| Cate | Term | Coun | Count i | P-value | Enrichment s |
|---|---|---|---|---|---|
| GO | extracellular region | 181 | 1730 | 2.32E-09 | 6.27166781 |
| GO | response to glucocorticoid stimulus | 17 | 71 | 4.23E-06 | 5.72349811 |
| GO | integral to plasma membrane | 103 | 969 | 4.39E-06 | 4.80518264 |
| GO | extracellular space | 75 | 647 | 4.61E-06 | 4.87892193 |
| GO | complement activation, classical pathway | 10 | 27 | 6.18E-06 | 6.22340428 |
| GO | cell surface | 33 | 214 | 9.22E-06 | 5.00545963 |
| GO | negative regulation of cell proliferation | 39 | 287 | 3.09E-05 | 4.56887372 |
| GO | sequence-specific DNA binding | 57 | 487 | 4.83E-05 | 4.31407689 |
| GO | transcription factor activity | 94 | 922 | 5.83E-05 | 4.14536776 |
| GO | response to lipopolysaccharide | 19 | 105 | 8.24E-05 | 4.58512879 |
| GO | response to protein stimulus | 11 | 42 | 8.68E-05 | 4.97635904 |
| GO | positive regulation of peptidyl-tyrosine phosphorylation | 11 | 42 | 8.68E-05 | 4.97635904 |
| GO | membrane | 302 | 3643 | 8.69E-05 | 3.87128531 |
| GO | transmembrane receptor protein tyrosine phosphatase activity | 7 | 18 | 0.000112 | 5.39167485 |
| GO | response to progesterone stimulus | 8 | 24 | 0.000127 | 5.14754434 |
| GO | innate immune response | 19 | 109 | 0.000138 | 4.39661919 |
| GO | negative regulation of ERK1 and ERK2 cascade | 5 | 9 | 0.000148 | 5.79343807 |
| GO | Rho guanyl-nucleotide exchange factor activity | 14 | 68 | 0.00017 | 4.50238222 |
| GO | integral to membrane | 315 | 3857 | 0.000179 | 3.67260466 |
| GO | rhythmic process | 6 | 14 | 0.000188 | 5.34311137 |
| GO | steroid hormone receptor activity | 11 | 46 | 0.00021 | 4.59564659 |
| GO | positive regulation of NF-kappaB transcription factor activity | 11 | 47 | 0.000258 | 4.5070577 |
| GO | negative regulation of fibroblast growth factor receptor signaling path | 4 | 6 | 0.000291 | 5.80864705 |
| GO | cardiac muscle cell proliferation | 4 | 6 | 0.000291 | 5.80864705 |
| GO | pathogen-associated molecular pattern dependent induction by symb | 4 | 6 | 0.000291 | 5.80864705 |
| GO | transcription repressor activity | 25 | 173 | 0.000304 | 3.98784591 |
| GO | piRNA binding | 3 | 3 | 0.000319 | 6.39509339 |
| GO | insulin-like growth factor binding protein complex | 3 | 3 | 0.000319 | 6.39509339 |
| GO | mesodermal cell fate determination | 3 | 3 | 0.000319 | 6.39509339 |
| GO | positive regulation of macrophage cytokine production | 3 | 3 | 0.000319 | 6.39509339 |
| GO | response to glucose stimulus | 12 | 57 | 0.000393 | 4.26011511 |
| GO | ligand-dependent nuclear receptor activity | 8 | 28 | 0.000421 | 4.56130989 |
| GO | response to light stimulus | 6 | 16 | 0.000444 | 4.86280549 |
| GO | positive regulation of gene-specific transcription from RNA polymeras | 16 | 92 | 0.000466 | 4.02222337 |
| GO | positive regulation of smooth muscle cell proliferation | 8 | 29 | 0.000547 | 4.43176129 |
| GO | positive regulation of osteoclast differentiation | 4 | 7 | 0.000643 | 5.27551414 |
| GO | negative regulation of cell death | 4 | 7 | 0.000643 | 5.27551414 |
| GO | cellular response to lipopolysaccharide | 4 | 7 | 0.000643 | 5.27551414 |
| GO | microglial cell activation during immune response | 4 | 7 | 0.000643 | 5.27551414 |
| GO | signal transduction | 157 | 1796 | 0.000654 | 3.3653997 |
| GO | regulation of apoptosis | 18 | 114 | 0.00071 | 3.80020595 |
| GO | ion transport | 54 | 505 | 0.000721 | 3.48246795 |
| GO | positive regulation of tumor necrosis factor production | 5 | 12 | 0.000781 | 4.78302593 |
| GO | lipoprotein metabolic process | 6 | 18 | 0.000915 | 4.45719923 |
| GO | regulation of Rho protein signal transduction | 13 | 71 | 0.000939 | 3.83879701 |
| GO | plasma membrane | 228 | 2763 | 0.001019 | 3.19319655 |
| GO | voltage-gated ion channel activity | 21 | 147 | 0.001035 | 3.59379216 |
| GO | anchored to membrane | 17 | 109 | 0.001136 | 3.63530314 |

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|---|---|---|---|---|---|
| GO | positive regulation of chemokine production | 5 | 13 | 0.001198 | 4.52035837 |
| GO | epithelial cell maturation involved in prostate gland development | 3 | 4 | 0.001209 | 5.40302105 |
| GO | activin receptor activity, type I | 3 | 4 | 0.001209 | 5.40302105 |
| GO | secretory columnal luminar epithelial cell differentiation involved in pr | 3 | 4 | 0.001209 | 5.40302105 |
| GO | positive regulation of toll-like receptor signaling pathway | 3 | 4 | 0.001209 | 5.40302105 |
| GO | apical plasma membrane | 22 | 159 | 0.001222 | 3.51336832 |
| GO | immune response | 35 | 303 | 0.001637 | 3.27957156 |
| GO | response to retinoic acid | 8 | 34 | 0.001706 | 3.86102647 |
| GO | response to cytokine stimulus | 10 | 50 | 0.001784 | 3.69387928 |
| GO | positive regulation of transcription from RNA polymerase II promoter | 34 | 295 | 0.001964 | 3.21764375 |
| GO | retinol metabolic process | 4 | 9 | 0.002071 | 4.47220331 |
| GO | response to fatty acid | 4 | 9 | 0.002071 | 4.47220331 |
| GO | ligand-regulated transcription factor activity | 4 | 9 | 0.002071 | 4.47220331 |
| GO | positive regulation of interleukin-12 production | 4 | 9 | 0.002071 | 4.47220331 |
| GO | circadian rhythm | 8 | 35 | 0.002081 | 3.75974575 |
| GO | positive regulation of interleukin-6 production | 6 | 21 | 0.002241 | 3.94948136 |
| GO | multicellular organismal development | 83 | 890 | 0.002322 | 3.01643691 |
| GO | filopodium assembly | 5 | 15 | 0.002491 | 4.06852596 |
| GO | cell adhesion | 53 | 522 | 0.002514 | 3.04663053 |
| GO | scavenger receptor activity | 9 | 44 | 0.00254 | 3.58423773 |
| GO | negative regulation of nerve growth factor receptor signaling pathway | 3 | 5 | 0.002869 | 4.71159348 |
| GO | insulin binding | 3 | 5 | 0.002869 | 4.71159348 |
| GO | placenta blood vessel development | 3 | 5 | 0.002869 | 4.71159348 |
| GO | lipopolysaccharide receptor activity | 3 | 5 | 0.002869 | 4.71159348 |
| GO | regulation of transcription, DNA-dependent | 92 | 1013 | 0.003009 | 2.91294452 |
| GO | response to drug | 27 | 225 | 0.003112 | 3.08861225 |
| GO | positive regulation of Ras protein signal transduction | 4 | 10 | 0.003266 | 4.15714422 |
| GO | receptor signaling protein tyrosine kinase activity | 4 | 10 | 0.003266 | 4.15714422 |
| GO | positive regulation of tyrosine phosphorylation of Stat3 protein | 4 | 10 | 0.003266 | 4.15714422 |
| GO | positive regulation of interleukin-8 production | 4 | 10 | 0.003266 | 4.15714422 |
| GO | response to cAMP | 9 | 46 | 0.003492 | 3.42567314 |
| GO | potassium channel regulator activity | 6 | 23 | 0.003706 | 3.6610393 |
| GO | odontogenesis | 6 | 23 | 0.003706 | 3.6610393 |
| GO | regulation of cell proliferation | 12 | 73 | 0.003733 | 3.25782225 |
| GO | response to organic cyclic substance | 14 | 92 | 0.003772 | 3.193921 |
| GO | membrane raft | 15 | 103 | 0.004249 | 3.11660156 |
| GO | regulation of long-term neuronal synaptic plasticity | 5 | 17 | 0.004577 | 3.69047681 |
| GO | negative regulation of Ras GTPase activity | 2 | 2 | 0.004668 | 5.22143439 |
| GO | bud elongation involved in lung branching | 2 | 2 | 0.004668 | 5.22143439 |
| GO | blood vessel endothelial cell proliferation involved in sprouting angiog | 2 | 2 | 0.004668 | 5.22143439 |
| GO | positive regulation of dopamine uptake | 2 | 2 | 0.004668 | 5.22143439 |
| GO | establishment of blood-nerve barrier | 2 | 2 | 0.004668 | 5.22143439 |
| GO | lymph vessel development | 2 | 2 | 0.004668 | 5.22143439 |
| GO | positive regulation of glycoprotein biosynthetic process | 2 | 2 | 0.004668 | 5.22143439 |
| GO | positive regulation of interleukin-3 biosynthetic process | 2 | 2 | 0.004668 | 5.22143439 |
| GO | serotonin secretion | 2 | 2 | 0.004668 | 5.22143439 |
| GO | Ral guanyl-nucleotide exchange factor activity | 2 | 2 | 0.004668 | 5.22143439 |
| GO | regulation of low-density lipoprotein receptor catabolic process | 2 | 2 | 0.004668 | 5.22143439 |
| GO | prostate gland stromal morphogenesis | 2 | 2 | 0.004668 | 5.22143439 |

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|---|---|---|---|---|---|
| GO | hepatic immune response | 2 | 2 | 0.004668 | 5.22143439 |
| GO | response to iron(II) ion | 2 | 2 | 0.004668 | 5.22143439 |
| GO | axon target recognition | 2 | 2 | 0.004668 | 5.22143439 |
| GO | RNA destabilization | 2 | 2 | 0.004668 | 5.22143439 |
| GO | response to exogenous dsRNA | 4 | 11 | 0.004857 | 3.88209859 |
| GO | neural crest cell development | 4 | 11 | 0.004857 | 3.88209859 |
| GO | cell fate determination | 4 | 11 | 0.004857 | 3.88209859 |
| GO | myoblast fusion | 4 | 11 | 0.004857 | 3.88209859 |
| GO | proteinaceous extracellular matrix | 26 | 223 | 0.00538 | 2.87181754 |
| GO | regulation of blood pressure | 9 | 49 | 0.005419 | 3.20318458 |
| GO | regulation of hydrogen peroxide metabolic process | 3 | 6 | 0.005446 | 4.19059941 |
| GO | response to peptidoglycan | 3 | 6 | 0.005446 | 4.19059941 |
| GO | positive regulation of organ growth | 3 | 6 | 0.005446 | 4.19059941 |
| GO | chromatin DNA binding | 3 | 6 | 0.005446 | 4.19059941 |
| GO | insulin-like growth factor I binding | 3 | 6 | 0.005446 | 4.19059941 |
| GO | lipid binding | 16 | 116 | 0.005518 | 2.97892851 |
| GO | phosphatidylinositol binding | 5 | 18 | 0.005985 | 3.52272361 |
| GO | metal ion binding | 213 | 2658 | 0.006011 | 2.59675014 |
| GO | sarcolemma | 10 | 59 | 0.006254 | 3.08345325 |
| GO | positive regulation of apoptosis | 15 | 108 | 0.006635 | 2.91332224 |
| GO | cell-cell signaling | 27 | 238 | 0.006655 | 2.77443809 |
| GO | lung development | 10 | 60 | 0.007057 | 3.02270894 |
| GO | response to hypoxia | 18 | 140 | 0.007087 | 2.83421857 |
| GO | zinc ion binding | 154 | 1867 | 0.007194 | 2.54919044 |
| GO | B cell differentiation | 7 | 34 | 0.007213 | 3.18080871 |
| GO | palate development | 7 | 34 | 0.007213 | 3.18080871 |
| GO | protein amino acid dephosphorylation | 16 | 120 | 0.007642 | 2.82995576 |
| GO | leukotriene biosynthetic process | 5 | 19 | 0.007673 | 3.36668991 |
| GO | insulin-like growth factor binding | 5 | 19 | 0.007673 | 3.36668991 |
| GO | response to estradiol stimulus | 10 | 61 | 0.007937 | 2.96317511 |
| GO | basement membrane | 10 | 61 | 0.007937 | 2.96317511 |
| GO | kidney development | 10 | 61 | 0.007937 | 2.96317511 |
| GO | positive regulation of cell proliferation | 31 | 290 | 0.008997 | 2.62147079 |
| GO | transmembrane receptor protein tyrosine phosphatase signaling pathw | 3 | 7 | 0.009049 | 3.77745366 |
| GO | negative regulation of smooth muscle cell migration | 3 | 7 | 0.009049 | 3.77745366 |
| GO | GTP-Rho binding | 3 | 7 | 0.009049 | 3.77745366 |
| GO | positive regulation of pseudopodium assembly | 3 | 7 | 0.009049 | 3.77745366 |
| GO | P granule | 3 | 7 | 0.009049 | 3.77745366 |
| GO | piRNA metabolic process | 3 | 7 | 0.009049 | 3.77745366 |
| GO | natriuresis | 3 | 7 | 0.009049 | 3.77745366 |
| GO | drinking behavior | 3 | 7 | 0.009049 | 3.77745366 |
| GO | regulation of organ growth | 3 | 7 | 0.009049 | 3.77745366 |
| GO | neurotransmitter biosynthetic process | 3 | 7 | 0.009049 | 3.77745366 |
| GO | positive regulation of glycolysis | 3 | 7 | 0.009049 | 3.77745366 |
| GO | osteoclast differentiation | 3 | 7 | 0.009049 | 3.77745366 |
| GO | positive regulation of fatty acid beta-oxidation | 3 | 7 | 0.009049 | 3.77745366 |
| GO | calcium-activated potassium channel activity | 4 | 13 | 0.009427 | 3.42090875 |
| GO | insulin-like growth factor receptor binding | 4 | 13 | 0.009427 | 3.42090875 |
| GO | inflammatory response | 25 | 222 | 0.009603 | 2.62895529 |

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|---|---|---|---|---|---|
| GO | integral to Golgi membrane | 8 | 45 | 0.010411 | 2.91242389 |
| GO | protein dimerization activity | 12 | 84 | 0.01154 | 2.71212167 |
| GO | branching morphogenesis of a tube | 5 | 21 | 0.011985 | 3.08425664 |
| GO | negative regulation of BMP signaling pathway | 5 | 21 | 0.011985 | 3.08425664 |
| GO | induction of apoptosis | 20 | 170 | 0.01228 | 2.55865965 |
| GO | cell fate commitment | 6 | 29 | 0.012282 | 2.95890235 |
| GO | positive regulation of vasodilation | 4 | 14 | 0.012495 | 3.22414322 |
| GO | negative regulation of tumor necrosis factor production | 4 | 14 | 0.012495 | 3.22414322 |
| GO | cytoskeletal adaptor activity | 4 | 14 | 0.012495 | 3.22414322 |
| GO | complement activation, alternative pathway | 4 | 14 | 0.012495 | 3.22414322 |
| GO | negative regulation of transcription from RNA polymerase II promoter | 25 | 227 | 0.012514 | 2.50976116 |
| GO | transcription activator activity | 25 | 227 | 0.012514 | 2.50976116 |
| GO | epidermis development | 11 | 75 | 0.012619 | 2.69310063 |
| GO | double-stranded DNA binding | 11 | 75 | 0.012619 | 2.69310063 |
| GO | axon | 16 | 127 | 0.012895 | 2.58256753 |
| GO | endoplasmic reticulum membrane | 49 | 518 | 0.013107 | 2.40015136 |
| GO | regulation of potassium ion transport | 2 | 3 | 0.013367 | 4.10700924 |
| GO | homotypic cell-cell adhesion | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of lipopolysaccharide-mediated signaling pathway | 2 | 3 | 0.013367 | 4.10700924 |
| GO | regulation of MAP kinase activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | ubiquitin-protein ligase regulator activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | activin receptor complex | 2 | 3 | 0.013367 | 4.10700924 |
| GO | dense core granule | 2 | 3 | 0.013367 | 4.10700924 |
| GO | positive regulation of monocyte differentiation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of extracellular matrix disassembly | 2 | 3 | 0.013367 | 4.10700924 |
| GO | endothelial cell activation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | regulation of pathway-restricted SMAD protein phosphorylation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | dopamine receptor activity, coupled via Gi/Go | 2 | 3 | 0.013367 | 4.10700924 |
| GO | response to histamine | 2 | 3 | 0.013367 | 4.10700924 |
| GO | nitric oxide transport | 2 | 3 | 0.013367 | 4.10700924 |
| GO | positive regulation of sarcomere organization | 2 | 3 | 0.013367 | 4.10700924 |
| GO | brain segmentation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | positive regulation of granulocyte macrophage colony-stimulating fact | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of low-density lipoprotein particle clearance | 2 | 3 | 0.013367 | 4.10700924 |
| GO | glutamate decarboxylase activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | cerebral cortex neuron differentiation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of T-helper 2 cell differentiation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | interleukin-6 receptor complex | 2 | 3 | 0.013367 | 4.10700924 |
| GO | interleukin-6-mediated signaling pathway | 2 | 3 | 0.013367 | 4.10700924 |
| GO | germ cell programmed cell death | 2 | 3 | 0.013367 | 4.10700924 |
| GO | laminin-11 complex | 2 | 3 | 0.013367 | 4.10700924 |
| GO | protein-lysine 6-oxidase activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | common-partner SMAD protein phosphorylation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | positive regulation of keratinocyte differentiation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | pancreatic polypeptide receptor activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | xenobiotic-transporting ATPase activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of B cell apoptosis | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of T-helper 2 type immune response | 2 | 3 | 0.013367 | 4.10700924 |
| GO | negative regulation of prostatic bud formation | 2 | 3 | 0.013367 | 4.10700924 |

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|---|---|---|---|---|---|
| GO | microglial cell activation | 2 | 3 | 0.013367 | 4.10700924 |
| GO | cellular response to lipoteichoic acid | 2 | 3 | 0.013367 | 4.10700924 |
| GO | low voltage-gated calcium channel activity | 2 | 3 | 0.013367 | 4.10700924 |
| GO | regulation of protein binding | 3 | 8 | 0.013749 | 3.43779811 |
| GO | positive regulation of SMAD protein nuclear translocation | 3 | 8 | 0.013749 | 3.43779811 |
| GO | regulation of ossification | 3 | 8 | 0.013749 | 3.43779811 |
| GO | negative regulation of calcium ion transport via voltage-gated calcium | 3 | 8 | 0.013749 | 3.43779811 |
| GO | oxidative demethylation | 3 | 8 | 0.013749 | 3.43779811 |
| GO | retinal metabolic process | 3 | 8 | 0.013749 | 3.43779811 |
| GO | diuresis | 3 | 8 | 0.013749 | 3.43779811 |
| GO | heart trabecula formation | 3 | 8 | 0.013749 | 3.43779811 |
| GO | positive regulation of NF-kappaB import into nucleus | 3 | 8 | 0.013749 | 3.43779811 |
| GO | integrin-mediated signaling pathway | 9 | 57 | 0.01458 | 2.68310357 |
| GO | lyase activity | 13 | 97 | 0.014654 | 2.56968202 |
| GO | endomembrane system | 11 | 77 | 0.015215 | 2.59617825 |
| GO | ureteric bud development | 7 | 39 | 0.015332 | 2.75323672 |
| GO | positive regulation of gene-specific transcription | 7 | 39 | 0.015332 | 2.75323672 |
| GO | regulation of mitotic cell cycle | 4 | 15 | 0.016133 | 3.04494013 |
| GO | neural tube development | 4 | 15 | 0.016133 | 3.04494013 |
| GO | cholesterol metabolic process | 9 | 58 | 0.016244 | 2.62432456 |
| GO | SMAD binding | 6 | 31 | 0.016951 | 2.7646427 |
| GO | intracellular | 145 | 1794 | 0.017287 | 2.20069861 |
| GO | blood vessel development | 7 | 40 | 0.017519 | 2.6758052 |
| GO | positive regulation of glucose import | 5 | 23 | 0.017697 | 2.83424487 |
| GO | negative regulation of cell adhesion | 5 | 23 | 0.017697 | 2.83424487 |
| GO | SH3/SH2 adaptor activity | 8 | 50 | 0.019214 | 2.57156168 |
| GO | response to estrogen stimulus | 8 | 50 | 0.019214 | 2.57156168 |
| GO | blood vessel morphogenesis | 3 | 9 | 0.019587 | 3.15096855 |
| GO | cytoplasmic sequestering of transcription factor | 3 | 9 | 0.019587 | 3.15096855 |
| GO | oxidoreductase activity | 40 | 418 | 0.019668 | 2.24030443 |
| GO | negative regulation of MAP kinase activity | 4 | 16 | 0.02037 | 2.88058782 |
| GO | positive regulation of endothelial cell migration | 4 | 16 | 0.02037 | 2.88058782 |
| GO | membrane depolarization | 4 | 16 | 0.02037 | 2.88058782 |
| GO | SMAD protein signal transduction | 4 | 16 | 0.02037 | 2.88058782 |
| GO | positive regulation of vasoconstriction | 4 | 16 | 0.02037 | 2.88058782 |
| GO | negative regulation of transcription, DNA-dependent | 12 | 91 | 0.020871 | 2.40697893 |
| GO | positive regulation of nitric oxide biosynthetic process | 5 | 24 | 0.021128 | 2.71932149 |
| GO | response to insulin stimulus | 8 | 51 | 0.021467 | 2.50831541 |
| GO | cell growth | 7 | 42 | 0.022535 | 2.52777829 |
| GO | heart development | 14 | 114 | 0.023447 | 2.31114214 |
| GO | skeletal system development | 15 | 125 | 0.023501 | 2.29600632 |
| GO | response to peptide hormone stimulus | 9 | 62 | 0.0243 | 2.40070986 |
| GO | positive regulation of transcription factor activity | 5 | 25 | 0.024964 | 2.61024504 |
| GO | brown fat cell differentiation | 5 | 25 | 0.024964 | 2.61024504 |
| GO | activation of JUN kinase activity | 5 | 25 | 0.024964 | 2.61024504 |
| GO | organ morphogenesis | 14 | 115 | 0.02508 | 2.27579921 |
| GO | positive regulation of calcium-mediated signaling | 4 | 17 | 0.025229 | 2.72893467 |
| GO | nitrogen compound metabolic process | 4 | 17 | 0.025229 | 2.72893467 |
| GO | endoderm development | 4 | 17 | 0.025229 | 2.72893467 |

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|---|---|---|---|---|---|
| GO | 1-acylglycerophosphocholine O-acyltransferase activity | 2 | 4 | 0.025525 | 3.42142987 |
| GO | proton-transporting two-sector ATPase complex, proton-transporting | 2 | 4 | 0.025525 | 3.42142987 |
| GO | positive regulation of fatty acid oxidation | 2 | 4 | 0.025525 | 3.42142987 |
| GO | MyD88-dependent toll-like receptor signaling pathway | 2 | 4 | 0.025525 | 3.42142987 |
| GO | alcohol dehydrogenase activity, zinc-dependent | 2 | 4 | 0.025525 | 3.42142987 |
| GO | glial cell migration | 2 | 4 | 0.025525 | 3.42142987 |
| GO | phospholipid translocation | 2 | 4 | 0.025525 | 3.42142987 |
| GO | caffeine oxidase activity | 2 | 4 | 0.025525 | 3.42142987 |
| GO | drug catabolic process | 2 | 4 | 0.025525 | 3.42142987 |
| GO | Gram-positive bacterial cell surface binding | 2 | 4 | 0.025525 | 3.42142987 |
| GO | intercellular canaliculus | 2 | 4 | 0.025525 | 3.42142987 |
| GO | behavioral response to ethanol | 2 | 4 | 0.025525 | 3.42142987 |
| GO | cerebral cortex GABAergic interneuron migration | 2 | 4 | 0.025525 | 3.42142987 |
| GO | dopamine receptor activity | 2 | 4 | 0.025525 | 3.42142987 |
| GO | cellular sodium ion homeostasis | 2 | 4 | 0.025525 | 3.42142987 |
| GO | positive regulation of cardiac muscle hypertrophy | 2 | 4 | 0.025525 | 3.42142987 |
| GO | regulation of blood volume by renin-angiotensin | 2 | 4 | 0.025525 | 3.42142987 |
| GO | bioluminescence | 2 | 4 | 0.025525 | 3.42142987 |
| GO | hindgut morphogenesis | 2 | 4 | 0.025525 | 3.42142987 |
| GO | head morphogenesis | 2 | 4 | 0.025525 | 3.42142987 |
| GO | monocyte chemotaxis | 2 | 4 | 0.025525 | 3.42142987 |
| GO | negative regulation of collagen biosynthetic process | 2 | 4 | 0.025525 | 3.42142987 |
| GO | carbon dioxide transport | 2 | 4 | 0.025525 | 3.42142987 |
| GO | cellular response to dexamethasone stimulus | 2 | 4 | 0.025525 | 3.42142987 |
| GO | plasma membrane organization | 2 | 4 | 0.025525 | 3.42142987 |
| GO | fibril | 2 | 4 | 0.025525 | 3.42142987 |
| GO | negative regulation of myeloid cell differentiation | 2 | 4 | 0.025525 | 3.42142987 |
| GO | nucleotide-binding oligomerization domain containing 2 signaling path | 2 | 4 | 0.025525 | 3.42142987 |
| GO | response to muramyl dipeptide | 2 | 4 | 0.025525 | 3.42142987 |
| GO | peptide YY receptor activity | 2 | 4 | 0.025525 | 3.42142987 |
| GO | regulation of Wnt receptor signaling pathway through beta-catenin | 2 | 4 | 0.025525 | 3.42142987 |
| GO | negative regulation of appetite | 2 | 4 | 0.025525 | 3.42142987 |
| GO | negative regulation of sequestering of triglyceride | 2 | 4 | 0.025525 | 3.42142987 |
| GO | negative regulation of membrane protein ectodomain proteolysis | 2 | 4 | 0.025525 | 3.42142987 |
| GO | urinary bladder development | 2 | 4 | 0.025525 | 3.42142987 |
| GO | peptide:hydrogen symporter activity | 2 | 4 | 0.025525 | 3.42142987 |
| GO | cobalamin transport | 2 | 4 | 0.025525 | 3.42142987 |
| GO | positive regulation of nitric-oxide synthase biosynthetic process | 2 | 4 | 0.025525 | 3.42142987 |
| GO | lipopolysaccharide receptor complex | 2 | 4 | 0.025525 | 3.42142987 |
| GO | positive regulation of bone resorption | 2 | 4 | 0.025525 | 3.42142987 |
| GO | activation of MAPK activity | 8 | 53 | 0.026522 | 2.38615188 |
| GO | dopamine metabolic process | 3 | 10 | 0.026582 | 2.90367785 |
| GO | prostaglandin biosynthetic process | 3 | 10 | 0.026582 | 2.90367785 |
| GO | fatty acid transport | 3 | 10 | 0.026582 | 2.90367785 |
| GO | R-SMAD binding | 3 | 10 | 0.026582 | 2.90367785 |
| GO | prostate gland epithelium morphogenesis | 3 | 10 | 0.026582 | 2.90367785 |
| GO | defense response to Gram-negative bacterium | 3 | 10 | 0.026582 | 2.90367785 |
| GO | phosphoinositide 3-kinase binding | 3 | 10 | 0.026582 | 2.90367785 |
| GO | metalloendopeptidase inhibitor activity | 3 | 10 | 0.026582 | 2.90367785 |

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|---|---|---|---|---|---|
| GO | response to virus | 13 | 105 | 0.026674 | 2.25832995 |
| GO | peptidase activity | 43 | 465 | 0.026842 | 2.08724947 |
| GO | sugar binding | 18 | 161 | 0.026865 | 2.19422191 |
| GO | protein binding | 459 | 6249 | 0.027837 | 1.9517952 |
| GO | brush border membrane | 5 | 26 | 0.02922 | 2.50646932 |
| GO | endopeptidase inhibitor activity | 5 | 26 | 0.02922 | 2.50646932 |
| GO | neuropeptide signaling pathway | 11 | 85 | 0.029718 | 2.23596124 |
| GO | apoptosis | 41 | 444 | 0.030655 | 2.02736874 |
| GO | platelet-derived growth factor receptor signaling pathway | 4 | 18 | 0.030728 | 2.58824799 |
| GO | protein ubiquitination involved in ubiquitin-dependent protein catabo | 4 | 18 | 0.030728 | 2.58824799 |
| GO | endocrine pancreas development | 4 | 18 | 0.030728 | 2.58824799 |
| GO | response to corticosterone stimulus | 4 | 18 | 0.030728 | 2.58824799 |
| GO | pituitary gland development | 4 | 18 | 0.030728 | 2.58824799 |
| GO | cellular process | 4 | 18 | 0.030728 | 2.58824799 |
| GO | cortical cytoskeleton | 4 | 18 | 0.030728 | 2.58824799 |
| GO | protein amino acid glycosylation | 9 | 65 | 0.031965 | 2.24388376 |
| GO | iron ion binding | 9 | 65 | 0.031965 | 2.24388376 |
| GO | transforming growth factor beta receptor signaling pathway | 8 | 55 | 0.032349 | 2.26934106 |
| GO | transmembrane receptor activity | 13 | 108 | 0.032664 | 2.14850996 |
| GO | odontogenesis of dentine-containing tooth | 6 | 36 | 0.03361 | 2.33989753 |
| GO | response to cold | 5 | 27 | 0.033907 | 2.40751839 |
| GO | retinol dehydrogenase activity | 3 | 11 | 0.034729 | 2.68693381 |
| GO | negative regulation of osteoclast differentiation | 3 | 11 | 0.034729 | 2.68693381 |
| GO | sphingolipid biosynthetic process | 3 | 11 | 0.034729 | 2.68693381 |
| GO | transforming growth factor beta receptor activity | 3 | 11 | 0.034729 | 2.68693381 |
| GO | positive regulation of cellular protein metabolic process | 3 | 11 | 0.034729 | 2.68693381 |
| GO | arachidonic acid secretion | 3 | 11 | 0.034729 | 2.68693381 |
| GO | peptide hormone processing | 3 | 11 | 0.034729 | 2.68693381 |
| GO | positive regulation of interleukin-1 beta secretion | 3 | 11 | 0.034729 | 2.68693381 |
| GO | basal lamina | 3 | 11 | 0.034729 | 2.68693381 |
| GO | I-kappaB phosphorylation | 3 | 11 | 0.034729 | 2.68693381 |
| GO | cellular response to insulin stimulus | 7 | 46 | 0.035363 | 2.25569969 |
| GO | external side of plasma membrane | 14 | 121 | 0.036698 | 2.07080173 |
| GO | neutrophil chemotaxis | 4 | 19 | 0.036875 | 2.45711416 |
| GO | positive regulation of MAP kinase activity | 4 | 19 | 0.036875 | 2.45711416 |
| GO | positive regulation of JNK cascade | 4 | 19 | 0.036875 | 2.45711416 |
| GO | serine-type endopeptidase activity | 16 | 144 | 0.037188 | 2.04126778 |
| GO | integrin complex | 5 | 28 | 0.039033 | 2.31297528 |
| GO | lung morphogenesis | 2 | 5 | 0.040629 | 2.93915777 |
| GO | activation of MAPKKK activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | branching involved in mammary gland duct morphogenesis | 2 | 5 | 0.040629 | 2.93915777 |
| GO | positive regulation of sodium ion transport | 2 | 5 | 0.040629 | 2.93915777 |
| GO | monoterpenoid metabolic process | 2 | 5 | 0.040629 | 2.93915777 |
| GO | serine C-palmitoyltransferase activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | serine C-palmitoyltransferase complex | 2 | 5 | 0.040629 | 2.93915777 |
| GO | pattern recognition receptor activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | inhibition of adenylate cyclase activity by dopamine receptor signaling | 2 | 5 | 0.040629 | 2.93915777 |
| GO | nerve-nerve synaptic transmission | 2 | 5 | 0.040629 | 2.93915777 |
| GO | fear response | 2 | 5 | 0.040629 | 2.93915777 |

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|---|---|---|---|---|---|
| GO | protein tyrosine/threonine phosphatase activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | mitogen-activated protein kinase binding | 2 | 5 | 0.040629 | 2.93915777 |
| GO | microfibril | 2 | 5 | 0.040629 | 2.93915777 |
| GO | paraxial mesoderm formation | 2 | 5 | 0.040629 | 2.93915777 |
| GO | neutrophil mediated immunity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | positive regulation of immunoglobulin secretion | 2 | 5 | 0.040629 | 2.93915777 |
| GO | negative regulation of transporter activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | negative regulation of focal adhesion assembly | 2 | 5 | 0.040629 | 2.93915777 |
| GO | response to cholesterol | 2 | 5 | 0.040629 | 2.93915777 |
| GO | amine oxidase activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | regulation of cardiac muscle contraction | 2 | 5 | 0.040629 | 2.93915777 |
| GO | entrainment of circadian clock | 2 | 5 | 0.040629 | 2.93915777 |
| GO | prostaglandin E receptor activity | 2 | 5 | 0.040629 | 2.93915777 |
| GO | negative regulation of growth of symbiont in host | 2 | 5 | 0.040629 | 2.93915777 |
| GO | cell-matrix adhesion | 9 | 68 | 0.041163 | 2.09528969 |
| GO | protein homodimerization activity | 34 | 365 | 0.041173 | 1.89607134 |
| GO | negative regulation of cell migration | 6 | 38 | 0.042479 | 2.18964653 |
| GO | response to mechanical stimulus | 6 | 38 | 0.042479 | 2.18964653 |
| GO | transcription factor binding | 18 | 170 | 0.042732 | 1.94806018 |
| GO | cytokine-mediated signaling pathway | 7 | 48 | 0.043287 | 2.13003653 |
| GO | retina development in camera-type eye | 4 | 20 | 0.043678 | 2.33436646 |
| GO | tumor necrosis factor receptor binding | 4 | 20 | 0.043678 | 2.33436646 |
| GO | drug metabolic process | 3 | 12 | 0.044007 | 2.49439933 |
| GO | photoreceptor inner segment | 3 | 12 | 0.044007 | 2.49439933 |
| GO | response to pH | 3 | 12 | 0.044007 | 2.49439933 |
| GO | negative regulation of macrophage derived foam cell differentiation | 3 | 12 | 0.044007 | 2.49439933 |
| GO | positive regulation of interferon-beta production | 3 | 12 | 0.044007 | 2.49439933 |
| GO | metanephros development | 5 | 29 | 0.044606 | 2.22247287 |
| GO | protein targeting | 5 | 29 | 0.044606 | 2.22247287 |
| GO | in utero embryonic development | 15 | 136 | 0.045041 | 1.94544286 |
| GO | Golgi membrane | 32 | 343 | 0.045655 | 1.84760542 |
| GO | transport vesicle | 6 | 39 | 0.047414 | 2.11803392 |
| GO | calcium ion transport | 13 | 114 | 0.047442 | 1.93887619 |
| GO | receptor activity | 93 | 1148 | 0.047686 | 1.75396703 |
| GO | elevation of cytosolic calcium ion concentration | 11 | 92 | 0.048847 | 1.95146746 |
| GO | brain development | 13 | 115 | 0.050292 | 1.90514552 |
| GO | negative regulation of gene-specific transcription from RNA polymeras | 8 | 60 | 0.050569 | 1.99790727 |
| GO | adult locomotory behavior | 5 | 30 | 0.050631 | 2.13568644 |
| GO | dorsal/ventral pattern formation | 5 | 30 | 0.050631 | 2.13568644 |
| GO | positive regulation of inflammatory response | 4 | 21 | 0.051135 | 2.21903192 |
| GO | ventricular cardiac muscle tissue morphogenesis | 4 | 21 | 0.051135 | 2.21903192 |
| GO | negative regulation of gene-specific transcription | 4 | 21 | 0.051135 | 2.21903192 |
| GO | proteolysis | 38 | 423 | 0.051314 | 1.77101609 |
| GO | response to hydrogen peroxide | 6 | 40 | 0.05269 | 2.04857614 |
| GO | negative regulation of smooth muscle cell proliferation | 3 | 13 | 0.05438 | 2.32145913 |
| GO | hormone metabolic process | 3 | 13 | 0.05438 | 2.32145913 |
| GO | MAP kinase tyrosine/serine/threonine phosphatase activity | 3 | 13 | 0.05438 | 2.32145913 |
| GO | regulation of inflammatory response | 3 | 13 | 0.05438 | 2.32145913 |
| GO | negative regulation of Wnt receptor signaling pathway through beta-c | 3 | 13 | 0.05438 | 2.32145913 |

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|---|---|---|---|---|---|
| GO | embryonic cranial skeleton morphogenesis | 3 | 13 | 0.05438 | 2.32145913 |
| GO | inorganic anion exchanger activity | 3 | 13 | 0.05438 | 2.32145913 |
| GO | activation of NF-kappaB-inducing kinase activity | 3 | 13 | 0.05438 | 2.32145913 |
| GO | intracellular protein kinase cascade | 11 | 94 | 0.055565 | 1.8746873 |
| GO | embryonic development | 9 | 72 | 0.055986 | 1.90854926 |
| GO | positive regulation of MAPKKK cascade | 5 | 31 | 0.057108 | 2.05232749 |
| GO | heart morphogenesis | 5 | 31 | 0.057108 | 2.05232749 |
| GO | negative regulation of Ras protein signal transduction | 2 | 6 | 0.058221 | 2.57255176 |
| GO | prostate epithelial cord arborization involved in prostate glandular aci | 2 | 6 | 0.058221 | 2.57255176 |
| GO | negative regulation of interleukin-12 production | 2 | 6 | 0.058221 | 2.57255176 |
| GO | response to amine stimulus | 2 | 6 | 0.058221 | 2.57255176 |
| GO | negative regulation of protein secretion | 2 | 6 | 0.058221 | 2.57255176 |
| GO | peristalsis | 2 | 6 | 0.058221 | 2.57255176 |
| GO | regulation of synaptic transmission, GABAergic | 2 | 6 | 0.058221 | 2.57255176 |
| GO | regulation of dopamine metabolic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | positive regulation of fatty acid biosynthetic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | inositol phosphate-mediated signaling | 2 | 6 | 0.058221 | 2.57255176 |
| GO | mitochondrial membrane organization | 2 | 6 | 0.058221 | 2.57255176 |
| GO | positive regulation of mast cell degranulation | 2 | 6 | 0.058221 | 2.57255176 |
| GO | leukotriene metabolic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | lipoxygenase activity | 2 | 6 | 0.058221 | 2.57255176 |
| GO | glycosaminoglycan catabolic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | heparan sulfate proteoglycan biosynthetic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | neuron fate specification | 2 | 6 | 0.058221 | 2.57255176 |
| GO | exocrine pancreas development | 2 | 6 | 0.058221 | 2.57255176 |
| GO | positive regulation of myoblast differentiation | 2 | 6 | 0.058221 | 2.57255176 |
| GO | interleukin-6 receptor binding | 2 | 6 | 0.058221 | 2.57255176 |
| GO | positive regulation of acute inflammatory response | 2 | 6 | 0.058221 | 2.57255176 |
| GO | water transmembrane transporter activity | 2 | 6 | 0.058221 | 2.57255176 |
| GO | SMAD protein nuclear translocation | 2 | 6 | 0.058221 | 2.57255176 |
| GO | somatic stem cell division | 2 | 6 | 0.058221 | 2.57255176 |
| GO | negative regulation of erythrocyte differentiation | 2 | 6 | 0.058221 | 2.57255176 |
| GO | maintenance of gastrointestinal epithelium | 2 | 6 | 0.058221 | 2.57255176 |
| GO | dopamine biosynthetic process | 2 | 6 | 0.058221 | 2.57255176 |
| GO | negative regulation of cholesterol storage | 2 | 6 | 0.058221 | 2.57255176 |
| GO | protein thiol-disulfide exchange | 2 | 6 | 0.058221 | 2.57255176 |
| GO | regulation of branching involved in prostate gland morphogenesis | 2 | 6 | 0.058221 | 2.57255176 |
| GO | branching involved in embryonic placenta morphogenesis | 2 | 6 | 0.058221 | 2.57255176 |
| GO | cobalt ion transport | 2 | 6 | 0.058221 | 2.57255176 |
| GO | Rho GTPase activator activity | 4 | 22 | 0.059242 | 2.11029161 |
| GO | gluconeogenesis | 4 | 22 | 0.059242 | 2.11029161 |
| GO | negative regulation of NF-kappaB transcription factor activity | 4 | 22 | 0.059242 | 2.11029161 |
| GO | cysteine-type endopeptidase inhibitor activity | 4 | 22 | 0.059242 | 2.11029161 |
| GO | blood vessel remodeling | 4 | 22 | 0.059242 | 2.11029161 |
| GO | activation of phospholipase C activity | 4 | 22 | 0.059242 | 2.11029161 |
| GO | basal plasma membrane | 4 | 22 | 0.059242 | 2.11029161 |
| GO | voltage-gated calcium channel complex | 4 | 22 | 0.059242 | 2.11029161 |
| GO | positive regulation of cell migration | 8 | 62 | 0.059401 | 1.89661467 |
| GO | extracellular matrix organization | 8 | 62 | 0.059401 | 1.89661467 |

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|---|---|---|---|---|---|
| GO | G-protein coupled receptor activity | 32 | 352 | 0.060733 | 1.69312561 |
| GO | anti-apoptosis | 18 | 178 | 0.061715 | 1.74101138 |
| GO | positive regulation of anti-apoptosis | 5 | 32 | 0.064037 | 1.97213867 |
| GO | spermatid development | 5 | 32 | 0.064037 | 1.97213867 |
| GO | apical part of cell | 6 | 42 | 0.06427 | 1.91563311 |
| GO | cytokine activity | 15 | 143 | 0.06445 | 1.73843571 |
| GO | transcription repressor binding | 3 | 14 | 0.065804 | 2.16465914 |
| GO | response to starvation | 3 | 14 | 0.065804 | 2.16465914 |
| GO | regulation of sensory perception of pain | 3 | 14 | 0.065804 | 2.16465914 |
| GO | regulation of vasoconstriction | 3 | 14 | 0.065804 | 2.16465914 |
| GO | regulation of neuronal synaptic plasticity | 3 | 14 | 0.065804 | 2.16465914 |
| GO | positive regulation of protein secretion | 3 | 14 | 0.065804 | 2.16465914 |
| GO | artery morphogenesis | 3 | 14 | 0.065804 | 2.16465914 |
| GO | eye development | 3 | 14 | 0.065804 | 2.16465914 |
| GO | negative regulation of mitotic cell cycle | 3 | 14 | 0.065804 | 2.16465914 |
| GO | sialyltransferase activity | 3 | 14 | 0.065804 | 2.16465914 |
| GO | DNA damage response, signal transduction by p53 class mediator resu | 3 | 14 | 0.065804 | 2.16465914 |
| GO | response to ATP | 3 | 14 | 0.065804 | 2.16465914 |
| GO | proteasome core complex | 3 | 14 | 0.065804 | 2.16465914 |
| GO | guanyl-nucleotide exchange factor activity | 13 | 120 | 0.066302 | 1.74126282 |
| GO | galactosyltransferase activity | 4 | 23 | 0.067988 | 2.00745043 |
| GO | activation of MAPKK activity | 4 | 23 | 0.067988 | 2.00745043 |
| GO | voltage-gated calcium channel activity | 4 | 23 | 0.067988 | 2.00745043 |
| GO | negative regulation of cell migration involved in sprouting angiogenesi | 1 | 1 | 0.068348 | 3.69201445 |
| GO | 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | racemase and epimerase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | lung growth | 1 | 1 | 0.068348 | 3.69201445 |
| GO | ATP-binding and phosphorylation-dependent chloride channel activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | channel-conductance-controlling ATPase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | actin modification | 1 | 1 | 0.068348 | 3.69201445 |
| GO | myosin II binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of synapse organization | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of innate immune response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of macrophage cytokine production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of macrophage tolerance induction | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of protein complex disassembly | 1 | 1 | 0.068348 | 3.69201445 |
| GO | acyl carnitine transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | sphinganine metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | sphingolipid delta-4 desaturase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | sphingosine hydroxylase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | neuronal RNA granule | 1 | 1 | 0.068348 | 3.69201445 |
| GO | collagen type VIII | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbamoyl phosphate biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbamoyl-phosphate synthase (ammonia) activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbamoyl-phosphate synthase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | citrulline biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | nitric oxide metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | mammary gland fat development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of mononuclear cell proliferation | 1 | 1 | 0.068348 | 3.69201445 |

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|---|---|---|---|---|---|
| GO | regulation of macrophage derived foam cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | reproductive developmental process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of blood vessel remodeling | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of collagen catabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of elastin catabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of histolysis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of tissue remodeling | 1 | 1 | 0.068348 | 3.69201445 |
| GO | beta2-adrenergic receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular amide metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | urea metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of endothelial cell migration | 1 | 1 | 0.068348 | 3.69201445 |
| GO | induction of bacterial agglutination | 1 | 1 | 0.068348 | 3.69201445 |
| GO | zymogen binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | establishment of localization | 1 | 1 | 0.068348 | 3.69201445 |
| GO | invadopodium membrane | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of T cell mediated immunity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | dopamine D2 receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | dopamine D4 receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | toxin receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | angiotensin mediated vasoconstriction involved in regulation of syster | 1 | 1 | 0.068348 | 3.69201445 |
| GO | renal response to blood flow involved in circulatory renin-angiotensin | 1 | 1 | 0.068348 | 3.69201445 |
| GO | response to muscle activity involved in regulation of muscle adaptatio | 1 | 1 | 0.068348 | 3.69201445 |
| GO | type 2 angiotensin receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of elastin biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | activation of phospholipase D activity by G-protein coupled receptor p | 1 | 1 | 0.068348 | 3.69201445 |
| GO | endothelin A receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of nitric-oxide synthase biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | protein kinase C deactivation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | O-glycan processing, core 3 | 1 | 1 | 0.068348 | 3.69201445 |
| GO | rhombomere 3 formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | rhombomere 5 formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | axial mesoderm formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | notochord cell development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of cellular metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of cellular metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of angiotensin metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | synapse maturation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | hemopoietic stem cell proliferation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of type I hypersensitivity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | pancreatic D cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | pancreatic E cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cytoskeleton-dependent intracellular transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | latrotoxin receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | low-density lipoprotein receptor catabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glutamate catabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | protein-pyridoxal-5-phosphate linkage | 1 | 1 | 0.068348 | 3.69201445 |
| GO | exocrine system development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | intrinsic to plasma membrane | 1 | 1 | 0.068348 | 3.69201445 |
| GO | racemase and epimerase activity, acting on carbohydrates and derivat | 1 | 1 | 0.068348 | 3.69201445 |

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|---|---|---|---|---|---|
| GO | UDP-glucuronate 5'-epimerase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | vitamin transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | vitamin transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | FADH2 metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | intracellular pH elevation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactosa | 1 | 1 | 0.068348 | 3.69201445 |
| GO | anterior semicircular canal development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | lateral semicircular canal development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | pallium development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | ferritin receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | iron ion transmembrane transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of interleukin-10 biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | histidine ammonia-lyase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | radial spoke | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glycolate metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | muscle hypertrophy | 1 | 1 | 0.068348 | 3.69201445 |
| GO | myotube cell development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | satellite cell maintenance involved in skeletal muscle regeneration | 1 | 1 | 0.068348 | 3.69201445 |
| GO | intussusceptive angiogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | butyryl-CoA dehydrogenase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glucagon secretion | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of B cell activation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | ciliary neurotrophic factor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of activation of Janus kinase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbon dioxide transmembrane transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbon dioxide transmembrane transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular hyperosmotic response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to inorganic substance | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to mechanical stimulus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to nitric oxide | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to salt stress | 1 | 1 | 0.068348 | 3.69201445 |
| GO | establishment or maintenance of actin cytoskeleton polarity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | maintenance of symbiont-containing vacuole via substance secreted b | 1 | 1 | 0.068348 | 3.69201445 |
| GO | nitric oxide transmembrane transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | symbiont-containing vacuole membrane | 1 | 1 | 0.068348 | 3.69201445 |
| GO | transepithelial water transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | insulin receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of developmental growth | 1 | 1 | 0.068348 | 3.69201445 |
| GO | transformation of host cell by virus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | leading edge cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of synaptic growth at neuromuscular junction | 1 | 1 | 0.068348 | 3.69201445 |
| GO | stem cell factor receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | GMP binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | laminin-5 complex | 1 | 1 | 0.068348 | 3.69201445 |
| GO | morphogenesis of a polarized epithelium | 1 | 1 | 0.068348 | 3.69201445 |
| GO | axon extension involved in regeneration | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of phospholipase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to vitamin A | 1 | 1 | 0.068348 | 3.69201445 |
| GO | steryl-sulfatase activity | 1 | 1 | 0.068348 | 3.69201445 |

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|---|---|---|---|---|---|
| GO | mannosidase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | protein channel activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | inner acrosomal membrane | 1 | 1 | 0.068348 | 3.69201445 |
| GO | G0 to G1 transition | 1 | 1 | 0.068348 | 3.69201445 |
| GO | double-stranded methylated DNA binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of myeloid leukocyte differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to magnetism | 1 | 1 | 0.068348 | 3.69201445 |
| GO | lung epithelial cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | neuroblast fate determination | 1 | 1 | 0.068348 | 3.69201445 |
| GO | noradrenergic neuron fate commitment | 1 | 1 | 0.068348 | 3.69201445 |
| GO | oligodendrocyte cell fate commitment | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of timing of subpallium neuron differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | response to epidermal growth factor stimulus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | methylenetetrahydrofolate reductase (NADPH) activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | nitrilase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | aortic valve morphogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | endocardium morphogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | foregut morphogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of epithelial cell proliferation involved in prostate gland dev | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of somitogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | generation of ovulation cycle rhythm | 1 | 1 | 0.068348 | 3.69201445 |
| GO | 2'-5'-oligoadenylate synthetase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | relaxation of cardiac muscle | 1 | 1 | 0.068348 | 3.69201445 |
| GO | protein amino acid hydroxylation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | tetrahydrobiopterin metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | tyrosine biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | interleukin-20 receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of epidermal cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | peptidylamidoglycolate lyase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | peptidylglycine monooxygenase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | carbohydrate response element binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glucose mediated signaling pathway | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of oxidative phosphorylation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | spot adherens junction | 1 | 1 | 0.068348 | 3.69201445 |
| GO | 1-phosphatidylinositol-4-phosphate 3-kinase, class IA complex | 1 | 1 | 0.068348 | 3.69201445 |
| GO | branchiomeric skeletal muscle development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | hydroxylysine biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | granule cell precursor tangential migration | 1 | 1 | 0.068348 | 3.69201445 |
| GO | melanin-concentrating hormone activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | type 1 melanin-concentrating hormone receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of translation in response to oxidative stress | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of calcium-dependent cell-cell adhesion | 1 | 1 | 0.068348 | 3.69201445 |
| GO | lactosylceramide 4-alpha-galactosyltransferase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | thyroid stimulating hormone secreting cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cell fate commitment involved in the formation of primary germ layer | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of catenin protein nuclear translocation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of canonical Wnt receptor signaling pathway involved in he | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of methylation-dependent chromatin silencing | 1 | 1 | 0.068348 | 3.69201445 |
| GO | RNA 5'-end processing | 1 | 1 | 0.068348 | 3.69201445 |

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| GO | sphingoid biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | barrier septum formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | unidimensional cell growth | 1 | 1 | 0.068348 | 3.69201445 |
| GO | inorganic diphosphate transmembrane transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | asymmetric cell division | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of complement activation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase activ | 1 | 1 | 0.068348 | 3.69201445 |
| GO | neuromedin U binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | columnar/cuboidal epithelial cell development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of calcium ion transport via store-operated calciur | 1 | 1 | 0.068348 | 3.69201445 |
| GO | flavin-linked sulfhydryl oxidase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of mast cell activation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cytotoxic T cell degranulation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | retinol transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | retinol transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | spermatogonial cell division | 1 | 1 | 0.068348 | 3.69201445 |
| GO | response to cGMP | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of germinal center formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of memory T cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | complement binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of mitochondrion organization | 1 | 1 | 0.068348 | 3.69201445 |
| GO | activation of immune response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cytokine production involved in immune response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | detection of muramyl dipeptide | 1 | 1 | 0.068348 | 3.69201445 |
| GO | immunoglobulin production during immune response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | macrophage inflammatory protein-1 alpha production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | muramyl dipeptide binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of interleukin-18 production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of toll-like receptor 2 signaling pathway | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glutamate:sodium symporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | branch elongation involved in ureteric bud branching | 1 | 1 | 0.068348 | 3.69201445 |
| GO | bronchus development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | bud dilation involved in lung branching | 1 | 1 | 0.068348 | 3.69201445 |
| GO | epithelial cell proliferation involved in lung morphogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | intermediate mesodermal cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | mammary gland formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of branching involved in ureteric bud morphogene | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of glomerulus development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | trachea formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | creatine transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | creatine transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | creatine:sodium symporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | channel inhibitor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of amino acid transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | oligopeptide transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | antibiotic transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | antibiotic transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | dipeptide transporter activity | 1 | 1 | 0.068348 | 3.69201445 |

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| GO | dipeptide transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | high affinity oligopeptide transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of dopamine uptake | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of monooxygenase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of norepinephrine uptake | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of serotonin uptake | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of thrombin receptor signaling pathway | 1 | 1 | 0.068348 | 3.69201445 |
| GO | neutral lipid metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | phospholipase D inhibitor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of acyl-CoA biosynthetic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of phospholipase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of synaptic vesicle priming | 1 | 1 | 0.068348 | 3.69201445 |
| GO | thromboxane-A synthase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | respiratory burst involved in inflammatory response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | radial pattern formation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | definitive erythrocyte differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | response to luteinizing hormone stimulus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | transforming growth factor beta receptor activity, type III | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cellular response to bacterial lipopeptide | 1 | 1 | 0.068348 | 3.69201445 |
| GO | chloramphenicol transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | triacylated lipopeptide binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | detection of virus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | detection of fungus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | innate immune response-activating signal transduction | 1 | 1 | 0.068348 | 3.69201445 |
| GO | intestinal epithelial structure maintenance | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of interleukin-17 production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of interleukin-23 production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of interleukin-1 production | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of nucleotide-binding oligomerization domain cont | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of nucleotide-binding oligomerization domain cont | 1 | 1 | 0.068348 | 3.69201445 |
| GO | production of nitric oxide involved in inflammatory response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of type IIa hypersensitivity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | ionotropic glutamate receptor complex | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of mesenchymal cell proliferation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of cytokine secretion during immune response | 1 | 1 | 0.068348 | 3.69201445 |
| GO | receptor tyrosine kinase-like orphan receptor binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of nuclear-transcribed mRNA poly(A) tail shortenin | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of nuclease activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | oxidoreductase activity, acting on the CH-OH group of donors, quinon | 1 | 1 | 0.068348 | 3.69201445 |
| GO | calcitonin binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | semicircular canal morphogenesis | 1 | 1 | 0.068348 | 3.69201445 |
| GO | vestibular reflex | 1 | 1 | 0.068348 | 3.69201445 |
| GO | hydroxypyruvate isomerase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | calcium-dependent cysteine-type endopeptidase inhibitor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | CMP-N-acetylneuraminate monooxygenase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | patched ligand maturation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of skeletal muscle tissue development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | ribonuclease T2 activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | BMP signaling pathway involved in spinal cord dorsal/ventral patterni | 1 | 1 | 0.068348 | 3.69201445 |

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| GO | floor plate development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | galactosylgalactosylglucosylceramide beta-D-acetylgalactosaminyltran | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of protein oligomerization | 1 | 1 | 0.068348 | 3.69201445 |
| GO | phosphatidic acid binding | 1 | 1 | 0.068348 | 3.69201445 |
| GO | negative regulation of Golgi to plasma membrane protein transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | trans-Golgi network transport vesicle membrane | 1 | 1 | 0.068348 | 3.69201445 |
| GO | pyruvate secondary active transmembrane transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | pyruvate transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | opsonin receptor activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | nicotinate phosphoribosyltransferase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | phosphorus-oxygen lyase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glucose 1-dehydrogenase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | guanine deaminase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | detection of hormone stimulus | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glycoprotein transporter activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | glycoprotein transport | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of cholesterol esterification | 1 | 1 | 0.068348 | 3.69201445 |
| GO | sterol-transporting ATPase activity | 1 | 1 | 0.068348 | 3.69201445 |
| GO | regulation of striated muscle cell differentiation | 1 | 1 | 0.068348 | 3.69201445 |
| GO | rhombomere 6 development | 1 | 1 | 0.068348 | 3.69201445 |
| GO | cytokine metabolic process | 1 | 1 | 0.068348 | 3.69201445 |
| GO | meiotic cohesin complex | 1 | 1 | 0.068348 | 3.69201445 |
| GO | positive regulation of I-kappaB kinase/NF-kappaB cascade | 12 | 109 | 0.068635 | 1.73201304 |
| GO | cell cortex | 9 | 75 | 0.069117 | 1.77612679 |
| GO | calcium-mediated signaling | 5 | 33 | 0.071416 | 1.89488958 |
| GO | learning or memory | 5 | 33 | 0.071416 | 1.89488958 |
| GO | lipid metabolic process | 20 | 206 | 0.071456 | 1.64352049 |
| GO | chloride channel complex | 7 | 54 | 0.073533 | 1.7870745 |
| GO | oxidation reduction | 44 | 515 | 0.074186 | 1.5580508 |
| GO | ubiquitin protein ligase binding | 6 | 44 | 0.077226 | 1.78993003 |
| GO | drug binding | 6 | 44 | 0.077226 | 1.78993003 |
| GO | hydrolase activity, acting on glycosyl bonds | 6 | 44 | 0.077226 | 1.78993003 |
| GO | response to interleukin-1 | 4 | 24 | 0.077361 | 1.90991387 |
| GO | defense response to Gram-positive bacterium | 4 | 24 | 0.077361 | 1.90991387 |
| GO | response to metal ion | 2 | 7 | 0.077889 | 2.27939317 |
| GO | positive regulation of ossification | 2 | 7 | 0.077889 | 2.27939317 |
| GO | chitin catabolic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | chitinase activity | 2 | 7 | 0.077889 | 2.27939317 |
| GO | retinoic acid binding | 2 | 7 | 0.077889 | 2.27939317 |
| GO | axon regeneration | 2 | 7 | 0.077889 | 2.27939317 |
| GO | fibril organization | 2 | 7 | 0.077889 | 2.27939317 |
| GO | dopamine binding | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of peptidyl-serine phosphorylation | 2 | 7 | 0.077889 | 2.27939317 |
| GO | exogenous drug catabolic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of cAMP biosynthetic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | smooth muscle cell differentiation | 2 | 7 | 0.077889 | 2.27939317 |
| GO | detection of light stimulus involved in visual perception | 2 | 7 | 0.077889 | 2.27939317 |
| GO | bHLH transcription factor binding | 2 | 7 | 0.077889 | 2.27939317 |
| GO | embryonic process involved in female pregnancy | 2 | 7 | 0.077889 | 2.27939317 |

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|---|---|---|---|---|---|
| GO | central nervous system neuron development | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of T cell receptor signaling pathway | 2 | 7 | 0.077889 | 2.27939317 |
| GO | cellular homeostasis | 2 | 7 | 0.077889 | 2.27939317 |
| GO | pancreatic juice secretion | 2 | 7 | 0.077889 | 2.27939317 |
| GO | positive regulation of interleukin-12 biosynthetic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | wound healing, spreading of epidermal cells | 2 | 7 | 0.077889 | 2.27939317 |
| GO | positive regulation of Notch signaling pathway | 2 | 7 | 0.077889 | 2.27939317 |
| GO | response to selenium ion | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of myoblast differentiation | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of synaptic transmission, GABAergic | 2 | 7 | 0.077889 | 2.27939317 |
| GO | aggresome | 2 | 7 | 0.077889 | 2.27939317 |
| GO | 3',5'-cyclic-GMP phosphodiesterase activity | 2 | 7 | 0.077889 | 2.27939317 |
| GO | phototransduction, visible light | 2 | 7 | 0.077889 | 2.27939317 |
| GO | chromatoid body | 2 | 7 | 0.077889 | 2.27939317 |
| GO | CARD domain binding | 2 | 7 | 0.077889 | 2.27939317 |
| GO | negative regulation of interferon-gamma production | 2 | 7 | 0.077889 | 2.27939317 |
| GO | hyperosmotic response | 2 | 7 | 0.077889 | 2.27939317 |
| GO | positive regulation of chemokine biosynthetic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | positive regulation of interferon-beta biosynthetic process | 2 | 7 | 0.077889 | 2.27939317 |
| GO | regulation of mRNA stability | 2 | 7 | 0.077889 | 2.27939317 |
| GO | transmembrane receptor protein serine/threonine kinase activity | 2 | 7 | 0.077889 | 2.27939317 |
| GO | response to biotic stimulus | 3 | 15 | 0.078221 | 2.0213543 |
| GO | water transport | 3 | 15 | 0.078221 | 2.0213543 |
| GO | cellular response to heat | 3 | 15 | 0.078221 | 2.0213543 |
| GO | positive regulation of phagocytosis | 3 | 15 | 0.078221 | 2.0213543 |
| GO | response to vitamin D | 3 | 15 | 0.078221 | 2.0213543 |
| GO | polysome | 3 | 15 | 0.078221 | 2.0213543 |
| GO | phosphatidylinositol-4,5-bisphosphate binding | 3 | 15 | 0.078221 | 2.0213543 |
| GO | extrinsic to membrane | 5 | 34 | 0.07924 | 1.82037319 |
| GO | perikaryon | 5 | 34 | 0.07924 | 1.82037319 |
| GO | lipid transport | 8 | 66 | 0.079814 | 1.70484899 |
| GO | anatomical structure morphogenesis | 11 | 101 | 0.083773 | 1.6197354 |
| GO | glucose homeostasis | 6 | 45 | 0.084217 | 1.72955338 |
| GO | GTPase activity | 19 | 198 | 0.084525 | 1.54773173 |
| GO | epidermal growth factor receptor signaling pathway | 4 | 25 | 0.087341 | 1.81716987 |
| GO | mammary gland development | 4 | 25 | 0.087341 | 1.81716987 |
| GO | skeletal system morphogenesis | 4 | 25 | 0.087341 | 1.81716987 |
| GO | feeding behavior | 4 | 25 | 0.087341 | 1.81716987 |
| GO | positive regulation of B cell proliferation | 4 | 25 | 0.087341 | 1.81716987 |
| GO | positive regulation of protein amino acid phosphorylation | 5 | 35 | 0.087503 | 1.74840286 |
| GO | steroid metabolic process | 8 | 68 | 0.091405 | 1.61387119 |
| GO | regulation of small GTPase mediated signal transduction | 6 | 46 | 0.091545 | 1.67071297 |
| GO | carbonate dehydratase activity | 3 | 16 | 0.091572 | 1.88947898 |
| GO | glycosaminoglycan binding | 3 | 16 | 0.091572 | 1.88947898 |
| GO | negative regulation of blood pressure | 3 | 16 | 0.091572 | 1.88947898 |
| GO | antigen binding | 3 | 16 | 0.091572 | 1.88947898 |
| GO | neurogenesis | 3 | 16 | 0.091572 | 1.88947898 |
| GO | carbohydrate binding | 3 | 16 | 0.091572 | 1.88947898 |
| GO | gap junction | 3 | 16 | 0.091572 | 1.88947898 |

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|---|---|---|---|---|---|
| GO | neuron fate commitment | 3 | 16 | 0.091572 | 1.88947898 |
| GO | negative regulation of protein amino acid phosphorylation | 3 | 16 | 0.091572 | 1.88947898 |
| GO | negative regulation of endothelial cell proliferation | 3 | 16 | 0.091572 | 1.88947898 |
| GO | regulation of cell growth | 7 | 57 | 0.092377 | 1.63176254 |
| GO | liver development | 7 | 57 | 0.092377 | 1.63176254 |
| GO | ion channel activity | 15 | 151 | 0.092713 | 1.5150815 |
| GO | calcium ion binding | 50 | 605 | 0.093517 | 1.41623362 |
| GO | skeletal muscle tissue development | 5 | 36 | 0.096195 | 1.67880982 |
| GO | ovarian follicle development | 5 | 36 | 0.096195 | 1.67880982 |
| GO | insulin receptor signaling pathway | 5 | 36 | 0.096195 | 1.67880982 |
| GO | extracellular matrix structural constituent | 8 | 69 | 0.097545 | 1.56951049 |
| GO | negative regulation of apoptosis | 14 | 140 | 0.097659 | 1.48959411 |
| GO | cell differentiation | 40 | 474 | 0.097833 | 1.40146099 |
| GO | cellular response to hormone stimulus | 4 | 26 | 0.097908 | 1.72877463 |
| GO | branching involved in ureteric bud morphogenesis | 4 | 26 | 0.097908 | 1.72877463 |
| GO | negative regulation of epithelial cell proliferation | 4 | 26 | 0.097908 | 1.72877463 |
| GO | chloride channel activity | 7 | 58 | 0.099204 | 1.5820587 |
| GO | oxidoreductase activity, acting on single donors with incorporation of | 7 | 58 | 0.099204 | 1.5820587 |
| GO | UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransfera | 2 | 8 | 0.099269 | 2.03645393 |
| GO | phosphate transport | 2 | 8 | 0.099269 | 2.03645393 |
| GO | regulation of calcium ion-dependent exocytosis | 2 | 8 | 0.099269 | 2.03645393 |
| GO | secretory granule membrane | 2 | 8 | 0.099269 | 2.03645393 |
| GO | embryonic viscerocranium morphogenesis | 2 | 8 | 0.099269 | 2.03645393 |
| GO | behavioral response to cocaine | 2 | 8 | 0.099269 | 2.03645393 |
| GO | positive regulation of neuroblast proliferation | 2 | 8 | 0.099269 | 2.03645393 |
| GO | regulation of heart rate | 2 | 8 | 0.099269 | 2.03645393 |
| GO | regulation of sodium ion transport | 2 | 8 | 0.099269 | 2.03645393 |
| GO | phosphoinositide 3-kinase cascade | 2 | 8 | 0.099269 | 2.03645393 |
| GO | cellular response to hydrogen peroxide | 2 | 8 | 0.099269 | 2.03645393 |
| GO | histone acetyltransferase complex | 2 | 8 | 0.099269 | 2.03645393 |
| GO | negative regulation of programmed cell death | 2 | 8 | 0.099269 | 2.03645393 |
| GO | protein autoprocessing | 2 | 8 | 0.099269 | 2.03645393 |
| GO | positive regulation of chondrocyte differentiation | 2 | 8 | 0.099269 | 2.03645393 |
| GO | positive regulation of leukocyte chemotaxis | 2 | 8 | 0.099269 | 2.03645393 |
| GO | regulation of embryonic development | 2 | 8 | 0.099269 | 2.03645393 |
| GO | positive regulation of leukocyte migration | 2 | 8 | 0.099269 | 2.03645393 |
| GO | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity | 2 | 8 | 0.099269 | 2.03645393 |
| GO | glycosphingolipid biosynthetic process | 2 | 8 | 0.099269 | 2.03645393 |
| GO | glycerophosphodiester phosphodiesterase activity | 2 | 8 | 0.099269 | 2.03645393 |
| GO | phosphatidylinositol-3-phosphate binding | 2 | 8 | 0.099269 | 2.03645393 |
| GO | mesonephros development | 2 | 8 | 0.099269 | 2.03645393 |
| GO | peptidoglycan binding | 2 | 8 | 0.099269 | 2.03645393 |
| GO | positive regulation of endocytosis | 2 | 8 | 0.099269 | 2.03645393 |
| GO | regulation of dopamine secretion | 2 | 8 | 0.099269 | 2.03645393 |
| GO | syntaxin-1 binding | 2 | 8 | 0.099269 | 2.03645393 |
| GO | cobalamin binding | 2 | 8 | 0.099269 | 2.03645393 |
| GO | negative regulation of endothelial cell migration | 2 | 8 | 0.099269 | 2.03645393 |
| GO | calcium channel complex | 2 | 8 | 0.099269 | 2.03645393 |
| GO | protein amino acid phosphorylation | 41 | 488 | 0.099532 | 1.38957171 |

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|---|---|---|---|---|---|
| GO | endoplasmic reticulum | 70 | 880 | 0.102142 | 1.34789252 |
| GO | heparin binding | 11 | 105 | 0.103256 | 1.48273034 |
| GO | response to ethanol | 8 | 70 | 0.103912 | 1.52586823 |
| GO | oxygen binding | 5 | 37 | 0.105307 | 1.61144096 |
| GO | positive regulation of pathway-restricted SMAD protein phosphorylati | 3 | 17 | 0.105788 | 1.76739253 |
| GO | aspartic-type endopeptidase activity | 3 | 17 | 0.105788 | 1.76739253 |
| GO | sphingolipid metabolic process | 3 | 17 | 0.105788 | 1.76739253 |
| GO | social behavior | 3 | 17 | 0.105788 | 1.76739253 |
| GO | actin filament capping | 3 | 17 | 0.105788 | 1.76739253 |
| GO | negative regulation of osteoblast differentiation | 3 | 17 | 0.105788 | 1.76739253 |
| GO | transcription corepressor activity | 14 | 142 | 0.106427 | 1.4335163 |
| GO | negative regulation of signal transduction | 6 | 48 | 0.107195 | 1.55733646 |
| GO | adherens junction | 4 | 27 | 0.109039 | 1.64434121 |
| GO | endocytic vesicle | 4 | 27 | 0.109039 | 1.64434121 |
| GO | positive regulation of fibroblast proliferation | 4 | 27 | 0.109039 | 1.64434121 |
| GO | SH2 domain binding | 4 | 27 | 0.109039 | 1.64434121 |
| GO | transmembrane receptor protein tyrosine kinase signaling pathway | 8 | 71 | 0.110505 | 1.48292065 |
| GO | GTPase activator activity | 15 | 156 | 0.113798 | 1.3819275 |
| GO | positive regulation of angiogenesis | 5 | 38 | 0.114827 | 1.54615705 |
| GO | digestion | 6 | 49 | 0.115504 | 1.5026615 |
| GO | phospholipid binding | 6 | 49 | 0.115504 | 1.5026615 |
| GO | tight junction | 8 | 72 | 0.11732 | 1.44064511 |
| GO | actin filament organization | 4 | 28 | 0.120707 | 1.5635304 |
| GO | memory | 4 | 28 | 0.120707 | 1.5635304 |
| GO | positive regulation of DNA replication | 4 | 28 | 0.120707 | 1.5635304 |
| GO | sensory perception of pain | 4 | 28 | 0.120707 | 1.5635304 |
| GO | beta-amyloid binding | 3 | 18 | 0.1208 | 1.65377237 |
| GO | cornified envelope | 3 | 18 | 0.1208 | 1.65377237 |
| GO | integral to membrane of membrane fraction | 3 | 18 | 0.1208 | 1.65377237 |
| GO | establishment or maintenance of cell polarity | 3 | 18 | 0.1208 | 1.65377237 |
| GO | polypeptide N-acetylgalactosaminyltransferase activity | 3 | 18 | 0.1208 | 1.65377237 |
| GO | inner ear development | 3 | 18 | 0.1208 | 1.65377237 |
| GO | inward rectifier potassium channel activity | 3 | 18 | 0.1208 | 1.65377237 |
| GO | cytoskeleton organization | 7 | 61 | 0.121282 | 1.43858443 |
| GO | axonogenesis | 7 | 61 | 0.121282 | 1.43858443 |
| GO | NADPH oxidase complex | 2 | 9 | 0.122036 | 1.82973378 |
| GO | intracellular part | 2 | 9 | 0.122036 | 1.82973378 |
| GO | negative regulation of interleukin-6 production | 2 | 9 | 0.122036 | 1.82973378 |
| GO | negative regulation of protein catabolic process | 2 | 9 | 0.122036 | 1.82973378 |
| GO | embryonic foregut morphogenesis | 2 | 9 | 0.122036 | 1.82973378 |
| GO | retinal binding | 2 | 9 | 0.122036 | 1.82973378 |
| GO | respiratory burst | 2 | 9 | 0.122036 | 1.82973378 |
| GO | associative learning | 2 | 9 | 0.122036 | 1.82973378 |
| GO | phosphoinositide metabolic process | 2 | 9 | 0.122036 | 1.82973378 |
| GO | low-density lipoprotein particle remodeling | 2 | 9 | 0.122036 | 1.82973378 |
| GO | telencephalon development | 2 | 9 | 0.122036 | 1.82973378 |
| GO | fucosyltransferase activity | 2 | 9 | 0.122036 | 1.82973378 |
| GO | detection of calcium ion | 2 | 9 | 0.122036 | 1.82973378 |
| GO | regulation of MAPKKK cascade | 2 | 9 | 0.122036 | 1.82973378 |

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|---|---|---|---|---|---|
| GO | phospholipase binding | 2 | 9 | 0.122036 | 1.82973378 |
| GO | neuropeptide Y receptor activity | 2 | 9 | 0.122036 | 1.82973378 |
| GO | calcium-transporting ATPase activity | 2 | 9 | 0.122036 | 1.82973378 |
| GO | ATP hydrolysis coupled proton transport | 2 | 9 | 0.122036 | 1.82973378 |
| GO | GTP biosynthetic process | 2 | 9 | 0.122036 | 1.82973378 |
| GO | nucleoside diphosphate kinase activity | 2 | 9 | 0.122036 | 1.82973378 |
| GO | UTP biosynthetic process | 2 | 9 | 0.122036 | 1.82973378 |
| GO | lipopolysaccharide binding | 2 | 9 | 0.122036 | 1.82973378 |
| GO | M band | 2 | 9 | 0.122036 | 1.82973378 |
| GO | male meiosis I | 2 | 9 | 0.122036 | 1.82973378 |
| GO | RNA polymerase II transcription factor activity, enhancer binding | 5 | 39 | 0.12474 | 1.48283112 |
| GO | peptidase inhibitor activity | 9 | 85 | 0.125678 | 1.37438654 |
| GO | Golgi apparatus | 62 | 784 | 0.127321 | 1.21632917 |
| GO | embryonic axis specification | 1 | 2 | 0.132028 | 2.41918886 |
| GO | coreceptor, soluble ligand activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | mast cell activation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | endoplasmic reticulum Sec complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | iodide transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | superoxide-generating NADPH oxidase activator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of gluconeogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | prenylated protein tyrosine phosphatase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of axon regeneration | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of protein complex disassembly | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of toll-like receptor signaling pathway | 1 | 2 | 0.132028 | 2.41918886 |
| GO | heme transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | chloride channel regulator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | acyl carnitine transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | myosin II complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | insulin processing | 1 | 2 | 0.132028 | 2.41918886 |
| GO | anion homeostasis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to oleic acid | 1 | 2 | 0.132028 | 2.41918886 |
| GO | complement receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | macrophage colony stimulating factor receptor binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of odontogenesis of dentine-containing tooth | 1 | 2 | 0.132028 | 2.41918886 |
| GO | heat generation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of smooth muscle contraction | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of skeletal muscle tissue growth | 1 | 2 | 0.132028 | 2.41918886 |
| GO | vasodilation by norepinephrine-epinephrine involved in regulation of | 1 | 2 | 0.132028 | 2.41918886 |
| GO | (S)-limonene 6-monooxygenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | (S)-limonene 7-monooxygenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 4-hydroxyacetophenone monooxygenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | monocarboxylic acid metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | primary lung bud formation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | retinoic acid biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | alkaloid catabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | ceramide cholinephosphotransferase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | sphingomyelin synthase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | transferrin transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of dopamine receptor signaling pathway | 1 | 2 | 0.132028 | 2.41918886 |

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|---|---|---|---|---|---|
| GO | neurological system process involved in regulation of systemic arterial | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of sodium:hydrogen antiporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | acetyltransferase activator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | brain renin-angiotensin system | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of NAD(P)H oxidase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of blood vessel size by renin-angiotensin | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of renal output by angiotensin | 1 | 2 | 0.132028 | 2.41918886 |
| GO | renin-angiotensin regulation of aldosterone production | 1 | 2 | 0.132028 | 2.41918886 |
| GO | smooth muscle cell proliferation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of prostaglandin-endoperoxidase synthase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | rhythmic excitation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosan | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to heparin | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to mycophenolic acid | 1 | 2 | 0.132028 | 2.41918886 |
| GO | rhythmic behavior | 1 | 2 | 0.132028 | 2.41918886 |
| GO | notochord formation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | protein-DNA complex assembly | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular protein catabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glutamate uptake involved in synaptic transmission | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of transferase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to interleukin-15 | 1 | 2 | 0.132028 | 2.41918886 |
| GO | IgE receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | pancreatic A cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | pancreatic B cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | dolichol kinase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | lacrimal gland development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | paraxial mesodermal cell fate commitment | 1 | 2 | 0.132028 | 2.41918886 |
| GO | arachidonate 5-lipoxygenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | alpha-L-fucosidase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of receptor recycling | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glutamate decarboxylation to succinate | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of amyloid precursor protein biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glucagon receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | forebrain neuron fate commitment | 1 | 2 | 0.132028 | 2.41918886 |
| GO | hydrogen peroxide metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of integrin biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | voltage-gated proton channel activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glycolipid metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | purine nucleotide metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glutaminase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | C5a anaphylatoxin receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | artery development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | smoothened signaling pathway involved in spinal cord motor neuron c | 1 | 2 | 0.132028 | 2.41918886 |
| GO | smoothened signaling pathway involved in ventral spinal cord interneu | 1 | 2 | 0.132028 | 2.41918886 |
| GO | DNA nucleotidylexotransferase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glutamate-ammonia ligase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glutamine biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | voluntary musculoskeletal movement | 1 | 2 | 0.132028 | 2.41918886 |
| GO | Pyrin domain binding | 1 | 2 | 0.132028 | 2.41918886 |

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|---|---|---|---|---|---|
| GO | cytokinesis, completion of separation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | aldehyde oxidase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | xanthine dehydrogenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | epithelial-mesenchymal signaling involved in prostate gland developm | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 20-alpha-hydroxysteroid dehydrogenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | hyaluronan catabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | hormone secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cilium movement | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of steroid hormone receptor signaling pathway | 1 | 2 | 0.132028 | 2.41918886 |
| GO | Type I pneumocyte differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | protein tyrosine phosphatase activator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-2 binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-4 receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-7 receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | neutrophil apoptosis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of vascular endothelial growth factor production | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-6 binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-6 receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to copper ion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to mercury ion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cerebrospinal fluid secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glycerol transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | intracellular cGMP activated cation channel activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of saliva secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | renal water transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | interleukin-10 receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 3-phosphoinositide-dependent protein kinase binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of respiratory burst | 1 | 2 | 0.132028 | 2.41918886 |
| GO | ganglioside metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to potassium ion starvation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | acetylcholine receptor regulator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | lymphoid progenitor cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of transcription from RNA polymerase I promoter | 1 | 2 | 0.132028 | 2.41918886 |
| GO | laminin-3 complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | clathrin-coated endocytic vesicle membrane | 1 | 2 | 0.132028 | 2.41918886 |
| GO | phospholipase activator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | leukotriene-C4 synthase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | paraxial mesoderm morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular biogenic amine metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of serotonin secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of dopamine metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to aluminum ion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | slow-twitch skeletal muscle fiber contraction | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of mast cell apoptosis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of mast cell proliferation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cerebral cortex GABAergic interneuron differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | olfactory pit development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | subpallium neuron fate commitment | 1 | 2 | 0.132028 | 2.41918886 |
| GO | macrophage colony stimulating factor receptor activity | 1 | 2 | 0.132028 | 2.41918886 |

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| GO | Bcl3/NF-kappaB2 complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | follicular dendritic cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | nucleotide-binding oligomerization domain containing 1 signaling path | 1 | 2 | 0.132028 | 2.41918886 |
| GO | D-serine transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | aconitate hydratase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | iron-responsive element binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of photoreceptor cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of transcription of Notch receptor target | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to insecticide | 1 | 2 | 0.132028 | 2.41918886 |
| GO | nerve growth factor production | 1 | 2 | 0.132028 | 2.41918886 |
| GO | dopamine uptake | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of actin filament bundle assembly | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of release of cytochrome c from mitochondria | 1 | 2 | 0.132028 | 2.41918886 |
| GO | protein K63-linked ubiquitination | 1 | 2 | 0.132028 | 2.41918886 |
| GO | embryonic body morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to chlorate | 1 | 2 | 0.132028 | 2.41918886 |
| GO | detection of light stimulus | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of plasma membrane long-chain fatty acid transpo | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cytoplasmic cyclin-dependent protein kinase holoenzyme complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | myoblast cell fate commitment | 1 | 2 | 0.132028 | 2.41918886 |
| GO | PML body organization | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of MHC class I biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | anatomical structure development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | embryonic epithelial tube formation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | somatotropin secreting cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | hydroxymethylglutaryl-CoA lyase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | BMP signaling pathway involved in heart induction | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cardiac cell fate determination | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of gene silencing by miRNA | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of receptor biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 1-alkylglycerophosphocholine O-acetyltransferase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | germ-line stem cell maintenance | 1 | 2 | 0.132028 | 2.41918886 |
| GO | establishment of epithelial cell polarity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | oxidoreductase activity, acting on sulfur group of donors, disulfide as | 1 | 2 | 0.132028 | 2.41918886 |
| GO | activation of phospholipase A2 activity by calcium-mediated signaling | 1 | 2 | 0.132028 | 2.41918886 |
| GO | neuromedin U receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | inositol trisphosphate biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | prostaglandin F receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of epinephrine secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of norepinephrine secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | prostaglandin-endoperoxide synthase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular pigment accumulation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | myosin V binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | natural killer cell degranulation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | embryonic retina morphogenesis in camera-type eye | 1 | 2 | 0.132028 | 2.41918886 |
| GO | female genitalia morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | angiotensin maturation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of isotype switching to IgE isotypes | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of mast cell cytokine production | 1 | 2 | 0.132028 | 2.41918886 |

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| GO | regulation of Rho GTPase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 3-hydroxybutyrate dehydrogenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | vitamin metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 3-oxoacid CoA-transferase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | ketone body catabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of biosynthetic process of antibacterial peptides ac | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of neutrophil chemotaxis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | protein-disulfide reductase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cardiac septum development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cloacal septation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of kidney development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | telencephalon regionalization | 1 | 2 | 0.132028 | 2.41918886 |
| GO | urea transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | proton-dependent oligopeptide secondary active transmembrane trar | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of exocytosis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of platelet-derived growth factor receptor signalin | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of inositol phosphate biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of glutamate secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of isotype switching to IgE isotypes | 1 | 2 | 0.132028 | 2.41918886 |
| GO | platelet degranulation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | syntaxin-2 binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | lactate transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | B cell receptor complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | beta selection | 1 | 2 | 0.132028 | 2.41918886 |
| GO | homeostasis of number of cells | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of oxygen and reactive oxygen species metabolic p | 1 | 2 | 0.132028 | 2.41918886 |
| GO | negative regulation of T cell differentiation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of transcription involved in lymphatic endothelial cell fate c | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to follicle-stimulating hormone stimulus | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cell surface pattern recognition receptor signaling pathway | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to diacylated bacterial lipopeptide | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to triacylated bacterial lipopeptide | 1 | 2 | 0.132028 | 2.41918886 |
| GO | detection of diacylated bacterial lipopeptide | 1 | 2 | 0.132028 | 2.41918886 |
| GO | detection of triacylated bacterial lipopeptide | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of interleukin-18 production | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to bacterial lipoprotein | 1 | 2 | 0.132028 | 2.41918886 |
| GO | Toll-like receptor 1-Toll-like receptor 2 protein complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | response to lipoteichoic acid | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of activation of membrane attack complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | cellular response to interferon-gamma | 1 | 2 | 0.132028 | 2.41918886 |
| GO | hypophysis morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | lateral sprouting involved in mammary gland duct morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of response to cytokine stimulus | 1 | 2 | 0.132028 | 2.41918886 |
| GO | myosin light chain binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of chemotaxis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | Stn1-Ten1 complex | 1 | 2 | 0.132028 | 2.41918886 |
| GO | receptor recycling | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of circadian sleep/wake cycle, non-REM sleep | 1 | 2 | 0.132028 | 2.41918886 |
| GO | stereocilia ankle link complex | 1 | 2 | 0.132028 | 2.41918886 |

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|---|---|---|---|---|---|
| GO | actin nucleation | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of secretion | 1 | 2 | 0.132028 | 2.41918886 |
| GO | two-component response regulator activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | striated muscle thick filament | 1 | 2 | 0.132028 | 2.41918886 |
| GO | initial segment | 1 | 2 | 0.132028 | 2.41918886 |
| GO | pantothenate metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | ATPase activity, coupled to transmembrane movement of ions | 1 | 2 | 0.132028 | 2.41918886 |
| GO | adenylylsulfate kinase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | sulfate adenylyltransferase (ATP) activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | activin receptor activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | development of primary female sexual characteristics | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | lipoteichoic acid binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | nicotinamide metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | leg morphogenesis | 1 | 2 | 0.132028 | 2.41918886 |
| GO | 6-phosphogluconolactonase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | glucose-6-phosphate dehydrogenase activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of cholesterol biosynthetic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | toxin transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of skeletal muscle fiber development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | microspike assembly | 1 | 2 | 0.132028 | 2.41918886 |
| GO | clathrin heavy chain binding | 1 | 2 | 0.132028 | 2.41918886 |
| GO | positive regulation of embryonic development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | sensory organ development | 1 | 2 | 0.132028 | 2.41918886 |
| GO | L-ascorbate:sodium symporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | L-ascorbic acid metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | L-ascorbic acid transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | L-ascorbic acid transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | molecular hydrogen transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | nucleobase transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | nucleobase transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | sodium-dependent L-ascorbate transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | sodium-dependent multivitamin transmembrane transporter activity | 1 | 2 | 0.132028 | 2.41918886 |
| GO | transepithelial L-ascorbic acid transport | 1 | 2 | 0.132028 | 2.41918886 |
| GO | regulation of carbohydrate metabolic process | 1 | 2 | 0.132028 | 2.41918886 |
| GO | respiratory gaseous exchange | 4 | 29 | 0.132883 | 1.4860434 |
| GO | positive regulation of ERK1 and ERK2 cascade | 4 | 29 | 0.132883 | 1.4860434 |
| GO | negative regulation of neuron apoptosis | 6 | 51 | 0.133053 | 1.39702606 |
| GO | male gonad development | 5 | 40 | 0.135033 | 1.42134709 |
| GO | regulation of signal transduction | 3 | 19 | 0.136536 | 1.54753841 |
| GO | lipid particle | 3 | 19 | 0.136536 | 1.54753841 |
| GO | protein amino acid O-linked glycosylation | 3 | 19 | 0.136536 | 1.54753841 |
| GO | negative regulation of cell differentiation | 3 | 19 | 0.136536 | 1.54753841 |
| GO | spleen development | 3 | 19 | 0.136536 | 1.54753841 |
| GO | protein heterodimerization activity | 18 | 199 | 0.136557 | 1.24218143 |
| GO | defense response | 7 | 63 | 0.137283 | 1.34727968 |
| GO | cell surface receptor linked signaling pathway | 15 | 161 | 0.137508 | 1.25329609 |
| GO | actin binding | 24 | 278 | 0.141386 | 1.19695967 |
| GO | monooxygenase activity | 6 | 52 | 0.142275 | 1.34595308 |

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|---|---|---|---|---|---|
| GO | central nervous system development | 10 | 100 | 0.145088 | 1.25760325 |
| GO | one-carbon metabolic process | 4 | 30 | 0.145537 | 1.41161573 |
| GO | response to organic nitrogen | 4 | 30 | 0.145537 | 1.41161573 |
| GO | insulin receptor binding | 4 | 30 | 0.145537 | 1.41161573 |
| GO | negative regulation of protein kinase activity | 5 | 41 | 0.145689 | 1.36159858 |
| GO | cholesterol homeostasis | 5 | 41 | 0.145689 | 1.36159858 |
| GO | death receptor binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | negative regulation of ossification | 2 | 10 | 0.145899 | 1.65021148 |
| GO | phagocytic vesicle membrane | 2 | 10 | 0.145899 | 1.65021148 |
| GO | receptor internalization | 2 | 10 | 0.145899 | 1.65021148 |
| GO | elevation of cytosolic calcium ion concentration involved in G-protein | 2 | 10 | 0.145899 | 1.65021148 |
| GO | cytoplasmic part | 2 | 10 | 0.145899 | 1.65021148 |
| GO | negative regulation of blood coagulation | 2 | 10 | 0.145899 | 1.65021148 |
| GO | negative regulation of hormone secretion | 2 | 10 | 0.145899 | 1.65021148 |
| GO | heparan sulfate proteoglycan binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | vascular endothelial growth factor receptor signaling pathway | 2 | 10 | 0.145899 | 1.65021148 |
| GO | regulation of exocytosis | 2 | 10 | 0.145899 | 1.65021148 |
| GO | phosphotyrosine binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | limb morphogenesis | 2 | 10 | 0.145899 | 1.65021148 |
| GO | positive regulation of glycogen biosynthetic process | 2 | 10 | 0.145899 | 1.65021148 |
| GO | lipoprotein binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | receptor tyrosine kinase binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | transforming growth factor beta receptor binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | limb development | 2 | 10 | 0.145899 | 1.65021148 |
| GO | CTP biosynthetic process | 2 | 10 | 0.145899 | 1.65021148 |
| GO | transforming growth factor beta binding | 2 | 10 | 0.145899 | 1.65021148 |
| GO | potassium ion transport | 14 | 151 | 0.151483 | 1.1913065 |
| GO | GTP binding | 29 | 347 | 0.152254 | 1.13431562 |
| GO | B cell activation | 3 | 20 | 0.152923 | 1.44779831 |
| GO | positive regulation of bone mineralization | 3 | 20 | 0.152923 | 1.44779831 |
| GO | adult walking behavior | 3 | 20 | 0.152923 | 1.44779831 |
| GO | response to amphetamine | 3 | 20 | 0.152923 | 1.44779831 |
| GO | positive regulation of mitosis | 3 | 20 | 0.152923 | 1.44779831 |
| GO | positive regulation of neuron apoptosis | 3 | 20 | 0.152923 | 1.44779831 |
| GO | tissue regeneration | 3 | 20 | 0.152923 | 1.44779831 |
| GO | response to steroid hormone stimulus | 3 | 20 | 0.152923 | 1.44779831 |
| GO | L-ascorbic acid binding | 3 | 20 | 0.152923 | 1.44779831 |
| GO | actin cytoskeleton organization | 11 | 114 | 0.155894 | 1.19434428 |
| GO | regulation of cell cycle | 5 | 42 | 0.156692 | 1.30348792 |
| GO | calcium-dependent protein binding | 4 | 31 | 0.158637 | 1.34001228 |
| GO | transcription from RNA polymerase II promoter | 16 | 178 | 0.159161 | 1.14416413 |
| GO | Wnt receptor signaling pathway | 9 | 90 | 0.161066 | 1.19275155 |
| GO | serine-type endopeptidase inhibitor activity | 9 | 90 | 0.161066 | 1.19275155 |
| GO | calmodulin binding | 13 | 140 | 0.161127 | 1.15343799 |
| GO | cysteine-type endopeptidase activity | 6 | 54 | 0.161563 | 1.24704217 |
| GO | protein localization | 6 | 54 | 0.161563 | 1.24704217 |
| GO | endocytosis | 10 | 103 | 0.165762 | 1.15897145 |
| GO | inner ear morphogenesis | 5 | 43 | 0.168023 | 1.24692519 |
| GO | Notch signaling pathway | 5 | 43 | 0.168023 | 1.24692519 |

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|---|---|---|---|---|---|
| GO | glucose metabolic process | 5 | 43 | 0.168023 | 1.24692519 |
| GO | angiogenesis | 11 | 116 | 0.169161 | 1.1336167 |
| GO | synaptic transmission | 15 | 167 | 0.169308 | 1.10446241 |
| GO | microsome | 19 | 219 | 0.1694 | 1.08589716 |
| GO | protein kinase inhibitor activity | 3 | 21 | 0.169887 | 1.3538072 |
| GO | calcium-dependent phospholipid binding | 3 | 21 | 0.169887 | 1.3538072 |
| GO | Wnt receptor signaling pathway, calcium modulating pathway | 3 | 21 | 0.169887 | 1.3538072 |
| GO | threonine-type endopeptidase activity | 3 | 21 | 0.169887 | 1.3538072 |
| GO | polysaccharide binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | morphogenesis of an epithelium | 2 | 11 | 0.170604 | 1.49176904 |
| GO | ceramide biosynthetic process | 2 | 11 | 0.170604 | 1.49176904 |
| GO | retinol binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | DNA methylation involved in gamete generation | 2 | 11 | 0.170604 | 1.49176904 |
| GO | cell recognition | 2 | 11 | 0.170604 | 1.49176904 |
| GO | guanylate kinase activity | 2 | 11 | 0.170604 | 1.49176904 |
| GO | T cell costimulation | 2 | 11 | 0.170604 | 1.49176904 |
| GO | long-chain fatty acid-CoA ligase activity | 2 | 11 | 0.170604 | 1.49176904 |
| GO | regulation of blood vessel size | 2 | 11 | 0.170604 | 1.49176904 |
| GO | kinesin binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | Rho GTPase binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | positive regulation of DNA binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | low-density lipoprotein receptor binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | protein maturation by peptide bond cleavage | 2 | 11 | 0.170604 | 1.49176904 |
| GO | gap junction channel activity | 2 | 11 | 0.170604 | 1.49176904 |
| GO | laminin binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | regulation of neurotransmitter secretion | 2 | 11 | 0.170604 | 1.49176904 |
| GO | cell volume homeostasis | 2 | 11 | 0.170604 | 1.49176904 |
| GO | hemidesmosome assembly | 2 | 11 | 0.170604 | 1.49176904 |
| GO | negative regulation of DNA binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | somatic stem cell maintenance | 2 | 11 | 0.170604 | 1.49176904 |
| GO | vasodilation | 2 | 11 | 0.170604 | 1.49176904 |
| GO | 3',5'-cyclic-nucleotide phosphodiesterase activity | 2 | 11 | 0.170604 | 1.49176904 |
| GO | face morphogenesis | 2 | 11 | 0.170604 | 1.49176904 |
| GO | phosphatidylserine binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | activin binding | 2 | 11 | 0.170604 | 1.49176904 |
| GO | protein amino acid autophosphorylation | 8 | 79 | 0.170925 | 1.16183906 |
| GO | ossification | 6 | 55 | 0.171606 | 1.19911195 |
| GO | neural tube closure | 4 | 32 | 0.172152 | 1.27102323 |
| GO | regulation of transcription from RNA polymerase II promoter | 18 | 207 | 0.174813 | 1.06677146 |
| GO | response to hormone stimulus | 5 | 44 | 0.179664 | 1.19182747 |
| GO | cell-cell junction | 6 | 56 | 0.181901 | 1.15214171 |
| GO | lysosome | 13 | 144 | 0.185812 | 1.04679907 |
| GO | JNK cascade | 4 | 33 | 0.186046 | 1.20446062 |
| GO | acrosomal vesicle | 4 | 33 | 0.186046 | 1.20446062 |
| GO | T cell activation | 4 | 33 | 0.186046 | 1.20446062 |
| GO | potassium channel activity | 4 | 33 | 0.186046 | 1.20446062 |
| GO | determination of left/right symmetry | 4 | 33 | 0.186046 | 1.20446062 |
| GO | positive regulation of translation | 3 | 22 | 0.187358 | 1.26493749 |
| GO | multicellular organism growth | 3 | 22 | 0.187358 | 1.26493749 |

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|---|---|---|---|---|---|
| GO | positive regulation of neuron differentiation | 3 | 22 | 0.187358 | 1.26493749 |
| GO | mesoderm formation | 3 | 22 | 0.187358 | 1.26493749 |
| GO | regulation of ubiquitin-protein ligase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | progesterone metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | double-stranded RNA adenosine deaminase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | polo kinase kinase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of myelination | 1 | 3 | 0.191359 | 1.81892509 |
| GO | heme transporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular chloride ion homeostasis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | creatine kinase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of protein export from nucleus | 1 | 3 | 0.191359 | 1.81892509 |
| GO | sphingosine metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | kininogen binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | response to interleukin-4 | 1 | 3 | 0.191359 | 1.81892509 |
| GO | adenylate cyclase binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | desensitization of G-protein coupled receptor protein signaling pathw | 1 | 3 | 0.191359 | 1.81892509 |
| GO | diet induced thermogenesis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | norepinephrine binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | organic acid metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | oxidoreductase activity, acting on paired donors, with incorporation o | 1 | 3 | 0.191359 | 1.81892509 |
| GO | Gram-negative bacterial cell surface binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of cell-cell adhesion mediated by integrin | 1 | 3 | 0.191359 | 1.81892509 |
| GO | branching morphogenesis of a nerve | 1 | 3 | 0.191359 | 1.81892509 |
| GO | ovarian follicle rupture | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of natriuresis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of norepinephrine secretion | 1 | 3 | 0.191359 | 1.81892509 |
| GO | endothelin B receptor binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | rhombomere 3 development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of blood vessel endothelial cell migration | 1 | 3 | 0.191359 | 1.81892509 |
| GO | N-terminal peptidyl-lysine acetylation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of protein import into nucleus, translocation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | age-dependent response to oxidative stress | 1 | 3 | 0.191359 | 1.81892509 |
| GO | macrophage activation during immune response | 1 | 3 | 0.191359 | 1.81892509 |
| GO | transforming growth factor beta receptor complex assembly | 1 | 3 | 0.191359 | 1.81892509 |
| GO | adenosylhomocysteinase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | conditioned taste aversion | 1 | 3 | 0.191359 | 1.81892509 |
| GO | 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activi | 1 | 3 | 0.191359 | 1.81892509 |
| GO | apolipoprotein receptor binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of receptor internalization | 1 | 3 | 0.191359 | 1.81892509 |
| GO | very-low-density lipoprotein receptor binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | phosphatidylserine metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | protein amino acid O-linked glycosylation via serine | 1 | 3 | 0.191359 | 1.81892509 |
| GO | protein amino acid O-linked glycosylation via threonine | 1 | 3 | 0.191359 | 1.81892509 |
| GO | heparin biosynthetic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cerebral cortex tangential migration | 1 | 3 | 0.191359 | 1.81892509 |
| GO | AMP deaminase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | forebrain dorsal/ventral pattern formation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | smoothened signaling pathway involved in dorsal/ventral neural tube | 1 | 3 | 0.191359 | 1.81892509 |
| GO | tube development | 1 | 3 | 0.191359 | 1.81892509 |

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|---|---|---|---|---|---|
| GO | activation of phospholipase C activity by muscarinic acetylcholine rece | 1 | 3 | 0.191359 | 1.81892509 |
| GO | bone development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | beta-glucuronidase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cilium axoneme assembly | 1 | 3 | 0.191359 | 1.81892509 |
| GO | myoblast proliferation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of androgen receptor signaling pathway | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of smooth muscle cell apoptosis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | Type II pneumocyte differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | skeletal muscle tissue growth | 1 | 3 | 0.191359 | 1.81892509 |
| GO | interleukin-2 receptor activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of chemokine biosynthetic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular response to cAMP | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular response to retinoic acid | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular response to stress | 1 | 3 | 0.191359 | 1.81892509 |
| GO | glycerol transport | 1 | 3 | 0.191359 | 1.81892509 |
| GO | multicellular organismal water homeostasis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | potassium ion transmembrane transporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | insulin receptor complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | PTB domain binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | CD8-positive, alpha-beta T cell differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | alphav-beta3 integrin-vitronectin complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | vascular endothelial growth factor receptor 2 binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | inositol-1,4,5-trisphosphate receptor activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | osteoblast proliferation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of transcription from RNA polymerase II promoter, | 1 | 3 | 0.191359 | 1.81892509 |
| GO | clustering of voltage-gated sodium channels | 1 | 3 | 0.191359 | 1.81892509 |
| GO | neurotransmitter receptor metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | small conductance calcium-activated potassium channel activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | myeloid progenitor cell differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of long-term neuronal synaptic plasticity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | laminin-10 complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of stress fiber assembly | 1 | 3 | 0.191359 | 1.81892509 |
| GO | IgE binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | actinin binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | elastic fiber assembly | 1 | 3 | 0.191359 | 1.81892509 |
| GO | activin responsive factor complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | zygotic specification of dorsal/ventral axis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of epithelial cell migration | 1 | 3 | 0.191359 | 1.81892509 |
| GO | somite specification | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of melanocyte differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | stem cell factor receptor binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | spinal cord oligodendrocyte cell fate specification | 1 | 3 | 0.191359 | 1.81892509 |
| GO | myosin light chain kinase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | ionotropic glutamate receptor binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | axon extension involved in development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | I-kappaB/NF-kappaB complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of NF-kappaB import into nucleus | 1 | 3 | 0.191359 | 1.81892509 |
| GO | multicellular organismal response to stress | 1 | 3 | 0.191359 | 1.81892509 |

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|---|---|---|---|---|---|
| GO | negative regulation of calcium ion transport into cytosol | 1 | 3 | 0.191359 | 1.81892509 |
| GO | nitric-oxide synthase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | tetrahydrobiopterin binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | neurotrophin binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | phenylalanine 4-monooxygenase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | rRNA methyltransferase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | rRNA modification | 1 | 3 | 0.191359 | 1.81892509 |
| GO | calmodulin-dependent cyclic-nucleotide phosphodiesterase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cell-substrate junction | 1 | 3 | 0.191359 | 1.81892509 |
| GO | growth hormone receptor signaling pathway | 1 | 3 | 0.191359 | 1.81892509 |
| GO | phosphoinositide 3-kinase regulator activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | smooth muscle cell migration | 1 | 3 | 0.191359 | 1.81892509 |
| GO | procollagen-lysine 5-dioxygenase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | centrosome localization | 1 | 3 | 0.191359 | 1.81892509 |
| GO | limb bud formation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of synaptic transmission, dopaminergic | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of circadian sleep/wake cycle, REM sleep | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cobalt ion binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | mesenchymal to epithelial transition | 1 | 3 | 0.191359 | 1.81892509 |
| GO | tertiary branching involved in mammary gland duct morphogenesis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | miRNA binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | response to nematode | 1 | 3 | 0.191359 | 1.81892509 |
| GO | DNA damage induced protein phosphorylation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | inorganic phosphate transmembrane transporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | outer membrane | 1 | 3 | 0.191359 | 1.81892509 |
| GO | intracellular calcium activated chloride channel activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | reduction of food intake in response to dietary excess | 1 | 3 | 0.191359 | 1.81892509 |
| GO | activation of Ral GTPase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | Ral GTPase activator activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | platelet activating factor receptor activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | chaperone cofactor-dependent protein refolding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | somatic diversification of immunoglobulins | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cyclooxygenase pathway | 1 | 3 | 0.191359 | 1.81892509 |
| GO | uterus development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | midgut development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | retinoid-X receptor activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | ventricular cardiac muscle cell differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | vitamin D response element binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of retinal cell programmed cell death | 1 | 3 | 0.191359 | 1.81892509 |
| GO | detection of biotic stimulus | 1 | 3 | 0.191359 | 1.81892509 |
| GO | innate immune response in mucosa | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of interleukin-17 production | 1 | 3 | 0.191359 | 1.81892509 |
| GO | beta-galactoside alpha-2,3-sialyltransferase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular response to water deprivation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | Rap GTPase activator activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | D-aspartate import | 1 | 3 | 0.191359 | 1.81892509 |
| GO | endocardial cushion development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of cartilage development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | prostate gland morphogenesis | 1 | 3 | 0.191359 | 1.81892509 |

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|---|---|---|---|---|---|
| GO | renal system process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | specification of organ position | 1 | 3 | 0.191359 | 1.81892509 |
| GO | trachea development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | protein anchor | 1 | 3 | 0.191359 | 1.81892509 |
| GO | basic amino acid transmembrane transporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | mitochondrial ATP synthesis coupled electron transport | 1 | 3 | 0.191359 | 1.81892509 |
| GO | negative regulation of histone acetylation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of neurotransmitter secretion | 1 | 3 | 0.191359 | 1.81892509 |
| GO | intrinsic to internal side of plasma membrane | 1 | 3 | 0.191359 | 1.81892509 |
| GO | clathrin sculpted acetylcholine transport vesicle membrane | 1 | 3 | 0.191359 | 1.81892509 |
| GO | thioredoxin peroxidase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cardiac epithelial to mesenchymal transition | 1 | 3 | 0.191359 | 1.81892509 |
| GO | inhibin-betaglycan-ActRII complex | 1 | 3 | 0.191359 | 1.81892509 |
| GO | response to molecule of fungal origin | 1 | 3 | 0.191359 | 1.81892509 |
| GO | detection of lipopolysaccharide | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of interferon-alpha production | 1 | 3 | 0.191359 | 1.81892509 |
| GO | myofibril assembly | 1 | 3 | 0.191359 | 1.81892509 |
| GO | granulosa cell differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | cellular response to calcium ion | 1 | 3 | 0.191359 | 1.81892509 |
| GO | epithelial cell proliferation involved in mammary gland duct elongatio | 1 | 3 | 0.191359 | 1.81892509 |
| GO | frizzled binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of protein kinase C signaling cascade | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of T cell chemotaxis | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of branching involved in mammary gland duct morphogene | 1 | 3 | 0.191359 | 1.81892509 |
| GO | acetate-CoA ligase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | calcitonin receptor activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | microtubule-based flagellum part | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of interleukin-1 alpha secretion | 1 | 3 | 0.191359 | 1.81892509 |
| GO | inner ear receptor stereocilium organization | 1 | 3 | 0.191359 | 1.81892509 |
| GO | fibroblast migration | 1 | 3 | 0.191359 | 1.81892509 |
| GO | peptide transporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | peptide transport | 1 | 3 | 0.191359 | 1.81892509 |
| GO | diacylglycerol metabolic process | 1 | 3 | 0.191359 | 1.81892509 |
| GO | second-messenger-mediated signaling | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of megakaryocyte differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | syndecan binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | sodium:bicarbonate symporter activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | axon hillock | 1 | 3 | 0.191359 | 1.81892509 |
| GO | pantetheine hydrolase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | spongiotrophoblast differentiation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | sulfate assimilation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | regulation of actin polymerization or depolymerization | 1 | 3 | 0.191359 | 1.81892509 |
| GO | positive regulation of activin receptor signaling pathway | 1 | 3 | 0.191359 | 1.81892509 |
| GO | phosphatidylinositol-4-phosphate binding | 1 | 3 | 0.191359 | 1.81892509 |
| GO | transforming growth factor beta receptor activity, type I | 1 | 3 | 0.191359 | 1.81892509 |
| GO | intrinsic to Golgi membrane | 1 | 3 | 0.191359 | 1.81892509 |
| GO | NAD+ nucleosidase activity | 1 | 3 | 0.191359 | 1.81892509 |
| GO | histone H3 deacetylation | 1 | 3 | 0.191359 | 1.81892509 |
| GO | histone H4 deacetylation | 1 | 3 | 0.191359 | 1.81892509 |

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|---|---|---|---|---|---|
| GO | rhombomere 5 development | 1 | 3 | 0.191359 | 1.81892509 |
| GO | receptor binding | 18 | 211 | 0.195819 | 0.9817225 |
| GO | cholesterol transport | 2 | 12 | 0.195923 | 1.35008603 |
| GO | Rac GTPase binding | 2 | 12 | 0.195923 | 1.35008603 |
| GO | microvillus membrane | 2 | 12 | 0.195923 | 1.35008603 |
| GO | keratinocyte proliferation | 2 | 12 | 0.195923 | 1.35008603 |
| GO | positive regulation of macrophage derived foam cell differentiation | 2 | 12 | 0.195923 | 1.35008603 |
| GO | lysosphingolipid and lysophosphatidic acid receptor activity | 2 | 12 | 0.195923 | 1.35008603 |
| GO | neuromuscular synaptic transmission | 2 | 12 | 0.195923 | 1.35008603 |
| GO | eye photoreceptor cell development | 2 | 12 | 0.195923 | 1.35008603 |
| GO | positive regulation of caspase activity | 2 | 12 | 0.195923 | 1.35008603 |
| GO | tissue homeostasis | 2 | 12 | 0.195923 | 1.35008603 |
| GO | insulin receptor substrate binding | 2 | 12 | 0.195923 | 1.35008603 |
| GO | low-density lipoprotein particle | 2 | 12 | 0.195923 | 1.35008603 |
| GO | melanocyte differentiation | 2 | 12 | 0.195923 | 1.35008603 |
| GO | positive regulation of calcium ion transport | 2 | 12 | 0.195923 | 1.35008603 |
| GO | retinoic acid receptor signaling pathway | 2 | 12 | 0.195923 | 1.35008603 |
| GO | positive regulation of stress-activated MAPK cascade | 2 | 12 | 0.195923 | 1.35008603 |
| GO | anion transmembrane transporter activity | 2 | 12 | 0.195923 | 1.35008603 |
| GO | caspase inhibitor activity | 2 | 12 | 0.195923 | 1.35008603 |
| GO | protein tyrosine phosphatase activity | 8 | 82 | 0.19678 | 1.05055361 |
| GO | positive regulation of transcription | 13 | 146 | 0.198792 | 0.99465529 |
| GO | sulfotransferase activity | 4 | 34 | 0.200287 | 1.14015543 |
| GO | PML body | 4 | 34 | 0.200287 | 1.14015543 |
| GO | activation of protein kinase C activity by G-protein coupled receptor p | 4 | 34 | 0.200287 | 1.14015543 |
| GO | humoral immune response | 4 | 34 | 0.200287 | 1.14015543 |
| GO | response to calcium ion | 5 | 46 | 0.203796 | 1.08572624 |
| GO | Z disc | 5 | 46 | 0.203796 | 1.08572624 |
| GO | regulation of ARF GTPase activity | 3 | 23 | 0.205263 | 1.180656 |
| GO | developmental growth | 3 | 23 | 0.205263 | 1.180656 |
| GO | neuromuscular process controlling balance | 3 | 23 | 0.205263 | 1.180656 |
| GO | cell maturation | 3 | 23 | 0.205263 | 1.180656 |
| GO | positive regulation of osteoblast differentiation | 3 | 23 | 0.205263 | 1.180656 |
| GO | steroid binding | 3 | 23 | 0.205263 | 1.180656 |
| GO | positive regulation of insulin secretion | 3 | 23 | 0.205263 | 1.180656 |
| GO | neurotransmitter secretion | 3 | 23 | 0.205263 | 1.180656 |
| GO | blood coagulation | 7 | 71 | 0.210379 | 1.01174538 |
| GO | FAD binding | 7 | 71 | 0.210379 | 1.01174538 |
| GO | positive regulation of transcription, DNA-dependent | 11 | 122 | 0.212029 | 0.95796191 |
| GO | organ regeneration | 4 | 35 | 0.21484 | 1.07795524 |
| GO | embryonic limb morphogenesis | 4 | 35 | 0.21484 | 1.07795524 |
| GO | extracellular matrix | 4 | 35 | 0.21484 | 1.07795524 |
| GO | binding | 39 | 500 | 0.215673 | 0.86673618 |
| GO | hydrolase activity, acting on acid anhydrides, catalyzing transmembran | 5 | 47 | 0.216247 | 1.03458604 |
| GO | SH3 domain binding | 9 | 97 | 0.217539 | 0.95612469 |
| GO | heme binding | 10 | 110 | 0.218999 | 0.94040082 |
| GO | transferase activity, transferring glycosyl groups | 13 | 149 | 0.219003 | 0.91784064 |
| GO | response to nutrient | 7 | 72 | 0.220401 | 0.97274096 |
| GO | histone deacetylase activity | 2 | 13 | 0.221658 | 1.22200951 |

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|---|---|---|---|---|---|
| GO | bone mineralization | 2 | 13 | 0.221658 | 1.22200951 |
| GO | induction of an organ | 2 | 13 | 0.221658 | 1.22200951 |
| GO | positive regulation of actin filament polymerization | 2 | 13 | 0.221658 | 1.22200951 |
| GO | superoxide metabolic process | 2 | 13 | 0.221658 | 1.22200951 |
| GO | acetylcholine receptor activity | 2 | 13 | 0.221658 | 1.22200951 |
| GO | lipid storage | 2 | 13 | 0.221658 | 1.22200951 |
| GO | carboxypeptidase activity | 2 | 13 | 0.221658 | 1.22200951 |
| GO | positive regulation of phosphoinositide 3-kinase cascade | 2 | 13 | 0.221658 | 1.22200951 |
| GO | middle ear morphogenesis | 2 | 13 | 0.221658 | 1.22200951 |
| GO | positive regulation of smooth muscle contraction | 2 | 13 | 0.221658 | 1.22200951 |
| GO | negative regulation of proteolysis | 2 | 13 | 0.221658 | 1.22200951 |
| GO | positive regulation vascular endothelial growth factor production | 2 | 13 | 0.221658 | 1.22200951 |
| GO | camera-type eye morphogenesis | 2 | 13 | 0.221658 | 1.22200951 |
| GO | negative regulation of fat cell differentiation | 2 | 13 | 0.221658 | 1.22200951 |
| GO | labyrinthine layer blood vessel development | 2 | 13 | 0.221658 | 1.22200951 |
| GO | MAP kinase kinase activity | 2 | 13 | 0.221658 | 1.22200951 |
| GO | RNA catabolic process | 2 | 13 | 0.221658 | 1.22200951 |
| GO | synaptic transmission, glutamatergic | 2 | 13 | 0.221658 | 1.22200951 |
| GO | oogenesis | 2 | 13 | 0.221658 | 1.22200951 |
| GO | protein targeting to membrane | 2 | 13 | 0.221658 | 1.22200951 |
| GO | T cell proliferation | 2 | 13 | 0.221658 | 1.22200951 |
| GO | ARF GTPase activator activity | 3 | 24 | 0.223535 | 1.10050625 |
| GO | G-protein signaling, coupled to cAMP nucleotide second messenger | 3 | 24 | 0.223535 | 1.10050625 |
| GO | negative regulation of inflammatory response | 3 | 24 | 0.223535 | 1.10050625 |
| GO | visual learning | 3 | 24 | 0.223535 | 1.10050625 |
| GO | lung alveolus development | 3 | 24 | 0.223535 | 1.10050625 |
| GO | response to gamma radiation | 3 | 24 | 0.223535 | 1.10050625 |
| GO | learning | 3 | 24 | 0.223535 | 1.10050625 |
| GO | proteolysis involved in cellular protein catabolic process | 3 | 24 | 0.223535 | 1.10050625 |
| GO | fatty acid biosynthetic process | 5 | 48 | 0.228927 | 0.9846364 |
| GO | phosphoprotein phosphatase activity | 4 | 36 | 0.229671 | 1.0177221 |
| GO | somitogenesis | 4 | 36 | 0.229671 | 1.0177221 |
| GO | response to organic substance | 4 | 36 | 0.229671 | 1.0177221 |
| GO | response to stress | 10 | 112 | 0.235344 | 0.88067891 |
| GO | female pregnancy | 6 | 61 | 0.236676 | 0.93038753 |
| GO | phospholipid biosynthetic process | 5 | 49 | 0.241816 | 0.93582048 |
| GO | wound healing | 5 | 49 | 0.241816 | 0.93582048 |
| GO | metallocarboxypeptidase activity | 3 | 25 | 0.242107 | 1.0240947 |
| GO | protein phosphatase binding | 3 | 25 | 0.242107 | 1.0240947 |
| GO | leukocyte cell-cell adhesion | 3 | 25 | 0.242107 | 1.0240947 |
| GO | symporter activity | 10 | 113 | 0.243681 | 0.85124131 |
| GO | activation of adenylate cyclase activity by G-protein signaling pathway | 4 | 37 | 0.244745 | 0.95933085 |
| GO | protein amino acid sulfation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | CTD phosphatase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | branching involved in prostate gland morphogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | 9-cis-retinoic acid biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | base conversion or substitution editing | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of respiratory burst | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cellular glucose homeostasis | 1 | 4 | 0.246637 | 1.4398387 |

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| GO | positive regulation of histone acetylation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | DNA damage response, signal transduction | 1 | 4 | 0.246637 | 1.4398387 |
| GO | mammary duct terminal end bud growth | 1 | 4 | 0.246637 | 1.4398387 |
| GO | piP-body | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of peptidase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | heterocycle metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | nose development | 1 | 4 | 0.246637 | 1.4398387 |
| GO | sphingomyelin biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | zymogen granule membrane | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of cAMP metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of dopamine uptake | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of kinase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | JUN kinase binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | toxin metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | astrocyte activation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | peptide hormone secretion | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of cell size | 1 | 4 | 0.246637 | 1.4398387 |
| GO | vein smooth muscle contraction | 1 | 4 | 0.246637 | 1.4398387 |
| GO | eukaryotic translation elongation factor 1 complex | 1 | 4 | 0.246637 | 1.4398387 |
| GO | facial nerve structural organization | 1 | 4 | 0.246637 | 1.4398387 |
| GO | Schwann cell differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phosphopyruvate hydratase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phosphopyruvate hydratase complex | 1 | 4 | 0.246637 | 1.4398387 |
| GO | peroxisome proliferator activated receptor binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | response to cobalt ion | 1 | 4 | 0.246637 | 1.4398387 |
| GO | histone demethylase activity (H3-K9 specific) | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cAMP response element binding protein binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | lipoxygenase pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | inner ear receptor cell differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cerebral cortex radially oriented cell migration | 1 | 4 | 0.246637 | 1.4398387 |
| GO | forebrain neuron development | 1 | 4 | 0.246637 | 1.4398387 |
| GO | NADP metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of systemic arterial blood pressure by renin-angiotensin | 1 | 4 | 0.246637 | 1.4398387 |
| GO | optic nerve morphogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of T-helper 1 cell differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of estrogen receptor signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | testosterone 17-beta-dehydrogenase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | chondroitin sulfate proteoglycan biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | lung lobe morphogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of granule cell precursor proliferation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | water homeostasis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | ciliary neurotrophic factor receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | lateral ventricle development | 1 | 4 | 0.246637 | 1.4398387 |
| GO | insulin-like growth factor II binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of gene-specific transcription | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cell-cell adhesion mediated by integrin | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cell-substrate junction assembly | 1 | 4 | 0.246637 | 1.4398387 |
| GO | calcium ion transmembrane transporter activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | platelet dense tubular network membrane | 1 | 4 | 0.246637 | 1.4398387 |

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| GO | positive regulation by host of viral transcription | 1 | 4 | 0.246637 | 1.4398387 |
| GO | saliva secretion | 1 | 4 | 0.246637 | 1.4398387 |
| GO | myeloid leukocyte differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of Rac protein signal transduction | 1 | 4 | 0.246637 | 1.4398387 |
| GO | response to mineralocorticoid stimulus | 1 | 4 | 0.246637 | 1.4398387 |
| GO | very-low-density lipoprotein receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | dopamine catabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | androgen binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | bone remodeling | 1 | 4 | 0.246637 | 1.4398387 |
| GO | JUN kinase kinase kinase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cell-cell junction maintenance | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of lipid storage | 1 | 4 | 0.246637 | 1.4398387 |
| GO | toll-like receptor 4 signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | CCAAT-binding factor complex | 1 | 4 | 0.246637 | 1.4398387 |
| GO | arginine binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | compartment pattern formation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of glial cell differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of neurogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of developmental process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | neurotrophin receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of respiratory gaseous exchange | 1 | 4 | 0.246637 | 1.4398387 |
| GO | ADP biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | mitochondrial proton-transporting ATP synthase complex, catalytic co | 1 | 4 | 0.246637 | 1.4398387 |
| GO | nerve growth factor processing | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of BMP signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | secretion by cell | 1 | 4 | 0.246637 | 1.4398387 |
| GO | catecholamine biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | aggresome assembly | 1 | 4 | 0.246637 | 1.4398387 |
| GO | norepinephrine metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of lipid biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | rRNA (adenine-N6,N6-)-dimethyltransferase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cGMP-mediated signaling | 1 | 4 | 0.246637 | 1.4398387 |
| GO | intercalated disc | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phosphoglucomutase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | ErbB-3 class receptor binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | auditory receptor cell stereocilium organization | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of histone deacetylation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | tube morphogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of fatty acid metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | platelet activating factor biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | pi-body | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phosphorylase kinase regulator activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | transmembrane receptor protein tyrosine kinase signaling protein acti | 1 | 4 | 0.246637 | 1.4398387 |
| GO | tight junction assembly | 1 | 4 | 0.246637 | 1.4398387 |
| GO | calcium- and calmodulin-dependent protein kinase complex | 1 | 4 | 0.246637 | 1.4398387 |
| GO | activation of store-operated calcium channel activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | embryonic organ morphogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of cardiac muscle cell proliferation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | vagina development | 1 | 4 | 0.246637 | 1.4398387 |

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| GO | melatonin receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | retinoic acid receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | mechanoreceptor differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of TOR signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of humoral immune response mediated by circulat | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of TOR signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | alpha-N-acetylneuraminate alpha-2,8-sialyltransferase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | L-glutamate import | 1 | 4 | 0.246637 | 1.4398387 |
| GO | lens induction in camera-type eye | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of mitosis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of cell death | 1 | 4 | 0.246637 | 1.4398387 |
| GO | chloride transmembrane transporter activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | urea transport | 1 | 4 | 0.246637 | 1.4398387 |
| GO | arachidonic acid binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | platelet aggregation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | synaptic vesicle maturation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of gamma-delta T cell differentiation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | chromaffin granule membrane | 1 | 4 | 0.246637 | 1.4398387 |
| GO | progesterone receptor signaling pathway | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of interferon-alpha biosynthetic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of platelet activation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | muscle thin filament tropomyosin | 1 | 4 | 0.246637 | 1.4398387 |
| GO | luteinization | 1 | 4 | 0.246637 | 1.4398387 |
| GO | dendritic spine membrane | 1 | 4 | 0.246637 | 1.4398387 |
| GO | gene expression | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of cellular pH reduction | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of adenylate cyclase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cellular response to glucose starvation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | maintenance of organ identity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | blood vessel maturation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | peripheral to membrane of membrane fraction | 1 | 4 | 0.246637 | 1.4398387 |
| GO | protein phosphatase type 1 complex | 1 | 4 | 0.246637 | 1.4398387 |
| GO | [heparan sulfate]-glucosamine N-sulfotransferase activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | actin filament severing | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cyclic nucleotide metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | negative regulation of plasma membrane long-chain fatty acid transpc | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of glucose metabolic process | 1 | 4 | 0.246637 | 1.4398387 |
| GO | release of cytoplasmic sequestered NF-kappaB | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of mitochondrial depolarization | 1 | 4 | 0.246637 | 1.4398387 |
| GO | cellular response to protein stimulus | 1 | 4 | 0.246637 | 1.4398387 |
| GO | vacuolar acidification | 1 | 4 | 0.246637 | 1.4398387 |
| GO | sequestering of actin monomers | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phosphatidylinositol-5-phosphate binding | 1 | 4 | 0.246637 | 1.4398387 |
| GO | long term synaptic depression | 1 | 4 | 0.246637 | 1.4398387 |
| GO | response to hydroperoxide | 1 | 4 | 0.246637 | 1.4398387 |
| GO | thrombospondin receptor activity | 1 | 4 | 0.246637 | 1.4398387 |
| GO | intracellular cholesterol transport | 1 | 4 | 0.246637 | 1.4398387 |
| GO | phospholipid transporter activity | 1 | 4 | 0.246637 | 1.4398387 |

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| GO | peptidyl-lysine deacetylation | 1 | 4 | 0.246637 | 1.4398387 |
| GO | positive regulation of cell migration involved in sprouting angiogenesis | 1 | 4 | 0.246637 | 1.4398387 |
| GO | clathrin coat | 1 | 4 | 0.246637 | 1.4398387 |
| GO | regulation of protein transport | 1 | 4 | 0.246637 | 1.4398387 |
| GO | lateral element | 1 | 4 | 0.246637 | 1.4398387 |
| GO | temperature homeostasis | 2 | 14 | 0.247634 | 1.10517506 |
| GO | glutamine metabolic process | 2 | 14 | 0.247634 | 1.10517506 |
| GO | endosome to lysosome transport | 2 | 14 | 0.247634 | 1.10517506 |
| GO | behavioral fear response | 2 | 14 | 0.247634 | 1.10517506 |
| GO | nitric oxide mediated signal transduction | 2 | 14 | 0.247634 | 1.10517506 |
| GO | response to testosterone stimulus | 2 | 14 | 0.247634 | 1.10517506 |
| GO | protein-chromophore linkage | 2 | 14 | 0.247634 | 1.10517506 |
| GO | sulfur metabolic process | 2 | 14 | 0.247634 | 1.10517506 |
| GO | embryonic heart tube development | 2 | 14 | 0.247634 | 1.10517506 |
| GO | calmodulin-dependent protein kinase activity | 2 | 14 | 0.247634 | 1.10517506 |
| GO | regulation of action potential in neuron | 2 | 14 | 0.247634 | 1.10517506 |
| GO | positive regulation of protein catabolic process | 2 | 14 | 0.247634 | 1.10517506 |
| GO | neuroblast proliferation | 2 | 14 | 0.247634 | 1.10517506 |
| GO | transmembrane transporter activity | 2 | 14 | 0.247634 | 1.10517506 |
| GO | ATP catabolic process | 2 | 14 | 0.247634 | 1.10517506 |
| GO | decidualization | 2 | 14 | 0.247634 | 1.10517506 |
| GO | cell fate specification | 2 | 14 | 0.247634 | 1.10517506 |
| GO | dystrophin-associated glycoprotein complex | 2 | 14 | 0.247634 | 1.10517506 |
| GO | pathway-restricted SMAD protein phosphorylation | 2 | 14 | 0.247634 | 1.10517506 |
| GO | single-stranded RNA binding | 2 | 14 | 0.247634 | 1.10517506 |
| GO | transcription factor complex | 12 | 140 | 0.249175 | 0.81728188 |
| GO | fatty acid metabolic process | 7 | 75 | 0.251415 | 0.85915296 |
| GO | promoter binding | 9 | 101 | 0.252835 | 0.82901024 |
| GO | response to oxidative stress | 9 | 101 | 0.252835 | 0.82901024 |
| GO | chloride transport | 5 | 50 | 0.254893 | 0.88808529 |
| GO | activation of caspase activity | 5 | 50 | 0.254893 | 0.88808529 |
| GO | Golgi cisterna membrane | 6 | 63 | 0.25987 | 0.84718805 |
| GO | positive regulation of gene expression | 4 | 38 | 0.260029 | 0.90266757 |
| GO | collagen fibril organization | 3 | 26 | 0.260915 | 0.95107994 |
| GO | GDP binding | 3 | 26 | 0.260915 | 0.95107994 |
| GO | NAD+ ADP-ribosyltransferase activity | 3 | 26 | 0.260915 | 0.95107994 |
| GO | hemopoiesis | 5 | 51 | 0.268136 | 0.84138139 |
| GO | copper ion binding | 5 | 51 | 0.268136 | 0.84138139 |
| GO | forebrain development | 5 | 51 | 0.268136 | 0.84138139 |
| GO | protein complex binding | 8 | 90 | 0.27242 | 0.77404613 |
| GO | response to nicotine | 2 | 15 | 0.273697 | 0.99776846 |
| GO | voltage-gated chloride channel activity | 2 | 15 | 0.273697 | 0.99776846 |
| GO | actin filament bundle assembly | 2 | 15 | 0.273697 | 0.99776846 |
| GO | embryonic forelimb morphogenesis | 2 | 15 | 0.273697 | 0.99776846 |
| GO | phospholipid-translocating ATPase activity | 2 | 15 | 0.273697 | 0.99776846 |
| GO | positive regulation of catalytic activity | 2 | 15 | 0.273697 | 0.99776846 |
| GO | digestive tract development | 2 | 15 | 0.273697 | 0.99776846 |
| GO | cellular component organization | 2 | 15 | 0.273697 | 0.99776846 |
| GO | cellular response to extracellular stimulus | 2 | 15 | 0.273697 | 0.99776846 |

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| GO | myeloid cell differentiation | 2 | 15 | 0.273697 | 0.99776846 |
| GO | neuromuscular junction development | 2 | 15 | 0.273697 | 0.99776846 |
| GO | hair follicle development | 2 | 15 | 0.273697 | 0.99776846 |
| GO | chondrocyte differentiation | 2 | 15 | 0.273697 | 0.99776846 |
| GO | ATPase binding | 2 | 15 | 0.273697 | 0.99776846 |
| GO | oxidoreductase activity, acting on paired donors, with incorporation o | 2 | 15 | 0.273697 | 0.99776846 |
| GO | regulation of protein amino acid phosphorylation | 2 | 15 | 0.273697 | 0.99776846 |
| GO | regulation of immune response | 2 | 15 | 0.273697 | 0.99776846 |
| GO | positive regulation of cytokine secretion | 2 | 15 | 0.273697 | 0.99776846 |
| GO | epithelial cell differentiation | 4 | 39 | 0.275491 | 0.84762832 |
| GO | ER-Golgi intermediate compartment | 4 | 39 | 0.275491 | 0.84762832 |
| GO | cytoskeletal protein binding | 4 | 39 | 0.275491 | 0.84762832 |
| GO | interspecies interaction between organisms | 22 | 280 | 0.278823 | 0.68295535 |
| GO | ATP synthesis coupled proton transport | 3 | 27 | 0.2799 | 0.88116403 |
| GO | enzyme inhibitor activity | 3 | 27 | 0.2799 | 0.88116403 |
| GO | negative regulation of neuron differentiation | 3 | 27 | 0.2799 | 0.88116403 |
| GO | cell-cell adherens junction | 3 | 27 | 0.2799 | 0.88116403 |
| GO | negative regulation of cell growth | 8 | 91 | 0.28242 | 0.74134092 |
| GO | ubiquitin-protein ligase activity | 12 | 145 | 0.288106 | 0.69027851 |
| GO | dendritic spine | 4 | 40 | 0.291097 | 0.79411803 |
| GO | hormone activity | 7 | 79 | 0.294592 | 0.71506294 |
| GO | response to wounding | 5 | 53 | 0.295041 | 0.75088555 |
| GO | ATP biosynthetic process | 5 | 53 | 0.295041 | 0.75088555 |
| GO | negative regulation of myotube differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mitogen-activated protein kinase kinase binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mRNA modification | 1 | 5 | 0.298138 | 1.16672207 |
| GO | opioid peptide activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of protein complex assembly | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sodium ion binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sodium-dependent phosphate transmembrane transporter activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | transepithelial chloride transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | respiratory electron transport chain | 1 | 5 | 0.298138 | 1.16672207 |
| GO | barbed-end actin filament capping | 1 | 5 | 0.298138 | 1.16672207 |
| GO | calcium- and calmodulin-responsive adenylate cyclase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | interleukin-1-mediated signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of cytokine-mediated signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | folic acid transporter activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | toxin binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of neuron apoptosis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | ethanol oxidation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sphingosine-1-phosphate phosphatase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | monocyte activation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of macrophage differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of heart contraction | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of potassium ion transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | oxidoreductase activity, acting on paired donors, with incorporation o | 1 | 5 | 0.298138 | 1.16672207 |
| GO | embryonic camera-type eye development | 1 | 5 | 0.298138 | 1.16672207 |
| GO | activation of phospholipase C activity by dopamine receptor signaling | 1 | 5 | 0.298138 | 1.16672207 |
| GO | circadian regulation of gene expression | 1 | 5 | 0.298138 | 1.16672207 |

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| GO | G-protein signaling, coupled to cGMP nucleotide second messenger | 1 | 5 | 0.298138 | 1.16672207 |
| GO | type 1 angiotensin receptor binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | artery smooth muscle contraction | 1 | 5 | 0.298138 | 1.16672207 |
| GO | leukocyte activation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of systemic arterial blood pressure by endothelin | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mammary gland involution | 1 | 5 | 0.298138 | 1.16672207 |
| GO | transmembrane-ephrin receptor activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | musculoskeletal movement | 1 | 5 | 0.298138 | 1.16672207 |
| GO | fibroblast growth factor receptor activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | axon midline choice point recognition | 1 | 5 | 0.298138 | 1.16672207 |
| GO | cell morphogenesis involved in neuron differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | glycosaminoglycan metabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mesenchymal cell differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | lymphangiogenesis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | activation of JNKK activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | anterograde axon cargo transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | response to gravity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | lysosomal transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of receptor activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of transferase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | ER to Golgi transport vesicle membrane | 1 | 5 | 0.298138 | 1.16672207 |
| GO | AP-1 adaptor complex | 1 | 5 | 0.298138 | 1.16672207 |
| GO | SCF-dependent proteasomal ubiquitin-dependent protein catabolic pr | 1 | 5 | 0.298138 | 1.16672207 |
| GO | vitamin D binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | purine base metabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of protein import into nucleus | 1 | 5 | 0.298138 | 1.16672207 |
| GO | spinal cord dorsal/ventral patterning | 1 | 5 | 0.298138 | 1.16672207 |
| GO | virion binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | virus-host interaction | 1 | 5 | 0.298138 | 1.16672207 |
| GO | peptidyl-citrulline biosynthetic process from peptidyl-arginine | 1 | 5 | 0.298138 | 1.16672207 |
| GO | protein-arginine deiminase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | azurophil granule | 1 | 5 | 0.298138 | 1.16672207 |
| GO | S100 alpha binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | cell killing | 1 | 5 | 0.298138 | 1.16672207 |
| GO | CRD-mediated mRNA stability complex | 1 | 5 | 0.298138 | 1.16672207 |
| GO | CRD-mediated mRNA stabilization | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of astrocyte differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | monocyte differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | motile secondary cilium | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of insulin-like growth factor receptor signaling pat | 1 | 5 | 0.298138 | 1.16672207 |
| GO | chorio-allantoic fusion | 1 | 5 | 0.298138 | 1.16672207 |
| GO | ciliary neurotrophic factor-mediated signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of interleukin-8 production | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of protein amino acid autophosphorylation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | glycosphingolipid metabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of developmental pigmentation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | lipoprotein catabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | low-density lipoprotein particle clearance | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of GTPase activity | 1 | 5 | 0.298138 | 1.16672207 |

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| GO | pericardium development | 1 | 5 | 0.298138 | 1.16672207 |
| GO | primary microRNA processing | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | transforming growth factor beta receptor, pathway-specific cytoplasm | 1 | 5 | 0.298138 | 1.16672207 |
| GO | steroid catabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sulfuric ester hydrolase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of osteoclast differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | E-box binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | spinal cord association neuron differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | nerve growth factor receptor signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | germinal center formation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of Notch signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sprouting angiogenesis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | reduction of cytosolic calcium ion concentration | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of cardiac muscle hypertrophy | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of prostaglandin secretion | 1 | 5 | 0.298138 | 1.16672207 |
| GO | nerve growth factor binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | peptide metabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of cell cycle arrest | 1 | 5 | 0.298138 | 1.16672207 |
| GO | glycolipid binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | glycolipid transporter activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of triglyceride biosynthetic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of establishment of protein localization in plasma r | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of cytokine production | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of defense response to virus by host | 1 | 5 | 0.298138 | 1.16672207 |
| GO | microvillus assembly | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of smoothened signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | oocyte development | 1 | 5 | 0.298138 | 1.16672207 |
| GO | serine-type carboxypeptidase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | DNA-directed RNA polymerase II, holoenzyme | 1 | 5 | 0.298138 | 1.16672207 |
| GO | cellular amino acid and derivative metabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of T cell activation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | sodium-independent organic anion transmembrane transporter activit | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of bone mineralization | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of triglyceride catabolic process | 1 | 5 | 0.298138 | 1.16672207 |
| GO | melanosome localization | 1 | 5 | 0.298138 | 1.16672207 |
| GO | ammonium transmembrane transporter activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of Rho protein signal transduction | 1 | 5 | 0.298138 | 1.16672207 |
| GO | glutamate secretion | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of neuroblast proliferation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | neuron recognition | 1 | 5 | 0.298138 | 1.16672207 |
| GO | detection of chemical stimulus involved in sensory perception of bitte | 1 | 5 | 0.298138 | 1.16672207 |
| GO | thioredoxin-disulfide reductase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | BMP receptor binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mesenchymal to epithelial transition involved in metanephros morpho | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of chondrocyte differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of oligodendrocyte differentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of branching involved in ureteric bud morphogene | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of smooth muscle cell differentiation | 1 | 5 | 0.298138 | 1.16672207 |

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| GO | tongue morphogenesis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | anion exchanger activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | cellular ion homeostasis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | oligopeptide transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | drug transport | 1 | 5 | 0.298138 | 1.16672207 |
| GO | long-term synaptic potentiation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | positive regulation of receptor recycling | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of locomotion | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of macrophage activation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | tau protein binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | spectrin-associated cytoskeleton | 1 | 5 | 0.298138 | 1.16672207 |
| GO | induction of apoptosis by hormones | 1 | 5 | 0.298138 | 1.16672207 |
| GO | somatostatin receptor activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | definitive hemopoiesis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of cellular component movement | 1 | 5 | 0.298138 | 1.16672207 |
| GO | response to prostaglandin E stimulus | 1 | 5 | 0.298138 | 1.16672207 |
| GO | toll-like receptor signaling pathway | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of short-term neuronal synaptic plasticity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | mammary gland branching involved in thelarche | 1 | 5 | 0.298138 | 1.16672207 |
| GO | 1-alkyl-2-acetylglycerophosphocholine esterase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | intramembranous ossification | 1 | 5 | 0.298138 | 1.16672207 |
| GO | phosphatidylinositol transporter activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | endoderm formation | 1 | 5 | 0.298138 | 1.16672207 |
| GO | muscle organ morphogenesis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | negative regulation of kinase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | regulation of calcium ion transport via voltage-gated calcium channel | 1 | 5 | 0.298138 | 1.16672207 |
| GO | secondary active monocarboxylate transmembrane transporter activit | 1 | 5 | 0.298138 | 1.16672207 |
| GO | peptidoglycan receptor activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | N-acetylglucosamine 6-O-sulfotransferase activity | 1 | 5 | 0.298138 | 1.16672207 |
| GO | cellular metal ion homeostasis | 1 | 5 | 0.298138 | 1.16672207 |
| GO | nitric-oxide synthase binding | 1 | 5 | 0.298138 | 1.16672207 |
| GO | segment specification | 1 | 5 | 0.298138 | 1.16672207 |
| GO | camera-type eye development | 3 | 28 | 0.299003 | 0.81408553 |
| GO | single fertilization | 3 | 28 | 0.299003 | 0.81408553 |
| GO | positive regulation of axonogenesis | 2 | 16 | 0.299715 | 0.89837015 |
| GO | vitamin D receptor binding | 2 | 16 | 0.299715 | 0.89837015 |
| GO | nicotinic acetylcholine-activated cation-selective channel activity | 2 | 16 | 0.299715 | 0.89837015 |
| GO | nicotinic acetylcholine-gated receptor-channel complex | 2 | 16 | 0.299715 | 0.89837015 |
| GO | phosphatidylinositol-3,4,5-trisphosphate binding | 2 | 16 | 0.299715 | 0.89837015 |
| GO | negative regulation of insulin secretion | 2 | 16 | 0.299715 | 0.89837015 |
| GO | receptor complex | 2 | 16 | 0.299715 | 0.89837015 |
| GO | gamete generation | 2 | 16 | 0.299715 | 0.89837015 |
| GO | response to morphine | 2 | 16 | 0.299715 | 0.89837015 |
| GO | lateral plasma membrane | 2 | 16 | 0.299715 | 0.89837015 |
| GO | smoothened signaling pathway | 2 | 16 | 0.299715 | 0.89837015 |
| GO | response to nutrient levels | 2 | 16 | 0.299715 | 0.89837015 |
| GO | internal side of plasma membrane | 2 | 16 | 0.299715 | 0.89837015 |
| GO | calcium-dependent cysteine-type endopeptidase activity | 2 | 16 | 0.299715 | 0.89837015 |
| GO | response to axon injury | 2 | 16 | 0.299715 | 0.89837015 |

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| GO | mitochondrial envelope | 2 | 16 | 0.299715 | 0.89837015 |
| GO | eukaryotic cell surface binding | 2 | 16 | 0.299715 | 0.89837015 |
| GO | stereocilium | 2 | 16 | 0.299715 | 0.89837015 |
| GO | mRNA binding | 4 | 41 | 0.306817 | 0.74204953 |
| GO | cellular defense response | 5 | 54 | 0.308661 | 0.70700984 |
| GO | proton transport | 5 | 54 | 0.308661 | 0.70700984 |
| GO | basolateral plasma membrane | 9 | 107 | 0.308862 | 0.64801212 |
| GO | actin cytoskeleton | 11 | 134 | 0.308876 | 0.63258503 |
| GO | cell proliferation | 22 | 286 | 0.313206 | 0.57903666 |
| GO | histone deacetylase complex | 3 | 29 | 0.318171 | 0.74961393 |
| GO | protein kinase C binding | 3 | 29 | 0.318171 | 0.74961393 |
| GO | keratinocyte differentiation | 3 | 29 | 0.318171 | 0.74961393 |
| GO | transcriptional repressor complex | 3 | 29 | 0.318171 | 0.74961393 |
| GO | behavior | 3 | 29 | 0.318171 | 0.74961393 |
| GO | protein homooligomerization | 6 | 68 | 0.32007 | 0.65103418 |
| GO | post-embryonic development | 5 | 55 | 0.322367 | 0.66399739 |
| GO | chemokine activity | 4 | 42 | 0.32262 | 0.69134274 |
| GO | histone deacetylation | 2 | 17 | 0.325572 | 0.80585039 |
| GO | positive regulation of cell-substrate adhesion | 2 | 17 | 0.325572 | 0.80585039 |
| GO | positive regulation of proteasomal ubiquitin-dependent protein catab | 2 | 17 | 0.325572 | 0.80585039 |
| GO | activation of protein kinase A activity | 2 | 17 | 0.325572 | 0.80585039 |
| GO | DNA damage response, signal transduction resulting in induction of ap | 2 | 17 | 0.325572 | 0.80585039 |
| GO | regulation of pH | 2 | 17 | 0.325572 | 0.80585039 |
| GO | regulation of angiogenesis | 2 | 17 | 0.325572 | 0.80585039 |
| GO | NF-kappaB binding | 2 | 17 | 0.325572 | 0.80585039 |
| GO | rough endoplasmic reticulum | 2 | 17 | 0.325572 | 0.80585039 |
| GO | anchored to plasma membrane | 2 | 17 | 0.325572 | 0.80585039 |
| GO | nuclear body | 2 | 17 | 0.325572 | 0.80585039 |
| GO | caspase activator activity | 2 | 17 | 0.325572 | 0.80585039 |
| GO | 2 iron, 2 sulfur cluster binding | 2 | 17 | 0.325572 | 0.80585039 |
| GO | fatty acid binding | 2 | 17 | 0.325572 | 0.80585039 |
| GO | positive regulation of cell differentiation | 2 | 17 | 0.325572 | 0.80585039 |
| GO | embryonic pattern specification | 2 | 17 | 0.325572 | 0.80585039 |
| GO | embryonic hindlimb morphogenesis | 2 | 17 | 0.325572 | 0.80585039 |
| GO | epithelial to mesenchymal transition | 2 | 17 | 0.325572 | 0.80585039 |
| GO | regulation of excitatory postsynaptic membrane potential | 2 | 17 | 0.325572 | 0.80585039 |
| GO | glycerol metabolic process | 2 | 17 | 0.325572 | 0.80585039 |
| GO | negative regulation of insulin receptor signaling pathway | 2 | 17 | 0.325572 | 0.80585039 |
| GO | coreceptor activity | 2 | 17 | 0.325572 | 0.80585039 |
| GO | myofibril | 2 | 17 | 0.325572 | 0.80585039 |
| GO | ribonuclease activity | 2 | 17 | 0.325572 | 0.80585039 |
| GO | cell junction | 29 | 387 | 0.329917 | 0.51883318 |
| GO | cell death | 10 | 123 | 0.331858 | 0.57111086 |
| GO | transcription coactivator activity | 15 | 192 | 0.333655 | 0.53957741 |
| GO | transporter activity | 22 | 290 | 0.3368 | 0.51098066 |
| GO | protein tyrosine/serine/threonine phosphatase activity | 3 | 30 | 0.337352 | 0.68754501 |
| GO | cell morphogenesis | 3 | 30 | 0.337352 | 0.68754501 |
| GO | gene silencing by RNA | 3 | 30 | 0.337352 | 0.68754501 |
| GO | BMP signaling pathway | 4 | 43 | 0.338476 | 0.64192388 |

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|---|---|---|---|---|---|
| GO | cell-cell adhesion | 6 | 70 | 0.344735 | 0.57683556 |
| GO | growth factor activity | 12 | 152 | 0.345241 | 0.51992217 |
| GO | structural constituent of tooth enamel | 1 | 6 | 0.346122 | 0.95450412 |
| GO | alcohol dehydrogenase (NAD) activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | protein phosphatase 2B binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cellular phosphate ion homeostasis | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to fructose stimulus | 1 | 6 | 0.346122 | 0.95450412 |
| GO | bicarbonate transport | 1 | 6 | 0.346122 | 0.95450412 |
| GO | fatty acid oxidation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | acylglycerol lipase activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | alcohol metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of translational initiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to dietary excess | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glycogen catabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to glucagon stimulus | 1 | 6 | 0.346122 | 0.95450412 |
| GO | retinoic acid metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | activation of transmembrane receptor protein tyrosine kinase activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | synaptic vesicle transport | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of synaptic transmission, glutamatergic | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of growth hormone secretion | 1 | 6 | 0.346122 | 0.95450412 |
| GO | regulation of inhibitory postsynaptic membrane potential | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of epidermal growth factor receptor signaling path | 1 | 6 | 0.346122 | 0.95450412 |
| GO | vasoconstriction | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glycoprotein biosynthetic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glucocorticoid receptor binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | neuromuscular process controlling posture | 1 | 6 | 0.346122 | 0.95450412 |
| GO | spinal cord motor neuron differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of synaptic transmission, GABAergic | 1 | 6 | 0.346122 | 0.95450412 |
| GO | germ cell migration | 1 | 6 | 0.346122 | 0.95450412 |
| GO | actomyosin structure organization | 1 | 6 | 0.346122 | 0.95450412 |
| GO | histone H3-K9 demethylation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | histone H4-K5 acetylation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | histone H4-K8 acetylation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | high-density lipoprotein binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | arachidonic acid metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | nuclear envelope lumen | 1 | 6 | 0.346122 | 0.95450412 |
| GO | fucose metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | extrinsic to external side of plasma membrane | 1 | 6 | 0.346122 | 0.95450412 |
| GO | AP-2 adaptor complex | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glycoprotein catabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | regulation of synaptic transmission, glutamatergic | 1 | 6 | 0.346122 | 0.95450412 |
| GO | transmembrane receptor protein tyrosine kinase adaptor protein activ | 1 | 6 | 0.346122 | 0.95450412 |
| GO | phagocytic vesicle | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of survival gene product expression | 1 | 6 | 0.346122 | 0.95450412 |
| GO | epithelial cell development | 1 | 6 | 0.346122 | 0.95450412 |
| GO | hyaluronoglucosaminidase activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | lung vasculature development | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of insulin-like growth factor receptor signaling path | 1 | 6 | 0.346122 | 0.95450412 |
| GO | ammonia transmembrane transporter activity | 1 | 6 | 0.346122 | 0.95450412 |

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| GO | ammonium transport | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cellular response to hypoxia | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cellular response to UV | 1 | 6 | 0.346122 | 0.95450412 |
| GO | activation of protein kinase B activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | lipoic acid binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to manganese ion | 1 | 6 | 0.346122 | 0.95450412 |
| GO | plasma membrane enriched fraction | 1 | 6 | 0.346122 | 0.95450412 |
| GO | striated muscle cell differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | endothelial cell differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glutathione binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | catecholamine metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | enucleate erythrocyte differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | forebrain neuron differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to folic acid | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cytoplasmic sequestering of NF-kappaB | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cadmium ion binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of glutamate secretion | 1 | 6 | 0.346122 | 0.95450412 |
| GO | response to fluid shear stress | 1 | 6 | 0.346122 | 0.95450412 |
| GO | L-phenylalanine catabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | startle response | 1 | 6 | 0.346122 | 0.95450412 |
| GO | peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glycolipid transport | 1 | 6 | 0.346122 | 0.95450412 |
| GO | rough endoplasmic reticulum membrane | 1 | 6 | 0.346122 | 0.95450412 |
| GO | antigen processing and presentation of endogenous peptide antigen v | 1 | 6 | 0.346122 | 0.95450412 |
| GO | meiotic prophase I | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of T cell activation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | DNA packaging | 1 | 6 | 0.346122 | 0.95450412 |
| GO | complement activation, lectin pathway | 1 | 6 | 0.346122 | 0.95450412 |
| GO | parturition | 1 | 6 | 0.346122 | 0.95450412 |
| GO | cytidine deaminase activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | apical junction complex | 1 | 6 | 0.346122 | 0.95450412 |
| GO | exocytic vesicle | 1 | 6 | 0.346122 | 0.95450412 |
| GO | erythrocyte development | 1 | 6 | 0.346122 | 0.95450412 |
| GO | glycosphingolipid binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of interleukin-2 production | 1 | 6 | 0.346122 | 0.95450412 |
| GO | sodium channel regulator activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | negative regulation of striated muscle tissue development | 1 | 6 | 0.346122 | 0.95450412 |
| GO | ubiquitin-ubiquitin ligase activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | Hsp70 protein binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | amine metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | enzyme linked receptor protein signaling pathway | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of alpha-beta T cell differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of B cell differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | macrophage activation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of tumor necrosis factor biosynthetic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | podosome | 1 | 6 | 0.346122 | 0.95450412 |
| GO | store-operated calcium channel activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | C-X-C chemokine receptor activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | DNA N-glycosylase activity | 1 | 6 | 0.346122 | 0.95450412 |

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| GO | thyroid hormone receptor activity | 1 | 6 | 0.346122 | 0.95450412 |
| GO | hyaluronan metabolic process | 1 | 6 | 0.346122 | 0.95450412 |
| GO | juxtaparanode region of axon | 1 | 6 | 0.346122 | 0.95450412 |
| GO | mammary gland epithelial cell proliferation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | proton-transporting V-type ATPase, V0 domain | 1 | 6 | 0.346122 | 0.95450412 |
| GO | trophoblast giant cell differentiation | 1 | 6 | 0.346122 | 0.95450412 |
| GO | phosphatidylinositol-3,5-bisphosphate binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | positive regulation of BMP signaling pathway | 1 | 6 | 0.346122 | 0.95450412 |
| GO | phospholipid homeostasis | 1 | 6 | 0.346122 | 0.95450412 |
| GO | bile acid binding | 1 | 6 | 0.346122 | 0.95450412 |
| GO | locomotory behavior | 5 | 57 | 0.349956 | 0.58042152 |
| GO | neuron migration | 5 | 57 | 0.349956 | 0.58042152 |
| GO | DNA damage checkpoint | 2 | 18 | 0.351168 | 0.71929675 |
| GO | regulation of insulin secretion | 2 | 18 | 0.351168 | 0.71929675 |
| GO | embryonic placenta development | 2 | 18 | 0.351168 | 0.71929675 |
| GO | response to inorganic substance | 2 | 18 | 0.351168 | 0.71929675 |
| GO | pancreas development | 2 | 18 | 0.351168 | 0.71929675 |
| GO | WW domain binding | 2 | 18 | 0.351168 | 0.71929675 |
| GO | protein import into nucleus, translocation | 2 | 18 | 0.351168 | 0.71929675 |
| GO | ADP binding | 2 | 18 | 0.351168 | 0.71929675 |
| GO | proton-transporting ATPase activity, rotational mechanism | 2 | 18 | 0.351168 | 0.71929675 |
| GO | SNARE complex | 2 | 18 | 0.351168 | 0.71929675 |
| GO | anion transport | 2 | 18 | 0.351168 | 0.71929675 |
| GO | cytolysis | 2 | 18 | 0.351168 | 0.71929675 |
| GO | recycling endosome | 2 | 18 | 0.351168 | 0.71929675 |
| GO | pattern specification process | 4 | 44 | 0.354357 | 0.5937249 |
| GO | protein stabilization | 3 | 31 | 0.3565 | 0.62769707 |
| GO | cation binding | 3 | 31 | 0.3565 | 0.62769707 |
| GO | phospholipid metabolic process | 3 | 31 | 0.3565 | 0.62769707 |
| GO | NADP or NADPH binding | 3 | 31 | 0.3565 | 0.62769707 |
| GO | embryonic digit morphogenesis | 3 | 31 | 0.3565 | 0.62769707 |
| GO | ATPase activity, coupled to transmembrane movement of substances | 3 | 31 | 0.3565 | 0.62769707 |
| GO | early endosome | 7 | 85 | 0.361881 | 0.51281184 |
| GO | intracellular signaling pathway | 14 | 182 | 0.362991 | 0.46063268 |
| GO | regulation of cell shape | 5 | 58 | 0.363801 | 0.53979284 |
| GO | blood circulation | 4 | 45 | 0.370236 | 0.54668287 |
| GO | regulation of G-protein coupled receptor protein signaling pathway | 3 | 32 | 0.375571 | 0.5699078 |
| GO | peptide binding | 3 | 32 | 0.375571 | 0.5699078 |
| GO | peptidyl-tyrosine phosphorylation | 3 | 32 | 0.375571 | 0.5699078 |
| GO | G2/M transition of mitotic cell cycle | 2 | 19 | 0.376419 | 0.63796267 |
| GO | negative regulation of adenylate cyclase activity | 2 | 19 | 0.376419 | 0.63796267 |
| GO | patterning of blood vessels | 2 | 19 | 0.376419 | 0.63796267 |
| GO | protein processing | 2 | 19 | 0.376419 | 0.63796267 |
| GO | heterophilic cell-cell adhesion | 2 | 19 | 0.376419 | 0.63796267 |
| GO | collagen catabolic process | 2 | 19 | 0.376419 | 0.63796267 |
| GO | cadherin binding | 2 | 19 | 0.376419 | 0.63796267 |
| GO | photoreceptor outer segment | 2 | 19 | 0.376419 | 0.63796267 |
| GO | regulation of synaptic plasticity | 2 | 19 | 0.376419 | 0.63796267 |
| GO | response to amino acid stimulus | 2 | 19 | 0.376419 | 0.63796267 |

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| GO | lipid transporter activity | 2 | 19 | 0.376419 | 0.63796267 |
| GO | cell migration | 5 | 59 | 0.377657 | 0.49989664 |
| GO | synaptic vesicle | 4 | 46 | 0.386088 | 0.50073952 |
| GO | protein complex assembly | 8 | 101 | 0.38621 | 0.43364765 |
| GO | protein trimerization | 1 | 7 | 0.390828 | 0.78133269 |
| GO | adenosine deaminase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | sodium:phosphate symporter activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | folic acid transport | 1 | 7 | 0.390828 | 0.78133269 |
| GO | long-chain fatty acid transport | 1 | 7 | 0.390828 | 0.78133269 |
| GO | regulation of Cdc42 GTPase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | adrenoceptor activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | negative regulation of multicellular organism growth | 1 | 7 | 0.390828 | 0.78133269 |
| GO | steroid hydroxylase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | ear development | 1 | 7 | 0.390828 | 0.78133269 |
| GO | adenohypophysis development | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of cholesterol esterification | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of heart rate | 1 | 7 | 0.390828 | 0.78133269 |
| GO | ephrin receptor signaling pathway | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of proteolysis | 1 | 7 | 0.390828 | 0.78133269 |
| GO | neurofilament cytoskeleton organization | 1 | 7 | 0.390828 | 0.78133269 |
| GO | regulation of cell size | 1 | 7 | 0.390828 | 0.78133269 |
| GO | surfactant homeostasis | 1 | 7 | 0.390828 | 0.78133269 |
| GO | histone H4-K12 acetylation | 1 | 7 | 0.390828 | 0.78133269 |
| GO | MOZ/MORF histone acetyltransferase complex | 1 | 7 | 0.390828 | 0.78133269 |
| GO | alpha(1,3)-fucosyltransferase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | negative regulation of catalytic activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | superoxide-generating NADPH oxidase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | enteric nervous system development | 1 | 7 | 0.390828 | 0.78133269 |
| GO | regulation of cell-matrix adhesion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | prostate gland growth | 1 | 7 | 0.390828 | 0.78133269 |
| GO | protein heterotetramerization | 1 | 7 | 0.390828 | 0.78133269 |
| GO | receptor clustering | 1 | 7 | 0.390828 | 0.78133269 |
| GO | LRR domain binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | laminin-1 complex | 1 | 7 | 0.390828 | 0.78133269 |
| GO | type I transforming growth factor beta receptor binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | sympathetic nervous system development | 1 | 7 | 0.390828 | 0.78133269 |
| GO | nucleosome disassembly | 1 | 7 | 0.390828 | 0.78133269 |
| GO | citrate metabolic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | anagen | 1 | 7 | 0.390828 | 0.78133269 |
| GO | morphogenesis of an epithelial sheet | 1 | 7 | 0.390828 | 0.78133269 |
| GO | death | 1 | 7 | 0.390828 | 0.78133269 |
| GO | neuron maturation | 1 | 7 | 0.390828 | 0.78133269 |
| GO | extracellular ATP-gated cation channel activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | purinergic nucleotide receptor activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | glycoprotein metabolic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | protein metabolic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | peptide biosynthetic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | semaphorin receptor activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | DNA damage response, signal transduction by p53 class mediator resu | 1 | 7 | 0.390828 | 0.78133269 |

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| GO | protein K48-linked deubiquitination | 1 | 7 | 0.390828 | 0.78133269 |
| GO | negative regulation of cell-matrix adhesion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | nerve development | 1 | 7 | 0.390828 | 0.78133269 |
| GO | negative regulation of cell size | 1 | 7 | 0.390828 | 0.78133269 |
| GO | glutamate binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | ankyrin binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | nuclear hormone receptor binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | dynein binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | synaptic transmission, dopaminergic | 1 | 7 | 0.390828 | 0.78133269 |
| GO | synaptic vesicle endocytosis | 1 | 7 | 0.390828 | 0.78133269 |
| GO | response to mercury ion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of alpha-beta T cell proliferation | 1 | 7 | 0.390828 | 0.78133269 |
| GO | type II transforming growth factor beta receptor binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | erythrocyte maturation | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of interleukin-10 production | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of interleukin-8 biosynthetic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of MHC class II biosynthetic process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | response to molecule of bacterial origin | 1 | 7 | 0.390828 | 0.78133269 |
| GO | membrane attack complex | 1 | 7 | 0.390828 | 0.78133269 |
| GO | AU-rich element binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | developmental pigmentation | 1 | 7 | 0.390828 | 0.78133269 |
| GO | secretion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | adult behavior | 1 | 7 | 0.390828 | 0.78133269 |
| GO | titin binding | 1 | 7 | 0.390828 | 0.78133269 |
| GO | detection of mechanical stimulus involved in sensory perception of so | 1 | 7 | 0.390828 | 0.78133269 |
| GO | neurological system process | 1 | 7 | 0.390828 | 0.78133269 |
| GO | pentose-phosphate shunt | 1 | 7 | 0.390828 | 0.78133269 |
| GO | positive regulation of cell-cell adhesion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | response to lipid | 1 | 7 | 0.390828 | 0.78133269 |
| GO | protein deacetylase activity | 1 | 7 | 0.390828 | 0.78133269 |
| GO | mitochondrial outer membrane translocase complex | 1 | 7 | 0.390828 | 0.78133269 |
| GO | clathrin coat assembly | 1 | 7 | 0.390828 | 0.78133269 |
| GO | sister chromatid cohesion | 1 | 7 | 0.390828 | 0.78133269 |
| GO | specific RNA polymerase II transcription factor activity | 3 | 33 | 0.394523 | 0.51403165 |
| GO | endosome | 16 | 215 | 0.399293 | 0.35473993 |
| GO | desmosome | 2 | 20 | 0.401252 | 0.56123017 |
| GO | dendrite development | 2 | 20 | 0.401252 | 0.56123017 |
| GO | connexon complex | 2 | 20 | 0.401252 | 0.56123017 |
| GO | positive regulation of protein kinase B signaling cascade | 2 | 20 | 0.401252 | 0.56123017 |
| GO | response to radiation | 2 | 20 | 0.401252 | 0.56123017 |
| GO | neural crest cell migration | 2 | 20 | 0.401252 | 0.56123017 |
| GO | phosphate metabolic process | 2 | 20 | 0.401252 | 0.56123017 |
| GO | neuron differentiation | 4 | 47 | 0.401887 | 0.45584076 |
| GO | exocytosis | 4 | 47 | 0.401887 | 0.45584076 |
| GO | response to heat | 4 | 47 | 0.401887 | 0.45584076 |
| GO | protein domain specific binding | 9 | 117 | 0.40689 | 0.36869127 |
| GO | positive regulation of cell growth | 3 | 34 | 0.41332 | 0.45993767 |
| GO | platelet alpha granule lumen | 3 | 34 | 0.41332 | 0.45993767 |
| GO | receptor signaling protein activity | 3 | 34 | 0.41332 | 0.45993767 |

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| GO | presynaptic membrane | 3 | 34 | 0.41332 | 0.45993767 |
| GO | visual perception | 14 | 189 | 0.417461 | 0.31350579 |
| GO | serine-type peptidase activity | 4 | 48 | 0.417611 | 0.41193633 |
| GO | integrin binding | 5 | 62 | 0.419113 | 0.38432911 |
| GO | ATPase activity, coupled to transmembrane movement of ions, phospl | 2 | 21 | 0.425606 | 0.48858248 |
| GO | aromatase activity | 2 | 21 | 0.425606 | 0.48858248 |
| GO | negative regulation of caspase activity | 2 | 21 | 0.425606 | 0.48858248 |
| GO | regulation of multicellular organism growth | 2 | 21 | 0.425606 | 0.48858248 |
| GO | defense response to virus | 2 | 21 | 0.425606 | 0.48858248 |
| GO | release of cytochrome c from mitochondria | 2 | 21 | 0.425606 | 0.48858248 |
| GO | positive regulation of mesenchymal cell proliferation | 2 | 21 | 0.425606 | 0.48858248 |
| GO | sensory perception of sound | 7 | 91 | 0.430199 | 0.32493141 |
| GO | induction of apoptosis by extracellular signals | 7 | 91 | 0.430199 | 0.32493141 |
| GO | negative regulation of transcription | 11 | 148 | 0.431903 | 0.2892346 |
| GO | transmembrane receptor protein tyrosine kinase activity | 3 | 35 | 0.431928 | 0.40750761 |
| GO | acute-phase response | 3 | 35 | 0.431928 | 0.40750761 |
| GO | excretion | 3 | 35 | 0.431928 | 0.40750761 |
| GO | U12-type spliceosomal complex | 1 | 8 | 0.432479 | 0.63510975 |
| GO | poly(A) RNA binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | creatine metabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | triglyceride catabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | retinoid binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | positive regulation of cell-matrix adhesion | 1 | 8 | 0.432479 | 0.63510975 |
| GO | regulation of catalytic activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | small GTPase binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | sexual reproduction | 1 | 8 | 0.432479 | 0.63510975 |
| GO | negative regulation of protein kinase B signaling cascade | 1 | 8 | 0.432479 | 0.63510975 |
| GO | prepulse inhibition | 1 | 8 | 0.432479 | 0.63510975 |
| GO | dopamine receptor signaling pathway | 1 | 8 | 0.432479 | 0.63510975 |
| GO | response to salt stress | 1 | 8 | 0.432479 | 0.63510975 |
| GO | non-membrane spanning protein tyrosine phosphatase activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | ephrin receptor binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | tail morphogenesis | 1 | 8 | 0.432479 | 0.63510975 |
| GO | protein-DNA complex | 1 | 8 | 0.432479 | 0.63510975 |
| GO | adenylate kinase activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | GABA receptor binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | histone H4-K16 acetylation | 1 | 8 | 0.432479 | 0.63510975 |
| GO | clathrin binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | protein homotrimerization | 1 | 8 | 0.432479 | 0.63510975 |
| GO | tumor necrosis factor-mediated signaling pathway | 1 | 8 | 0.432479 | 0.63510975 |
| GO | protein destabilization | 1 | 8 | 0.432479 | 0.63510975 |
| GO | histidine catabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | antigen processing and presentation of peptide antigen via MHC class | 1 | 8 | 0.432479 | 0.63510975 |
| GO | positive regulation of JAK-STAT cascade | 1 | 8 | 0.432479 | 0.63510975 |
| GO | male sex determination | 1 | 8 | 0.432479 | 0.63510975 |
| GO | synapse organization | 1 | 8 | 0.432479 | 0.63510975 |
| GO | epithelial cell proliferation | 1 | 8 | 0.432479 | 0.63510975 |
| GO | intestinal cholesterol absorption | 1 | 8 | 0.432479 | 0.63510975 |
| GO | embryonic hemopoiesis | 1 | 8 | 0.432479 | 0.63510975 |

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|---|---|---|---|---|---|
| GO | co-SMAD binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | SMAD protein complex assembly | 1 | 8 | 0.432479 | 0.63510975 |
| GO | neurotransmitter catabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | heterochromatin | 1 | 8 | 0.432479 | 0.63510975 |
| GO | response to lithium ion | 1 | 8 | 0.432479 | 0.63510975 |
| GO | hemostasis | 1 | 8 | 0.432479 | 0.63510975 |
| GO | nuclear localization sequence binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | positive regulation of cholesterol efflux | 1 | 8 | 0.432479 | 0.63510975 |
| GO | arginine catabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | central nervous system projection neuron axonogenesis | 1 | 8 | 0.432479 | 0.63510975 |
| GO | hydrogen-exporting ATPase activity, phosphorylative mechanism | 1 | 8 | 0.432479 | 0.63510975 |
| GO | phospholipase inhibitor activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | response to sucrose stimulus | 1 | 8 | 0.432479 | 0.63510975 |
| GO | cyclin binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | pharyngeal system development | 1 | 8 | 0.432479 | 0.63510975 |
| GO | RNA polymerase II transcription elongation factor activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | transferase activity, transferring nitrogenous groups | 1 | 8 | 0.432479 | 0.63510975 |
| GO | protein K63-linked deubiquitination | 1 | 8 | 0.432479 | 0.63510975 |
| GO | sodium:dicarboxylate symporter activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | hemopoietic progenitor cell differentiation | 1 | 8 | 0.432479 | 0.63510975 |
| GO | membrane-bounded vesicle | 1 | 8 | 0.432479 | 0.63510975 |
| GO | protein localization in nucleus | 1 | 8 | 0.432479 | 0.63510975 |
| GO | SNARE binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | antioxidant activity | 1 | 8 | 0.432479 | 0.63510975 |
| GO | immunoglobulin mediated immune response | 1 | 8 | 0.432479 | 0.63510975 |
| GO | cellular protein localization | 1 | 8 | 0.432479 | 0.63510975 |
| GO | diacylglycerol binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | intrinsic to membrane | 1 | 8 | 0.432479 | 0.63510975 |
| GO | transmembrane receptor protein serine/threonine kinase signaling pa | 1 | 8 | 0.432479 | 0.63510975 |
| GO | phosphatidylcholine binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | negative regulation of bone resorption | 1 | 8 | 0.432479 | 0.63510975 |
| GO | amyloid precursor protein catabolic process | 1 | 8 | 0.432479 | 0.63510975 |
| GO | actin monomer binding | 1 | 8 | 0.432479 | 0.63510975 |
| GO | cell redox homeostasis | 5 | 63 | 0.432841 | 0.34709641 |
| GO | PDZ domain binding | 4 | 49 | 0.433237 | 0.36897945 |
| GO | caveola | 4 | 49 | 0.433237 | 0.36897945 |
| GO | response to unfolded protein | 4 | 49 | 0.433237 | 0.36897945 |
| GO | protein serine/threonine kinase activity | 24 | 335 | 0.435806 | 0.24102365 |
| GO | nuclear envelope | 7 | 92 | 0.441537 | 0.29486273 |
| GO | protein tyrosine kinase activity | 6 | 78 | 0.444041 | 0.30072463 |
| GO | hormone-mediated signaling pathway | 4 | 50 | 0.448745 | 0.32692649 |
| GO | small GTPase mediated signal transduction | 14 | 193 | 0.448747 | 0.23188953 |
| GO | microvillus | 2 | 22 | 0.449431 | 0.41958338 |
| GO | calcium-independent cell-cell adhesion | 2 | 22 | 0.449431 | 0.41958338 |
| GO | photoreceptor cell maintenance | 2 | 22 | 0.449431 | 0.41958338 |
| GO | placenta development | 2 | 22 | 0.449431 | 0.41958338 |
| GO | pigmentation | 2 | 22 | 0.449431 | 0.41958338 |
| GO | eating behavior | 2 | 22 | 0.449431 | 0.41958338 |
| GO | histone-lysine N-methyltransferase activity | 2 | 22 | 0.449431 | 0.41958338 |

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|---|---|---|---|---|---|
| GO | transport | 36 | 511 | 0.449876 | 0.19087566 |
| GO | cellular amino acid metabolic process | 3 | 36 | 0.450315 | 0.35663439 |
| GO | I-kappaB kinase/NF-kappaB cascade | 3 | 36 | 0.450315 | 0.35663439 |
| GO | perinuclear region of cytoplasm | 22 | 309 | 0.453056 | 0.20011044 |
| GO | postsynaptic density | 6 | 79 | 0.456325 | 0.26828682 |
| GO | nervous system development | 27 | 382 | 0.456901 | 0.18249763 |
| GO | muscle organ development | 7 | 94 | 0.464094 | 0.23571406 |
| GO | cell projection | 7 | 94 | 0.464094 | 0.23571406 |
| GO | regulation of growth | 4 | 51 | 0.464116 | 0.28573671 |
| GO | secretory granule | 4 | 51 | 0.464116 | 0.28573671 |
| GO | cartilage development | 3 | 37 | 0.468453 | 0.30722074 |
| GO | protein catabolic process | 3 | 37 | 0.468453 | 0.30722074 |
| GO | protein localization at cell surface | 1 | 9 | 0.471284 | 0.50849902 |
| GO | androgen metabolic process | 1 | 9 | 0.471284 | 0.50849902 |
| GO | mitotic cell cycle | 1 | 9 | 0.471284 | 0.50849902 |
| GO | pseudopodium | 1 | 9 | 0.471284 | 0.50849902 |
| GO | adult feeding behavior | 1 | 9 | 0.471284 | 0.50849902 |
| GO | dendrite cytoplasm | 1 | 9 | 0.471284 | 0.50849902 |
| GO | macrophage differentiation | 1 | 9 | 0.471284 | 0.50849902 |
| GO | histone monoubiquitination | 1 | 9 | 0.471284 | 0.50849902 |
| GO | gonad development | 1 | 9 | 0.471284 | 0.50849902 |
| GO | lamellipodium membrane | 1 | 9 | 0.471284 | 0.50849902 |
| GO | positive regulation of JUN kinase activity | 1 | 9 | 0.471284 | 0.50849902 |
| GO | cellular response to reactive oxygen species | 1 | 9 | 0.471284 | 0.50849902 |
| GO | sleep | 1 | 9 | 0.471284 | 0.50849902 |
| GO | L-fucose catabolic process | 1 | 9 | 0.471284 | 0.50849902 |
| GO | positive regulation of receptor-mediated endocytosis | 1 | 9 | 0.471284 | 0.50849902 |
| GO | DNA damage response, signal transduction by p53 class mediator resu | 1 | 9 | 0.471284 | 0.50849902 |
| GO | specific granule | 1 | 9 | 0.471284 | 0.50849902 |
| GO | serotonin binding | 1 | 9 | 0.471284 | 0.50849902 |
| GO | positive regulation of tyrosine phosphorylation of Stat5 protein | 1 | 9 | 0.471284 | 0.50849902 |
| GO | proteoglycan biosynthetic process | 1 | 9 | 0.471284 | 0.50849902 |
| GO | regulation of peptidyl-tyrosine phosphorylation | 1 | 9 | 0.471284 | 0.50849902 |
| GO | muscarinic acetylcholine receptor signaling pathway | 1 | 9 | 0.471284 | 0.50849902 |
| GO | positive regulation of nitric-oxide synthase activity | 1 | 9 | 0.471284 | 0.50849902 |
| GO | branching involved in salivary gland morphogenesis | 1 | 9 | 0.471284 | 0.50849902 |
| GO | organ growth | 1 | 9 | 0.471284 | 0.50849902 |
| GO | axonal fasciculation | 1 | 9 | 0.471284 | 0.50849902 |
| GO | central nervous system neuron differentiation | 1 | 9 | 0.471284 | 0.50849902 |
| GO | MHC class I protein binding | 1 | 9 | 0.471284 | 0.50849902 |
| GO | vacuolar proton-transporting V-type ATPase complex | 1 | 9 | 0.471284 | 0.50849902 |
| GO | insulin-like growth factor receptor signaling pathway | 1 | 9 | 0.471284 | 0.50849902 |
| GO | maintenance of protein location in nucleus | 1 | 9 | 0.471284 | 0.50849902 |
| GO | female gonad development | 1 | 9 | 0.471284 | 0.50849902 |
| GO | organic anion transmembrane transporter activity | 1 | 9 | 0.471284 | 0.50849902 |
| GO | grooming behavior | 1 | 9 | 0.471284 | 0.50849902 |
| GO | response to pain | 1 | 9 | 0.471284 | 0.50849902 |
| GO | apical protein localization | 1 | 9 | 0.471284 | 0.50849902 |
| GO | melanosome transport | 1 | 9 | 0.471284 | 0.50849902 |

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| GO | negative regulation of S phase of mitotic cell cycle | 1 | 9 | 0.471284 | 0.50849902 |
| GO | detection of bacterium | 1 | 9 | 0.471284 | 0.50849902 |
| GO | dicarboxylic acid transport | 1 | 9 | 0.471284 | 0.50849902 |
| GO | epithelial tube branching involved in lung morphogenesis | 1 | 9 | 0.471284 | 0.50849902 |
| GO | smooth muscle tissue development | 1 | 9 | 0.471284 | 0.50849902 |
| GO | muscle cell differentiation | 1 | 9 | 0.471284 | 0.50849902 |
| GO | positive regulation of release of sequestered calcium ion into cytosol | 1 | 9 | 0.471284 | 0.50849902 |
| GO | spectrin | 1 | 9 | 0.471284 | 0.50849902 |
| GO | T-helper 1 type immune response | 1 | 9 | 0.471284 | 0.50849902 |
| GO | cleavage furrow | 1 | 9 | 0.471284 | 0.50849902 |
| GO | DNA-(apurinic or apyrimidinic site) lyase activity | 1 | 9 | 0.471284 | 0.50849902 |
| GO | quinone binding | 1 | 9 | 0.471284 | 0.50849902 |
| GO | sensory perception of light stimulus | 1 | 9 | 0.471284 | 0.50849902 |
| GO | ER overload response | 1 | 9 | 0.471284 | 0.50849902 |
| GO | hedgehog receptor activity | 1 | 9 | 0.471284 | 0.50849902 |
| GO | two-component signal transduction system (phosphorelay) | 1 | 9 | 0.471284 | 0.50849902 |
| GO | oligosaccharide biosynthetic process | 1 | 9 | 0.471284 | 0.50849902 |
| GO | response to food | 1 | 9 | 0.471284 | 0.50849902 |
| GO | ovulation from ovarian follicle | 1 | 9 | 0.471284 | 0.50849902 |
| GO | phospholipid efflux | 1 | 9 | 0.471284 | 0.50849902 |
| GO | retinoid X receptor binding | 1 | 9 | 0.471284 | 0.50849902 |
| GO | condensed nuclear chromosome, centromeric region | 1 | 9 | 0.471284 | 0.50849902 |
| GO | sarcoplasmic reticulum | 2 | 23 | 0.472685 | 0.35386157 |
| GO | positive regulation of multicellular organism growth | 2 | 23 | 0.472685 | 0.35386157 |
| GO | protease binding | 2 | 23 | 0.472685 | 0.35386157 |
| GO | ER-associated protein catabolic process | 2 | 23 | 0.472685 | 0.35386157 |
| GO | erythrocyte differentiation | 2 | 23 | 0.472685 | 0.35386157 |
| GO | regulation of cell adhesion | 2 | 23 | 0.472685 | 0.35386157 |
| GO | Golgi stack | 2 | 23 | 0.472685 | 0.35386157 |
| GO | nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 5 | 66 | 0.473545 | 0.23895159 |
| GO | DNA binding | 96 | 1392 | 0.478792 | 0.09481585 |
| GO | signal transducer activity | 20 | 285 | 0.484792 | 0.12317081 |
| GO | carbohydrate metabolic process | 14 | 198 | 0.487656 | 0.13222615 |
| GO | microtubule cytoskeleton | 4 | 53 | 0.494376 | 0.20579677 |
| GO | cellular membrane organization | 4 | 53 | 0.494376 | 0.20579677 |
| GO | activation of adenylate cyclase activity | 2 | 24 | 0.495335 | 0.29109863 |
| GO | oxygen and reactive oxygen species metabolic process | 2 | 24 | 0.495335 | 0.29109863 |
| GO | peripheral nervous system development | 2 | 24 | 0.495335 | 0.29109863 |
| GO | histone H3 acetylation | 2 | 24 | 0.495335 | 0.29109863 |
| GO | cilium assembly | 2 | 24 | 0.495335 | 0.29109863 |
| GO | transmembrane transport | 34 | 492 | 0.499301 | 0.06746496 |
| GO | beta-catenin binding | 3 | 39 | 0.503887 | 0.21242552 |
| GO | insoluble fraction | 3 | 39 | 0.503887 | 0.21242552 |
| GO | G-protein signaling, coupled to cyclic nucleotide second messenger | 3 | 39 | 0.503887 | 0.21242552 |
| GO | aging | 6 | 83 | 0.504703 | 0.14259162 |
| GO | chromatin silencing | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cellular respiration | 1 | 10 | 0.507438 | 0.39674511 |
| GO | acetylcholine binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cognition | 1 | 10 | 0.507438 | 0.39674511 |

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|---|---|---|---|---|---|
| GO | ribonucleoprotein binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | urea cycle | 1 | 10 | 0.507438 | 0.39674511 |
| GO | positive regulation of cytokine production | 1 | 10 | 0.507438 | 0.39674511 |
| GO | positive regulation of collagen biosynthetic process | 1 | 10 | 0.507438 | 0.39674511 |
| GO | protein kinase B signaling cascade | 1 | 10 | 0.507438 | 0.39674511 |
| GO | carboxylic acid metabolic process | 1 | 10 | 0.507438 | 0.39674511 |
| GO | histone acetyltransferase binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | IkappaB kinase complex | 1 | 10 | 0.507438 | 0.39674511 |
| GO | MHC class I receptor activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | positive regulation of smooth muscle cell migration | 1 | 10 | 0.507438 | 0.39674511 |
| GO | acyl-CoA dehydrogenase activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | water channel activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | morphogenesis of embryonic epithelium | 1 | 10 | 0.507438 | 0.39674511 |
| GO | substrate adhesion-dependent cell spreading | 1 | 10 | 0.507438 | 0.39674511 |
| GO | I-SMAD binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | oxygen transporter activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | oxygen transport | 1 | 10 | 0.507438 | 0.39674511 |
| GO | lipopolysaccharide-mediated signaling pathway | 1 | 10 | 0.507438 | 0.39674511 |
| GO | stem cell maintenance | 1 | 10 | 0.507438 | 0.39674511 |
| GO | Golgi lumen | 1 | 10 | 0.507438 | 0.39674511 |
| GO | CUL4 RING ubiquitin ligase complex | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cAMP-dependent protein kinase complex | 1 | 10 | 0.507438 | 0.39674511 |
| GO | transmission of nerve impulse | 1 | 10 | 0.507438 | 0.39674511 |
| GO | isotype switching | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cardiac muscle tissue development | 1 | 10 | 0.507438 | 0.39674511 |
| GO | signalosome | 1 | 10 | 0.507438 | 0.39674511 |
| GO | L-glutamate transmembrane transporter activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | calcium ion homeostasis | 1 | 10 | 0.507438 | 0.39674511 |
| GO | platelet alpha granule membrane | 1 | 10 | 0.507438 | 0.39674511 |
| GO | platelet alpha granule | 1 | 10 | 0.507438 | 0.39674511 |
| GO | B cell receptor signaling pathway | 1 | 10 | 0.507438 | 0.39674511 |
| GO | interleukin-1 receptor binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | tumor necrosis factor receptor activity | 1 | 10 | 0.507438 | 0.39674511 |
| GO | complement activation | 1 | 10 | 0.507438 | 0.39674511 |
| GO | mRNA catabolic process | 1 | 10 | 0.507438 | 0.39674511 |
| GO | XY body | 1 | 10 | 0.507438 | 0.39674511 |
| GO | killing of cells of another organism | 1 | 10 | 0.507438 | 0.39674511 |
| GO | calcium ion-dependent exocytosis | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cytokine binding | 1 | 10 | 0.507438 | 0.39674511 |
| GO | embryonic digestive tract development | 1 | 10 | 0.507438 | 0.39674511 |
| GO | mRNA cap binding complex | 1 | 10 | 0.507438 | 0.39674511 |
| GO | NAD metabolic process | 1 | 10 | 0.507438 | 0.39674511 |
| GO | positive regulation of T cell activation | 1 | 10 | 0.507438 | 0.39674511 |
| GO | cellular component movement | 7 | 98 | 0.508499 | 0.12115542 |
| GO | dendrite | 9 | 128 | 0.514696 | 0.08836645 |
| GO | melanosome | 6 | 84 | 0.516562 | 0.11212658 |
| GO | mitochondrial intermembrane space | 2 | 25 | 0.517355 | 0.23101953 |
| GO | lipid biosynthetic process | 2 | 25 | 0.517355 | 0.23101953 |
| GO | glycoprotein binding | 2 | 25 | 0.517355 | 0.23101953 |

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|---|---|---|---|---|---|
| GO | heterotrimeric G-protein complex | 2 | 25 | 0.517355 | 0.23101953 |
| GO | fat cell differentiation | 2 | 25 | 0.517355 | 0.23101953 |
| GO | osteoblast differentiation | 2 | 25 | 0.517355 | 0.23101953 |
| GO | stress fiber | 2 | 25 | 0.517355 | 0.23101953 |
| GO | receptor-mediated endocytosis | 3 | 40 | 0.52114 | 0.16688897 |
| GO | catalytic activity | 8 | 114 | 0.521942 | 0.07754642 |
| GO | response to toxin | 4 | 55 | 0.523889 | 0.12888284 |
| GO | cytoplasmic membrane-bounded vesicle | 6 | 85 | 0.528309 | 0.08202449 |
| GO | voltage-gated potassium channel complex | 6 | 85 | 0.528309 | 0.08202449 |
| GO | magnesium ion binding | 11 | 159 | 0.528326 | 0.04186063 |
| GO | negative regulation of cell cycle | 3 | 41 | 0.53806 | 0.12250048 |
| GO | protein import into nucleus | 2 | 26 | 0.538725 | 0.17338525 |
| GO | triglyceride metabolic process | 2 | 26 | 0.538725 | 0.17338525 |
| GO | skin development | 2 | 26 | 0.538725 | 0.17338525 |
| GO | terminal button | 2 | 26 | 0.538725 | 0.17338525 |
| GO | embryo implantation | 2 | 26 | 0.538725 | 0.17338525 |
| GO | lamellipodium | 5 | 71 | 0.53903 | 0.06939483 |
| GO | focal adhesion | 6 | 86 | 0.539939 | 0.05227575 |
| GO | dipeptidyl-peptidase activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | motor axon guidance | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of axon extension | 1 | 11 | 0.541121 | 0.29660426 |
| GO | negative regulation of JNK cascade | 1 | 11 | 0.541121 | 0.29660426 |
| GO | fibroblast growth factor binding | 1 | 11 | 0.541121 | 0.29660426 |
| GO | DNA bending activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | maternal process involved in female pregnancy | 1 | 11 | 0.541121 | 0.29660426 |
| GO | sodium channel activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | SCF ubiquitin ligase complex | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of vascular endothelial growth factor receptor sign | 1 | 11 | 0.541121 | 0.29660426 |
| GO | myelin sheath | 1 | 11 | 0.541121 | 0.29660426 |
| GO | trophectodermal cell differentiation | 1 | 11 | 0.541121 | 0.29660426 |
| GO | delayed rectifier potassium channel activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | low-density lipoprotein receptor activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | actin filament polymerization | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of epithelial to mesenchymal transition | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of neurogenesis | 1 | 11 | 0.541121 | 0.29660426 |
| GO | methionine biosynthetic process | 1 | 11 | 0.541121 | 0.29660426 |
| GO | gamma-tubulin binding | 1 | 11 | 0.541121 | 0.29660426 |
| GO | FMN binding | 1 | 11 | 0.541121 | 0.29660426 |
| GO | nitric oxide biosynthetic process | 1 | 11 | 0.541121 | 0.29660426 |
| GO | oligodendrocyte differentiation | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of calcium ion transport into cytosol | 1 | 11 | 0.541121 | 0.29660426 |
| GO | Ras GTPase binding | 1 | 11 | 0.541121 | 0.29660426 |
| GO | intermediate filament cytoskeleton | 1 | 11 | 0.541121 | 0.29660426 |
| GO | neuropeptide receptor activity | 1 | 11 | 0.541121 | 0.29660426 |
| GO | replication fork | 1 | 11 | 0.541121 | 0.29660426 |
| GO | npBAF complex | 1 | 11 | 0.541121 | 0.29660426 |
| GO | cellular response to oxidative stress | 1 | 11 | 0.541121 | 0.29660426 |
| GO | response to magnesium ion | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of interferon-gamma biosynthetic process | 1 | 11 | 0.541121 | 0.29660426 |

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|---|---|---|---|---|---|
| GO | positive regulation of interferon-gamma production | 1 | 11 | 0.541121 | 0.29660426 |
| GO | initiation of viral infection | 1 | 11 | 0.541121 | 0.29660426 |
| GO | positive regulation of erythrocyte differentiation | 1 | 11 | 0.541121 | 0.29660426 |
| GO | phosphatidylinositol-3,4-bisphosphate binding | 1 | 11 | 0.541121 | 0.29660426 |
| GO | pyridine nucleotide biosynthetic process | 1 | 11 | 0.541121 | 0.29660426 |
| GO | P-P-bond-hydrolysis-driven protein transmembrane transporter activit | 1 | 11 | 0.541121 | 0.29660426 |
| GO | bile acid metabolic process | 1 | 11 | 0.541121 | 0.29660426 |
| GO | oocyte maturation | 1 | 11 | 0.541121 | 0.29660426 |
| GO | transcription regulator activity | 7 | 102 | 0.551579 | 0.01120772 |
| GO | synaptic vesicle membrane | 3 | 42 | 0.554633 | 0.07919755 |
| GO | JAK-STAT cascade | 2 | 27 | 0.559431 | 0.11798685 |
| GO | negative regulation of Wnt receptor signaling pathway | 2 | 27 | 0.559431 | 0.11798685 |
| GO | phagocytosis | 2 | 27 | 0.559431 | 0.11798685 |
| GO | cell aging | 2 | 27 | 0.559431 | 0.11798685 |
| GO | meiosis | 4 | 58 | 0.56653 | 0.01865991 |
| GO | structural constituent of muscle | 3 | 43 | 0.570845 | 0.03692257 |
| GO | ligand-dependent nuclear receptor binding | 1 | 12 | 0.572503 | 0.20577273 |
| GO | lysophospholipase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | response to chemical stimulus | 1 | 12 | 0.572503 | 0.20577273 |
| GO | endothelial cell migration | 1 | 12 | 0.572503 | 0.20577273 |
| GO | release of sequestered calcium ion into cytosol | 1 | 12 | 0.572503 | 0.20577273 |
| GO | ephrin receptor activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | acetyltransferase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | arylsulfatase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | glutamate receptor activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | estradiol 17-beta-dehydrogenase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | male meiosis | 1 | 12 | 0.572503 | 0.20577273 |
| GO | positive regulation of peptidyl-serine phosphorylation | 1 | 12 | 0.572503 | 0.20577273 |
| GO | cGMP biosynthetic process | 1 | 12 | 0.572503 | 0.20577273 |
| GO | activation of protein kinase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | platelet-derived growth factor receptor binding | 1 | 12 | 0.572503 | 0.20577273 |
| GO | smooth muscle contraction | 1 | 12 | 0.572503 | 0.20577273 |
| GO | endochondral ossification | 1 | 12 | 0.572503 | 0.20577273 |
| GO | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | 1 | 12 | 0.572503 | 0.20577273 |
| GO | mitochondrial ATP synthesis coupled proton transport | 1 | 12 | 0.572503 | 0.20577273 |
| GO | triglyceride homeostasis | 1 | 12 | 0.572503 | 0.20577273 |
| GO | axon terminus | 1 | 12 | 0.572503 | 0.20577273 |
| GO | costamere | 1 | 12 | 0.572503 | 0.20577273 |
| GO | histone methylation | 1 | 12 | 0.572503 | 0.20577273 |
| GO | iron-sulfur cluster binding | 1 | 12 | 0.572503 | 0.20577273 |
| GO | calcium channel regulator activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | positive regulation of cellular component movement | 1 | 12 | 0.572503 | 0.20577273 |
| GO | voltage-gated sodium channel complex | 1 | 12 | 0.572503 | 0.20577273 |
| GO | positive regulation of innate immune response | 1 | 12 | 0.572503 | 0.20577273 |
| GO | dorsal/ventral neural tube patterning | 1 | 12 | 0.572503 | 0.20577273 |
| GO | nBAF complex | 1 | 12 | 0.572503 | 0.20577273 |
| GO | alpha-tubulin binding | 1 | 12 | 0.572503 | 0.20577273 |
| GO | ferrous iron binding | 1 | 12 | 0.572503 | 0.20577273 |
| GO | glutamate signaling pathway | 1 | 12 | 0.572503 | 0.20577273 |

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|---|---|---|---|---|---|
| GO | T cell receptor complex | 1 | 12 | 0.572503 | 0.20577273 |
| GO | negative regulation of cyclin-dependent protein kinase activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | regulation of muscle contraction | 1 | 12 | 0.572503 | 0.20577273 |
| GO | NLS-bearing substrate import into nucleus | 1 | 12 | 0.572503 | 0.20577273 |
| GO | mammary gland alveolus development | 1 | 12 | 0.572503 | 0.20577273 |
| GO | regulation of lipid metabolic process | 1 | 12 | 0.572503 | 0.20577273 |
| GO | cholesterol transporter activity | 1 | 12 | 0.572503 | 0.20577273 |
| GO | protein oligomerization | 2 | 28 | 0.579464 | 0.06464066 |
| GO | activation of phospholipase C activity by G-protein coupled receptor p | 2 | 28 | 0.579464 | 0.06464066 |
| GO | negative regulation of transforming growth factor beta receptor signa | 2 | 28 | 0.579464 | 0.06464066 |
| GO | small GTPase regulator activity | 2 | 28 | 0.579464 | 0.06464066 |
| GO | antigen processing and presentation | 2 | 28 | 0.579464 | 0.06464066 |
| GO | regulation of cell migration | 2 | 28 | 0.579464 | 0.06464066 |
| GO | ruffle membrane | 2 | 29 | 0.598819 | 0.01318446 |
| GO | chaperone binding | 2 | 29 | 0.598819 | 0.01318446 |
| GO | cyclin-dependent protein kinase activity | 2 | 29 | 0.598819 | 0.01318446 |
| GO | phosphate binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | cAMP biosynthetic process | 1 | 13 | 0.60174 | 0.12255989 |
| GO | folic acid binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | cell wall macromolecule catabolic process | 1 | 13 | 0.60174 | 0.12255989 |
| GO | regulation of cell differentiation | 1 | 13 | 0.60174 | 0.12255989 |
| GO | bone resorption | 1 | 13 | 0.60174 | 0.12255989 |
| GO | steroid hormone receptor signaling pathway | 1 | 13 | 0.60174 | 0.12255989 |
| GO | epidermal growth factor receptor binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | positive regulation of hormone secretion | 1 | 13 | 0.60174 | 0.12255989 |
| GO | endosome organization | 1 | 13 | 0.60174 | 0.12255989 |
| GO | receptor signaling complex scaffold activity | 1 | 13 | 0.60174 | 0.12255989 |
| GO | fibroblast growth factor receptor binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | superoxide anion generation | 1 | 13 | 0.60174 | 0.12255989 |
| GO | serotonin receptor activity | 1 | 13 | 0.60174 | 0.12255989 |
| GO | glial cell differentiation | 1 | 13 | 0.60174 | 0.12255989 |
| GO | myoblast differentiation | 1 | 13 | 0.60174 | 0.12255989 |
| GO | extracellular matrix binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | oligodendrocyte development | 1 | 13 | 0.60174 | 0.12255989 |
| GO | hydrogen ion transporting ATP synthase activity, rotational mechanisn | 1 | 13 | 0.60174 | 0.12255989 |
| GO | protein autoubiquitination | 1 | 13 | 0.60174 | 0.12255989 |
| GO | retrograde transport, endosome to Golgi | 1 | 13 | 0.60174 | 0.12255989 |
| GO | transcription elongation factor complex | 1 | 13 | 0.60174 | 0.12255989 |
| GO | regulation of protein kinase activity | 1 | 13 | 0.60174 | 0.12255989 |
| GO | organic anion transport | 1 | 13 | 0.60174 | 0.12255989 |
| GO | regulation of smooth muscle contraction | 1 | 13 | 0.60174 | 0.12255989 |
| GO | hippo signaling pathway | 1 | 13 | 0.60174 | 0.12255989 |
| GO | negative regulation of phosphorylation | 1 | 13 | 0.60174 | 0.12255989 |
| GO | low-density lipoprotein binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | myosin binding | 1 | 13 | 0.60174 | 0.12255989 |
| GO | lipid homeostasis | 1 | 13 | 0.60174 | 0.12255989 |
| GO | T cell homeostasis | 1 | 13 | 0.60174 | 0.12255989 |
| GO | response to bacterium | 1 | 13 | 0.60174 | 0.12255989 |
| GO | high-density lipoprotein particle remodeling | 1 | 13 | 0.60174 | 0.12255989 |

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|---|---|---|---|---|---|
| GO | DNA-directed RNA polymerase II, core complex | 1 | 14 | 0.628979 | 0.04569098 |
| GO | senescence | 1 | 14 | 0.628979 | 0.04569098 |
| GO | dynein complex | 1 | 14 | 0.628979 | 0.04569098 |
| GO | nuclear heterochromatin | 1 | 14 | 0.628979 | 0.04569098 |
| GO | DNA methylation | 1 | 14 | 0.628979 | 0.04569098 |
| GO | cellular response to starvation | 1 | 14 | 0.628979 | 0.04569098 |
| GO | membrane protein ectodomain proteolysis | 1 | 14 | 0.628979 | 0.04569098 |
| GO | regulation of action potential | 1 | 14 | 0.628979 | 0.04569098 |
| GO | anatomical structure formation involved in morphogenesis | 1 | 14 | 0.628979 | 0.04569098 |
| GO | positive regulation of transforming growth factor beta receptor signali | 1 | 14 | 0.628979 | 0.04569098 |
| GO | regulation of transforming growth factor beta receptor signaling pathv | 1 | 14 | 0.628979 | 0.04569098 |
| GO | phosphoinositide phosphorylation | 1 | 14 | 0.628979 | 0.04569098 |
| GO | 3'-5' exonuclease activity | 1 | 14 | 0.628979 | 0.04569098 |
| GO | cytokine production | 1 | 14 | 0.628979 | 0.04569098 |
| GO | microtubule-based flagellum | 1 | 14 | 0.628979 | 0.04569098 |
| GO | response to interferon-gamma | 1 | 14 | 0.628979 | 0.04569098 |
| GO | tropomyosin binding | 1 | 14 | 0.628979 | 0.04569098 |
| GO | filamentous actin | 1 | 14 | 0.628979 | 0.04569098 |
| GO | voltage-gated potassium channel activity | 3 | 63 | 0.989 | -0.6530869 |
| GO | chromatin modification | 11 | 204 | 0.989 | -0.8209609 |
| GO | chromatin organization | 1 | 19 | 0.989 | -0.2716131 |
| GO | chromatin remodeling | 2 | 46 | 0.989 | -0.6692339 |
| GO | cytoplasm | 293 | 4355 | 0.989 | -0.318496 |
| GO | hydrolase activity | 61 | 917 | 0.989 | -0.2247214 |
| GO | nucleus | 305 | 4735 | 0.989 | -1.2382054 |
| GO | regulation of transcription | 64 | 956 | 0.989 | -0.1763453 |
| GO | specific transcriptional repressor activity | 2 | 38 | 0.989 | -0.3843114 |
| GO | homophilic cell adhesion | 8 | 135 | 0.989 | -0.4199774 |
| GO | Wnt receptor signaling pathway through beta-catenin | 1 | 23 | 0.989 | -0.4729329 |
| GO | RNA splicing | 5 | 251 | 0.989 | -3.0606908 |
| GO | carbohydrate biosynthetic process | 1 | 17 | 0.989 | -0.1556918 |
| GO | transferase activity | 57 | 1127 | 0.989 | -2.4376244 |
| GO | lysosomal membrane | 2 | 83 | 0.989 | -1.6011028 |
| GO | soluble fraction | 20 | 315 | 0.989 | -0.3444081 |
| GO | cellular_component | 34 | 528 | 0.989 | -0.3651737 |
| GO | cytosol | 59 | 1230 | 0.989 | -2.9289359 |
| GO | acyltransferase activity | 5 | 133 | 0.989 | -1.4104393 |
| GO | integral to endoplasmic reticulum membrane | 2 | 46 | 0.989 | -0.6692339 |
| GO | cytoskeleton | 39 | 635 | 0.989 | -0.7039731 |
| GO | ATP binding | 87 | 1426 | 0.989 | -1.1418424 |
| GO | negative regulation of transcription factor activity | 1 | 30 | 0.989 | -0.7605964 |
| GO | protein kinase activity | 7 | 170 | 0.989 | -1.4102369 |
| GO | microtubule | 9 | 233 | 0.989 | -1.8089579 |
| GO | intracellular protein transport | 2 | 174 | 0.989 | -2.9856027 |
| GO | protein transporter activity | 2 | 69 | 0.989 | -1.2980687 |
| GO | protein transport | 25 | 388 | 0.989 | -0.308779 |
| GO | ER to Golgi vesicle-mediated transport | 1 | 41 | 0.989 | -1.1165976 |
| GO | vesicle-mediated transport | 6 | 165 | 0.989 | -1.635216 |
| GO | membrane fraction | 31 | 472 | 0.989 | -0.2327974 |

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|---|---|---|---|---|---|
| GO | hydrogen ion transmembrane transporter activity | 1 | 20 | 0.989 | -0.325338 |
| GO | mitochondrion | 51 | 1193 | 0.989 | -3.6193147 |
| GO | Cajal body | 1 | 38 | 0.989 | -1.0278009 |
| GO | ligase activity | 16 | 303 | 0.989 | -1.0807961 |
| GO | nuclear speck | 4 | 111 | 0.989 | -1.3530016 |
| GO | double-stranded RNA binding | 2 | 31 | 0.989 | -0.0846181 |
| GO | mRNA processing | 5 | 231 | 0.989 | -2.83014 |
| GO | nucleolus | 41 | 692 | 0.989 | -0.9663498 |
| GO | nucleoplasm | 12 | 455 | 0.989 | -3.5913344 |
| GO | RNA binding | 17 | 562 | 0.989 | -3.6333204 |
| GO | RNA processing | 3 | 80 | 0.989 | -1.0956941 |
| GO | axon guidance | 4 | 71 | 0.989 | -0.4017804 |
| GO | endoplasmic reticulum lumen | 3 | 68 | 0.989 | -0.7932213 |
| GO | biological_process | 36 | 547 | 0.989 | -0.2383713 |
| GO | sodium ion transport | 7 | 129 | 0.989 | -0.6360887 |
| GO | cell cycle | 19 | 458 | 0.989 | -2.3061836 |
| GO | female gamete generation | 1 | 15 | 0.989 | -0.0258174 |
| GO | regulation of gene expression | 2 | 32 | 0.989 | -0.1312076 |
| GO | nucleotide binding | 110 | 1859 | 0.989 | -1.650776 |
| GO | ATPase activity | 8 | 128 | 0.989 | -0.2630822 |
| GO | cholesterol biosynthetic process | 1 | 25 | 0.989 | -0.5620556 |
| GO | cytoplasmic vesicle membrane | 4 | 61 | 0.989 | -0.0860063 |
| GO | early endosome membrane | 1 | 37 | 0.989 | -0.9969995 |
| GO | enzyme binding | 7 | 114 | 0.989 | -0.2947195 |
| GO | androgen receptor binding | 1 | 29 | 0.989 | -0.723245 |
| GO | androgen receptor signaling pathway | 1 | 39 | 0.989 | -1.0579801 |
| GO | ligand-dependent nuclear receptor transcription coactivator activity | 1 | 31 | 0.989 | -0.7969334 |
| GO | mitochondrion organization | 1 | 25 | 0.989 | -0.5620556 |
| GO | RNA polymerase II transcription mediator activity | 1 | 28 | 0.989 | -0.6848042 |
| GO | transcription initiation from RNA polymerase II promoter | 1 | 64 | 0.989 | -1.6742596 |
| GO | DNA repair | 2 | 182 | 0.989 | -3.0812562 |
| GO | molecular_function | 27 | 577 | 0.989 | -2.0836371 |
| GO | identical protein binding | 22 | 338 | 0.989 | -0.2396045 |
| GO | inhibition of adenylate cyclase activity by G-protein signaling pathway | 2 | 30 | 0.989 | -0.0365257 |
| GO | chromosome, telomeric region | 1 | 23 | 0.989 | -0.4729329 |
| GO | response to DNA damage stimulus | 3 | 78 | 0.989 | -1.0481326 |
| GO | neuron projection morphogenesis | 1 | 17 | 0.989 | -0.1556918 |
| GO | cell communication | 5 | 90 | 0.989 | -0.4820701 |
| GO | phosphoinositide binding | 3 | 56 | 0.989 | -0.438846 |
| GO | cellular calcium ion homeostasis | 4 | 60 | 0.989 | -0.0516961 |
| GO | extracellular ligand-gated ion channel activity | 3 | 46 | 0.989 | -0.0842472 |
| GO | postsynaptic membrane | 7 | 149 | 0.989 | -1.0377 |
| GO | synapse | 16 | 255 | 0.989 | -0.3569683 |
| GO | G-protein coupled receptor protein signaling pathway | 43 | 725 | 0.989 | -0.9832936 |
| GO | electron carrier activity | 10 | 149 | 0.989 | -0.0599297 |
| GO | protein disulfide oxidoreductase activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | olfactory receptor activity | 5 | 290 | 0.989 | -3.4755007 |
| GO | response to stimulus | 17 | 477 | 0.989 | -2.867116 |
| GO | sensory perception of smell | 6 | 305 | 0.989 | -3.3960898 |

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|---|---|---|---|---|---|
| GO | mitochondrial inner membrane | 10 | 231 | 0.989 | -1.5184843 |
| GO | MLL1 complex | 1 | 26 | 0.989 | -0.6043094 |
| GO | cell cycle arrest | 5 | 108 | 0.989 | -0.9107392 |
| GO | neuron projection development | 2 | 41 | 0.989 | -0.4970486 |
| GO | peptidyl-serine phosphorylation | 1 | 26 | 0.989 | -0.6043094 |
| GO | Rab GTPase activator activity | 2 | 44 | 0.989 | -0.6024802 |
| GO | regulation of Rab GTPase activity | 2 | 44 | 0.989 | -0.6024802 |
| GO | post-translational protein modification | 1 | 27 | 0.989 | -0.6451903 |
| GO | regulation of protein metabolic process | 2 | 42 | 0.989 | -0.5329476 |
| GO | heat shock protein binding | 4 | 62 | 0.989 | -0.1197661 |
| GO | nucleic acid binding | 9 | 254 | 0.989 | -2.092831 |
| GO | protein folding | 5 | 139 | 0.989 | -1.5182271 |
| GO | ribosome | 3 | 172 | 0.989 | -2.6577232 |
| GO | actin filament binding | 3 | 50 | 0.989 | -0.2342323 |
| GO | metabolic process | 31 | 455 | 0.989 | -0.0185063 |
| GO | metallopeptidase activity | 6 | 88 | 0.989 | -0.0061982 |
| GO | protein modification process | 9 | 145 | 0.989 | -0.3007814 |
| GO | structural molecule activity | 8 | 196 | 0.989 | -1.5353745 |
| GO | mitochondrial matrix | 5 | 147 | 0.989 | -1.6560591 |
| GO | mitochondrial nucleoid | 1 | 31 | 0.989 | -0.7969334 |
| GO | protein complex | 8 | 153 | 0.989 | -0.7904272 |
| GO | cytoplasmic vesicle | 14 | 229 | 0.989 | -0.435165 |
| GO | homeostasis of number of cells within a tissue | 1 | 15 | 0.989 | -0.0258174 |
| GO | positive regulation of protein kinase activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | regulation of translation | 3 | 61 | 0.989 | -0.5942032 |
| GO | spermatogenesis | 16 | 261 | 0.989 | -0.4541866 |
| GO | microtubule motor activity | 3 | 76 | 0.989 | -0.9995167 |
| GO | microtubule-based movement | 3 | 84 | 0.989 | -1.187871 |
| GO | hyaluronic acid binding | 1 | 19 | 0.989 | -0.2716131 |
| GO | Rho protein signal transduction | 2 | 36 | 0.989 | -0.3044533 |
| GO | binding of sperm to zona pellucida | 1 | 15 | 0.989 | -0.0258174 |
| GO | autophagy | 2 | 36 | 0.989 | -0.3044533 |
| GO | histone binding | 3 | 44 | 0.989 | -0.0043777 |
| GO | ruffle | 3 | 53 | 0.989 | -0.339292 |
| GO | cysteine-type peptidase activity | 3 | 76 | 0.989 | -0.9995167 |
| GO | structural constituent of ribosome | 1 | 146 | 0.989 | -2.9560895 |
| GO | translation | 2 | 197 | 0.989 | -3.2537784 |
| GO | ubiquitin thiolesterase activity | 3 | 68 | 0.989 | -0.7932213 |
| GO | ubiquitin-dependent protein catabolic process | 5 | 139 | 0.989 | -1.5182271 |
| GO | intrinsic to endoplasmic reticulum membrane | 1 | 16 | 0.989 | -0.0927387 |
| GO | RNA polymerase II transcription factor activity | 8 | 126 | 0.989 | -0.2167289 |
| GO | kinase activity | 2 | 117 | 0.989 | -2.2037494 |
| GO | metalloendopeptidase activity | 6 | 102 | 0.989 | -0.3822225 |
| GO | microtubule binding | 1 | 58 | 0.989 | -1.5447389 |
| GO | motor activity | 3 | 64 | 0.989 | -0.6818948 |
| GO | post-Golgi vesicle-mediated transport | 2 | 37 | 0.989 | -0.3448894 |
| GO | aminopeptidase activity | 1 | 28 | 0.989 | -0.6848042 |
| GO | collagen binding | 2 | 34 | 0.989 | -0.2202801 |
| GO | response to cocaine | 1 | 16 | 0.989 | -0.0927387 |

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|---|---|---|---|---|---|
| GO | synapse assembly | 2 | 33 | 0.989 | -0.1763973 |
| GO | regulation of neuron differentiation | 1 | 19 | 0.989 | -0.2716131 |
| GO | regulation of heart contraction | 2 | 32 | 0.989 | -0.1312076 |
| GO | inactivation of MAPK activity | 1 | 20 | 0.989 | -0.325338 |
| GO | glucose transport | 1 | 22 | 0.989 | -0.4257707 |
| GO | translation elongation factor activity | 1 | 20 | 0.989 | -0.325338 |
| GO | translational elongation | 1 | 87 | 0.989 | -2.1062764 |
| GO | T cell differentiation | 1 | 19 | 0.989 | -0.2716131 |
| GO | myelination | 1 | 29 | 0.989 | -0.723245 |
| GO | vasculogenesis | 2 | 42 | 0.989 | -0.5329476 |
| GO | regulation of translational initiation | 1 | 24 | 0.989 | -0.518309 |
| GO | translation factor activity, nucleic acid binding | 1 | 21 | 0.989 | -0.3766422 |
| GO | translation initiation factor activity | 1 | 49 | 0.989 | -1.3315436 |
| GO | translational initiation | 1 | 36 | 0.989 | -0.965541 |
| GO | glycolysis | 1 | 41 | 0.989 | -1.1165976 |
| GO | synaptosome | 5 | 91 | 0.989 | -0.5078876 |
| GO | histone acetyltransferase activity | 2 | 38 | 0.989 | -0.3843114 |
| GO | histone H4 acetylation | 1 | 15 | 0.989 | -0.0258174 |
| GO | ceramide metabolic process | 1 | 16 | 0.989 | -0.0927387 |
| GO | ER-Golgi intermediate compartment membrane | 1 | 17 | 0.989 | -0.1556918 |
| GO | lysosome organization | 1 | 22 | 0.989 | -0.4257707 |
| GO | positive regulation of epithelial cell proliferation | 2 | 34 | 0.989 | -0.2202801 |
| GO | mitochondrial outer membrane | 5 | 81 | 0.989 | -0.2365984 |
| GO | neuronal cell body | 10 | 148 | 0.989 | -0.0377794 |
| GO | peroxisomal membrane | 1 | 41 | 0.989 | -1.1165976 |
| GO | peroxisome | 1 | 92 | 0.989 | -2.1900444 |
| GO | chromosome, centromeric region | 1 | 47 | 0.989 | -1.2803951 |
| GO | fibroblast growth factor receptor signaling pathway | 2 | 33 | 0.989 | -0.1763973 |
| GO | positive regulation of cell cycle | 1 | 15 | 0.989 | -0.0258174 |
| GO | cell development | 1 | 15 | 0.989 | -0.0258174 |
| GO | mesoderm development | 1 | 27 | 0.989 | -0.6451903 |
| GO | microtubule associated complex | 1 | 25 | 0.989 | -0.5620556 |
| GO | protein C-terminus binding | 9 | 146 | 0.989 | -0.3222596 |
| GO | mitochondrial membrane | 1 | 51 | 0.989 | -1.3811973 |
| GO | protein kinase binding | 7 | 113 | 0.989 | -0.2704575 |
| GO | GTPase binding | 1 | 15 | 0.989 | -0.0258174 |
| GO | G-protein-coupled receptor binding | 1 | 24 | 0.989 | -0.518309 |
| GO | chromatin assembly or disassembly | 1 | 36 | 0.989 | -0.965541 |
| GO | chromatin binding | 7 | 156 | 0.989 | -1.166763 |
| GO | chromatin | 4 | 81 | 0.989 | -0.6778477 |
| GO | single-stranded DNA binding | 3 | 49 | 0.989 | -0.1978616 |
| GO | protein binding, bridging | 2 | 44 | 0.989 | -0.6024802 |
| GO | nuclear matrix | 2 | 62 | 0.989 | -1.1279564 |
| GO | nuclear membrane | 5 | 87 | 0.989 | -0.4029584 |
| GO | ubiquitin ligase complex | 3 | 54 | 0.989 | -0.3730548 |
| GO | late endosome | 2 | 43 | 0.989 | -0.5680787 |
| GO | GABA-A receptor activity | 1 | 19 | 0.989 | -0.2716131 |
| GO | gamma-aminobutyric acid signaling pathway | 1 | 20 | 0.989 | -0.325338 |
| GO | pyridoxal phosphate binding | 2 | 51 | 0.989 | -0.8255526 |

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|---|---|---|---|---|---|
| GO | vesicle membrane | 1 | 15 | 0.989 | -0.0258174 |
| GO | manganese ion binding | 1 | 32 | 0.989 | -0.8323231 |
| GO | Rab GTPase binding | 2 | 33 | 0.989 | -0.1763973 |
| GO | isomerase activity | 4 | 99 | 0.989 | -1.1046924 |
| GO | generation of precursor metabolites and energy | 3 | 55 | 0.989 | -0.4062317 |
| GO | peptide hormone binding | 1 | 22 | 0.989 | -0.4257707 |
| GO | electron transport chain | 4 | 86 | 0.989 | -0.8042978 |
| GO | male genitalia development | 1 | 17 | 0.989 | -0.1556918 |
| GO | purine ribonucleoside monophosphate biosynthetic process | 1 | 17 | 0.989 | -0.1556918 |
| GO | chemotaxis | 7 | 117 | 0.989 | -0.3662918 |
| GO | neuron apoptosis | 1 | 16 | 0.989 | -0.0927387 |
| GO | anterior/posterior pattern formation | 4 | 81 | 0.989 | -0.6778477 |
| GO | cilium | 2 | 90 | 0.989 | -1.7381864 |
| GO | embryonic skeletal system morphogenesis | 2 | 36 | 0.989 | -0.3044533 |
| GO | histone deacetylase binding | 2 | 39 | 0.989 | -0.4227773 |
| GO | mediator complex | 1 | 31 | 0.989 | -0.7969334 |
| GO | proximal/distal pattern formation | 1 | 22 | 0.989 | -0.4257707 |
| GO | DNA replication | 3 | 146 | 0.989 | -2.2976321 |
| GO | DNA-directed DNA polymerase activity | 1 | 30 | 0.989 | -0.7605964 |
| GO | guanyl nucleotide binding | 1 | 17 | 0.989 | -0.1556918 |
| GO | protein amino acid ADP-ribosylation | 1 | 22 | 0.989 | -0.4257707 |
| GO | cellular iron ion homeostasis | 1 | 24 | 0.989 | -0.518309 |
| GO | induction of apoptosis by intracellular signals | 1 | 15 | 0.989 | -0.0258174 |
| GO | protein ubiquitination | 4 | 85 | 0.989 | -0.7795502 |
| GO | negative regulation of T cell proliferation | 1 | 18 | 0.989 | -0.2151789 |
| GO | glutathione transferase activity | 1 | 17 | 0.989 | -0.1556918 |
| GO | biosynthetic process | 2 | 49 | 0.989 | -0.7647026 |
| GO | cell division | 6 | 246 | 0.989 | -2.7500096 |
| GO | midbody | 1 | 25 | 0.989 | -0.5620556 |
| GO | spindle | 3 | 90 | 0.989 | -1.319481 |
| GO | MHC class I protein complex | 1 | 18 | 0.989 | -0.2151789 |
| GO | NAD or NADH binding | 1 | 37 | 0.989 | -0.9969995 |
| GO | positive regulation of mitotic cell cycle | 1 | 16 | 0.989 | -0.0927387 |
| GO | heterogeneous nuclear ribonucleoprotein complex | 1 | 15 | 0.989 | -0.0258174 |
| GO | ribonucleoprotein complex | 1 | 95 | 0.989 | -2.2389329 |
| GO | spliceosomal complex | 1 | 118 | 0.989 | -2.5854018 |
| GO | steroid biosynthetic process | 1 | 30 | 0.989 | -0.7605964 |
| GO | unfolded protein binding | 4 | 103 | 0.989 | -1.1901847 |
| GO | G1/S transition of mitotic cell cycle | 2 | 42 | 0.989 | -0.5329476 |
| GO | hippocampus development | 1 | 20 | 0.989 | -0.325338 |
| GO | lipid catabolic process | 5 | 90 | 0.989 | -0.4820701 |
| GO | activation of pro-apoptotic gene products | 1 | 22 | 0.989 | -0.4257707 |
| GO | cilium axoneme | 1 | 26 | 0.989 | -0.6043094 |
| GO | phosphoinositide-mediated signaling | 2 | 33 | 0.989 | -0.1763973 |
| GO | Ras protein signal transduction | 4 | 64 | 0.989 | -0.1857124 |
| GO | negative regulation of translation | 1 | 18 | 0.989 | -0.2151789 |
| GO | acyl-CoA binding | 1 | 15 | 0.989 | -0.0258174 |
| GO | fatty acid beta-oxidation | 1 | 21 | 0.989 | -0.3766422 |
| GO | platelet activation | 1 | 24 | 0.989 | -0.518309 |

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|---|---|---|---|---|---|
| GO | positive regulation of T cell proliferation | 1 | 27 | 0.989 | -0.6451903 |
| GO | brush border | 1 | 22 | 0.989 | -0.4257707 |
| GO | cytokine receptor activity | 1 | 17 | 0.989 | -0.1556918 |
| GO | endosome membrane | 5 | 92 | 0.989 | -0.5334396 |
| GO | negative regulation of gene expression | 1 | 23 | 0.989 | -0.4729329 |
| GO | response to activity | 1 | 18 | 0.989 | -0.2151789 |
| GO | response to tumor necrosis factor | 1 | 17 | 0.989 | -0.1556918 |
| GO | sarcoplasmic reticulum membrane | 1 | 17 | 0.989 | -0.1556918 |
| GO | nuclear chromatin | 1 | 16 | 0.989 | -0.0927387 |
| GO | nuclear chromosome | 1 | 23 | 0.989 | -0.4729329 |
| GO | structural constituent of cytoskeleton | 2 | 73 | 0.989 | -1.3891833 |
| GO | protein secretion | 1 | 16 | 0.989 | -0.0927387 |
| GO | intracellular membrane-bounded organelle | 8 | 127 | 0.989 | -0.2399943 |
| GO | transcription | 1 | 69 | 0.989 | -1.7759985 |
| GO | focal adhesion assembly | 1 | 15 | 0.989 | -0.0258174 |
| GO | coated pit | 2 | 41 | 0.989 | -0.4970486 |
| GO | actin filament | 1 | 28 | 0.989 | -0.6848042 |
| GO | regulation of GTPase activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | collagen | 1 | 22 | 0.989 | -0.4257707 |
| GO | enzyme activator activity | 1 | 40 | 0.989 | -1.0875691 |
| GO | nuclear outer membrane | 1 | 20 | 0.989 | -0.325338 |
| GO | gastrulation | 1 | 15 | 0.989 | -0.0258174 |
| GO | insulin secretion | 1 | 23 | 0.989 | -0.4729329 |
| GO | protein N-terminus binding | 3 | 72 | 0.989 | -0.8988756 |
| GO | cerebral cortex development | 1 | 16 | 0.989 | -0.0927387 |
| GO | muscle contraction | 6 | 97 | 0.989 | -0.2540433 |
| GO | myosin complex | 2 | 41 | 0.989 | -0.4970486 |
| GO | regulation of protein localization | 1 | 18 | 0.989 | -0.2151789 |
| GO | centrosome | 2 | 117 | 0.989 | -2.2037494 |
| GO | neuron development | 1 | 27 | 0.989 | -0.6451903 |
| GO | 4 iron, 4 sulfur cluster binding | 1 | 25 | 0.989 | -0.5620556 |
| GO | tricarboxylic acid cycle | 1 | 21 | 0.989 | -0.3766422 |
| GO | hair follicle morphogenesis | 1 | 16 | 0.989 | -0.0927387 |
| GO | cation transport | 2 | 65 | 0.989 | -1.202663 |
| GO | nucleotidyltransferase activity | 2 | 71 | 0.989 | -1.344131 |
| GO | mitochondrial proton-transporting ATP synthase complex | 1 | 16 | 0.989 | -0.0927387 |
| GO | endopeptidase activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | amino acid binding | 1 | 15 | 0.989 | -0.0258174 |
| GO | cellular amino acid biosynthetic process | 1 | 24 | 0.989 | -0.518309 |
| GO | cofactor binding | 1 | 19 | 0.989 | -0.2716131 |
| GO | acid-amino acid ligase activity | 2 | 34 | 0.989 | -0.2202801 |
| GO | kinase binding | 1 | 27 | 0.989 | -0.6451903 |
| GO | neuron projection | 2 | 60 | 0.989 | -1.0764977 |
| GO | protein polyubiquitination | 1 | 25 | 0.989 | -0.5620556 |
| GO | chromosome | 2 | 135 | 0.989 | -2.4736529 |
| GO | nucleosome assembly | 1 | 65 | 0.989 | -1.6950268 |
| GO | nucleosome | 1 | 52 | 0.989 | -1.4054996 |
| GO | trans-Golgi network | 3 | 51 | 0.989 | -0.269908 |
| GO | SNAP receptor activity | 1 | 20 | 0.989 | -0.325338 |

| | | | | | |
|---|---|---|---|---|---|
| GO | peptidyl-prolyl cis-trans isomerase activity | 1 | 32 | 0.989 | -0.8323231 |
| GO | phototransduction | 1 | 21 | 0.989 | -0.3766422 |
| GO | calcium channel activity | 3 | 44 | 0.989 | -0.0043777 |
| GO | microtubule organizing center | 4 | 96 | 0.989 | -1.0385911 |
| GO | lactation | 1 | 28 | 0.989 | -0.6848042 |
| GO | negative regulation of angiogenesis | 1 | 28 | 0.989 | -0.6848042 |
| GO | response to UV | 1 | 30 | 0.989 | -0.7605964 |
| GO | sex differentiation | 1 | 23 | 0.989 | -0.4729329 |
| GO | cis-Golgi network | 1 | 17 | 0.989 | -0.1556918 |
| GO | methyltransferase activity | 2 | 106 | 0.989 | -2.02441 |
| GO | N-acetyltransferase activity | 1 | 20 | 0.989 | -0.325338 |
| GO | spindle pole | 2 | 50 | 0.989 | -0.7953911 |
| GO | endoplasmic reticulum unfolded protein response | 1 | 20 | 0.989 | -0.325338 |
| GO | ubiquitin-specific protease activity | 1 | 28 | 0.989 | -0.6848042 |
| GO | ATP-dependent helicase activity | 2 | 61 | 0.989 | -1.1024 |
| GO | helicase activity | 5 | 107 | 0.989 | -0.8887029 |
| GO | filopodium | 1 | 25 | 0.989 | -0.5620556 |
| GO | intracellular transport | 1 | 17 | 0.989 | -0.1556918 |
| GO | cAMP binding | 1 | 17 | 0.989 | -0.1556918 |
| GO | cAMP-dependent protein kinase regulator activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | MAPKKK cascade | 1 | 31 | 0.989 | -0.7969334 |
| GO | cytokinesis | 1 | 34 | 0.989 | -0.9004979 |
| GO | cardiac muscle contraction | 1 | 17 | 0.989 | -0.1556918 |
| GO | anaphase-promoting complex-dependent proteasomal ubiquitin-depe | 3 | 63 | 0.989 | -0.6530869 |
| GO | negative regulation of ubiquitin-protein ligase activity involved in mitc | 3 | 62 | 0.989 | -0.6238613 |
| GO | positive regulation of ubiquitin-protein ligase activity involved in mitot | 3 | 65 | 0.989 | -0.7102992 |
| GO | proteasome complex | 3 | 56 | 0.989 | -0.438846 |
| GO | triglyceride lipase activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | late endosome membrane | 1 | 51 | 0.989 | -1.3811973 |
| GO | protein amino acid N-linked glycosylation | 1 | 15 | 0.989 | -0.0258174 |
| GO | ARF guanyl-nucleotide exchange factor activity | 1 | 17 | 0.989 | -0.1556918 |
| GO | regulation of ARF protein signal transduction | 1 | 16 | 0.989 | -0.0927387 |
| GO | peroxidase activity | 1 | 17 | 0.989 | -0.1556918 |
| GO | dephosphorylation | 1 | 21 | 0.989 | -0.3766422 |
| GO | embryonic skeletal system development | 1 | 23 | 0.989 | -0.4729329 |
| GO | voltage-gated sodium channel activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | metal ion transmembrane transporter activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | metal ion transport | 1 | 20 | 0.989 | -0.325338 |
| GO | zinc ion transport | 1 | 24 | 0.989 | -0.518309 |
| GO | defense response to bacterium | 4 | 75 | 0.989 | -0.5163078 |
| GO | positive regulation of protein ubiquitination | 1 | 25 | 0.989 | -0.5620556 |
| GO | vesicle | 1 | 17 | 0.989 | -0.1556918 |
| GO | chemoattractant activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | germ cell development | 1 | 22 | 0.989 | -0.4257707 |
| GO | growth | 1 | 29 | 0.989 | -0.723245 |
| GO | positive regulation of endothelial cell proliferation | 2 | 31 | 0.989 | -0.0846181 |
| GO | neurotransmitter transport | 1 | 40 | 0.989 | -1.0875691 |
| GO | amino acid transport | 1 | 46 | 0.989 | -1.2542207 |
| GO | SWI/SNF complex | 1 | 15 | 0.989 | -0.0258174 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| GO | growth cone | 3 | 58 | 0.989 | -0.502473 |
| GO | keratinization | 1 | 31 | 0.989 | -0.7969334 |
| GO | vesicle docking involved in exocytosis | 1 | 19 | 0.989 | -0.2716131 |
| GO | mannose binding | 1 | 16 | 0.989 | -0.0927387 |
| GO | non-membrane spanning protein tyrosine kinase activity | 1 | 40 | 0.989 | -1.0875691 |
| GO | endocytic vesicle membrane | 1 | 22 | 0.989 | -0.4257707 |
| GO | hydrogen peroxide catabolic process | 1 | 16 | 0.989 | -0.0927387 |
| GO | thymus development | 1 | 23 | 0.989 | -0.4729329 |
| GO | response to zinc ion | 1 | 18 | 0.989 | -0.2151789 |
| GO | C-C chemokine receptor activity | 1 | 16 | 0.989 | -0.0927387 |
| GO | cell leading edge | 1 | 17 | 0.989 | -0.1556918 |
| GO | DNA fragmentation involved in apoptotic nuclear change | 1 | 18 | 0.989 | -0.2151789 |
| GO | base-excision repair | 1 | 19 | 0.989 | -0.2716131 |
| GO | damaged DNA binding | 1 | 44 | 0.989 | -1.2005828 |
| GO | nucleotide-excision repair | 1 | 26 | 0.989 | -0.6043094 |
| GO | iron ion transport | 1 | 22 | 0.989 | -0.4257707 |
| GO | flagellum | 1 | 19 | 0.989 | -0.2716131 |
| GO | phospholipid transport | 1 | 18 | 0.989 | -0.2151789 |
| GO | nuclear chromosome, telomeric region | 1 | 16 | 0.989 | -0.0927387 |
| GO | telomere maintenance | 1 | 19 | 0.989 | -0.2716131 |
| GO | cell adhesion molecule binding | 1 | 15 | 0.989 | -0.0258174 |
| GO | nucleoside metabolic process | 1 | 16 | 0.989 | -0.0927387 |
| GO | nucleoside-triphosphatase activity | 1 | 59 | 0.989 | -1.5669486 |
| GO | protein serine/threonine phosphatase activity | 1 | 37 | 0.989 | -0.9969995 |
| GO | estrogen receptor binding | 1 | 15 | 0.989 | -0.0258174 |
| GO | diacylglycerol kinase activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | fertilization | 1 | 17 | 0.989 | -0.1556918 |
| GO | mRNA 3'-UTR binding | 1 | 17 | 0.989 | -0.1556918 |
| GO | high-density lipoprotein particle | 1 | 19 | 0.989 | -0.2716131 |
| GO | very-low-density lipoprotein particle | 1 | 19 | 0.989 | -0.2716131 |
| GO | T cell receptor signaling pathway | 1 | 22 | 0.989 | -0.4257707 |
| GO | endonuclease activity | 1 | 57 | 0.989 | -1.5222605 |
| GO | gastrulation with mouth forming second | 1 | 21 | 0.989 | -0.3766422 |
| GO | positive regulation of cell adhesion | 1 | 20 | 0.989 | -0.325338 |
| GO | cellular membrane fusion | 1 | 22 | 0.989 | -0.4257707 |
| GO | neuropeptide hormone activity | 1 | 21 | 0.989 | -0.3766422 |
| GO | mitosis | 1 | 199 | 0.989 | -3.5585578 |
| GO | MAP kinase kinase kinase activity | 1 | 15 | 0.989 | -0.0258174 |
| GO | growth factor binding | 1 | 23 | 0.989 | -0.4729329 |
| GO | peptidyl-threonine phosphorylation | 1 | 18 | 0.989 | -0.2151789 |
| GO | neuromuscular junction | 1 | 24 | 0.989 | -0.518309 |
| GO | endosome transport | 1 | 21 | 0.989 | -0.3766422 |
| GO | thyroid hormone receptor binding | 1 | 25 | 0.989 | -0.5620556 |
| GO | RNA metabolic process | 1 | 19 | 0.989 | -0.2716131 |
| GO | N-acetylglucosamine metabolic process | 1 | 15 | 0.989 | -0.0258174 |
| GO | cholesterol binding | 1 | 18 | 0.989 | -0.2151789 |
| GO | cholesterol efflux | 1 | 19 | 0.989 | -0.2716131 |
| GO | reverse cholesterol transport | 1 | 15 | 0.989 | -0.0258174 |
| GO | histone methyltransferase complex | 1 | 17 | 0.989 | -0.1556918 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| GO | phosphoprotein phosphatase inhibitor activity | 1 | 18 | 0.989 | -0.2151789 |
| GO | protein targeting to mitochondrion | 1 | 25 | 0.989 | -0.5620556 |
| GO | regulation of endocytosis | 1 | 15 | 0.989 | -0.0258174 |
| GO | male germ cell nucleus | 1 | 15 | 0.989 | -0.0258174 |
| GO | reciprocal meiotic recombination | 1 | 22 | 0.989 | -0.4257707 |
| GO | synapsis | 1 | 5 | 0.298138 | 1.16672207 |

score (z)