRECT | proteasome_complex | RT | 19 | 0.9 | 6.0E-6 | 1.1E-4 |
| | UP_KW_BIOLOGICAL_PROCESS | ER-Golgi_transport | RT | 29 | 1.4 | 6.5E-6 | 8.4E-5 |
| | UP_KW_BIOLOGICAL_PROCESS | Unfolded_protein_response | RT | 18 | 0.9 | 6.8E-6 | 8.4E-5 |
| | GOTERM_BP_DIRECT | nucleus_organization | RT | 12 | 0.6 | 7.7E-6 | 7.8E-4 |
| | GOTERM_BP_DIRECT | viral_budding_via_host_ESCRT_complex | RT | 12 | 0.6 | 7.7E-6 | 7.8E-4 |
| | GOTERM_CC_DIRECT | azurophil_granule_membrane | RT | 19 | 0.9 | 7.9E-6 | 1.4E-4 |
| | GOTERM_CC_DIRECT | RNA_polymerase_II_transcription_factor_complex | RT | 30 | 1.5 | 8.0E-6 | 1.4E-4 |
| | GOTERM_MF_DIRECT | transcription_coactivator_activity | RT | 53 | 2.6 | 8.4E-6 | 5.3E-4 |
| | UP_SEQ_FEATURE | TOPO_DOM:Lumenal | RT | 101 | 4.9 | 8.5E-6 | 4.5E-3 |
| | GOTERM_BP_DIRECT | ubiquitin-dependent_protein_catabolic_process_via_the_multivesicular_body_sorting_pathway | RT | 14 | 0.7 | 8.9E-6 | 8.8E-4 |
| | UP_SEQ_FEATURE | MOTIF:Q motif | RT | 15 | 0.7 | 9.0E-6 | 4.5E-3 |
| | GOTERM_BP_DIRECT | regulation_of_translation | RT | 26 | 1.3 | 9.8E-6 | 9.6E-4 |
| | INTERPRO | Thioredoxin-like_sf | RT | 31 | 1.5 | 1.0E-5 | 1.1E-2 |
| | GOTERM_BP_DIRECT | endoplasmic_reticulum_unfolded_protein_response | RT | 17 | 0.8 | 1.1E-5 | 1.0E-3 |
| | UP_SEQ_FEATURE | DOMAIN:Thioredoxin | RT | 16 | 0.8 | 1.2E-5 | 5.7E-3 |
| | GOTERM_BP_DIRECT | cellular_response_to_DNA_damage_stimulus | RT | 55 | 2.7 | 1.2E-5 | 1.2E-3 |
| | GOTERM_BP_DIRECT | regulation_of_mitotic_spindle_assembly | RT | 12 | 0.6 | 1.2E-5 | 1.2E-3 |
| | UP_SEQ_FEATURE | DOMAIN:Ig-like C1-type | RT | 15 | 0.7 | 1.3E-5 | 5.7E-3 |
| | GOTERM_BP_DIRECT | regulation_of_centrosome_duplication | RT | 11 | 0.5 | 1.3E-5 | 1.2E-3 |
| | INTERPRO | Znf_RING/FYVE/PHD | RT | 79 | 3.8 | 1.4E-5 | 1.1E-2 |
| | GOTERM_BP_DIRECT | ERAD_pathway | RT | 25 | 1.2 | 1.4E-5 | 1.3E-3 |
| | GOTERM_CC_DIRECT | MHC_class_II_protein_complex | RT | 12 | 0.6 | 1.5E-5 | 2.5E-4 |
| | KEGG_PATHWAY | Alzheimer_disease | RT | 78 | 3.8 | 1.5E-5 | 1.4E-4 |
| | UP_KW_BIOLOGICAL_PROCESS | Autophagy | RT | 40 | 1.9 | 1.5E-5 | 1.7E-4 |
| | GOTERM_CC_DIRECT | cytoplasmic_stress_granule | RT | 25 | 1.2 | 1.5E-5 | 2.5E-4 |
| | INTERPRO | Thioredoxin_domain | RT | 15 | 0.7 | 1.5E-5 | 1.1E-2 |
| | UP_KW_BIOLOGICAL_PROCESS | Electron_transport | RT | 30 | 1.5 | 1.6E-5 | 1.7E-4 |
| | UP_SEQ_FEATURE | MOTIF:Effector region | RT | 25 | 1.2 | 1.6E-5 | 6.7E-3 |
| | GOTERM_MF_DIRECT | protein_homodimerization_activity | RT | 116 | 5.7 | 1.6E-5 | 9.7E-4 |
| | KEGG_PATHWAY | Tuberculosis | RT | 44 | 2.1 | 1.8E-5 | 1.6E-4 |
| | GOTERM_CC_DIRECT | multivesicular_body | RT | 16 | 0.8 | 1.8E-5 | 3.0E-4 |
| | GOTERM_BP_DIRECT | ribosomal_large_subunit_biogenesis | RT | 14 | 0.7 | 1.9E-5 | 1.7E-3 |
| | GOTERM_MF_DIRECT | nucleic_acid_binding | RT | 58 | 2.8 | 2.1E-5 | 1.2E-3 |
| | INTERPRO | MHC_I_a_C | RT | 7 | 0.3 | 2.1E-5 | 1.3E-2 |
| | GOTERM_BP_DIRECT | protein_ubiquitination | RT | 77 | 3.8 | 2.1E-5 | 1.9E-3 |
| | INTERPRO | RNA-helicase_DEAD-box_CS | RT | 12 | 0.6 | 2.4E-5 | 1.3E-2 |
| | UP_SEQ_FEATURE | DOMAIN:Ubiquitin-like | RT | 19 | 0.9 | 2.5E-5 | 1.0E-2 |
| | GOTERM_CC_DIRECT | chromosome_telomeric_region | RT | 36 | 1.8 | 2.5E-5 | 4.0E-4 |
| | KEGG_PATHWAY | Chemical_carcinogenesis - reactive_oxygen_species | RT | 51 | 2.5 | 2.5E-5 | 2.2E-4 |
| | KEGG_PATHWAY | Allograft_rejection | RT | 16 | 0.8 | 2.6E-5 | 2.2E-4 |
| | GOTERM_CC_DIRECT | ubiquitin_ligase_complex | RT | 27 | 1.3 | 2.7E-5 | 4.3E-4 |
| | UP_KW_DOMAIN | Transit_peptide | RT | 81 | 3.9 | 2.8E-5 | 4.3E-4 |
| | GOTERM_BP_DIRECT | cellular_response_to_UV | RT | 18 | 0.9 | 3.0E-5 | 2.5E-3 |
| | GOTERM_BP_DIRECT | ER_to_Golgi_vesicle-mediated_transport | RT | 29 | 1.4 | 3.0E-5 | 2.5E-3 |
| | GOTERM_BP_DIRECT | chromatin_remodeling | RT | 59 | 2.9 | 3.0E-5 | 2.5E-3 |
| | KEGG_PATHWAY | Type_I_diabetes_mellitus | RT | 17 | 0.8 | 3.3E-5 | 2.8E-4 |
| | BIOCARTA | CTL-mediated immune response against target cells | RT | 11 | 0.5 | 3.5E-5 | 4.0E-3 |
| | BIOCARTA | The_Co-Stimulatory_Signal_During_T-cell_Activation | RT | 13 | 0.6 | 3.5E-5 | 4.0E-3 |
| | GOTERM_BP_DIRECT | positive_regulation_of_exosomal_secretion | RT | 9 | 0.4 | 3.6E-5 | 2.8E-3 |
| | GOTERM_BP_DIRECT | positive_regulation_of_cytoplasmic_translation | RT | 9 | 0.4 | 3.6E-5 | 2.8E-3 |
| | GOTERM_BP_DIRECT | intrinsic_apoptotic_signaling_pathway | RT | 14 | 0.7 | 3.8E-5 | 3.0E-3 |
| | KEGG_PATHWAY | Diabetic_cardiomyopathy | RT | 47 | 2.3 | 3.9E-5 | 3.2E-4 |
| | GOTERM_CC_DIRECT | late_endosome_membrane | RT | 32 | 1.6 | 4.0E-5 | 6.3E-4 |
| | GOTERM_BP_DIRECT | defense_response_to_virus | RT | 45 | 2.2 | 4.0E-5 | 3.1E-3 |
| | GOTERM_CC_DIRECT | kinetochore | RT | 33 | 1.6 | 4.0E-5 | 6.3E-4 |
| | UP_KW_PTM | ADP-ribosylation | RT | 37 | 1.8 | 4.1E-5 | 2.1E-4 |
| | BIOCARTA | Activation_of_Csk_by_cAMP-dependent_Protein_Kinase_Inhibits_Signaling_through_the_T_Cell_Receptor | RT | 14 | 0.7 | 4.5E-5 | 4.0E-3 |
| | INTERPRO | Ribosomal_zn-bd | RT | 8 | 0.4 | 4.5E-5 | 2.0E-2 |
| | UP_SEQ_FEATURE | CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO) | RT | 25 | 1.2 | 4.5E-5 | 1.7E-2 |
| | UP_SEQ_FEATURE | MOTIF:DEAD box | RT | 13 | 0.6 | 4.8E-5 | 1.7E-2 |
| | UP_SEQ_FEATURE | REGION:Alpha-2 | RT | 9 | 0.4 | 4.9E-5 | 1.7E-2 |
| | UP_SEQ_FEATURE | REGION:Alpha-1 | RT | 9 | 0.4 | 4.9E-5 | 1.7E-2 |
| | INTERPRO | Znf_PHD-finger | RT | 21 | 1.0 | 4.9E-5 | 2.0E-2 |
| | GOTERM_BP_DIRECT | positive_regulation_of_T_cell_activation | RT | 13 | 0.6 | 5.0E-5 | 3.9E-3 |
| | KEGG_PATHWAY | Spliceosome | RT | 49 | 2.4 | 5.1E-5 | 4.1E-4 |
| | SMART | PHD | RT | 23 | 1.1 | 5.2E-5 | 1.3E-2 |
| | GOTERM_CC_DIRECT | Flemming_body | RT | 13 | 0.6 | 5.2E-5 | 7.9E-4 |
| | GOTERM_CC_DIRECT | mitochondrial_membrane | RT | 34 | 1.7 | 5.3E-5 | 7.9E-4 |
| | INTERPRO | Ubiquitin-like_domsf | RT | 38 | 1.9 | 5.3E-5 | 2.0E-2 |
| | GOTERM_BP_DIRECT | circadian regulation_of_gene_expression | RT | 20 | 1.0 | 5.5E-5 | 4.1E-3 |
| | GOTERM_BP_DIRECT | retrograde_transport_endosome_to_Golgi | RT | 23 | 1.1 | 5.5E-5 | 4.1E-3 |
| | GOTERM_BP_DIRECT | lysosomal_lumen_acidification | RT | 11 | 0.5 | 5.5E-5 | 4.1E-3 |
| | INTERPRO | Znf_PHD | RT | 23 | 1.1 | 5.6E-5 | 2.0E-2 |
| | UP_SEQ_FEATURE | DOMAIN:PCI | RT | 11 | 0.5 | 6.0E-5 | 2.0E-2 |
| | GOTERM_BP_DIRECT | tumor_necrosis_factor-mediated_signaling_pathway | RT | 18 | 0.9 | 6.1E-5 | 4.4E-3 |
| | GOTERM_BP_DIRECT | nuclear_envelope_reassembly | RT | 10 | 0.5 | 6.3E-5 | 4.5E-3 |
| | GOTERM_BP_DIRECT | negative_regulation_of_transcription_elongation_from_RNA_polymerase_II_promoter | RT | 10 | 0.5 | 6.3E-5 | 4.5E-3 |
| | KEGG_PATHWAY | Lysosome | RT | 34 | 1.7 | 6.5E-5 | 5.1E-4 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|--|----|-------|-------|------|---------|-----------|
| | GOTERM_BP_DIRECT | viral budding from plasma membrane | RT | | 9 | 0.4 | 6.5E-5 | 4.5E-3 |
| | GOTERM_BP_DIRECT | mitophagy | RT | | 15 | 0.7 | 6.7E-5 | 4.5E-3 |
| | GOTERM_BP_DIRECT | negative regulation of viral genome replication | RT | | 15 | 0.7 | 6.7E-5 | 4.5E-3 |
| | GOTERM_BP_DIRECT | negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay | RT | | 7 | 0.3 | 6.7E-5 | 4.5E-3 |
| | KEGG_PATHWAY | Non-alcoholic fatty liver disease | RT | | 38 | 1.9 | 6.9E-5 | 5.3E-4 |
| | BIOCARTA | T Cell Receptor Signaling Pathway | RT | | 21 | 1.0 | 7.0E-5 | 4.6E-3 |
| | GOTERM_BP_DIRECT | erythrocyte differentiation | RT | | 17 | 0.8 | 7.0E-5 | 4.6E-3 |
| | GOTERM_MF_DIRECT | T cell receptor binding | RT | | 8 | 0.4 | 7.1E-5 | 4.0E-3 |
| | GOTERM_CC_DIRECT | U2-type catalytic step 2 spliceosome | RT | | 12 | 0.6 | 7.1E-5 | 1.1E-3 |
| | GOTERM_CC_DIRECT | P-body | RT | | 24 | 1.2 | 7.7E-5 | 1.1E-3 |
| | GOTERM_BP_DIRECT | proteolysis involved in cellular protein catabolic process | RT | | 16 | 0.8 | 8.0E-5 | 5.2E-3 |
| | GOTERM_MF_DIRECT | GDP binding | RT | | 21 | 1.0 | 8.6E-5 | 4.5E-3 |
| | GOTERM_MF_DIRECT | ubiquitin ligase inhibitor activity | RT | | 7 | 0.3 | 8.7E-5 | 4.5E-3 |
| | INTERPRO | Znf FYVE PHD | RT | | 30 | 1.5 | 8.7E-5 | 2.7E-2 |
| | GOTERM_CC_DIRECT | large ribosomal subunit | RT | | 9 | 0.4 | 8.9E-5 | 1.3E-3 |
| | INTERPRO | MHC I a a1/a2 | RT | | 8 | 0.4 | 9.0E-5 | 2.7E-2 |
| | GOTERM_BP_DIRECT | regulation of cell cycle | RT | | 45 | 2.2 | 9.1E-5 | 5.9E-3 |
| | INTERPRO | Thioredoxin CS | RT | | 9 | 0.4 | 9.4E-5 | 2.7E-2 |
| | GOTERM_MF_DIRECT | RNA polymerase II sequence-specific DNA binding transcription factor binding | RT | | 38 | 1.9 | 9.7E-5 | 4.9E-3 |
| | GOTERM_BP_DIRECT | positive regulation of interleukin-2 production | RT | | 13 | 0.6 | 9.8E-5 | 6.2E-3 |
| | UP_KW_BIOLOGICAL_PROCESS | Cell division | RT | | 75 | 3.7 | 1.0E-4 | 9.7E-4 |
| | KEGG_PATHWAY | Graft-versus-host disease | RT | | 16 | 0.8 | 1.0E-4 | 7.3E-4 |
| | KEGG_PATHWAY | Osteoclast differentiation | RT | | 34 | 1.7 | 1.0E-4 | 7.3E-4 |
| | KEGG_PATHWAY | Legionellosis | RT | | 19 | 0.9 | 1.0E-4 | 7.3E-4 |
| | KEGG_PATHWAY | Chagas disease | RT | | 28 | 1.4 | 1.0E-4 | 7.3E-4 |
| | GOTERM_CC_DIRECT | secretory granule membrane | RT | | 24 | 1.2 | 1.1E-4 | 1.5E-3 |
| | GOTERM_MF_DIRECT | rRNA binding | RT | | 15 | 0.7 | 1.1E-4 | 5.3E-3 |
| | GOTERM_BP_DIRECT | positive regulation of telomere maintenance | RT | | 9 | 0.4 | 1.1E-4 | 7.0E-3 |
| | GOTERM_CC_DIRECT | clathrin-coated endocytic vesicle membrane | RT | | 19 | 0.9 | 1.2E-4 | 1.7E-3 |
| | UP_SEQ_FEATURE | DOMAIN:RHD | RT | | 7 | 0.3 | 1.2E-4 | 3.9E-2 |
| | GOTERM_BP_DIRECT | positive regulation of interferon-alpha production | RT | | 11 | 0.5 | 1.2E-4 | 7.7E-3 |
| | KEGG_PATHWAY | TNF signaling pathway | RT | | 30 | 1.5 | 1.3E-4 | 8.7E-4 |
| | UP_SEQ_FEATURE | DOMAIN:DEAD-box RNA helicase Q | RT | | 12 | 0.6 | 1.3E-4 | 4.0E-2 |
| | GOTERM_BP_DIRECT | negative regulation of proteasomal ubiquitin-dependent protein catabolic process | RT | | 13 | 0.6 | 1.3E-4 | 8.0E-3 |
| | GOTERM_BP_DIRECT | activation of innate immune response | RT | | 13 | 0.6 | 1.3E-4 | 8.0E-3 |
| | GOTERM_BP_DIRECT | regulation of translational initiation | RT | | 12 | 0.6 | 1.3E-4 | 8.0E-3 |
| | INTERPRO | RHD DNA bind dom_sf | RT | | 7 | 0.3 | 1.3E-4 | 3.3E-2 |
| | INTERPRO | RHD dimer | RT | | 7 | 0.3 | 1.3E-4 | 3.3E-2 |
| | INTERPRO | RHD DNA bind dom | RT | | 7 | 0.3 | 1.3E-4 | 3.3E-2 |
| | UP_KW_BIOLOGICAL_PROCESS | Antiviral defense | RT | | 32 | 1.6 | 1.4E-4 | 1.2E-3 |
| | UP_KW_BIOLOGICAL_PROCESS | Respiratory chain | RT | | 20 | 1.0 | 1.4E-4 | 1.2E-3 |
| | GOTERM_MF_DIRECT | MHC class II receptor activity | RT | | 8 | 0.4 | 1.4E-4 | 6.2E-3 |
| | UP_SEQ_FEATURE | REGION:Leucine-zipper | RT | | 26 | 1.3 | 1.4E-4 | 4.2E-2 |
| | GOTERM_MF_DIRECT | ATPase activity | RT | | 71 | 3.5 | 1.4E-4 | 6.2E-3 |
| | GOTERM_MF_DIRECT | Hsp90 protein binding | RT | | 15 | 0.7 | 1.4E-4 | 6.2E-3 |
| | GOTERM_MF_DIRECT | cysteine-type endopeptidase activity | RT | | 19 | 0.9 | 1.4E-4 | 6.2E-3 |
| | GOTERM_BP_DIRECT | regulation of apoptotic process | RT | | 43 | 2.1 | 1.4E-4 | 8.6E-3 |
| | INTERPRO | SAP_dom_sf | RT | | 11 | 0.5 | 1.5E-4 | 3.4E-2 |
| | GOTERM_CC_DIRECT | azurophil granule lumen | RT | | 22 | 1.1 | 1.5E-4 | 2.0E-3 |
| | GOTERM_CC_DIRECT | specific granule membrane | RT | | 22 | 1.1 | 1.5E-4 | 2.0E-3 |
| | UP_KW_DISEASE | Intellectual disability | RT | | 121 | 5.9 | 1.5E-4 | 5.4E-3 |
| | UP_SEQ_FEATURE | LIPID:Phosphatidylethanolamine amidated glycine; alternate | RT | | 6 | 0.3 | 1.5E-4 | 4.2E-2 |
| | UP_SEQ_FEATURE | LIPID:Phosphatidylserine amidated glycine; alternate | RT | | 6 | 0.3 | 1.5E-4 | 4.2E-2 |
| | GOTERM_BP_DIRECT | positive regulation of signal transduction by p53 class mediator | RT | | 7 | 0.3 | 1.5E-4 | 9.0E-3 |
| | SMART | RAN | RT | | 22 | 1.1 | 1.5E-4 | 2.3E-2 |
| | GOTERM_CC_DIRECT | eukaryotic translation initiation factor 3 complex, eIF3m | RT | | 6 | 0.3 | 1.6E-4 | 2.1E-3 |
| | UP_KW_LIGAND | Nucleotide-binding | RT | | 233 | 11.4 | 1.6E-4 | 6.4E-3 |
| | UP_KW_DISEASE | Leber hereditary optic neuropathy | RT | | 8 | 0.4 | 1.6E-4 | 5.4E-3 |
| | INTERPRO | Zinc finger PHD-type_CS | RT | | 19 | 0.9 | 1.6E-4 | 3.6E-2 |
| | GOTERM_CC_DIRECT | late endosome | RT | | 31 | 1.5 | 1.6E-4 | 2.2E-3 |
| | UP_SEQ_FEATURE | REGION:Connecting peptide | RT | | 13 | 0.6 | 1.6E-4 | 4.4E-2 |
| | KEGG_PATHWAY | Lipid and atherosclerosis | RT | | 47 | 2.3 | 1.7E-4 | 1.1E-3 |
| | GOTERM_CC_DIRECT | endoplasmic reticulum-Golgi intermediate compartment | RT | | 20 | 1.0 | 1.7E-4 | 2.2E-3 |
| | GOTERM_BP_DIRECT | plasma membrane repair | RT | | 11 | 0.5 | 1.8E-4 | 1.0E-2 |
| | UP_KW_DOMAIN | Redox-active center | RT | | 15 | 0.7 | 1.8E-4 | 1.9E-3 |
| | GOTERM_BP_DIRECT | mitochondrial ATP synthesis coupled proton transport | RT | | 18 | 0.9 | 1.8E-4 | 1.0E-2 |
| | GOTERM_BP_DIRECT | autophagosome assembly | RT | | 19 | 0.9 | 1.8E-4 | 1.0E-2 |
| | GOTERM_CC_DIRECT | membrane coat | RT | | 10 | 0.5 | 1.8E-4 | 2.4E-3 |
| | SMART | SAP | RT | | 10 | 0.5 | 1.9E-4 | 2.3E-2 |
| | GOTERM_BP_DIRECT | positive regulation of RNA splicing | RT | | 8 | 0.4 | 1.9E-4 | 1.1E-2 |
| | BIOCARTA | Lck and Fyn tyrosine kinases in initiation of TCR Activation | RT | | 9 | 0.4 | 1.9E-4 | 1.0E-2 |
| | GOTERM_MF_DIRECT | tumor necrosis factor-activated receptor activity | RT | | 7 | 0.3 | 2.0E-4 | 8.2E-3 |
| | UP_KW_CELLULAR_COMPONENT | Golgi apparatus | RT | | 140 | 6.8 | 2.1E-4 | 1.5E-3 |
| | KEGG_PATHWAY | Protein export | RT | | 13 | 0.6 | 2.1E-4 | 1.4E-3 |
| | GOTERM_MF_DIRECT | binding, bridging | RT | | 38 | 1.9 | 2.1E-4 | 8.7E-3 |
| | INTERPRO | Small_GTP-bd_dom | RT | | 34 | 1.7 | 2.2E-4 | 4.6E-2 |
| | KEGG_PATHWAY | Hepatitis C | RT | | 37 | 1.8 | 2.4E-4 | 1.5E-3 |
| | GOTERM_BP_DIRECT | stress granule assembly | RT | | 11 | 0.5 | 2.5E-4 | 1.4E-2 |
| | UP_SEQ_FEATURE | DOMAIN:RRM 3 | RT | | 15 | 0.7 | 2.5E-4 | 6.7E-2 |
| | UP_KW_DOMAIN | Zinc-finger | RT | | 205 | 10.0 | 2.6E-4 | 2.0E-3 |
| | KEGG_PATHWAY | Vibrio cholerae infection | RT | | 17 | 0.8 | 2.6E-4 | 1.7E-3 |
| | GOTERM_CC_DIRECT | Prp19 complex | RT | | 8 | 0.4 | 2.7E-4 | 3.4E-3 |
| | KEGG_PATHWAY | Inflammatory bowel disease | RT | | 20 | 1.0 | 2.7E-4 | 1.7E-3 |
| | UP_SEQ_FEATURE | DOMAIN:PHD-type | RT | | 19 | 0.9 | 2.8E-4 | 7.0E-2 |
| | INTERPRO | RNA_helicase_DEAD_Q_motif | RT | | 12 | 0.6 | 2.8E-4 | 4.8E-2 |
| | INTERPRO | ARM-type_fold | RT | | 58 | 2.8 | 2.8E-4 | 4.8E-2 |
| | GOTERM_BP_DIRECT | cellular response to epidermal growth factor stimulus | RT | | 14 | 0.7 | 2.8E-4 | 1.5E-2 |
| | GOTERM_BP_DIRECT | mitotic metaphase plate congression | RT | | 14 | 0.7 | 2.8E-4 | 1.5E-2 |
| | INTERPRO | PCI_dom | RT | | 10 | 0.5 | 2.8E-4 | 4.8E-2 |
| | INTERPRO | SAP_dom | RT | | 10 | 0.5 | 2.8E-4 | 4.8E-2 |
| | INTERPRO | MHC II a/b_N | RT | | 10 | 0.5 | 2.8E-4 | 4.8E-2 |
| | GOTERM_BP_DIRECT | viral release from host cell | RT | | 9 | 0.4 | 2.9E-4 | 1.6E-2 |
| | KEGG_PATHWAY | mRNA surveillance pathway | RT | | 26 | 1.3 | 2.9E-4 | 1.8E-3 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|--|----|-------|-------|-----|---------|-----------|
| | GOTERM_CC_DIRECT | protein-DNA complex | RT | | 13 | 0.6 | 3.0E-4 | 3.8E-3 |
| | GOTERM_MF_DIRECT | peptide antigen binding | RT | | 15 | 0.7 | 3.1E-4 | 1.2E-2 |
| | UP_SEQ_FEATURE | DOMAIN:bZIP | RT | | 14 | 0.7 | 3.1E-4 | 7.5E-2 |
| | GOTERM_BP_DIRECT | IRE5-dependent viral translational initiation | RT | | 7 | 0.3 | 3.1E-4 | 1.6E-2 |
| | GOTERM_BP_DIRECT | CRD-mediated mRNA stabilization | RT | | 7 | 0.3 | 3.1E-4 | 1.6E-2 |
| | GOTERM_BP_DIRECT | vesicle fusion with vacuole | RT | | 7 | 0.3 | 3.1E-4 | 1.6E-2 |
| | GOTERM_BP_DIRECT | protein localization to chromosome, telomeric region | RT | | 7 | 0.3 | 3.1E-4 | 1.6E-2 |
| | GOTERM_BP_DIRECT | multivesicular body-lysosome fusion | RT | | 7 | 0.3 | 3.1E-4 | 1.6E-2 |
| | UP_SEQ_FEATURE | DOMAIN:Helicase C-terminal | RT | | 24 | 1.2 | 3.1E-4 | 7.5E-2 |
| | SMART | HELiC | RT | | 24 | 1.2 | 3.2E-4 | 2.9E-2 |
| | KEGG_PATHWAY | Mitophagy - animal | RT | | 27 | 1.3 | 3.2E-4 | 1.9E-3 |
| | UP_KW_BIOLOGICAL_PROCESS | Translation regulation | RT | | 31 | 1.5 | 3.2E-4 | 2.6E-3 |
| | GOTERM_BP_DIRECT | positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay | RT | | 8 | 0.4 | 3.3E-4 | 1.6E-2 |
| | GOTERM_BP_DIRECT | ribosomal small subunit assembly | RT | | 8 | 0.4 | 3.3E-4 | 1.6E-2 |
| | GOTERM_MF_DIRECT | protein disulfide oxidoreductase activity | RT | | 10 | 0.5 | 3.3E-4 | 1.3E-2 |
| | GOTERM_CC_DIRECT | endoplasmic reticulum-Golgi intermediate compartment membrane | RT | | 20 | 1.0 | 3.4E-4 | 4.1E-3 |
| | GOTERM_CC_DIRECT | cytoplasmic ribonucleoprotein granule | RT | | 20 | 1.0 | 3.4E-4 | 4.1E-3 |
| | GOTERM_BP_DIRECT | protein deubiquitination | RT | | 21 | 1.0 | 3.4E-4 | 1.7E-2 |
| | INTERPRO | Helicase_C | RT | | 24 | 1.2 | 3.4E-4 | 5.5E-2 |
| | GOTERM_BP_DIRECT | macromolecular complex assembly | RT | | 29 | 1.4 | 3.6E-4 | 1.8E-2 |
| | UP_SEQ_FEATURE | DOMAIN:SAP | RT | | 10 | 0.5 | 3.6E-4 | 8.4E-2 |
| | SMART | ZnF_RBZ | RT | | 9 | 0.4 | 3.6E-4 | 2.9E-2 |
| | GOTERM_MF_DIRECT | thyroid hormone receptor binding | RT | | 11 | 0.5 | 3.7E-4 | 1.3E-2 |
| | GOTERM_MF_DIRECT | mRNA 3'-UTR AU-rich region binding | RT | | 11 | 0.5 | 3.7E-4 | 1.3E-2 |
| | GOTERM_BP_DIRECT | ubiquitin-dependent ERAD pathway | RT | | 19 | 0.9 | 3.8E-4 | 1.8E-2 |
| | KEGG_PATHWAY | Leishmaniasis | RT | | 22 | 1.1 | 3.8E-4 | 2.3E-3 |
| | GOTERM_CC_DIRECT | F-actin capping_protein complex | RT | | 6 | 0.3 | 3.9E-4 | 4.7E-3 |
| | UP_SEQ_FEATURE | DISULFID:Redox-active | RT | | 15 | 0.7 | 3.9E-4 | 9.0E-2 |
| | GOTERM_BP_DIRECT | protein polyubiquitination | RT | | 32 | 1.6 | 3.9E-4 | 1.9E-2 |
| | INTERPRO | Atg8-like | RT | | 6 | 0.3 | 4.0E-4 | 6.3E-2 |
| | UP_KW_CELLULAR_COMPONENT | Proteasome | RT | | 16 | 0.8 | 4.0E-4 | 2.5E-3 |
| | GOTERM_BP_DIRECT | extrinsic apoptotic signaling pathway via death domain receptors | RT | | 13 | 0.6 | 4.1E-4 | 2.0E-2 |
| | GOTERM_MF_DIRECT | ubiquitin-protein transferase activity | RT | | 43 | 2.1 | 4.1E-4 | 1.4E-2 |
| | UP_SEQ_FEATURE | DOMAIN:RanBP2-type | RT | | 8 | 0.4 | 4.1E-4 | 9.0E-2 |
| | UP_SEQ_FEATURE | REPEAT:1-4 | RT | | 8 | 0.4 | 4.1E-4 | 9.0E-2 |
| | GOTERM_MF_DIRECT | double-stranded DNA binding | RT | | 25 | 1.2 | 4.2E-4 | 1.4E-2 |
| | SMART | DEXDc | RT | | 24 | 1.2 | 4.2E-4 | 2.9E-2 |
| | GOTERM_CC_DIRECT | transcription factor AP-1 complex | RT | | 5 | 0.2 | 4.2E-4 | 5.0E-3 |
| | INTERPRO | DEAD/DEAH_box_helicase_dom | RT | | 18 | 0.9 | 4.2E-4 | 6.4E-2 |
| | GOTERM_MF_DIRECT | small GTPase binding | RT | | 51 | 2.5 | 4.3E-4 | 1.5E-2 |
| | GOTERM_CC_DIRECT | CCR4-NOT complex | RT | | 8 | 0.4 | 4.4E-4 | 5.2E-3 |
| | GOTERM_BP_DIRECT | antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | RT | | 9 | 0.4 | 4.4E-4 | 2.0E-2 |
| | GOTERM_BP_DIRECT | late endosome to lysosome transport | RT | | 9 | 0.4 | 4.4E-4 | 2.0E-2 |
| | GOTERM_BP_DIRECT | barbed-end actin filament capping | RT | | 9 | 0.4 | 4.4E-4 | 2.0E-2 |
| | GOTERM_BP_DIRECT | positive regulation of ER-associated ubiquitin-dependent protein catabolic process | RT | | 6 | 0.3 | 4.5E-4 | 2.1E-2 |
| | GOTERM_BP_DIRECT | negative regulation of transcription from RNA polymerase I promoter | RT | | 6 | 0.3 | 4.5E-4 | 2.1E-2 |
| | GOTERM_BP_DIRECT | positive regulation of type I interferon production | RT | | 12 | 0.6 | 4.5E-4 | 2.1E-2 |
| | UP_SEQ_FEATURE | REGION:Self-association | RT | | 7 | 0.3 | 4.6E-4 | 9.7E-2 |
| | GOTERM_MF_DIRECT | double-stranded RNA binding | RT | | 19 | 0.9 | 4.6E-4 | 1.5E-2 |
| | INTERPRO | Translation_prot_SH3-like_sf | RT | | 8 | 0.4 | 4.6E-4 | 6.7E-2 |
| | BIOCARTA | T_Cytotoxic Cell Surface Molecules | RT | | 9 | 0.4 | 4.7E-4 | 1.8E-2 |
| | BIOCARTA | T_Helper Cell Surface Molecules | RT | | 9 | 0.4 | 4.7E-4 | 1.8E-2 |
| | GOTERM_BP_DIRECT | positive regulation of TORC1 signaling | RT | | 15 | 0.7 | 4.8E-4 | 2.1E-2 |
| | GOTERM_BP_DIRECT | negative regulation of protein ubiquitination | RT | | 16 | 0.8 | 4.9E-4 | 2.2E-2 |
| | GOTERM_CC_DIRECT | transport vesicle | RT | | 22 | 1.1 | 5.0E-4 | 5.9E-3 |
| | INTERPRO | Helicase_ATP-bd | RT | | 24 | 1.2 | 5.1E-4 | 7.2E-2 |
| | GOTERM_CC_DIRECT | postsynaptic density | RT | | 41 | 2.0 | 5.2E-4 | 6.0E-3 |
| | GOTERM_CC_DIRECT | retromer complex | RT | | 9 | 0.4 | 5.2E-4 | 6.0E-3 |
| | UP_SEQ_FEATURE | DOMAIN:RING-type | RT | | 37 | 1.8 | 5.3E-4 | 1.1E-1 |
| | GOTERM_BP_DIRECT | protein targeting to ER | RT | | 8 | 0.4 | 5.3E-4 | 2.3E-2 |
| | GOTERM_BP_DIRECT | peptide antigen assembly with MHC class II protein complex | RT | | 8 | 0.4 | 5.3E-4 | 2.3E-2 |
| | GOTERM_BP_DIRECT | protein K48-linked ubiquitination | RT | | 19 | 0.9 | 5.3E-4 | 2.3E-2 |
| | UP_KW_MOLECULAR_FUNCTION | rRNA-binding | RT | | 11 | 0.5 | 5.3E-4 | 5.8E-3 |
| | GOTERM_CC_DIRECT | tertiary granule membrane | RT | | 18 | 0.9 | 5.5E-4 | 6.2E-3 |
| | KEGG_PATHWAY | Autoimmune thyroid disease | RT | | 17 | 0.8 | 5.5E-4 | 3.2E-3 |
| | GOTERM_CC_DIRECT | membrane raft | RT | | 37 | 1.8 | 5.6E-4 | 6.2E-3 |
| | GOTERM_BP_DIRECT | cellular response to nitrogen starvation | RT | | 7 | 0.3 | 5.7E-4 | 2.4E-2 |
| | GOTERM_BP_DIRECT | negative thymic T cell selection | RT | | 7 | 0.3 | 5.7E-4 | 2.4E-2 |
| | UP_KW_BIOLOGICAL_PROCESS | Protein biosynthesis | RT | | 33 | 1.6 | 5.7E-4 | 4.3E-3 |
| | GOTERM_BP_DIRECT | platelet aggregation | RT | | 14 | 0.7 | 5.7E-4 | 2.4E-2 |
| | UP_KW_CELLULAR_COMPONENT | MHC II | RT | | 9 | 0.4 | 5.8E-4 | 3.2E-3 |
| | GOTERM_BP_DIRECT | tricarboxylic acid cycle | RT | | 12 | 0.6 | 5.9E-4 | 2.5E-2 |
| | UP_SEQ_FEATURE | DOMAIN:bZIP | RT | | 15 | 0.7 | 5.9E-4 | 1.2E-1 |
| | GOTERM_MF_DIRECT | misfolded protein binding | RT | | 9 | 0.4 | 6.0E-4 | 1.9E-2 |
| | GOTERM_CC_DIRECT | ficolin-1-rich granule membrane | RT | | 16 | 0.8 | 6.2E-4 | 6.8E-3 |
| | GOTERM_CC_DIRECT | cyclin-dependent protein kinase holoenzyme complex | RT | | 13 | 0.6 | 6.3E-4 | 6.9E-3 |
| | GOTERM_BP_DIRECT | signal transduction | RT | | 162 | 7.9 | 6.3E-4 | 2.6E-2 |
| | GOTERM_BP_DIRECT | mRNA splice site selection | RT | | 9 | 0.4 | 6.5E-4 | 2.7E-2 |
| | GOTERM_MF_DIRECT | RNA helicase activity | RT | | 19 | 0.9 | 6.5E-4 | 2.1E-2 |
| | GOTERM_BP_DIRECT | antigen processing and presentation of exogenous peptide antigen via MHC class II | RT | | 11 | 0.5 | 6.5E-4 | 2.7E-2 |
| | GOTERM_CC_DIRECT | mitochondrial nucleoid | RT | | 14 | 0.7 | 6.5E-4 | 7.0E-3 |
| | GOTERM_CC_DIRECT | nuclear matrix | RT | | 26 | 1.3 | 6.6E-4 | 7.0E-3 |
| | KEGG_PATHWAY | Citrate cycle (TCA cycle) | RT | | 12 | 0.6 | 6.6E-4 | 3.8E-3 |
| | GOTERM_MF_DIRECT | ribonucleoprotein complex binding | RT | | 12 | 0.6 | 6.6E-4 | 2.1E-2 |
| | GOTERM_BP_DIRECT | protein maturation | RT | | 13 | 0.6 | 6.7E-4 | 2.7E-2 |
| | GOTERM_CC_DIRECT | respiratory chain | RT | | 11 | 0.5 | 6.7E-4 | 7.1E-3 |
| | INTERPRO | Ubiquitin-like_dom | RT | | 16 | 0.8 | 6.7E-4 | 9.2E-2 |
| | SMART | ARF | RT | | 14 | 0.7 | 6.7E-4 | 4.1E-2 |
| | INTERPRO | bZIP_sf | RT | | 15 | 0.7 | 6.9E-4 | 9.2E-2 |
| | GOTERM_CC_DIRECT | cytoplasmic vesicle | RT | | 47 | 2.3 | 7.0E-4 | 7.3E-3 |
| | KEGG_PATHWAY | Spinocerebellar ataxia | RT | | 33 | 1.6 | 7.1E-4 | 4.0E-3 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----|-------|-------|-----|---------|-----------|
| | GOTERM_MF_DIRECT | GTPase activity | RT | | 58 | 2.8 | 7.3E-4 | 2.2E-2 |
| | GOTERM_CC_DIRECT | synapse | RT | | 73 | 3.6 | 7.5E-4 | 7.7E-3 |
| | GOTERM_CC_DIRECT | fibrillar center | RT | | 29 | 1.4 | 7.6E-4 | 7.7E-3 |
| | SMART | RAB | RT | | 30 | 1.5 | 7.6E-4 | 4.1E-2 |
| | UP_SEQ_FEATURE | DOMAIN:Serine/threonine specific protein phosphatases | RT | | 7 | 0.3 | 7.8E-4 | 1.5E-1 |
| | GOTERM_CC_DIRECT | MHC class I protein complex | RT | | 6 | 0.3 | 8.0E-4 | 8.0E-3 |
| | GOTERM_CC_DIRECT | nuclear telomere cap complex | RT | | 6 | 0.3 | 8.0E-4 | 8.0E-3 |
| | UP_SEQ_FEATURE | ZN_FING:C4-type | RT | | 16 | 0.8 | 8.2E-4 | 1.6E-1 |
| | GOTERM_MF_DIRECT | protein phosphatase binding | RT | | 21 | 1.0 | 8.2E-4 | 2.4E-2 |
| | GOTERM_BP_DIRECT | regulation of mitotic cell cycle | RT | | 17 | 0.8 | 8.3E-4 | 3.4E-2 |
| | INTERPRO | bZIP | RT | | 15 | 0.7 | 8.4E-4 | 1.1E-1 |
| | KEGG_PATHWAY | Pancreatic cancer | RT | | 21 | 1.0 | 8.6E-4 | 4.8E-3 |
| | UP_SEQ_FEATURE | MOTIF:Prevents secretion from ER | RT | | 15 | 0.7 | 8.7E-4 | 1.7E-1 |
| | GOTERM_BP_DIRECT | mRNA transcription from RNA polymerase II promoter | RT | | 14 | 0.7 | 8.7E-4 | 3.5E-2 |
| | GOTERM_BP_DIRECT | cellular response to heat | RT | | 15 | 0.7 | 8.8E-4 | 3.5E-2 |
| | GOTERM_BP_DIRECT | response to organic substance | RT | | 10 | 0.5 | 9.2E-4 | 3.6E-2 |
| | GOTERM_BP_DIRECT | protein modification process | RT | | 25 | 1.2 | 9.2E-4 | 3.6E-2 |
| | GOTERM_BP_DIRECT | negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | RT | | 9 | 0.4 | 9.3E-4 | 3.6E-2 |
| | GOTERM_BP_DIRECT | alpha-beta T cell activation | RT | | 6 | 0.3 | 9.3E-4 | 3.6E-2 |
| | GOTERM_BP_DIRECT | regulation of necroptotic process | RT | | 6 | 0.3 | 9.3E-4 | 3.6E-2 |
| | KEGG_PATHWAY | Rheumatoid arthritis | RT | | 24 | 1.2 | 9.4E-4 | 5.1E-3 |
| | UP_SEQ_FEATURE | TRANSIT:Mitochondrion | RT | | 78 | 3.8 | 9.6E-4 | 1.8E-1 |
| | UP_SEQ_FEATURE | REPEAT:1-3 | RT | | 8 | 0.4 | 9.7E-4 | 1.8E-1 |
| | UP_KW_CELLULAR_COMPONENT | Cytoskeleton | RT | | 185 | 9.0 | 9.8E-4 | 5.0E-3 |
| | GOTERM_BP_DIRECT | aerobic respiration | RT | | 17 | 0.8 | 9.8E-4 | 3.8E-2 |
| | UP_SEQ_FEATURE | DOMAIN:Helicase ATP-binding | RT | | 24 | 1.2 | 9.9E-4 | 1.8E-1 |
| | UP_SEQ_FEATURE | REPEAT:WD 6 | RT | | 42 | 2.0 | 1.0E-3 | 1.8E-1 |
| | GOTERM_MF_DIRECT | chromatin DNA binding | RT | | 20 | 1.0 | 1.0E-3 | 2.9E-2 |
| | INTERPRO | Longin-like_dom_sf | RT | | 10 | 0.5 | 1.0E-3 | 1.3E-1 |
| | KEGG_PATHWAY | Proteasome | RT | | 15 | 0.7 | 1.1E-3 | 5.9E-3 |
| | INTERPRO | Znf_RanBP2_sf | RT | | 9 | 0.4 | 1.1E-3 | 1.3E-1 |
| | INTERPRO | Rib_uL2_dom2 | RT | | 9 | 0.4 | 1.1E-3 | 1.3E-1 |
| | GOTERM_MF_DIRECT | GTPase binding | RT | | 12 | 0.6 | 1.1E-3 | 3.2E-2 |
| | UP_KW_CELLULAR_COMPONENT | MHC I | RT | | 6 | 0.3 | 1.1E-3 | 5.2E-3 |
| | UP_KW_LIGAND | GTP-binding | RT | | 58 | 2.8 | 1.1E-3 | 2.3E-2 |
| | UP_SEQ_FEATURE | DOMAIN:DUSP | RT | | 5 | 0.2 | 1.1E-3 | 1.9E-1 |
| | UP_SEQ_FEATURE | MOTIF:MIT-interacting motif | RT | | 5 | 0.2 | 1.1E-3 | 1.9E-1 |
| | GOTERM_CC_DIRECT | nuclear inner membrane | RT | | 15 | 0.7 | 1.1E-3 | 1.1E-2 |
| | UP_KW_DOMAIN | WD repeat | RT | | 42 | 2.0 | 1.1E-3 | 7.1E-3 |
| | GOTERM_MF_DIRECT | ubiquitin protein ligase activity | RT | | 57 | 2.8 | 1.2E-3 | 3.2E-2 |
| | GOTERM_CC_DIRECT | CRD-mediated mRNA stability complex | RT | | 5 | 0.2 | 1.2E-3 | 1.1E-2 |
| | GOTERM_CC_DIRECT | chromosome | RT | | 42 | 2.0 | 1.2E-3 | 1.1E-2 |
| | GOTERM_MF_DIRECT | histone binding | RT | | 36 | 1.8 | 1.2E-3 | 3.3E-2 |
| | BIOCARTA | IL_2_signaling_pathway | RT | | 12 | 0.6 | 1.2E-3 | 4.1E-2 |
| | KEGG_PATHWAY | Apoptosis - multiple species | RT | | 12 | 0.6 | 1.2E-3 | 6.5E-3 |
| | GOTERM_BP_DIRECT | regulation of mRNA processing | RT | | 8 | 0.4 | 1.2E-3 | 4.6E-2 |
| | GOTERM_BP_DIRECT | regulation of mRNA splicing, via spliceosome | RT | | 8 | 0.4 | 1.2E-3 | 4.6E-2 |
| | GOTERM_BP_DIRECT | translational elongation | RT | | 8 | 0.4 | 1.2E-3 | 4.6E-2 |
| | GOTERM_BP_DIRECT | T cell differentiation in thymus | RT | | 12 | 0.6 | 1.2E-3 | 4.6E-2 |
| | GOTERM_MF_DIRECT | NADH dehydrogenase (ubiquinone) activity | RT | | 13 | 0.6 | 1.2E-3 | 3.4E-2 |
| | GOTERM_CC_DIRECT | axon cytoplasm | RT | | 16 | 0.8 | 1.3E-3 | 1.2E-2 |
| | GOTERM_BP_DIRECT | positive regulation of apoptotic process | RT | | 51 | 2.5 | 1.3E-3 | 4.7E-2 |
| | GOTERM_BP_DIRECT | regulation of macroautophagy | RT | | 15 | 0.7 | 1.3E-3 | 4.7E-2 |
| | UP_KW_CELLULAR_COMPONENT | Chromosome | RT | | 90 | 4.4 | 1.3E-3 | 5.5E-3 |
| | UP_KW_BIOLOGICAL_PROCESS | Tricarboxylic acid cycle | RT | | 10 | 0.5 | 1.3E-3 | 9.2E-3 |
| | GOTERM_BP_DIRECT | vacuolar acidification | RT | | 9 | 0.4 | 1.3E-3 | 4.7E-2 |
| | GOTERM_CC_DIRECT | oligosaccharyltransferase complex | RT | | 7 | 0.3 | 1.3E-3 | 1.2E-2 |
| | GOTERM_CC_DIRECT | amphisome membrane | RT | | 7 | 0.3 | 1.3E-3 | 1.2E-2 |
| | GOTERM_BP_DIRECT | negative regulation of RNA splicing | RT | | 5 | 0.2 | 1.3E-3 | 4.7E-2 |
| | GOTERM_BP_DIRECT | chaperone-mediated autophagy | RT | | 5 | 0.2 | 1.3E-3 | 4.7E-2 |
| | GOTERM_CC_DIRECT | spindle | RT | | 28 | 1.4 | 1.3E-3 | 1.2E-2 |
| | SMART | PP2Ac | RT | | 7 | 0.3 | 1.3E-3 | 6.5E-2 |
| | INTERPRO | P-loop_NTPase | RT | | 119 | 5.8 | 1.3E-3 | 1.4E-1 |
| | INTERPRO | Ser/Thr-sp_prot-phosphatase | RT | | 7 | 0.3 | 1.4E-3 | 1.4E-1 |
| | INTERPRO | Snf7_fam | RT | | 7 | 0.3 | 1.4E-3 | 1.4E-1 |
| | INTERPRO | HSP70_C_sf | RT | | 7 | 0.3 | 1.4E-3 | 1.4E-1 |
| | GOTERM_CC_DIRECT | mitotic spindle | RT | | 27 | 1.3 | 1.4E-3 | 1.3E-2 |
| | KEGG_PATHWAY | Pathogenic Escherichia coli infection | RT | | 41 | 2.0 | 1.4E-3 | 7.4E-3 |
| | GOTERM_BP_DIRECT | positive regulation of erythrocyte differentiation | RT | | 11 | 0.5 | 1.4E-3 | 5.2E-2 |
| | GOTERM_BP_DIRECT | rhythmic process | RT | | 18 | 0.9 | 1.5E-3 | 5.2E-2 |
| | UP_SEQ_FEATURE | ZN_FING:C3H1-type | RT | | 15 | 0.7 | 1.5E-3 | 2.5E-1 |
| | SMART | BRLZ | RT | | 14 | 0.7 | 1.5E-3 | 6.6E-2 |
| | GOTERM_BP_DIRECT | protein dephosphorylation | RT | | 24 | 1.2 | 1.5E-3 | 5.3E-2 |
| | GOTERM_BP_DIRECT | maintenance of protein location in nucleus | RT | | 7 | 0.3 | 1.5E-3 | 5.4E-2 |
| | UP_KW_MOLECULAR_FUNCTION | Helicase | RT | | 29 | 1.4 | 1.5E-3 | 1.5E-2 |
| | UP_SEQ_FEATURE | REPEAT:WD | RT | | 36 | 1.8 | 1.6E-3 | 2.6E-1 |
| | GOTERM_MF_DIRECT | hydrolase activity | RT | | 47 | 2.3 | 1.6E-3 | 4.2E-2 |
| | BIOCARTA | Antigen Processing_and Presentation | RT | | 8 | 0.4 | 1.7E-3 | 4.9E-2 |
| | GOTERM_CC_DIRECT | mitochondrial inner membrane | RT | | 70 | 3.4 | 1.7E-3 | 1.5E-2 |
| | GOTERM_BP_DIRECT | mitochondrial fragmentation involved in apoptotic process | RT | | 6 | 0.3 | 1.7E-3 | 5.9E-2 |
| | GOTERM_BP_DIRECT | Golgi lumen acidification | RT | | 6 | 0.3 | 1.7E-3 | 5.9E-2 |
| | UP_SEQ_FEATURE | REPEAT:WD 5 | RT | | 42 | 2.0 | 1.7E-3 | 2.7E-1 |
| | KEGG_PATHWAY | Renal cell carcinoma | RT | | 19 | 0.9 | 1.7E-3 | 8.7E-3 |
| | GOTERM_BP_DIRECT | cellular response to interleukin-4 | RT | | 9 | 0.4 | 1.8E-3 | 6.0E-2 |
| | GOTERM_BP_DIRECT | cellular response to glucocorticoid stimulus | RT | | 9 | 0.4 | 1.8E-3 | 6.0E-2 |
| | GOTERM_BP_DIRECT | 3'-UTR-mediated mRNA destabilization | RT | | 8 | 0.4 | 1.8E-3 | 6.0E-2 |
| | KEGG_PATHWAY | Colorectal cancer | RT | | 22 | 1.1 | 1.8E-3 | 9.1E-3 |
| | GOTERM_BP_DIRECT | positive regulation of transcription initiation from RNA polymerase II promoter | RT | | 15 | 0.7 | 1.8E-3 | 6.2E-2 |
| | KEGG_PATHWAY | Cell cycle | RT | | 34 | 1.7 | 1.8E-3 | 9.1E-3 |
| | UP_SEQ_FEATURE | REPEAT:1-2 | RT | | 9 | 0.4 | 1.8E-3 | 2.9E-1 |
| | GOTERM_BP_DIRECT | positive regulation of telomere maintenance via telomerase | RT | | 11 | 0.5 | 1.8E-3 | 6.2E-2 |
| | UP_SEQ_FEATURE | DOMAIN:ARID | RT | | 7 | 0.3 | 1.9E-3 | 2.9E-1 |
| | GOTERM_BP_DIRECT | extrinsic apoptotic signaling pathway | RT | | 14 | 0.7 | 1.9E-3 | 6.3E-2 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----|-------|-------|-----|---------|-----------|
| | GOTERM_BP_DIRECT | T cell differentiation | RT | | 12 | 0.6 | 1.9E-3 | 6.3E-2 |
| | GOTERM_BP_DIRECT | regulation of mRNA stability | RT | | 12 | 0.6 | 1.9E-3 | 6.3E-2 |
| | GOTERM_BP_DIRECT | protein localization to nucleus | RT | | 12 | 0.6 | 1.9E-3 | 6.3E-2 |
| | GOTERM_BP_DIRECT | response to cytokine | RT | | 13 | 0.6 | 2.0E-3 | 6.3E-2 |
| | GOTERM_BP_DIRECT | positive regulation of protein kinase activity | RT | | 13 | 0.6 | 2.0E-3 | 6.3E-2 |
| | SMART | ARID | RT | | 7 | 0.3 | 2.0E-3 | 7.0E-2 |
| | SMART | BRIGHT | RT | | 7 | 0.3 | 2.0E-3 | 7.0E-2 |
| | INTERPRO | Znf_RanBP2 | RT | | 9 | 0.4 | 2.0E-3 | 1.9E-1 |
| | KEGG_PATHWAY | NF-kappa B signaling pathway | RT | | 25 | 1.2 | 2.0E-3 | 1.0E-2 |
| | INTERPRO | ARID_dom_sf | RT | | 7 | 0.3 | 2.1E-3 | 1.9E-1 |
| | INTERPRO | ARID_dom | RT | | 7 | 0.3 | 2.1E-3 | 1.9E-1 |
| | UP_SEQ_FEATURE | REPEAT:WD 4 | RT | | 42 | 2.0 | 2.1E-3 | 3.2E-1 |
| | GOTERM_BP_DIRECT | natural killer cell mediated cytotoxicity | RT | | 10 | 0.5 | 2.1E-3 | 6.8E-2 |
| | GOTERM_BP_DIRECT | telomere maintenance | RT | | 15 | 0.7 | 2.2E-3 | 6.9E-2 |
| | SMART | RHO | RT | | 25 | 1.2 | 2.2E-3 | 7.0E-2 |
| | GOTERM_CC_DIRECT | multivesicular body membrane | RT | | 10 | 0.5 | 2.2E-3 | 2.0E-2 |
| | UP_KW_CELLULAR_COMPONENT | Cyttoplasmic vesicle | RT | | 103 | 5.0 | 2.2E-3 | 8.9E-3 |
| | UP_SEQ_FEATURE | REGION:Basic motif | RT | | 14 | 0.7 | 2.3E-3 | 3.3E-1 |
| | GOTERM_MF_DIRECT | enzyme activator activity | RT | | 16 | 0.8 | 2.3E-3 | 5.9E-2 |
| | INTERPRO | Znf_RING | RT | | 48 | 2.3 | 2.3E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | regulation of cellular response to heat | RT | | 7 | 0.3 | 2.3E-3 | 7.4E-2 |
| | GOTERM_CC_DIRECT | vesicle | RT | | 31 | 1.5 | 2.4E-3 | 2.1E-2 |
| | UP_SEQ_FEATURE | DOMAIN:ADF-H | RT | | 6 | 0.3 | 2.4E-3 | 3.3E-1 |
| | UP_SEQ_FEATURE | TOPO_DOM:Mitochondrial intermembrane | RT | | 26 | 1.3 | 2.4E-3 | 3.3E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Chromosome partition | RT | | 14 | 0.7 | 2.4E-3 | 1.6E-2 |
| | GOTERM_BP_DIRECT | protein import into nucleus | RT | | 21 | 1.0 | 2.4E-3 | 7.6E-2 |
| | UP_SEQ_FEATURE | DOMAIN:STAT transcription factor protein interaction | RT | | 5 | 0.2 | 2.4E-3 | 3.3E-1 |
| | UP_SEQ_FEATURE | SITE:Cleavage; by ATG4B | RT | | 5 | 0.2 | 2.4E-3 | 3.3E-1 |
| | UP_SEQ_FEATURE | REPEAT:WD 3 | RT | | 42 | 2.0 | 2.4E-3 | 3.3E-1 |
| | UP_SEQ_FEATURE | REPEAT:1-1 | RT | | 9 | 0.4 | 2.4E-3 | 3.3E-1 |
| | UP_SEQ_FEATURE | ZN_FING:PHD-type | RT | | 13 | 0.6 | 2.5E-3 | 3.3E-1 |
| | GOTERM_CC_DIRECT | cytolytic granule | RT | | 6 | 0.3 | 2.5E-3 | 2.2E-2 |
| | GOTERM_CC_DIRECT | ESCRT III complex | RT | | 6 | 0.3 | 2.5E-3 | 2.2E-2 |
| | GOTERM_BP_DIRECT | protein localization to Golgi apparatus | RT | | 8 | 0.4 | 2.5E-3 | 7.8E-2 |
| | GOTERM_BP_DIRECT | positive regulation of proteolysis | RT | | 8 | 0.4 | 2.5E-3 | 7.8E-2 |
| | GOTERM_CC_DIRECT | PTW/PP1 phosphatase complex | RT | | 5 | 0.2 | 2.5E-3 | 2.2E-2 |
| | SMART | ADF | RT | | 6 | 0.3 | 2.5E-3 | 7.0E-2 |
| | SMART | STAT_int | RT | | 5 | 0.2 | 2.5E-3 | 7.0E-2 |
| | SMART | MHC_II_alpha | RT | | 5 | 0.2 | 2.5E-3 | 7.0E-2 |
| | GOTERM_BP_DIRECT | negative regulation of autophagy | RT | | 15 | 0.7 | 2.6E-3 | 7.9E-2 |
| | INTERPRO | KOW | RT | | 6 | 0.3 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | Ribosomal_eL8/eL30/eS12/Gad45 | RT | | 6 | 0.3 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | ADF-H | RT | | 6 | 0.3 | 2.6E-3 | 1.9E-1 |
| | UP_KW_PTM | S-nitrosylation | RT | | 17 | 0.8 | 2.6E-3 | 1.1E-2 |
| | INTERPRO | MHC_II_a_N | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_TF_prot_interaction | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_TF_coiled-coil | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_N_sf | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | Pept_C19_DUSP | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_TF_alpha | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_linker | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | DUSP-like_sf | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_TF_DNA-bd | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | INTERPRO | STAT_TF_DNA-bd_N | RT | | 5 | 0.2 | 2.6E-3 | 1.9E-1 |
| | SMART | RING | RT | | 41 | 2.0 | 2.6E-3 | 7.0E-2 |
| | GOTERM_MF_DIRECT | protein phosphatase regulator activity | RT | | 11 | 0.5 | 2.6E-3 | 6.6E-2 |
| | GOTERM_CC_DIRECT | U2-type precatalytic spliceosome | RT | | 13 | 0.6 | 2.6E-3 | 2.3E-2 |
| | GOTERM_BP_DIRECT | MAPK cascade | RT | | 23 | 1.1 | 2.7E-3 | 8.2E-2 |
| | GOTERM_CC_DIRECT | lysosomal lumen | RT | | 20 | 1.0 | 2.8E-3 | 2.4E-2 |
| | GOTERM_BP_DIRECT | endocytic recycling | RT | | 16 | 0.8 | 2.8E-3 | 8.4E-2 |
| | GOTERM_MF_DIRECT | estrogen receptor binding | RT | | 12 | 0.6 | 2.8E-3 | 6.9E-2 |
| | GOTERM_MF_DIRECT | protein serine/threonine phosphatase activity | RT | | 15 | 0.7 | 2.8E-3 | 6.9E-2 |
| | GOTERM_BP_DIRECT | interleukin-9-mediated signaling_pathway | RT | | 5 | 0.2 | 2.8E-3 | 8.4E-2 |
| | KEGG_PATHWAY | Non-small cell lung cancer | RT | | 19 | 0.9 | 2.8E-3 | 1.4E-2 |
| | GOTERM_BP_DIRECT | cotranslational protein targeting to membrane | RT | | 6 | 0.3 | 2.9E-3 | 8.4E-2 |
| | GOTERM_BP_DIRECT | positive regulation of RIG-I signaling_pathway | RT | | 6 | 0.3 | 2.9E-3 | 8.4E-2 |
| | GOTERM_BP_DIRECT | interleukin-15-mediated signaling_pathway | RT | | 6 | 0.3 | 2.9E-3 | 8.4E-2 |
| | GOTERM_BP_DIRECT | retrograde axonal transport | RT | | 6 | 0.3 | 2.9E-3 | 8.4E-2 |
| | GOTERM_BP_DIRECT | intracellular transport | RT | | 13 | 0.6 | 2.9E-3 | 8.4E-2 |
| | INTERPRO | p53-like_TF_DNA-bd_sf | RT | | 12 | 0.6 | 3.0E-3 | 2.2E-1 |
| | GOTERM_MF_DIRECT | pre-mRNA binding | RT | | 7 | 0.3 | 3.0E-3 | 7.2E-2 |
| | UP_KW_DISEASE | Parkinsonism | RT | | 13 | 0.6 | 3.0E-3 | 7.5E-2 |
| | BIOCARTA | Stathmin and breast cancer resistance to antimicrotubule agents | RT | | 12 | 0.6 | 3.0E-3 | 7.9E-2 |
| | SMART | PINT | RT | | 7 | 0.3 | 3.0E-3 | 7.5E-2 |
| | KEGG_PATHWAY | Yersinia infection | RT | | 30 | 1.5 | 3.0E-3 | 1.4E-2 |
| | GOTERM_BP_DIRECT | chromosome segregation | RT | | 20 | 1.0 | 3.1E-3 | 9.0E-2 |
| | SMART | RAS | RT | | 26 | 1.3 | 3.1E-3 | 7.5E-2 |
| | GOTERM_MF_DIRECT | K63-linked polyubiquitin binding | RT | | 9 | 0.4 | 3.2E-3 | 7.4E-2 |
| | GOTERM_MF_DIRECT | R-SMAD binding | RT | | 9 | 0.4 | 3.2E-3 | 7.4E-2 |
| | GOTERM_BP_DIRECT | I-kappaB kinase/NF-kappaB_signaling | RT | | 16 | 0.8 | 3.2E-3 | 9.4E-2 |
| | GOTERM_MF_DIRECT | RNA_polymerase_binding | RT | | 8 | 0.4 | 3.2E-3 | 7.4E-2 |
| | GOTERM_MF_DIRECT | polyubiquitin binding | RT | | 11 | 0.5 | 3.2E-3 | 7.4E-2 |
| | BIOCARTA | Rab GTPases Mark Targets In The Endocytic Machinery | RT | | 8 | 0.4 | 3.3E-3 | 8.0E-2 |
| | GOTERM_MF_DIRECT | disulfide oxidoreductase activity | RT | | 5 | 0.2 | 3.3E-3 | 7.5E-2 |
| | GOTERM_CC_DIRECT | histone acetyltransferase complex | RT | | 9 | 0.4 | 3.3E-3 | 2.9E-2 |
| | UP_SEQ_FEATURE | REGION:Interaction with VTA1 | RT | | 4 | 0.2 | 3.4E-3 | 4.4E-1 |
| | UP_SEQ_FEATURE | REGION:Interaction with Elongin BC complex | RT | | 4 | 0.2 | 3.4E-3 | 4.4E-1 |
| | GOTERM_BP_DIRECT | positive regulation of transcription elongation from RNA polymerase II_promoter | RT | | 13 | 0.6 | 3.4E-3 | 9.9E-2 |
| | GOTERM_BP_DIRECT | ribosomal large subunit assembly | RT | | 8 | 0.4 | 3.4E-3 | 9.9E-2 |
| | GOTERM_BP_DIRECT | positive regulation of B cell differentiation | RT | | 7 | 0.3 | 3.4E-3 | 9.9E-2 |
| | GOTERM_MF_DIRECT | GTP_binding | RT | | 62 | 3.0 | 3.4E-3 | 7.6E-2 |
| | GOTERM_CC_DIRECT | cytolytic granule membrane | RT | | 4 | 0.2 | 3.5E-3 | 2.9E-2 |
| | GOTERM_CC_DIRECT | ASAP complex | RT | | 4 | 0.2 | 3.5E-3 | 2.9E-2 |

| Sublist | Category | Term | RT Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----------|-------|------|---------|-----------|
| | GOTERM_BP_DIRECT | lysosome localization | RT | 10 | 0.5 | 3.5E-3 | 9.9E-2 |
| | GOTERM_CC_DIRECT | clathrin-coated vesicle membrane | RT | 10 | 0.5 | 3.5E-3 | 2.9E-2 |
| | GOTERM_CC_DIRECT | phagocytic vesicle | RT | 16 | 0.8 | 3.6E-3 | 3.0E-2 |
| | GOTERM_CC_DIRECT | mitochondrial respiratory chain complex I | RT | 13 | 0.6 | 3.7E-3 | 3.1E-2 |
| | UP_SEQ_FEATURE | COMPBIAS:Polar residues | RT | 725 | 35.3 | 3.7E-3 | 4.7E-1 |
| | UP_SEQ_FEATURE | CARBOHYD:(Microbial infection) N-beta-linked (GlcNAc) arginine | RT | 6 | 0.3 | 3.8E-3 | 4.7E-1 |
| | GOTERM_BP_DIRECT | negative regulation of mitotic cell cycle phase transition | RT | 4 | 0.2 | 3.8E-3 | 1.1E-1 |
| | UP_KW_MOLECULAR_FUNCTION | Thiol_protease | RT | 28 | 1.4 | 3.9E-3 | 3.4E-2 |
| | UP_SEQ_FEATURE | DOMAIN:TNFR-Cys | RT | 7 | 0.3 | 4.0E-3 | 4.9E-1 |
| | INTERPRO | Chaperone_TCP-1 | RT | 6 | 0.3 | 4.0E-3 | 2.9E-1 |
| | GOTERM_BP_DIRECT | negative regulation of T cell receptor signaling pathway | RT | 9 | 0.4 | 4.1E-3 | 1.1E-1 |
| | GOTERM_BP_DIRECT | protein refolding | RT | 9 | 0.4 | 4.1E-3 | 1.1E-1 |
| | GOTERM_MF_DIRECT | transcription corepressor activity | RT | 35 | 1.7 | 4.1E-3 | 8.8E-2 |
| | UP_SEQ_FEATURE | REPEAT:WD 1 | RT | 42 | 2.0 | 4.1E-3 | 5.0E-1 |
| | UP_SEQ_FEATURE | REPEAT:WD 2 | RT | 42 | 2.0 | 4.1E-3 | 5.0E-1 |
| | GOTERM_MF_DIRECT | SMAD binding | RT | 13 | 0.6 | 4.1E-3 | 8.8E-2 |
| | GOTERM_CC_DIRECT | proteasome accessory complex | RT | 7 | 0.3 | 4.1E-3 | 3.4E-2 |
| | GOTERM_MF_DIRECT | androgen receptor binding | RT | 9 | 0.4 | 4.1E-3 | 8.8E-2 |
| | GOTERM_CC_DIRECT | mitochondrial matrix | RT | 58 | 2.8 | 4.2E-3 | 3.4E-2 |
| | GOTERM_BP_DIRECT | mitotic spindle assembly | RT | 12 | 0.6 | 4.3E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | Lys63-specific deubiquitinase activity | RT | 7 | 0.3 | 4.3E-3 | 9.0E-2 |
| | GOTERM_BP_DIRECT | intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | RT | 10 | 0.5 | 4.4E-3 | 1.2E-1 |
| | GOTERM_BP_DIRECT | membrane fusion | RT | 10 | 0.5 | 4.4E-3 | 1.2E-1 |
| | KEGG_PATHWAY | Ferroptosis | RT | 13 | 0.6 | 4.4E-3 | 2.1E-2 |
| | INTERPRO | NA-bd_OB-fold | RT | 19 | 0.9 | 4.4E-3 | 3.1E-1 |
| | GOTERM_BP_DIRECT | negative regulation of tyrosine phosphorylation of STAT protein | RT | 6 | 0.3 | 4.5E-3 | 1.2E-1 |
| | GOTERM_BP_DIRECT | protein insertion into ER membrane | RT | 6 | 0.3 | 4.5E-3 | 1.2E-1 |
| | GOTERM_BP_DIRECT | late endosome to vacuole transport via multivesicular body sorting pathway | RT | 6 | 0.3 | 4.5E-3 | 1.2E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Stress response | RT | 24 | 1.2 | 4.6E-3 | 3.0E-2 |
| | GOTERM_MF_DIRECT | kinase binding | RT | 21 | 1.0 | 4.6E-3 | 9.4E-2 |
| | GOTERM_BP_DIRECT | telomere maintenance via telomerase | RT | 8 | 0.4 | 4.6E-3 | 1.2E-1 |
| | UP_KW_DISEASE | Proto-oncogene | RT | 43 | 2.1 | 4.7E-3 | 9.4E-2 |
| | SMART | WD40 | RT | 42 | 2.0 | 4.7E-3 | 1.0E-1 |
| | UP_SEQ_FEATURE | TOPO_DOM:Mitochondrial matrix | RT | 19 | 0.9 | 4.7E-3 | 5.6E-1 |
| | SMART | Znf_AN1 | RT | 5 | 0.2 | 4.7E-3 | 1.0E-1 |
| | INTERPRO | AN1-like_Znf | RT | 5 | 0.2 | 4.7E-3 | 3.2E-1 |
| | INTERPRO | Znf_AN1 | RT | 5 | 0.2 | 4.7E-3 | 3.2E-1 |
| | GOTERM_BP_DIRECT | regulation of T cell proliferation | RT | 7 | 0.3 | 4.9E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | positive regulation of ERAD pathway | RT | 7 | 0.3 | 4.9E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | vesicle transport along microtubule | RT | 7 | 0.3 | 4.9E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | nuclear migration | RT | 7 | 0.3 | 4.9E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | cellular response to unfolded protein | RT | 7 | 0.3 | 4.9E-3 | 1.3E-1 |
| | GOTERM_CC_DIRECT | kinetochore microtubule | RT | 8 | 0.4 | 5.1E-3 | 4.1E-2 |
| | INTERPRO | MHC_I/II-like_Ag-recog | RT | 12 | 0.6 | 5.1E-3 | 3.4E-1 |
| | GOTERM_BP_DIRECT | interleukin-2-mediated signaling pathway | RT | 5 | 0.2 | 5.2E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | posttranslational protein targeting to membrane, translocation | RT | 5 | 0.2 | 5.2E-3 | 1.3E-1 |
| | KEGG_PATHWAY | Ubiquitin mediated proteolysis | RT | 30 | 1.5 | 5.2E-3 | 2.4E-2 |
| | GOTERM_BP_DIRECT | NIK/NF-kappaB signaling | RT | 9 | 0.4 | 5.2E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | protein targeting to mitochondrion | RT | 9 | 0.4 | 5.2E-3 | 1.3E-1 |
| | SMART | TNFR | RT | 8 | 0.4 | 5.2E-3 | 1.1E-1 |
| | KEGG_PATHWAY | Chronic myeloid leukemia | RT | 19 | 0.9 | 5.3E-3 | 2.4E-2 |
| | GOTERM_BP_DIRECT | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | RT | 11 | 0.5 | 5.3E-3 | 1.4E-1 |
| | GOTERM_BP_DIRECT | cellular response to leukemia inhibitory factor | RT | 21 | 1.0 | 5.4E-3 | 1.4E-1 |
| | GOTERM_BP_DIRECT | regulation of mitochondrial membrane potential | RT | 10 | 0.5 | 5.4E-3 | 1.4E-1 |
| | INTERPRO | WD40 rpt | RT | 42 | 2.0 | 5.4E-3 | 3.6E-1 |
| | BIOCARTA | HIV Induced T Cell Apoptosis | RT | 7 | 0.3 | 5.6E-3 | 1.2E-1 |
| | UP_KW_DISEASE | Neurodegeneration | RT | 69 | 3.4 | 5.8E-3 | 9.7E-2 |
| | GOTERM_CC_DIRECT | alpha-beta T cell receptor complex | RT | 6 | 0.3 | 5.8E-3 | 4.6E-2 |
| | GOTERM_MF_DIRECT | Hsp70 protein binding | RT | 13 | 0.6 | 5.9E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | receptor signaling complex scaffold activity | RT | 10 | 0.5 | 5.9E-3 | 1.2E-1 |
| | GOTERM_BP_DIRECT | regulation of cell proliferation | RT | 26 | 1.3 | 5.9E-3 | 1.5E-1 |
| | BIOCARTA | D4-GDI Signaling Pathway | RT | 8 | 0.4 | 6.0E-3 | 1.2E-1 |
| | INTERPRO | HSP70_peptide-bd_sf | RT | 6 | 0.3 | 6.0E-3 | 3.9E-1 |
| | GOTERM_MF_DIRECT | phosphatidylethanolamine binding | RT | 7 | 0.3 | 6.1E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | myosin V binding | RT | 7 | 0.3 | 6.1E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | CD4 receptor binding | RT | 5 | 0.2 | 6.1E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | actin filament binding | RT | 36 | 1.8 | 6.2E-3 | 1.2E-1 |
| | GOTERM_MF_DIRECT | macromolecular complex binding | RT | 51 | 2.5 | 6.2E-3 | 1.2E-1 |
| | SMART | BROMO | RT | 11 | 0.5 | 6.4E-3 | 1.3E-1 |
| | GOTERM_BP_DIRECT | transcription from RNA polymerase II promoter | RT | 38 | 1.9 | 6.4E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | ribosome biogenesis | RT | 11 | 0.5 | 6.4E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | cellular respiration | RT | 11 | 0.5 | 6.4E-3 | 1.6E-1 |
| | UP_SEQ_FEATURE | REPEAT:TPR | RT | 19 | 0.9 | 6.5E-3 | 7.7E-1 |
| | GOTERM_BP_DIRECT | negative regulation of innate immune response | RT | 9 | 0.4 | 6.6E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | cellular response to interferon-beta | RT | 9 | 0.4 | 6.6E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | protein sumoylation | RT | 13 | 0.6 | 6.6E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | centrosome localization | RT | 7 | 0.3 | 6.7E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | positive regulation of T cell receptor signaling pathway | RT | 7 | 0.3 | 6.7E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | positive thymic T cell selection | RT | 6 | 0.3 | 6.7E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | interferon-gamma-mediated signaling pathway | RT | 6 | 0.3 | 6.7E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | positive regulation of nuclear-transcribed mRNA poly(A) tail shortening | RT | 6 | 0.3 | 6.7E-3 | 1.6E-1 |
| | GOTERM_CC_DIRECT | organelle membrane | RT | 9 | 0.4 | 6.8E-3 | 5.3E-2 |
| | GOTERM_MF_DIRECT | translation initiation factor binding | RT | 9 | 0.4 | 6.8E-3 | 1.3E-1 |
| | INTERPRO | G-protein_beta_WD-40_rep | RT | 19 | 0.9 | 6.9E-3 | 4.4E-1 |
| | UP_KW_LIGAND | Ubiquinone | RT | 10 | 0.5 | 7.0E-3 | 9.3E-2 |
| | GOTERM_BP_DIRECT | RNA_polymerase_II_transcriptional_preinitiation_complex_assembly | RT | 14 | 0.7 | 7.0E-3 | 1.7E-1 |
| | UP_KW_DOMAIN | Bromodomain | RT | 10 | 0.5 | 7.0E-3 | 3.6E-2 |
| | GOTERM_CC_DIRECT | tertiary_granule_lumen | RT | 13 | 0.6 | 7.0E-3 | 5.4E-2 |
| | GOTERM_BP_DIRECT | negative regulation of transcription from RNA polymerase II promoter | RT | 127 | 6.2 | 7.0E-3 | 1.7E-1 |
| | GOTERM_CC_DIRECT | autophagosome | RT | 16 | 0.8 | 7.0E-3 | 5.4E-2 |
| | GOTERM_CC_DIRECT | early_endosome_membrane | RT | 32 | 1.6 | 7.2E-3 | 5.6E-2 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----|-------|-------|------|---------|-----------|
| | GOTERM_BP_DIRECT | substantia nigra development | RT | | 12 | 0.6 | 7.2E-3 | 1.7E-1 |
| | INTERPRO | Small_GTPase | RT | | 25 | 1.2 | 7.2E-3 | 4.6E-1 |
| | GOTERM_BP_DIRECT | defense response | RT | | 17 | 0.8 | 7.3E-3 | 1.7E-1 |
| | UP_SEQ_FEATURE | MOTIF:Cx9C motif 2 | RT | | 7 | 0.3 | 7.4E-3 | 8.2E-1 |
| | UP_SEQ_FEATURE | ZN_FING:RanBP2-type | RT | | 7 | 0.3 | 7.4E-3 | 8.2E-1 |
| | UP_SEQ_FEATURE | MOTIF:Cx9C motif 1 | RT | | 7 | 0.3 | 7.4E-3 | 8.2E-1 |
| | UP_SEQ_FEATURE | REPEAT:WD 7 | RT | | 32 | 1.6 | 7.4E-3 | 8.2E-1 |
| | UP_SEQ_FEATURE | MUTAGEN:K->R: No effect on sumoylation. | RT | | 5 | 0.2 | 7.4E-3 | 8.2E-1 |
| | UP_SEQ_FEATURE | ZN_FING:PHD-type 2 | RT | | 10 | 0.5 | 7.6E-3 | 8.2E-1 |
| | KEGG_PATHWAY | Human papillomavirus infection | RT | | 58 | 2.8 | 7.6E-3 | 3.4E-2 |
| | INTERPRO | Znf_CCC | RT | | 14 | 0.7 | 7.6E-3 | 4.7E-1 |
| | GOTERM_CC_DIRECT | MHC class I peptide loading complex | RT | | 5 | 0.2 | 7.7E-3 | 5.8E-2 |
| | GOTERM_CC_DIRECT | mitochondrial intermembrane space | RT | | 17 | 0.8 | 7.7E-3 | 5.8E-2 |
| | GOTERM_BP_DIRECT | positive regulation of protein import into nucleus | RT | | 11 | 0.5 | 7.7E-3 | 1.8E-1 |
| | INTERPRO | Bromodomain | RT | | 11 | 0.5 | 7.8E-3 | 4.7E-1 |
| | GOTERM_BP_DIRECT | COPII vesicle coating | RT | | 8 | 0.4 | 7.8E-3 | 1.8E-1 |
| | UP_SEQ_FEATURE | DOMAIN:MHC class II alpha chain N-terminal | RT | | 4 | 0.2 | 7.8E-3 | 8.3E-1 |
| | INTERPRO | Chaperonin_TCP-1_CS | RT | | 5 | 0.2 | 7.9E-3 | 4.7E-1 |
| | GOTERM_CC_DIRECT | COP9 signalosome | RT | | 10 | 0.5 | 8.0E-3 | 6.0E-2 |
| | UP_SEQ_FEATURE | REPEAT:2-1 | RT | | 8 | 0.4 | 8.0E-3 | 8.3E-1 |
| | UP_SEQ_FEATURE | REPEAT:TNFR-Cys 1 | RT | | 8 | 0.4 | 8.0E-3 | 8.3E-1 |
| | UP_SEQ_FEATURE | REPEAT:TNFR-Cys 2 | RT | | 8 | 0.4 | 8.0E-3 | 8.3E-1 |
| | GOTERM_CC_DIRECT | cytoplasmic side of rough endoplasmic reticulum membrane | RT | | 4 | 0.2 | 8.0E-3 | 6.0E-2 |
| | GOTERM_BP_DIRECT | positive regulation of protein targeting to mitochondrion | RT | | 10 | 0.5 | 8.1E-3 | 1.9E-1 |
| | GOTERM_MF_DIRECT | promoter-specific chromatin binding | RT | | 15 | 0.7 | 8.1E-3 | 1.5E-1 |
| | GOTERM_MF_DIRECT | non-membrane spanning protein tyrosine phosphatase activity | RT | | 6 | 0.3 | 8.1E-3 | 1.5E-1 |
| | GOTERM_BP_DIRECT | positive regulation of lamellipodium assembly | RT | | 9 | 0.4 | 8.2E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | positive regulation of extrinsic apoptotic signaling pathway | RT | | 9 | 0.4 | 8.2E-3 | 1.9E-1 |
| | INTERPRO | RHD_CS | RT | | 4 | 0.2 | 8.2E-3 | 4.7E-1 |
| | INTERPRO | HnRNP-L/PTB | RT | | 4 | 0.2 | 8.2E-3 | 4.7E-1 |
| | INTERPRO | NFkB/Dor | RT | | 4 | 0.2 | 8.2E-3 | 4.7E-1 |
| | INTERPRO | PTBP1-like RRM2 | RT | | 4 | 0.2 | 8.2E-3 | 4.7E-1 |
| | INTERPRO | IPT_NFKappaB | RT | | 4 | 0.2 | 8.2E-3 | 4.7E-1 |
| | GOTERM_BP_DIRECT | DNA repair | RT | | 45 | 2.2 | 8.2E-3 | 1.9E-1 |
| | UP_KW_DOMAIN | SH2 domain | RT | | 19 | 0.9 | 8.2E-3 | 3.7E-2 |
| | GOTERM_CC_DIRECT | clathrin-coated endocytic vesicle | RT | | 8 | 0.4 | 8.4E-3 | 6.1E-2 |
| | GOTERM_CC_DIRECT | Cul4A-RING E3 ubiquitin ligase complex | RT | | 6 | 0.3 | 8.4E-3 | 6.1E-2 |
| | GOTERM_CC_DIRECT | proton-transporting V-type ATPase complex | RT | | 6 | 0.3 | 8.4E-3 | 6.1E-2 |
| | UP_KW_PTMM | Prenylation | RT | | 34 | 1.7 | 8.4E-3 | 3.2E-2 |
| | GOTERM_MF_DIRECT | telomeric DNA binding | RT | | 9 | 0.4 | 8.6E-3 | 1.5E-1 |
| | GOTERM_BP_DIRECT | negative regulation of erythrocyte differentiation | RT | | 5 | 0.2 | 8.6E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | late endosome to vacuole transport | RT | | 5 | 0.2 | 8.6E-3 | 1.9E-1 |
| | UP_SEQ_FEATURE | DOMAIN:C3H1-type | RT | | 12 | 0.6 | 8.6E-3 | 8.9E-1 |
| | INTERPRO | TNFR/NGFR_Cys rich reg | RT | | 8 | 0.4 | 8.7E-3 | 4.8E-1 |
| | INTERPRO | IPT_dom | RT | | 9 | 0.4 | 8.7E-3 | 4.8E-1 |
| | GOTERM_BP_DIRECT | negative regulation of IRE1-mediated unfolded protein response | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | AMP salvage | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | viral translational termination-reinitiation | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | positive regulation of endoplasmic reticulum unfolded protein response | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | posttranscriptional gene silencing | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | cellular sphingolipid homeostasis | RT | | 4 | 0.2 | 8.8E-3 | 1.9E-1 |
| | GOTERM_BP_DIRECT | endoplasmic reticulum calcium ion homeostasis | RT | | 7 | 0.3 | 8.9E-3 | 2.0E-1 |
| | GOTERM_BP_DIRECT | regulation of protein ubiquitination | RT | | 7 | 0.3 | 8.9E-3 | 2.0E-1 |
| | SMART | UBQ | RT | | 11 | 0.5 | 9.0E-3 | 1.7E-1 |
| | GOTERM_BP_DIRECT | negative regulation of gene expression | RT | | 46 | 2.2 | 9.1E-3 | 2.0E-1 |
| | KEGG_PATHWAY | p53 signaling pathway | RT | | 18 | 0.9 | 9.1E-3 | 4.0E-2 |
| | BIOCARTA | HIV-I Nef | RT | | 21 | 1.0 | 9.1E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | T cell costimulation | RT | | 11 | 0.5 | 9.2E-3 | 2.0E-1 |
| | GOTERM_BP_DIRECT | T cell proliferation | RT | | 11 | 0.5 | 9.2E-3 | 2.0E-1 |
| | INTERPRO | WD40 repeat_dom_sf | RT | | 45 | 2.2 | 9.2E-3 | 5.0E-1 |
| | INTERPRO | Bromodomain-like_sf | RT | | 11 | 0.5 | 9.2E-3 | 5.0E-1 |
| | BIOCARTA | IL-7 Signal Transduction | RT | | 9 | 0.4 | 9.3E-3 | 1.6E-1 |
| | GOTERM_BP_DIRECT | positive regulation of protein ubiquitination | RT | | 16 | 0.8 | 9.3E-3 | 2.0E-1 |
| | GOTERM_BP_DIRECT | intracellular pH reduction | RT | | 6 | 0.3 | 9.6E-3 | 2.1E-1 |
| | GOTERM_BP_DIRECT | endosomal lumen acidification | RT | | 6 | 0.3 | 9.6E-3 | 2.1E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Transcription regulation | RT | | 313 | 15.3 | 9.7E-3 | 6.0E-2 |
| | GOTERM_BP_DIRECT | retrograde vesicle-mediated transport, Golgi to ER | RT | | 12 | 0.6 | 9.9E-3 | 2.1E-1 |
| | GOTERM_BP_DIRECT | protein peptidyl-prolyl isomerization | RT | | 8 | 0.4 | 9.9E-3 | 2.1E-1 |
| | GOTERM_MF_DIRECT | WD40-repeat domain binding | RT | | 4 | 0.2 | 1.0E-2 | 1.7E-1 |
| | GOTERM_MF_DIRECT | acetyl-CoA C-acyltransferase activity | RT | | 4 | 0.2 | 1.0E-2 | 1.7E-1 |
| | GOTERM_CC_DIRECT | trans-Golgi network membrane | RT | | 20 | 1.0 | 1.0E-2 | 7.3E-2 |
| | GOTERM_MF_DIRECT | signaling adaptor activity | RT | | 14 | 0.7 | 1.0E-2 | 1.7E-1 |
| | BIOCARTA | TPO Signaling Pathway | RT | | 11 | 0.5 | 1.0E-2 | 1.6E-1 |
| | BIOCARTA | Caspase Cascade in Apoptosis | RT | | 11 | 0.5 | 1.0E-2 | 1.6E-1 |
| | GOTERM_CC_DIRECT | core mediator complex | RT | | 8 | 0.4 | 1.0E-2 | 7.6E-2 |
| | GOTERM_MF_DIRECT | kinase activity | RT | | 38 | 1.9 | 1.1E-2 | 1.8E-1 |
| | UP_SEQ_FEATURE | ZN_FING:PHD-type 1 | RT | | 10 | 0.5 | 1.1E-2 | 1.0E0 |
| | INTERPRO | WD40 repeat_CS | RT | | 25 | 1.2 | 1.1E-2 | 5.8E-1 |
| | INTERPRO | ADF-H/Gelsolin-like_dom_sf | RT | | 8 | 0.4 | 1.1E-2 | 5.8E-1 |
| | UP_SEQ_FEATURE | TRANSMEM:Helical; Anchor for type IV membrane protein | RT | | 14 | 0.7 | 1.1E-2 | 1.0E0 |
| | GOTERM_CC_DIRECT | centriolar satellite | RT | | 22 | 1.1 | 1.1E-2 | 8.2E-2 |
| | UP_SEQ_FEATURE | DOMAIN:Ribosomal protein eL8/eL30/eS12/Gadd45 | RT | | 5 | 0.2 | 1.1E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | REGION:Alpha-3 | RT | | 5 | 0.2 | 1.1E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | UNSURE:I or L | RT | | 5 | 0.2 | 1.1E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:CXXC-type | RT | | 5 | 0.2 | 1.1E-2 | 1.0E0 |
| | GOTERM_MF_DIRECT | S100 protein binding | RT | | 6 | 0.3 | 1.2E-2 | 1.9E-1 |
| | GOTERM_BP_DIRECT | positive regulation of T cell differentiation | RT | | 10 | 0.5 | 1.2E-2 | 2.5E-1 |
| | UP_SEQ_FEATURE | ZN_FING:RING-type | RT | | 33 | 1.6 | 1.2E-2 | 1.0E0 |
| | GOTERM_BP_DIRECT | negative regulation of DNA binding | RT | | 7 | 0.3 | 1.2E-2 | 2.5E-1 |
| | KEGG_PATHWAY | Epithelial cell signaling in Helicobacter pylori infection | RT | | 17 | 0.8 | 1.2E-2 | 5.2E-2 |
| | GOTERM_BP_DIRECT | immune response | RT | | 67 | 3.3 | 1.2E-2 | 2.5E-1 |
| | INTERPRO | Znf_CCC_sf | RT | | 10 | 0.5 | 1.2E-2 | 6.0E-1 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|---|----|-------|-------|------|---------|-----------|
| | INTERPRO | Ribosomal_eL30-like_sf | RT | | 6 | 0.3 | 1.2E-2 | 6.0E-1 |
| | INTERPRO | Hsp_70_fam | RT | | 6 | 0.3 | 1.2E-2 | 6.0E-1 |
| | INTERPRO | Heat_shock_70_CS | RT | | 6 | 0.3 | 1.2E-2 | 6.0E-1 |
| | GOTERM_BP_DIRECT | cellular_response_to_hypoxia | RT | | 24 | 1.2 | 1.2E-2 | 2.5E-1 |
| | GOTERM_CC_DIRECT | microtubule_organizing_center | RT | | 13 | 0.6 | 1.2E-2 | 8.7E-2 |
| | GOTERM_BP_DIRECT | positive_regulation_of_macroautophagy | RT | | 9 | 0.4 | 1.2E-2 | 2.5E-1 |
| | GOTERM_BP_DIRECT | protein_K11-linked_ubiquitination | RT | | 9 | 0.4 | 1.2E-2 | 2.5E-1 |
| | GOTERM_CC_DIRECT | rough_endoplasmic_reticulum | RT | | 9 | 0.4 | 1.2E-2 | 8.7E-2 |
| | GOTERM_BP_DIRECT | protein_localization_to_membrane | RT | | 8 | 0.4 | 1.2E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | regulation_of_double-strand_break_repair | RT | | 8 | 0.4 | 1.2E-2 | 2.6E-1 |
| | UP_SEQ_FEATURE | REPEAT:2-2 | RT | | 8 | 0.4 | 1.2E-2 | 1.0E0 |
| | GOTERM_MF_DIRECT | proton-transporting_ATPase_activity,_rotational_mechanism | RT | | 8 | 0.4 | 1.3E-2 | 2.1E-1 |
| | GOTERM_MF_DIRECT | protein_binding,_bridging_involved_in_substrate_recognition_for_ubiquitination | RT | | 13 | 0.6 | 1.3E-2 | 2.1E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_cysteine-type_endopeptidase_activity_involved_in_apoptotic_process | RT | | 11 | 0.5 | 1.3E-2 | 2.6E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Purine_salvage | RT | | 4 | 0.2 | 1.3E-2 | 7.6E-2 |
| | GOTERM_MF_DIRECT | protein_kinase_inhibitor_activity | RT | | 10 | 0.5 | 1.3E-2 | 2.1E-1 |
| | INTERPRO | Chromo-like_dom_sf | RT | | 9 | 0.4 | 1.3E-2 | 6.4E-1 |
| | GOTERM_CC_DIRECT | endoplasmic_reticulum_tubular_network | RT | | 7 | 0.3 | 1.3E-2 | 9.0E-2 |
| | GOTERM_MF_DIRECT | thiol-dependent_ubiquitin-specific_protease_activity | RT | | 21 | 1.0 | 1.3E-2 | 2.1E-1 |
| | GOTERM_CC_DIRECT | PcG_protein_complex | RT | | 8 | 0.4 | 1.3E-2 | 9.0E-2 |
| | GOTERM_MF_DIRECT | RNA_polymerase_II_core_binding | RT | | 9 | 0.4 | 1.3E-2 | 2.1E-1 |
| | GOTERM_BP_DIRECT | synaptic Vesicle_transport | RT | | 6 | 0.3 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_viral_entry_into_host_cell | RT | | 6 | 0.3 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_telomerase_RNA_localization_to_Cajal_body | RT | | 6 | 0.3 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | maturational_LSU-rRNA_from_tricistronic_rRNA_transcript_(SSU-rRNA,_5.8S_rRNA,_LSU-rRNA) | RT | | 6 | 0.3 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | membrane_budding | RT | | 6 | 0.3 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | endosome_transport_via_multivesicular_body_sorting_pathway | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_establishment_of_protein_localization_to_telomere | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_monocyte_differentiation | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_CD4-positive,_alpha-beta_T_cell_proliferation | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | regulation_of_T_cell_activation | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | GOTERM_BP_DIRECT | JAK-STAT cascade_involved_in_growth_hormone_signaling_pathway | RT | | 5 | 0.2 | 1.3E-2 | 2.6E-1 |
| | UP_KW_CELLULAR_COMPONENT | Telomere | RT | | 12 | 0.6 | 1.3E-2 | 4.9E-2 |
| | KEGG_PATHWAY | Pathways_in_cancer | RT | | 85 | 4.1 | 1.4E-2 | 5.9E-2 |
| | GOTERM_CC_DIRECT | mitochondrial_outer_membrane | RT | | 33 | 1.6 | 1.4E-2 | 9.5E-2 |
| | BIOCARTA | TNFR2_Signaling_Pathway | RT | | 9 | 0.4 | 1.4E-2 | 2.0E-1 |
| | INTERPRO | ATPase_NBD | RT | | 15 | 0.7 | 1.4E-2 | 6.8E-1 |
| | KEGG_PATHWAY | Toll-like_receptor_signaling_pathway | RT | | 23 | 1.1 | 1.4E-2 | 6.0E-2 |
| | GOTERM_BP_DIRECT | phosphorylation | RT | | 81 | 3.9 | 1.4E-2 | 2.8E-1 |
| | KEGG_PATHWAY | Natural_killer_cell-mediated_cytotoxicity | RT | | 26 | 1.3 | 1.4E-2 | 6.0E-2 |
| | UP_SEQ_FEATURE | DOMAIN:A20-type | RT | | 4 | 0.2 | 1.5E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:DDT | RT | | 4 | 0.2 | 1.5E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:Tudor-knot | RT | | 4 | 0.2 | 1.5E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | SITE:Cleavage; by CASP8 | RT | | 4 | 0.2 | 1.5E-2 | 1.0E0 |
| | GOTERM_BP_DIRECT | mitochondrial_electron_transport,_NADH_to_ubiquinone | RT | | 11 | 0.5 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | JAK-STAT cascade | RT | | 11 | 0.5 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | response_to_peptide_hormone | RT | | 11 | 0.5 | 1.5E-2 | 2.9E-1 |
| | GOTERM_CC_DIRECT | protein_phosphatase_4_complex | RT | | 4 | 0.2 | 1.5E-2 | 1.0E-1 |
| | GOTERM_CC_DIRECT | signal_peptidase_complex | RT | | 4 | 0.2 | 1.5E-2 | 1.0E-1 |
| | UP_SEQ_FEATURE | DOMAIN:Bromo | RT | | 10 | 0.5 | 1.5E-2 | 1.0E0 |
| | GOTERM_BP_DIRECT | regulation_of_innate immune_response | RT | | 7 | 0.3 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_translational_initiation | RT | | 7 | 0.3 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | negative_regulation_of_translational_initiation | RT | | 7 | 0.3 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | mitochondrion_morphogenesis | RT | | 7 | 0.3 | 1.5E-2 | 2.9E-1 |
| | SMART | DUSP | RT | | 4 | 0.2 | 1.5E-2 | 2.8E-1 |
| | UP_KW_MOLECULAR_FUNCTION | Rotamase | RT | | 11 | 0.5 | 1.5E-2 | 1.2E-1 |
| | INTERPRO | Tudor-knot | RT | | 4 | 0.2 | 1.5E-2 | 7.4E-1 |
| | KEGG_PATHWAY | Polycomb_repressive_complex | RT | | 19 | 0.9 | 1.5E-2 | 6.4E-2 |
| | UP_KW_BIOLOGICAL_PROCESS | mRNA_transport | RT | | 23 | 1.1 | 1.5E-2 | 8.7E-2 |
| | GOTERM_MF_DIRECT | p53_binding | RT | | 15 | 0.7 | 1.5E-2 | 2.3E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_interleukin-4_production | RT | | 8 | 0.4 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | positive_regulation_of_immune_globulin_production | RT | | 8 | 0.4 | 1.5E-2 | 2.9E-1 |
| | GOTERM_BP_DIRECT | regulation_of_circadian_rhythm | RT | | 14 | 0.7 | 1.5E-2 | 2.9E-1 |
| | GOTERM_MF_DIRECT | transcription_cofactor_binding | RT | | 10 | 0.5 | 1.5E-2 | 2.3E-1 |
| | GOTERM_MF_DIRECT | unmethylated_CpG_binding | RT | | 5 | 0.2 | 1.5E-2 | 2.3E-1 |
| | GOTERM_MF_DIRECT | peptide-lysine-N-acetyltransferase_activity | RT | | 5 | 0.2 | 1.5E-2 | 2.3E-1 |
| | GOTERM_BP_DIRECT | protein_secretion | RT | | 13 | 0.6 | 1.5E-2 | 2.9E-1 |
| | GOTERM_CC_DIRECT | endoplasmic_reticulum_quality_control_compartment | RT | | 6 | 0.3 | 1.5E-2 | 1.0E-1 |
| | GOTERM_BP_DIRECT | neuron_projection_development | RT | | 21 | 1.0 | 1.6E-2 | 2.9E-1 |
| | BIOCARTA | IL_17_Signaling_Pathway | RT | | 8 | 0.4 | 1.6E-2 | 2.2E-1 |
| | GOTERM_CC_DIRECT | euchromatin | RT | | 13 | 0.6 | 1.6E-2 | 1.1E-1 |
| | GOTERM_MF_DIRECT | cyclin-dependent_protein_serine/threonine_kinase_regulator_activity | RT | | 9 | 0.4 | 1.6E-2 | 2.4E-1 |
| | GOTERM_MF_DIRECT | histone_methyltransferase_binding | RT | | 6 | 0.3 | 1.6E-2 | 2.4E-1 |
| | GOTERM_CC_DIRECT | nuclear_chromosome | RT | | 8 | 0.4 | 1.6E-2 | 1.1E-1 |
| | UP_KW_DISEASE | Primary_mitochondrial_disease | RT | | 36 | 1.8 | 1.6E-2 | 2.3E-1 |
| | GOTERM_BP_DIRECT | peptide_antigen_assembly_with_MHC_class_I_protein_complex | RT | | 4 | 0.2 | 1.6E-2 | 3.0E-1 |
| | GOTERM_BP_DIRECT | protein_localization_to_endoplasmic_reticulum | RT | | 4 | 0.2 | 1.6E-2 | 3.0E-1 |
| | GOTERM_BP_DIRECT | regulation_of_T_cell_differentiation_in_thymus | RT | | 4 | 0.2 | 1.6E-2 | 3.0E-1 |
| | GOTERM_BP_DIRECT | endodermal_cell_fate_commitment | RT | | 4 | 0.2 | 1.6E-2 | 3.0E-1 |
| | GOTERM_BP_DIRECT | protection_from_natural_killer_cell-mediated_cytotoxicity | RT | | 4 | 0.2 | 1.6E-2 | 3.0E-1 |
| | SMART | IPT | RT | | 8 | 0.4 | 1.6E-2 | 2.9E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Transcription | RT | | 319 | 15.5 | 1.6E-2 | 8.9E-2 |
| | INTERPRO | ENTH_VHS | RT | | 8 | 0.4 | 1.7E-2 | 7.9E-1 |
| | UP_SEQ_FEATURE | ZNFING:CXXC-type | RT | | 5 | 0.2 | 1.7E-2 | 1.0E0 |
| | GOTERM_CC_DIRECT | endomembrane_system | RT | | 26 | 1.3 | 1.7E-2 | 1.1E-1 |
| | GOTERM_BP_DIRECT | type_I_interferon_signaling_pathway | RT | | 11 | 0.5 | 1.7E-2 | 3.1E-1 |
| | GOTERM_CC_DIRECT | chaperonin-containing_T-complex | RT | | 5 | 0.2 | 1.7E-2 | 1.1E-1 |
| | GOTERM_CC_DIRECT | endoplasmic_reticulum_chaperone_complex | RT | | 5 | 0.2 | 1.7E-2 | 1.1E-1 |
| | GOTERM_CC_DIRECT | NSL_complex | RT | | 5 | 0.2 | 1.7E-2 | 1.1E-1 |
| | GOTERM_CC_DIRECT | autolysosome | RT | | 5 | 0.2 | 1.7E-2 | 1.1E-1 |
| | KEGG_PATHWAY | RNA_degradation | RT | | 18 | 0.9 | 1.7E-2 | 7.1E-2 |

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|--------------------------|--|----|-------|-------|------|---------|-----------|
| | GOTERM_CC_DIRECT | aggresome | RT | | 9 | 0.4 | 1.8E-2 | 1.1E-1 |
| | GOTERM_BP_DIRECT | retrograde protein transport, ER to cytosol | RT | | 6 | 0.3 | 1.8E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | protein targeting to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway | RT | | 6 | 0.3 | 1.8E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | cellular response to chemokine | RT | | 6 | 0.3 | 1.8E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | nuclear envelope organization | RT | | 6 | 0.3 | 1.8E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | cellular response to nerve growth factor stimulus | RT | | 9 | 0.4 | 1.8E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | positive regulation of reactive oxygen species metabolic process | RT | | 9 | 0.4 | 1.8E-2 | 3.2E-1 |
| | GOTERM_CC_DIRECT | site of double-strand break | RT | | 17 | 0.8 | 1.8E-2 | 1.1E-1 |
| | KEGG_PATHWAY | Vasopressin-regulated water reabsorption | RT | | 12 | 0.6 | 1.8E-2 | 7.2E-2 |
| | UP_KW_BIOLOGICAL_PROCESS | DNA damage | RT | | 66 | 3.2 | 1.8E-2 | 9.3E-2 |
| | INTERPRO | TPR-like helical dom_sf | RT | | 34 | 1.7 | 1.8E-2 | 8.5E-1 |
| | GOTERM_MF_DIRECT | protein binding, bridging | RT | | 22 | 1.1 | 1.8E-2 | 2.6E-1 |
| | GOTERM_CC_DIRECT | cell cortex | RT | | 26 | 1.3 | 1.8E-2 | 1.1E-1 |
| | INTERPRO | SH2_dom_sf | RT | | 20 | 1.0 | 1.9E-2 | 8.7E-1 |
| | GOTERM_BP_DIRECT | clathrin-dependent endocytosis | RT | | 8 | 0.4 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | spliceosomal complex assembly | RT | | 8 | 0.4 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | protein targeting to lysosome | RT | | 8 | 0.4 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | DNA methylation | RT | | 8 | 0.4 | 1.9E-2 | 3.3E-1 |
| | GOTERM_CC_DIRECT | transcription factor complex | RT | | 33 | 1.6 | 1.9E-2 | 1.2E-1 |
| | GOTERM_CC_DIRECT | chromatin | RT | | 129 | 6.3 | 1.9E-2 | 1.2E-1 |
| | GOTERM_BP_DIRECT | intracellular estrogen receptor signaling pathway | RT | | 7 | 0.3 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | positive regulation of histone acetylation | RT | | 5 | 0.2 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | gamma-delta T cell activation | RT | | 5 | 0.2 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | cytoplasmic translational initiation | RT | | 5 | 0.2 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | positive regulation of protein localization to Cajal body | RT | | 5 | 0.2 | 1.9E-2 | 3.3E-1 |
| | GOTERM_BP_DIRECT | protein folding in endoplasmic reticulum | RT | | 5 | 0.2 | 1.9E-2 | 3.3E-1 |
| | GOTERM_CC_DIRECT | U2-type spliceosomal complex | RT | | 8 | 0.4 | 1.9E-2 | 1.2E-1 |
| | UP_KW_DISEASE | Parkinson disease | RT | | 8 | 0.4 | 1.9E-2 | 2.4E-1 |
| | BIOCARTA | Hypoxia and p53 in the Cardiovascular system | RT | | 11 | 0.5 | 1.9E-2 | 2.6E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Transport | RT | | 274 | 13.4 | 1.9E-2 | 9.8E-2 |
| | UP_SEQ_FEATURE | MOTIF:Di-lysine motif | RT | | 6 | 0.3 | 2.0E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:CHCH | RT | | 7 | 0.3 | 2.0E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | REPEAT:TNFR-Cys 3 | RT | | 7 | 0.3 | 2.0E-2 | 1.0E0 |
| | GOTERM_BP_DIRECT | regulation of cyclin-dependent protein serine/threonine kinase activity | RT | | 11 | 0.5 | 2.0E-2 | 3.4E-1 |
| | GOTERM_BP_DIRECT | protein N-linked glycosylation | RT | | 12 | 0.6 | 2.0E-2 | 3.4E-1 |
| | INTERPRO | MHC I-like Ag-recog | RT | | 8 | 0.4 | 2.0E-2 | 9.2E-1 |
| | INTERPRO | MHC I-like Ag-recog_sf | RT | | 8 | 0.4 | 2.0E-2 | 9.2E-1 |
| | GOTERM_BP_DIRECT | protein phosphorylation | RT | | 52 | 2.5 | 2.0E-2 | 3.5E-1 |
| | INTERPRO | GROEL-like equatorial_sf | RT | | 6 | 0.3 | 2.1E-2 | 9.5E-1 |
| | GOTERM_BP_DIRECT | positive regulation of defense response to virus by host | RT | | 9 | 0.4 | 2.1E-2 | 3.6E-1 |
| | GOTERM_BP_DIRECT | intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress | RT | | 9 | 0.4 | 2.1E-2 | 3.6E-1 |
| | GOTERM_MF_DIRECT | death receptor binding | RT | | 6 | 0.3 | 2.1E-2 | 3.0E-1 |
| | GOTERM_MF_DIRECT | lamin binding | RT | | 6 | 0.3 | 2.1E-2 | 3.0E-1 |
| | GOTERM_MF_DIRECT | ubiquitinyl hydrolase activity | RT | | 6 | 0.3 | 2.1E-2 | 3.0E-1 |
| | GOTERM_CC_DIRECT | transport vesicle membrane | RT | | 10 | 0.5 | 2.1E-2 | 1.3E-1 |
| | GOTERM_BP_DIRECT | endosomal transport | RT | | 14 | 0.7 | 2.2E-2 | 3.7E-1 |
| | KEGG_PATHWAY | Parathyroid hormone synthesis, secretion and action | RT | | 22 | 1.1 | 2.2E-2 | 8.8E-2 |
| | GOTERM_BP_DIRECT | positive regulation of protein catabolic process | RT | | 16 | 0.8 | 2.2E-2 | 3.8E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | Immunity | RT | | 132 | 6.4 | 2.2E-2 | 1.1E-1 |
| | UP_KW_BIOLOGICAL_PROCESS | DNA repair | RT | | 56 | 2.7 | 2.3E-2 | 1.1E-1 |
| | GOTERM_MF_DIRECT | peptidyl-prolyl cis-trans isomerase activity | RT | | 11 | 0.5 | 2.3E-2 | 3.2E-1 |
| | GOTERM_BP_DIRECT | positive regulation of DNA-templated transcription, elongation | RT | | 6 | 0.3 | 2.3E-2 | 3.9E-1 |
| | GOTERM_BP_DIRECT | cellular response to stress | RT | | 6 | 0.3 | 2.3E-2 | 3.9E-1 |
| | GOTERM_BP_DIRECT | synaptic vesicle lumen acidification | RT | | 6 | 0.3 | 2.3E-2 | 3.9E-1 |
| | UP_SEQ_FEATURE | REPEAT:Spectrin 17 | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:V-SNARE coiled-coil homology | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | REPEAT:Spectrin 15 | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | DOMAIN:v-SNARE coiled-coil homology | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | REGION:Membrane-binding amphipathic helix | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | UP_SEQ_FEATURE | REPEAT:Spectrin 16 | RT | | 5 | 0.2 | 2.3E-2 | 1.0E0 |
| | GOTERM_BP_DIRECT | positive regulation of interferon-gamma production | RT | | 15 | 0.7 | 2.3E-2 | 3.9E-1 |
| | GOTERM_BP_DIRECT | cellular response to insulin stimulus | RT | | 17 | 0.8 | 2.3E-2 | 3.9E-1 |
| | INTERPRO | SH2 | RT | | 19 | 0.9 | 2.4E-2 | 9.9E-1 |
| | GOTERM_MF_DIRECT | calcium-dependent protein binding | RT | | 16 | 0.8 | 2.4E-2 | 3.3E-1 |

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12 gene(s) from your list are not in the output.

Please cite DAVID within any publication that makes use of any methods inspired by DAVID.