

| term | tot | exp | obs | pValue | description | annotation |
|------------|-----|-----|-----|-----------|--|------------|
| GO:0006355 | 426 | 113 | 131 | 2.46E-002 | regulation of transcription, DNA-dependent | GO_BP |
| GO:0006351 | 137 | 36 | 48 | 1.63E-002 | transcription, DNA-dependent | GO_BP |
| GO:0001701 | 118 | 31 | 42 | 1.79E-002 | in utero embryonic development | GO_BP |
| GO:0006813 | 83 | 22 | 31 | 1.92E-002 | potassium ion transport | GO_BP |
| GO:0030324 | 62 | 16 | 25 | 1.21E-002 | lung development | GO_BP |
| GO:0030335 | 57 | 15 | 22 | 3.05E-002 | positive regulation of cell migration | GO_BP |
| GO:0010553 | 46 | 12 | 20 | 9.33E-003 | negative regulation of gene-specific transcription from RNA polymerase II promoter | GO_BP |
| GO:0090090 | 37 | 10 | 17 | 8.41E-003 | negative regulation of canonical Wnt receptor signaling pathway | GO_BP |
| GO:0045666 | 33 | 9 | 15 | 1.46E-002 | positive regulation of neuron differentiation | GO_BP |
| GO:0042593 | 32 | 8 | 14 | 2.60E-002 | glucose homeostasis | GO_BP |
| GO:0006334 | 23 | 6 | 13 | 2.20E-003 | nucleosome assembly | GO_BP |
| GO:0000902 | 30 | 8 | 13 | 3.41E-002 | cell morphogenesis | GO_BP |
| GO:0007492 | 20 | 5 | 12 | 1.62E-003 | endoderm development | GO_BP |
| GO:0030073 | 21 | 6 | 12 | 2.87E-003 | insulin secretion | GO_BP |
| GO:0016049 | 25 | 7 | 12 | 1.71E-002 | cell growth | GO_BP |
| GO:0042475 | 22 | 6 | 11 | 1.56E-002 | odontogenesis of dentine-containing tooth | GO_BP |
| GO:0006461 | 23 | 6 | 11 | 2.28E-002 | protein complex assembly | GO_BP |
| GO:0009968 | 21 | 6 | 10 | 3.06E-002 | negative regulation of signal transduction | GO_BP |
| GO:0001932 | 15 | 4 | 9 | 6.37E-003 | regulation of protein phosphorylation | GO_BP |
| GO:0001947 | 16 | 4 | 9 | 1.12E-002 | heart looping | GO_BP |
| GO:0021549 | 17 | 5 | 9 | 1.82E-002 | cerebellum development | GO_BP |
| GO:0030183 | 19 | 5 | 9 | 4.10E-002 | B cell differentiation | GO_BP |
| GO:0045786 | 19 | 5 | 9 | 4.10E-002 | negative regulation of cell cycle | GO_BP |
| GO:0007628 | 19 | 5 | 9 | 4.10E-002 | adult walking behavior | GO_BP |
| GO:0035050 | 12 | 3 | 8 | 4.13E-003 | embryonic heart tube development | GO_BP |
| GO:0048701 | 12 | 3 | 8 | 4.13E-003 | embryonic cranial skeleton morphogenesis | GO_BP |
| GO:0001656 | 14 | 4 | 8 | 1.48E-002 | metanephros development | GO_BP |
| GO:0043407 | 15 | 4 | 8 | 2.45E-002 | negative regulation of MAP kinase activity | GO_BP |
| GO:0031016 | 10 | 3 | 7 | 5.01E-003 | pancreas development | GO_BP |
| GO:0051146 | 11 | 3 | 7 | 1.06E-002 | striated muscle cell differentiation | GO_BP |
| GO:0030032 | 12 | 3 | 7 | 1.97E-002 | lamellipodium assembly | GO_BP |
| GO:0001755 | 12 | 3 | 7 | 1.97E-002 | neural crest cell migration | GO_BP |
| GO:0048066 | 7 | 2 | 6 | 1.87E-003 | developmental pigmentation | GO_BP |
| GO:0016265 | 8 | 2 | 6 | 5.80E-003 | death | GO_BP |
| GO:0010634 | 9 | 2 | 6 | 1.35E-002 | positive regulation of epithelial cell migration | GO_BP |
| GO:0010942 | 9 | 2 | 6 | 1.35E-002 | positive regulation of cell death | GO_BP |
| GO:0050930 | 9 | 2 | 6 | 1.35E-002 | induction of positive chemotaxis | GO_BP |
| GO:0030100 | 9 | 2 | 6 | 1.35E-002 | regulation of endocytosis | GO_BP |
| GO:0010951 | 11 | 3 | 6 | 4.50E-002 | negative regulation of endopeptidase activity | GO_BP |

| | | | | | | |
|------------|----|---|---|-----------|---|-------|
| GO:0009880 | 11 | 3 | 6 | 4.50E-002 | embryonic pattern specification | GO_BP |
| GO:0001824 | 11 | 3 | 6 | 4.50E-002 | blastocyst development | GO_BP |
| GO:0060325 | 11 | 3 | 6 | 4.50E-002 | face morphogenesis | GO_BP |
| GO:0007162 | 11 | 3 | 6 | 4.50E-002 | negative regulation of cell adhesion | GO_BP |
| GO:0050678 | 11 | 3 | 6 | 4.50E-002 | regulation of epithelial cell proliferation | GO_BP |
| GO:0045861 | 11 | 3 | 6 | 4.50E-002 | negative regulation of proteolysis | GO_BP |
| GO:0030878 | 11 | 3 | 6 | 4.50E-002 | thyroid gland development | GO_BP |
| GO:0042074 | 6 | 2 | 5 | 6.11E-003 | cell migration involved in gastrulation | GO_BP |
| GO:0002087 | 7 | 2 | 5 | 1.67E-002 | regulation of respiratory gaseous exchange by neurological system process | GO_BP |
| GO:0045879 | 7 | 2 | 5 | 1.67E-002 | negative regulation of smoothened signaling pathway | GO_BP |
| GO:0031146 | 8 | 2 | 5 | 3.49E-002 | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | GO_BP |
| GO:0007026 | 8 | 2 | 5 | 3.49E-002 | negative regulation of microtubule depolymerization | GO_BP |
| GO:0009948 | 8 | 2 | 5 | 3.49E-002 | anterior/posterior axis specification | GO_BP |
| GO:0048813 | 8 | 2 | 5 | 3.49E-002 | dendrite morphogenesis | GO_BP |
| GO:0048771 | 8 | 2 | 5 | 3.49E-002 | tissue remodeling | GO_BP |
| GO:0032886 | 4 | 1 | 4 | 4.94E-003 | regulation of microtubule-based process | GO_BP |
| GO:0051966 | 4 | 1 | 4 | 4.94E-003 | regulation of synaptic transmission, glutamatergic | GO_BP |
| GO:0035239 | 4 | 1 | 4 | 4.94E-003 | tube morphogenesis | GO_BP |
| GO:0032456 | 5 | 1 | 4 | 1.94E-002 | endocytic recycling | GO_BP |
| GO:0048596 | 5 | 1 | 4 | 1.94E-002 | embryonic camera-type eye morphogenesis | GO_BP |
| GO:0032940 | 5 | 1 | 4 | 1.94E-002 | secretion by cell | GO_BP |
| GO:0022027 | 6 | 2 | 4 | 4.61E-002 | interkinetic nuclear migration | GO_BP |
| GO:0042176 | 6 | 2 | 4 | 4.61E-002 | regulation of protein catabolic process | GO_BP |
| GO:0045576 | 6 | 2 | 4 | 4.61E-002 | mast cell activation | GO_BP |
| GO:0051929 | 6 | 2 | 4 | 4.61E-002 | positive regulation of calcium ion transport via voltage-gated calcium channel activity | GO_BP |
| GO:0006298 | 6 | 2 | 4 | 4.61E-002 | mismatch repair | GO_BP |
| GO:0006284 | 6 | 2 | 4 | 4.61E-002 | base-excision repair | GO_BP |
| GO:0007435 | 6 | 2 | 4 | 4.61E-002 | salivary gland morphogenesis | GO_BP |
| GO:0048511 | 6 | 2 | 4 | 4.61E-002 | rhythmic process | GO_BP |
| GO:0030193 | 6 | 2 | 4 | 4.61E-002 | regulation of blood coagulation | GO_BP |
| GO:0003407 | 3 | 1 | 3 | 1.86E-002 | neural retina development | GO_BP |
| GO:0007412 | 3 | 1 | 3 | 1.86E-002 | axon target recognition | GO_BP |
| GO:0016050 | 3 | 1 | 3 | 1.86E-002 | vesicle organization | GO_BP |
| GO:0003079 | 3 | 1 | 3 | 1.86E-002 | positive regulation of natriuresis | GO_BP |
| GO:0007529 | 3 | 1 | 3 | 1.86E-002 | establishment of synaptic specificity at neuromuscular junction | GO_BP |
| GO:0046323 | 3 | 1 | 3 | 1.86E-002 | glucose import | GO_BP |
| GO:0030300 | 3 | 1 | 3 | 1.86E-002 | regulation of intestinal cholesterol absorption | GO_BP |
| GO:0051891 | 3 | 1 | 3 | 1.86E-002 | positive regulation of cardioblast differentiation | GO_BP |
| GO:0015918 | 3 | 1 | 3 | 1.86E-002 | sterol transport | GO_BP |

| | | | | | | |
|------------|------|-----|-----|-----------|--|-------|
| GO:0016021 | 1589 | 424 | 461 | 8.81E-003 | integral to membrane | GO_CC |
| GO:0005622 | 743 | 198 | 226 | 8.51E-003 | intracellular | GO_CC |
| GO:0005887 | 132 | 35 | 49 | 5.03E-003 | integral to plasma membrane | GO_CC |
| GO:0030424 | 110 | 29 | 39 | 2.53E-002 | axon | GO_CC |
| GO:0005802 | 42 | 11 | 18 | 1.66E-002 | trans-Golgi network | GO_CC |
| GO:0005881 | 16 | 4 | 10 | 2.75E-003 | cytoplasmic microtubule | GO_CC |
| GO:0005913 | 21 | 6 | 10 | 3.16E-002 | cell-cell adherens junction | GO_CC |
| GO:0017053 | 17 | 5 | 9 | 1.88E-002 | transcriptional repressor complex | GO_CC |
| GO:0030315 | 19 | 5 | 9 | 4.23E-002 | T-tubule | GO_CC |
| GO:0000786 | 13 | 3 | 8 | 8.53E-003 | nucleosome | GO_CC |
| GO:0000793 | 16 | 4 | 8 | 3.89E-002 | condensed chromosome | GO_CC |
| GO:0000932 | 10 | 3 | 7 | 5.16E-003 | cytoplasmic mRNA processing body | GO_CC |
| GO:0005657 | 10 | 3 | 6 | 2.69E-002 | replication fork | GO_CC |
| GO:0000118 | 11 | 3 | 6 | 4.60E-002 | histone deacetylase complex | GO_CC |
| GO:0033276 | 8 | 2 | 5 | 3.56E-002 | transcription factor TFTC complex | GO_CC |
| GO:0000137 | 5 | 1 | 4 | 1.98E-002 | Golgi cis cisterna | GO_CC |
| GO:0008385 | 5 | 1 | 4 | 1.98E-002 | IkappaB kinase complex | GO_CC |
| GO:0042598 | 6 | 2 | 4 | 4.69E-002 | vesicular fraction | GO_CC |
| GO:0080008 | 6 | 2 | 4 | 4.69E-002 | CUL4 RING ubiquitin ligase complex | GO_CC |
| GO:0000300 | 3 | 1 | 3 | 1.89E-002 | peripheral to membrane of membrane fraction | GO_CC |
| GO:0032993 | 3 | 1 | 3 | 1.89E-002 | protein-DNA complex | GO_CC |
| GO:0001950 | 3 | 1 | 3 | 1.89E-002 | plasma membrane enriched fraction | GO_CC |
| GO:0019718 | 3 | 1 | 3 | 1.89E-002 | rough microsome | GO_CC |
| GO:0008270 | 813 | 217 | 241 | 2.65E-002 | zinc ion binding | GO_MF |
| GO:0003677 | 548 | 147 | 176 | 2.06E-003 | DNA binding | GO_MF |
| GO:0004872 | 435 | 116 | 135 | 2.21E-002 | receptor activity | GO_MF |
| GO:0003700 | 402 | 108 | 130 | 5.95E-003 | sequence-specific DNA binding transcription factor activity | GO_MF |
| GO:0008134 | 111 | 30 | 41 | 1.13E-002 | transcription factor binding | GO_MF |
| GO:0004842 | 101 | 27 | 35 | 4.76E-002 | ubiquitin-protein ligase activity | GO_MF |
| GO:0005244 | 68 | 18 | 25 | 4.42E-002 | voltage-gated ion channel activity | GO_MF |
| GO:0008083 | 60 | 16 | 23 | 3.25E-002 | growth factor activity | GO_MF |
| GO:0003690 | 44 | 12 | 20 | 5.69E-003 | double-stranded DNA binding | GO_MF |
| GO:0016566 | 29 | 8 | 14 | 1.05E-002 | specific transcriptional repressor activity | GO_MF |
| GO:0004221 | 33 | 9 | 14 | 3.68E-002 | ubiquitin thiolesterase activity | GO_MF |
| GO:0042826 | 29 | 8 | 13 | 2.71E-002 | histone deacetylase binding | GO_MF |
| GO:0016820 | 23 | 6 | 11 | 2.43E-002 | hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances | GO_MF |
| GO:0003697 | 25 | 7 | 11 | 4.68E-002 | single-stranded DNA binding | GO_MF |

| | | | | | | |
|------------|----|---|----|-----------|--|-------|
| GO:0046332 | 18 | 5 | 10 | 8.97E-003 | SMAD binding | GO_MF |
| GO:0019905 | 13 | 3 | 7 | 3.46E-002 | syntaxin binding | GO_MF |
| GO:0005160 | 7 | 2 | 6 | 1.96E-003 | transforming growth factor beta receptor binding | GO_MF |
| GO:0070491 | 10 | 3 | 6 | 2.73E-002 | repressing transcription factor binding | GO_MF |
| GO:0005388 | 6 | 2 | 5 | 6.36E-003 | calcium-transporting ATPase activity | GO_MF |
| GO:0031402 | 8 | 2 | 5 | 3.61E-002 | sodium ion binding | GO_MF |
| GO:0035257 | 5 | 1 | 4 | 2.01E-002 | nuclear hormone receptor binding | GO_MF |
| GO:0048406 | 5 | 1 | 4 | 2.01E-002 | nerve growth factor binding | GO_MF |
| GO:0042288 | 6 | 2 | 4 | 4.75E-002 | MHC class I protein binding | GO_MF |
| GO:0016922 | 6 | 2 | 4 | 4.75E-002 | ligand-dependent nuclear receptor binding | GO_MF |
| GO:0030676 | 3 | 1 | 3 | 1.91E-002 | Rac guanyl-nucleotide exchange factor activity | GO_MF |
| GO:0019887 | 3 | 1 | 3 | 1.91E-002 | protein kinase regulator activity | GO_MF |
| GO:0004571 | 3 | 1 | 3 | 1.91E-002 | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity | GO_MF |
| GO:0008401 | 3 | 1 | 3 | 1.91E-002 | retinoic acid 4-hydroxylase activity | GO_MF |
| GO:0005114 | 3 | 1 | 3 | 1.91E-002 | type II transforming growth factor beta receptor binding | GO_MF |

| | | | | | | |
|------|-----|----|----|-----------|---|------|
| 4144 | 127 | 33 | 44 | 2.17E-002 | Endocytosis | KEGG |
| 4120 | 84 | 22 | 31 | 2.04E-002 | Ubiquitin mediated proteolysis | KEGG |
| 4630 | 64 | 17 | 24 | 3.19E-002 | Jak-STAT signaling pathway | KEGG |
| 4350 | 49 | 13 | 22 | 3.66E-003 | TGF-beta signaling pathway | KEGG |
| 5212 | 42 | 11 | 19 | 6.11E-003 | Pancreatic cancer | KEGG |
| 4520 | 35 | 9 | 15 | 2.47E-002 | Adherens junction | KEGG |
| 4340 | 29 | 8 | 13 | 2.39E-002 | Hedgehog signaling pathway | KEGG |
| 5210 | 30 | 8 | 13 | 3.22E-002 | Colorectal cancer | KEGG |
| 3022 | 16 | 4 | 8 | 3.64E-002 | Basal transcription factors | KEGG |
| 410 | 16 | 4 | 8 | 3.64E-002 | beta-Alanine metabolism | KEGG |
| 450 | 11 | 3 | 6 | 4.37E-002 | Selenocompound metabolism | KEGG |
| 290 | 6 | 2 | 4 | 4.51E-002 | Valine, leucine and isoleucine biosynthesis | KEGG |