Table S3. GO enrichment analysis of the DE mRNAs in the network

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| GO ID | Description | GeneRatio (118) | BgRatio (23374) | pvalue |
| GO:0051240 | positive regulation of multicellular organismal process | 20 | 1147 | 1.20E-06 |
| GO:0045597 | positive regulation of cell differentiation | 14 | 730 | 1.90E-05 |
| GO:0010038 | response to metal ion | 7 | 180 | 3.70E-05 |
| GO:0032680 | regulation of tumor necrosis factor production | 5 | 78 | 4.70E-05 |
| GO:0035988 | chondrocyte proliferation | 3 | 15 | 5.50E-05 |
| GO:1903555 | regulation of tumor necrosis factor superfamily cytokine production | 5 | 81 | 5.70E-05 |
| GO:0009605 | response to external stimulus | 21 | 1650 | 7.40E-05 |
| GO:0010035 | response to inorganic substance | 8 | 275 | 7.90E-05 |
| GO:0032640 | tumor necrosis factor production | 5 | 87 | 8.00E-05 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production | 5 | 94 | 0.00012 |
| GO:2000738 | positive regulation of stem cell differentiation | 4 | 52 | 0.00014 |
| GO:1901701 | cellular response to oxygen-containing compound | 11 | 577 | 0.00017 |
| GO:1900271 | regulation of long-term synaptic potentiation | 3 | 23 | 0.00021 |
| GO:0051094 | positive regulation of developmental process | 15 | 1029 | 0.00021 |
| GO:1900272 | negative regulation of long-term synaptic potentiation | 2 | 5 | 0.00025 |
| GO:1902732 | positive regulation of chondrocyte proliferation | 2 | 5 | 0.00025 |
| GO:0023056 | positive regulation of signaling | 17 | 1291 | 0.00026 |
| GO:0010605 | negative regulation of macromolecule metabolic process | 22 | 1957 | 0.00029 |
| GO:0010647 | positive regulation of cell communication | 17 | 1309 | 0.00031 |
| GO:1901653 | cellular response to peptide | 6 | 181 | 0.00032 |
| GO:0007613 | memory | 4 | 65 | 0.00033 |
| GO:0007611 | learning or memory | 6 | 183 | 0.00034 |
| GO:0044793 | negative regulation by host of viral process | 2 | 6 | 0.00037 |
| GO:0070887 | cellular response to chemical stimulus | 23 | 2145 | 0.00041 |
| GO:0008286 | insulin receptor signaling pathway | 4 | 69 | 0.00041 |
| GO:0005513 | detection of calcium ion | 2 | 7 | 0.00052 |
| GO:1901699 | cellular response to nitrogen compound | 8 | 364 | 0.00053 |
| GO:0031348 | negative regulation of defense response | 5 | 131 | 0.00054 |
| GO:0009892 | negative regulation of metabolic process | 23 | 2188 | 0.00054 |
| GO:0050728 | negative regulation of inflammatory response | 4 | 75 | 0.00057 |
| GO:0050890 | cognition | 6 | 203 | 0.00059 |
| GO:0044708 | single-organism behavior | 8 | 374 | 0.00063 |
| GO:0009967 | positive regulation of signal transduction | 15 | 1166 | 0.00079 |
| GO:0032060 | bleb assembly | 2 | 9 | 0.00089 |
| GO:0010629 | negative regulation of gene expression | 15 | 1181 | 0.0009 |
| GO:0051090 | regulation of sequence-specific DNA binding transcription factor activity | 7 | 310 | 0.00101 |
| GO:0071417 | cellular response to organonitrogen compound | 7 | 310 | 0.00101 |
| GO:0051262 | protein tetramerization | 4 | 88 | 0.00104 |
| GO:0008219 | cell death | 19 | 1731 | 0.00106 |
| GO:0016265 | death | 19 | 1731 | 0.00106 |
| GO:0019731 | antibacterial humoral response | 2 | 10 | 0.00111 |
| GO:0007612 | learning | 4 | 91 | 0.00118 |
| GO:1902533 | positive regulation of intracellular signal transduction | 11 | 732 | 0.00121 |
| GO:0051592 | response to calcium ion | 4 | 93 | 0.00127 |
| GO:1900273 | positive regulation of long-term synaptic potentiation | 2 | 11 | 0.00135 |
| GO:0071310 | cellular response to organic substance | 19 | 1773 | 0.0014 |
| GO:0003008 | system process | 16 | 1370 | 0.00145 |
| GO:0048519 | negative regulation of biological process | 35 | 4254 | 0.00161 |
| GO:0050832 | defense response to fungus | 2 | 12 | 0.00161 |
| GO:0006897 | endocytosis | 9 | 537 | 0.00163 |
| GO:0060291 | long-term synaptic potentiation | 3 | 47 | 0.00173 |
| GO:0008306 | associative learning | 3 | 48 | 0.00184 |
| GO:1901652 | response to peptide | 6 | 255 | 0.00189 |
| GO:0014841 | skeletal muscle satellite cell proliferation | 2 | 13 | 0.0019 |
| GO:0014842 | regulation of skeletal muscle satellite cell proliferation | 2 | 13 | 0.0019 |
| GO:0071425 | hematopoietic stem cell proliferation | 2 | 13 | 0.0019 |
| GO:0097435 | fibril organization | 2 | 13 | 0.0019 |
| GO:0048584 | positive regulation of response to stimulus | 18 | 1682 | 0.00192 |
| GO:0051289 | protein homotetramerization | 3 | 50 | 0.00207 |
| GO:0031324 | negative regulation of cellular metabolic process | 20 | 1978 | 0.00208 |
| GO:0009887 | organ morphogenesis | 12 | 909 | 0.00217 |
| GO:0051239 | regulation of multicellular organismal process | 23 | 2432 | 0.00224 |
| GO:0019730 | antimicrobial humoral response | 2 | 15 | 0.00254 |
| GO:2000178 | negative regulation of neural precursor cell proliferation | 2 | 15 | 0.00254 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 9 | 577 | 0.00264 |
| GO:0032869 | cellular response to insulin stimulus | 4 | 114 | 0.00269 |
| GO:0006909 | phagocytosis | 4 | 115 | 0.00277 |
| GO:1904646 | cellular response to beta-amyloid | 2 | 16 | 0.0029 |
| GO:0044092 | negative regulation of molecular function | 11 | 822 | 0.00299 |
| GO:0012501 | programmed cell death | 17 | 1618 | 0.00313 |
| GO:0010466 | negative regulation of peptidase activity | 5 | 195 | 0.00314 |
| GO:0009620 | response to fungus | 2 | 17 | 0.00327 |
| GO:0014856 | skeletal muscle cell proliferation | 2 | 17 | 0.00327 |
| GO:0014857 | regulation of skeletal muscle cell proliferation | 2 | 17 | 0.00327 |
| GO:0045595 | regulation of cell differentiation | 16 | 1490 | 0.00336 |
| GO:0032501 | multicellular organismal process | 44 | 6004 | 0.00352 |
| GO:0008284 | positive regulation of cell proliferation | 9 | 604 | 0.00357 |
| GO:0045664 | regulation of neuron differentiation | 8 | 494 | 0.00363 |
| GO:0045777 | positive regulation of blood pressure | 2 | 18 | 0.00367 |
| GO:0071470 | cellular response to osmotic stress | 2 | 18 | 0.00367 |
| GO:0042221 | response to chemical | 27 | 3167 | 0.00392 |
| GO:0051253 | negative regulation of RNA metabolic process | 12 | 980 | 0.00399 |
| GO:0010628 | positive regulation of gene expression | 16 | 1520 | 0.00408 |
| GO:0044788 | modulation by host of viral process | 2 | 19 | 0.00409 |
| GO:0048513 | animal organ development | 24 | 2712 | 0.00423 |
| GO:0010720 | positive regulation of cell development | 7 | 400 | 0.00424 |
| GO:0003012 | muscle system process | 6 | 301 | 0.00429 |
| GO:0051346 | negative regulation of hydrolase activity | 6 | 302 | 0.00436 |
| GO:0045893 | positive regulation of transcription, DNA-templated | 14 | 1255 | 0.00436 |
| GO:0044707 | single-multicellular organism process | 40 | 5367 | 0.00438 |
| GO:0071398 | cellular response to fatty acid | 2 | 20 | 0.00452 |
| GO:0050777 | negative regulation of immune response | 3 | 66 | 0.00455 |
| GO:0032469 | endoplasmic reticulum calcium ion homeostasis | 2 | 21 | 0.00498 |
| GO:0050710 | negative regulation of cytokine secretion | 2 | 21 | 0.00498 |
| GO:1904645 | response to beta-amyloid | 2 | 21 | 0.00498 |
| GO:0006624 | vacuolar protein processing | 1 | 1 | 0.00505 |
| GO:0006863 | purine nucleobase transport | 1 | 1 | 0.00505 |
| GO:0009258 | 10-formyltetrahydrofolate catabolic process | 1 | 1 | 0.00505 |
| GO:0009397 | folic acid-containing compound catabolic process | 1 | 1 | 0.00505 |
| GO:0015851 | nucleobase transport | 1 | 1 | 0.00505 |
| GO:0015855 | pyrimidine nucleobase transport | 1 | 1 | 0.00505 |
| GO:0016199 | axon midline choice point recognition | 1 | 1 | 0.00505 |
| GO:0016340 | calcium-dependent cell-matrix adhesion | 1 | 1 | 0.00505 |
| GO:0018272 | protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal phosphate-L-lysine | 1 | 1 | 0.00505 |
| GO:0018352 | protein-pyridoxal-5-phosphate linkage | 1 | 1 | 0.00505 |
| GO:0021768 | nucleus accumbens development | 1 | 1 | 0.00505 |
| GO:0033023 | mast cell homeostasis | 1 | 1 | 0.00505 |
| GO:0033024 | mast cell apoptotic process | 1 | 1 | 0.00505 |
| GO:0033025 | regulation of mast cell apoptotic process | 1 | 1 | 0.00505 |
| GO:0033026 | negative regulation of mast cell apoptotic process | 1 | 1 | 0.00505 |
| GO:0035887 | aortic smooth muscle cell differentiation | 1 | 1 | 0.00505 |
| GO:0042560 | pteridine-containing compound catabolic process | 1 | 1 | 0.00505 |
| GO:0042710 | biofilm formation | 1 | 1 | 0.00505 |
| GO:0044010 | single-species biofilm formation | 1 | 1 | 0.00505 |
| GO:0044407 | single-species biofilm formation in or on host organism | 1 | 1 | 0.00505 |
| GO:0044524 | protein sulfhydration | 1 | 1 | 0.00505 |
| GO:0070267 | oncosis | 1 | 1 | 0.00505 |
| GO:0072658 | maintenance of protein location in membrane | 1 | 1 | 0.00505 |
| GO:0072660 | maintenance of protein location in plasma membrane | 1 | 1 | 0.00505 |
| GO:0090472 | dibasic protein processing | 1 | 1 | 0.00505 |
| GO:1900190 | regulation of single-species biofilm formation | 1 | 1 | 0.00505 |
| GO:1900191 | negative regulation of single-species biofilm formation | 1 | 1 | 0.00505 |
| GO:1900228 | regulation of single-species biofilm formation in or on host organism | 1 | 1 | 0.00505 |
| GO:1900229 | negative regulation of single-species biofilm formation in or on host organism | 1 | 1 | 0.00505 |
| GO:1901392 | regulation of transforming growth factor beta1 activation | 1 | 1 | 0.00505 |
| GO:1901394 | positive regulation of transforming growth factor beta1 activation | 1 | 1 | 0.00505 |
| GO:1902726 | positive regulation of skeletal muscle satellite cell differentiation | 1 | 1 | 0.00505 |
| GO:1904636 | response to ionomycin | 1 | 1 | 0.00505 |
| GO:1904637 | cellular response to ionomycin | 1 | 1 | 0.00505 |
| GO:1904823 | purine nucleobase transmembrane transport | 1 | 1 | 0.00505 |
| GO:1904829 | regulation of aortic smooth muscle cell differentiation | 1 | 1 | 0.00505 |
| GO:1904831 | positive regulation of aortic smooth muscle cell differentiation | 1 | 1 | 0.00505 |
| GO:2000446 | regulation of macrophage migration inhibitory factor signaling pathway | 1 | 1 | 0.00505 |
| GO:1903035 | negative regulation of response to wounding | 4 | 137 | 0.00518 |
| GO:0006936 | muscle contraction | 5 | 220 | 0.00523 |
| GO:0006915 | apoptotic process | 16 | 1561 | 0.00526 |
| GO:0042593 | glucose homeostasis | 4 | 139 | 0.00545 |
| GO:0045892 | negative regulation of transcription, DNA-templated | 11 | 891 | 0.00547 |
| GO:0032675 | regulation of interleukin-6 production | 3 | 72 | 0.00581 |
| GO:1901698 | response to nitrogen compound | 8 | 538 | 0.00601 |
| GO:0052547 | regulation of peptidase activity | 6 | 323 | 0.00601 |
| GO:0048523 | negative regulation of cellular process | 31 | 3927 | 0.00608 |
| GO:0048863 | stem cell differentiation | 6 | 328 | 0.00647 |
| GO:2000736 | regulation of stem cell differentiation | 4 | 146 | 0.00647 |
| GO:0031347 | regulation of defense response | 7 | 433 | 0.00647 |
| GO:0048713 | regulation of oligodendrocyte differentiation | 2 | 24 | 0.00649 |
| GO:0051092 | positive regulation of NF-kappaB transcription factor activity | 3 | 75 | 0.0065 |
| GO:1903508 | positive regulation of nucleic acid-templated transcription | 14 | 1316 | 0.00657 |
| GO:1901700 | response to oxygen-containing compound | 11 | 914 | 0.00658 |
| GO:0042330 | taxis | 8 | 548 | 0.00669 |
| GO:1902680 | positive regulation of RNA biosynthetic process | 14 | 1319 | 0.0067 |
| GO:0042472 | inner ear morphogenesis | 3 | 76 | 0.00675 |
| GO:0048522 | positive regulation of cellular process | 34 | 4463 | 0.00681 |
| GO:0032635 | interleukin-6 production | 3 | 77 | 0.00699 |
| GO:0030225 | macrophage differentiation | 2 | 25 | 0.00703 |
| GO:0072089 | stem cell proliferation | 4 | 150 | 0.00711 |
| GO:1903507 | negative regulation of nucleic acid-templated transcription | 11 | 927 | 0.00728 |
| GO:0098542 | defense response to other organism | 5 | 239 | 0.00736 |
| GO:0010595 | positive regulation of endothelial cell migration | 3 | 79 | 0.00751 |
| GO:0010557 | positive regulation of macromolecule biosynthetic process | 15 | 1481 | 0.00765 |
| GO:0007610 | behavior | 9 | 681 | 0.00769 |
| GO:0030335 | positive regulation of cell migration | 6 | 341 | 0.00776 |
| GO:0002687 | positive regulation of leukocyte migration | 3 | 80 | 0.00777 |
| GO:0010976 | positive regulation of neuron projection development | 4 | 154 | 0.00778 |
| GO:0002684 | positive regulation of immune system process | 9 | 683 | 0.00783 |
| GO:0032868 | response to insulin | 4 | 155 | 0.00796 |
| GO:0045934 | negative regulation of nucleobase-containing compound metabolic process | 12 | 1073 | 0.00805 |
| GO:0071375 | cellular response to peptide hormone stimulus | 4 | 156 | 0.00814 |
| GO:0032801 | receptor catabolic process | 2 | 27 | 0.00817 |
| GO:0007275 | multicellular organism development | 33 | 4347 | 0.00822 |
| GO:0007166 | cell surface receptor signaling pathway | 22 | 2549 | 0.00833 |
| GO:1902679 | negative regulation of RNA biosynthetic process | 11 | 945 | 0.00835 |
| GO:0030198 | extracellular matrix organization | 5 | 247 | 0.00842 |
| GO:0010951 | negative regulation of endopeptidase activity | 4 | 158 | 0.0085 |
| GO:0071222 | cellular response to lipopolysaccharide | 3 | 83 | 0.0086 |
| GO:0070542 | response to fatty acid | 2 | 28 | 0.00877 |
| GO:0071219 | cellular response to molecule of bacterial origin | 3 | 84 | 0.00888 |
| GO:0051254 | positive regulation of RNA metabolic process | 14 | 1367 | 0.00904 |
| GO:2000147 | positive regulation of cell motility | 6 | 353 | 0.00912 |
| GO:0045071 | negative regulation of viral genome replication | 2 | 29 | 0.00939 |
| GO:0045687 | positive regulation of glial cell differentiation | 2 | 29 | 0.00939 |
| GO:0032102 | negative regulation of response to external stimulus | 5 | 257 | 0.00989 |
| GO:0043277 | apoptotic cell clearance | 2 | 30 | 0.01002 |
| GO:0000294 | nuclear-transcribed mRNA catabolic process, endonucleolytic cleavage-dependent decay | 1 | 2 | 0.01007 |
| GO:0001966 | thigmotaxis | 1 | 2 | 0.01007 |
| GO:0002265 | astrocyte activation involved in immune response | 1 | 2 | 0.01007 |
| GO:0019732 | antifungal humoral response | 1 | 2 | 0.01007 |
| GO:0032902 | nerve growth factor production | 1 | 2 | 0.01007 |
| GO:0035691 | macrophage migration inhibitory factor signaling pathway | 1 | 2 | 0.01007 |
| GO:0036364 | transforming growth factor beta1 activation | 1 | 2 | 0.01007 |
| GO:0039019 | pronephric nephron development | 1 | 2 | 0.01007 |
| GO:0042222 | interleukin-1 biosynthetic process | 1 | 2 | 0.01007 |
| GO:0042538 | hyperosmotic salinity response | 1 | 2 | 0.01007 |
| GO:0045341 | MHC class I biosynthetic process | 1 | 2 | 0.01007 |
| GO:0045343 | regulation of MHC class I biosynthetic process | 1 | 2 | 0.01007 |
| GO:0045345 | positive regulation of MHC class I biosynthetic process | 1 | 2 | 0.01007 |
| GO:0045360 | regulation of interleukin-1 biosynthetic process | 1 | 2 | 0.01007 |
| GO:0045362 | positive regulation of interleukin-1 biosynthetic process | 1 | 2 | 0.01007 |
| GO:0048014 | Tie signaling pathway | 1 | 2 | 0.01007 |
| GO:0050720 | interleukin-1 beta biosynthetic process | 1 | 2 | 0.01007 |
| GO:0050722 | regulation of interleukin-1 beta biosynthetic process | 1 | 2 | 0.01007 |
| GO:0050725 | positive regulation of interleukin-1 beta biosynthetic process | 1 | 2 | 0.01007 |
| GO:0060414 | aorta smooth muscle tissue morphogenesis | 1 | 2 | 0.01007 |
| GO:0060945 | cardiac neuron differentiation | 1 | 2 | 0.01007 |
| GO:0060959 | cardiac neuron development | 1 | 2 | 0.01007 |
| GO:0070668 | positive regulation of mast cell proliferation | 1 | 2 | 0.01007 |
| GO:0071362 | cellular response to ether | 1 | 2 | 0.01007 |
| GO:0071475 | cellular hyperosmotic salinity response | 1 | 2 | 0.01007 |
| GO:0090299 | regulation of neural crest formation | 1 | 2 | 0.01007 |
| GO:0090300 | positive regulation of neural crest formation | 1 | 2 | 0.01007 |
| GO:1900069 | regulation of cellular hyperosmotic salinity response | 1 | 2 | 0.01007 |
| GO:1901000 | regulation of response to salt stress | 1 | 2 | 0.01007 |
| GO:1901390 | positive regulation of transforming growth factor beta activation | 1 | 2 | 0.01007 |
| GO:1902714 | negative regulation of interferon-gamma secretion | 1 | 2 | 0.01007 |
| GO:1902724 | positive regulation of skeletal muscle satellite cell proliferation | 1 | 2 | 0.01007 |
| GO:2000625 | regulation of miRNA catabolic process | 1 | 2 | 0.01007 |
| GO:2000627 | positive regulation of miRNA catabolic process | 1 | 2 | 0.01007 |
| GO:0051272 | positive regulation of cellular component movement | 6 | 362 | 0.01024 |
| GO:0010243 | response to organonitrogen compound | 7 | 473 | 0.01024 |
| GO:0006952 | defense response | 10 | 845 | 0.01055 |
| GO:0031328 | positive regulation of cellular biosynthetic process | 15 | 1538 | 0.01061 |
| GO:0002548 | monocyte chemotaxis | 2 | 31 | 0.01068 |
| GO:0006378 | mRNA polyadenylation | 2 | 31 | 0.01068 |
| GO:0008542 | visual learning | 2 | 31 | 0.01068 |
| GO:0032651 | regulation of interleukin-1 beta production | 2 | 31 | 0.01068 |
| GO:0042981 | regulation of apoptotic process | 13 | 1256 | 0.01087 |
| GO:0050727 | regulation of inflammatory response | 4 | 170 | 0.01091 |
| GO:0072091 | regulation of stem cell proliferation | 3 | 91 | 0.01104 |
| GO:0010092 | specification of organ identity | 2 | 32 | 0.01135 |
| GO:0045620 | negative regulation of lymphocyte differentiation | 2 | 32 | 0.01135 |
| GO:0040017 | positive regulation of locomotion | 6 | 371 | 0.01145 |
| GO:0009617 | response to bacterium | 6 | 372 | 0.01159 |
| GO:0010975 | regulation of neuron projection development | 6 | 373 | 0.01173 |
| GO:0071396 | cellular response to lipid | 6 | 374 | 0.01188 |
| GO:0043067 | regulation of programmed cell death | 13 | 1272 | 0.01198 |
| GO:0070265 | necrotic cell death | 2 | 33 | 0.01205 |
| GO:1900006 | positive regulation of dendrite development | 2 | 33 | 0.01205 |
| GO:0048568 | embryonic organ development | 6 | 377 | 0.01232 |
| GO:0050806 | positive regulation of synaptic transmission | 3 | 95 | 0.0124 |
| GO:0042127 | regulation of cell proliferation | 13 | 1278 | 0.01242 |
| GO:0002682 | regulation of immune system process | 11 | 1002 | 0.01256 |
| GO:0042471 | ear morphogenesis | 3 | 96 | 0.01275 |
| GO:0071216 | cellular response to biotic stimulus | 3 | 96 | 0.01275 |
| GO:1904018 | positive regulation of vasculature development | 3 | 96 | 0.01275 |
| GO:0032760 | positive regulation of tumor necrosis factor production | 2 | 34 | 0.01276 |
| GO:0009891 | positive regulation of biosynthetic process | 15 | 1573 | 0.01284 |
| GO:0052548 | regulation of endopeptidase activity | 5 | 275 | 0.01296 |
| GO:0033500 | carbohydrate homeostasis | 4 | 179 | 0.01298 |
| GO:0071804 | cellular potassium ion transport | 4 | 179 | 0.01298 |
| GO:0071805 | potassium ion transmembrane transport | 4 | 179 | 0.01298 |
| GO:0045944 | positive regulation of transcription from RNA polymerase II promoter | 10 | 873 | 0.01303 |
| GO:0010718 | positive regulation of epithelial to mesenchymal transition | 2 | 35 | 0.01349 |
| GO:0043631 | RNA polyadenylation | 2 | 35 | 0.01349 |
| GO:0050767 | regulation of neurogenesis | 8 | 621 | 0.01355 |
| GO:0006790 | sulfur compound metabolic process | 5 | 281 | 0.01411 |
| GO:0032611 | interleukin-1 beta production | 2 | 36 | 0.01423 |
| GO:0090503 | RNA phosphodiester bond hydrolysis, exonucleolytic | 2 | 36 | 0.01423 |
| GO:0051216 | cartilage development | 4 | 185 | 0.01449 |
| GO:0045861 | negative regulation of proteolysis | 5 | 283 | 0.01451 |
| GO:0050769 | positive regulation of neurogenesis | 5 | 284 | 0.01471 |
| GO:0031327 | negative regulation of cellular biosynthetic process | 12 | 1165 | 0.01475 |
| GO:0050768 | negative regulation of neurogenesis | 4 | 186 | 0.01476 |
| GO:0071495 | cellular response to endogenous stimulus | 11 | 1026 | 0.01476 |
| GO:0071229 | cellular response to acid chemical | 3 | 102 | 0.01499 |
| GO:0014015 | positive regulation of gliogenesis | 2 | 37 | 0.015 |
| GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine production | 2 | 37 | 0.015 |
| GO:0000103 | sulfate assimilation | 1 | 3 | 0.01507 |
| GO:0001994 | norepinephrine-epinephrine vasoconstriction involved in regulation of systemic arterial blood pressure | 1 | 3 | 0.01507 |
| GO:0002072 | optic cup morphogenesis involved in camera-type eye development | 1 | 3 | 0.01507 |
| GO:0002740 | negative regulation of cytokine secretion involved in immune response | 1 | 3 | 0.01507 |
| GO:0009256 | 10-formyltetrahydrofolate metabolic process | 1 | 3 | 0.01507 |
| GO:0010510 | regulation of acetyl-CoA biosynthetic process from pyruvate | 1 | 3 | 0.01507 |
| GO:0014005 | microglia development | 1 | 3 | 0.01507 |
| GO:0014034 | neural crest cell fate commitment | 1 | 3 | 0.01507 |
| GO:0030200 | heparan sulfate proteoglycan catabolic process | 1 | 3 | 0.01507 |
| GO:0030210 | heparin biosynthetic process | 1 | 3 | 0.01507 |
| GO:0032898 | neurotrophin production | 1 | 3 | 0.01507 |
| GO:0032914 | positive regulation of transforming growth factor beta1 production | 1 | 3 | 0.01507 |
| GO:0043152 | induction of bacterial agglutination | 1 | 3 | 0.01507 |
| GO:0045578 | negative regulation of B cell differentiation | 1 | 3 | 0.01507 |
| GO:0050713 | negative regulation of interleukin-1 beta secretion | 1 | 3 | 0.01507 |
| GO:0051563 | smooth endoplasmic reticulum calcium ion homeostasis | 1 | 3 | 0.01507 |
| GO:0051673 | membrane disruption in other organism | 1 | 3 | 0.01507 |
| GO:0055118 | negative regulation of cardiac muscle contraction | 1 | 3 | 0.01507 |
| GO:0060166 | olfactory pit development | 1 | 3 | 0.01507 |
| GO:0060332 | positive regulation of response to interferon-gamma | 1 | 3 | 0.01507 |
| GO:0060335 | positive regulation of interferon-gamma-mediated signaling pathway | 1 | 3 | 0.01507 |
| GO:0060423 | foregut regionalization | 1 | 3 | 0.01507 |
| GO:0060424 | lung field specification | 1 | 3 | 0.01507 |
| GO:0060492 | lung induction | 1 | 3 | 0.01507 |
| GO:0061031 | endodermal digestive tract morphogenesis | 1 | 3 | 0.01507 |
| GO:0070384 | Harderian gland development | 1 | 3 | 0.01507 |
| GO:0070666 | regulation of mast cell proliferation | 1 | 3 | 0.01507 |
| GO:1901552 | positive regulation of endothelial cell development | 1 | 3 | 0.01507 |
| GO:1902035 | positive regulation of hematopoietic stem cell proliferation | 1 | 3 | 0.01507 |
| GO:1902075 | cellular response to salt | 1 | 3 | 0.01507 |
| GO:1903142 | positive regulation of establishment of endothelial barrier | 1 | 3 | 0.01507 |
| GO:1903936 | cellular response to sodium arsenite | 1 | 3 | 0.01507 |
| GO:2001137 | positive regulation of endocytic recycling | 1 | 3 | 0.01507 |
| GO:0002683 | negative regulation of immune system process | 5 | 286 | 0.01512 |
| GO:0048518 | positive regulation of biological process | 37 | 5235 | 0.01525 |
| GO:0050896 | response to stimulus | 56 | 8727 | 0.01539 |
| GO:0048588 | developmental cell growth | 4 | 189 | 0.01556 |
| GO:0022610 | biological adhesion | 14 | 1462 | 0.01557 |
| GO:2000026 | regulation of multicellular organismal development | 15 | 1610 | 0.01559 |
| GO:0002763 | positive regulation of myeloid leukocyte differentiation | 2 | 38 | 0.01578 |
| GO:0040019 | positive regulation of embryonic development | 2 | 38 | 0.01578 |
| GO:0009890 | negative regulation of biosynthetic process | 12 | 1182 | 0.01635 |
| GO:0008283 | cell proliferation | 15 | 1621 | 0.01649 |
| GO:0006970 | response to osmotic stress | 2 | 39 | 0.01658 |
| GO:0019058 | viral life cycle | 4 | 194 | 0.01696 |
| GO:1903034 | regulation of response to wounding | 5 | 296 | 0.01728 |
| GO:0032088 | negative regulation of NF-kappaB transcription factor activity | 2 | 40 | 0.01739 |
| GO:2000648 | positive regulation of stem cell proliferation | 2 | 40 | 0.01739 |
| GO:0031123 | RNA 3'-end processing | 3 | 108 | 0.01745 |
| GO:0072358 | cardiovascular system development | 10 | 918 | 0.0179 |
| GO:0072359 | circulatory system development | 10 | 918 | 0.0179 |
| GO:0043062 | extracellular structure organization | 5 | 299 | 0.01797 |
| GO:2000113 | negative regulation of cellular macromolecule biosynthetic process | 11 | 1057 | 0.01801 |
| GO:0051172 | negative regulation of nitrogen compound metabolic process | 12 | 1199 | 0.01808 |
| GO:0001655 | urogenital system development | 5 | 301 | 0.01844 |
| GO:0051091 | positive regulation of sequence-specific DNA binding transcription factor activity | 4 | 199 | 0.01844 |
| GO:0051961 | negative regulation of nervous system development | 4 | 199 | 0.01844 |
| GO:0010941 | regulation of cell death | 13 | 1351 | 0.01886 |
| GO:0032456 | endocytic recycling | 2 | 42 | 0.01908 |
| GO:0032652 | regulation of interleukin-1 production | 2 | 42 | 0.01908 |
| GO:0060317 | cardiac epithelial to mesenchymal transition | 2 | 42 | 0.01908 |
| GO:1990267 | response to transition metal nanoparticle | 2 | 42 | 0.01908 |
| GO:0051259 | protein oligomerization | 6 | 417 | 0.01928 |
| GO:0045935 | positive regulation of nucleobase-containing compound metabolic process | 14 | 1505 | 0.01952 |
| GO:0010033 | response to organic substance | 19 | 2276 | 0.01961 |
| GO:0065008 | regulation of biological quality | 25 | 3255 | 0.01979 |
| GO:0032755 | positive regulation of interleukin-6 production | 2 | 43 | 0.01994 |
| GO:0045600 | positive regulation of fat cell differentiation | 2 | 43 | 0.01994 |
| GO:0055117 | regulation of cardiac muscle contraction | 2 | 43 | 0.01994 |
| GO:0003166 | bundle of His development | 1 | 4 | 0.02004 |
| GO:0003190 | atrioventricular valve formation | 1 | 4 | 0.02004 |
| GO:0003253 | cardiac neural crest cell migration involved in outflow tract morphogenesis | 1 | 4 | 0.02004 |
| GO:0007171 | activation of transmembrane receptor protein tyrosine kinase activity | 1 | 4 | 0.02004 |
| GO:0007406 | negative regulation of neuroblast proliferation | 1 | 4 | 0.02004 |
| GO:0008228 | opsonization | 1 | 4 | 0.02004 |
| GO:0009092 | homoserine metabolic process | 1 | 4 | 0.02004 |
| GO:0010961 | cellular magnesium ion homeostasis | 1 | 4 | 0.02004 |
| GO:0014004 | microglia differentiation | 1 | 4 | 0.02004 |
| GO:0014858 | positive regulation of skeletal muscle cell proliferation | 1 | 4 | 0.02004 |
| GO:0014859 | negative regulation of skeletal muscle cell proliferation | 1 | 4 | 0.02004 |
| GO:0016198 | axon choice point recognition | 1 | 4 | 0.02004 |
| GO:0016338 | calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules | 1 | 4 | 0.02004 |
| GO:0019343 | cysteine biosynthetic process via cystathionine | 1 | 4 | 0.02004 |
| GO:0019346 | transsulfuration | 1 | 4 | 0.02004 |
| GO:0023041 | neuronal signal transduction | 1 | 4 | 0.02004 |
| GO:0030167 | proteoglycan catabolic process | 1 | 4 | 0.02004 |
| GO:0030202 | heparin metabolic process | 1 | 4 | 0.02004 |
| GO:0031204 | posttranslational protein targeting to membrane, translocation | 1 | 4 | 0.02004 |
| GO:0032911 | negative regulation of transforming growth factor beta1 production | 1 | 4 | 0.02004 |
| GO:0033564 | anterior/posterior axon guidance | 1 | 4 | 0.02004 |
| GO:0035234 | ectopic germ cell programmed cell death | 1 | 4 | 0.02004 |
| GO:0043932 | ossification involved in bone remodeling | 1 | 4 | 0.02004 |
| GO:0044828 | negative regulation by host of viral genome replication | 1 | 4 | 0.02004 |
| GO:0045410 | positive regulation of interleukin-6 biosynthetic process | 1 | 4 | 0.02004 |
| GO:0045472 | response to ether | 1 | 4 | 0.02004 |
| GO:0045636 | positive regulation of melanocyte differentiation | 1 | 4 | 0.02004 |
| GO:0045714 | regulation of low-density lipoprotein particle receptor biosynthetic process | 1 | 4 | 0.02004 |
| GO:0045988 | negative regulation of striated muscle contraction | 1 | 4 | 0.02004 |
| GO:0046689 | response to mercury ion | 1 | 4 | 0.02004 |
| GO:0048087 | positive regulation of developmental pigmentation | 1 | 4 | 0.02004 |
| GO:0048143 | astrocyte activation | 1 | 4 | 0.02004 |
| GO:0048386 | positive regulation of retinoic acid receptor signaling pathway | 1 | 4 | 0.02004 |
| GO:0048793 | pronephros development | 1 | 4 | 0.02004 |
| GO:0050812 | regulation of acyl-CoA biosynthetic process | 1 | 4 | 0.02004 |
| GO:0050942 | positive regulation of pigment cell differentiation | 1 | 4 | 0.02004 |
| GO:0051006 | positive regulation of lipoprotein lipase activity | 1 | 4 | 0.02004 |
| GO:0060662 | salivary gland cavitation | 1 | 4 | 0.02004 |
| GO:0061047 | positive regulation of branching involved in lung morphogenesis | 1 | 4 | 0.02004 |
| GO:0061365 | positive regulation of triglyceride lipase activity | 1 | 4 | 0.02004 |
| GO:0070662 | mast cell proliferation | 1 | 4 | 0.02004 |
| GO:0071474 | cellular hyperosmotic response | 1 | 4 | 0.02004 |
| GO:1902074 | response to salt | 1 | 4 | 0.02004 |
| GO:1902723 | negative regulation of skeletal muscle satellite cell proliferation | 1 | 4 | 0.02004 |
| GO:1902730 | positive regulation of proteoglycan biosynthetic process | 1 | 4 | 0.02004 |
| GO:1902913 | positive regulation of neuroepithelial cell differentiation | 1 | 4 | 0.02004 |
| GO:1903935 | response to sodium arsenite | 1 | 4 | 0.02004 |
| GO:1904468 | negative regulation of tumor necrosis factor secretion | 1 | 4 | 0.02004 |
| GO:0010634 | positive regulation of epithelial cell migration | 3 | 114 | 0.02011 |
| GO:0043433 | negative regulation of sequence-specific DNA binding transcription factor activity | 3 | 114 | 0.02011 |
| GO:0051607 | defense response to virus | 3 | 114 | 0.02011 |
| GO:0051241 | negative regulation of multicellular organismal process | 9 | 803 | 0.02059 |
| GO:0080134 | regulation of response to stress | 11 | 1079 | 0.02063 |
| GO:0006935 | chemotaxis | 7 | 546 | 0.02091 |
| GO:0033002 | muscle cell proliferation | 3 | 116 | 0.02104 |
| GO:0051248 | negative regulation of protein metabolic process | 10 | 943 | 0.02113 |
| GO:0009267 | cellular response to starvation | 3 | 117 | 0.02152 |
| GO:0045666 | positive regulation of neuron differentiation | 4 | 209 | 0.02163 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 10 | 947 | 0.02168 |
| GO:0030858 | positive regulation of epithelial cell differentiation | 2 | 45 | 0.02172 |
| GO:0048708 | astrocyte differentiation | 2 | 45 | 0.02172 |
| GO:0050885 | neuromuscular process controlling balance | 2 | 45 | 0.02172 |
| GO:0009628 | response to abiotic stimulus | 9 | 811 | 0.02179 |
| GO:0016049 | cell growth | 6 | 430 | 0.02203 |
| GO:0007155 | cell adhesion | 13 | 1382 | 0.02226 |
| GO:0000122 | negative regulation of transcription from RNA polymerase II promoter | 7 | 554 | 0.02242 |
| GO:0061061 | muscle structure development | 7 | 554 | 0.02242 |
| GO:0042742 | defense response to bacterium | 3 | 119 | 0.02249 |
| GO:0044272 | sulfur compound biosynthetic process | 3 | 119 | 0.02249 |
| GO:0048583 | regulation of response to stimulus | 27 | 3633 | 0.02275 |
| GO:0043434 | response to peptide hormone | 4 | 213 | 0.023 |
| GO:0006954 | inflammatory response | 5 | 320 | 0.02329 |
| GO:0070374 | positive regulation of ERK1 and ERK2 cascade | 3 | 121 | 0.02348 |
| GO:0043086 | negative regulation of catalytic activity | 7 | 561 | 0.02381 |
| GO:0002062 | chondrocyte differentiation | 3 | 122 | 0.02399 |
| GO:0002685 | regulation of leukocyte migration | 3 | 122 | 0.02399 |
| GO:0043410 | positive regulation of MAPK cascade | 6 | 440 | 0.02432 |
| GO:1903901 | negative regulation of viral life cycle | 2 | 48 | 0.02451 |
| GO:0000738 | DNA catabolic process, exonucleolytic | 1 | 5 | 0.02499 |
| GO:0003139 | secondary heart field specification | 1 | 5 | 0.02499 |
| GO:0010891 | negative regulation of sequestering of triglyceride | 1 | 5 | 0.02499 |
| GO:0015791 | polyol transport | 1 | 5 | 0.02499 |
| GO:0030241 | skeletal muscle myosin thick filament assembly | 1 | 5 | 0.02499 |
| GO:0031665 | negative regulation of lipopolysaccharide-mediated signaling pathway | 1 | 5 | 0.02499 |
| GO:0032804 | negative regulation of low-density lipoprotein particle receptor catabolic process | 1 | 5 | 0.02499 |
| GO:0045080 | positive regulation of chemokine biosynthetic process | 1 | 5 | 0.02499 |
| GO:0045713 | low-density lipoprotein particle receptor biosynthetic process | 1 | 5 | 0.02499 |
| GO:0045793 | positive regulation of cell size | 1 | 5 | 0.02499 |
| GO:0048669 | collateral sprouting in absence of injury | 1 | 5 | 0.02499 |
| GO:0050711 | negative regulation of interleukin-1 secretion | 1 | 5 | 0.02499 |
| GO:0060431 | primary lung bud formation | 1 | 5 | 0.02499 |
| GO:0061046 | regulation of branching involved in lung morphogenesis | 1 | 5 | 0.02499 |
| GO:0070813 | hydrogen sulfide metabolic process | 1 | 5 | 0.02499 |
| GO:0070814 | hydrogen sulfide biosynthetic process | 1 | 5 | 0.02499 |
| GO:1902033 | regulation of hematopoietic stem cell proliferation | 1 | 5 | 0.02499 |
| GO:1903003 | positive regulation of protein deubiquitination | 1 | 5 | 0.02499 |
| GO:1990535 | neuron projection maintenance | 1 | 5 | 0.02499 |
| GO:2000317 | negative regulation of T-helper 17 type immune response | 1 | 5 | 0.02499 |
| GO:2000320 | negative regulation of T-helper 17 cell differentiation | 1 | 5 | 0.02499 |
| GO:2000630 | positive regulation of miRNA metabolic process | 1 | 5 | 0.02499 |
| GO:2000645 | negative regulation of receptor catabolic process | 1 | 5 | 0.02499 |
| GO:2001016 | positive regulation of skeletal muscle cell differentiation | 1 | 5 | 0.02499 |
| GO:0009888 | tissue development | 15 | 1708 | 0.02508 |
| GO:0010883 | regulation of lipid storage | 2 | 49 | 0.02547 |
| GO:0035272 | exocrine system development | 2 | 49 | 0.02547 |
| GO:0048525 | negative regulation of viral process | 2 | 49 | 0.02547 |
| GO:0010604 | positive regulation of macromolecule metabolic process | 21 | 2667 | 0.02562 |
| GO:0048731 | system development | 29 | 4016 | 0.02583 |
| GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling | 4 | 221 | 0.02588 |
| GO:0030097 | hemopoiesis | 8 | 702 | 0.02604 |
| GO:0042594 | response to starvation | 3 | 126 | 0.02607 |
| GO:0032612 | interleukin-1 production | 2 | 50 | 0.02644 |
| GO:0051960 | regulation of nervous system development | 8 | 706 | 0.02681 |
| GO:0010558 | negative regulation of macromolecule biosynthetic process | 11 | 1126 | 0.02715 |
| GO:0051962 | positive regulation of nervous system development | 5 | 335 | 0.02766 |
| GO:0007411 | axon guidance | 4 | 226 | 0.02779 |
| GO:0050900 | leukocyte migration | 4 | 226 | 0.02779 |
| GO:0030162 | regulation of proteolysis | 7 | 581 | 0.02809 |
| GO:0051851 | modification by host of symbiont morphology or physiology | 2 | 52 | 0.02844 |
| GO:0071347 | cellular response to interleukin-1 | 2 | 52 | 0.02844 |
| GO:0006813 | potassium ion transport | 4 | 228 | 0.02858 |
| GO:0014031 | mesenchymal cell development | 4 | 228 | 0.02858 |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | 14 | 1584 | 0.02871 |
| GO:0031669 | cellular response to nutrient levels | 3 | 131 | 0.0288 |
| GO:0030334 | regulation of cell migration | 8 | 716 | 0.02882 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 11 | 1139 | 0.02919 |
| GO:0060284 | regulation of cell development | 9 | 855 | 0.02929 |
| GO:0006942 | regulation of striated muscle contraction | 2 | 53 | 0.02946 |
| GO:0000459 | exonucleolytic trimming involved in rRNA processing | 1 | 6 | 0.02991 |
| GO:0000467 | exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 1 | 6 | 0.02991 |
| GO:0001955 | blood vessel maturation | 1 | 6 | 0.02991 |
| GO:0002227 | innate immune response in mucosa | 1 | 6 | 0.02991 |
| GO:0003149 | membranous septum morphogenesis | 1 | 6 | 0.02991 |
| GO:0003164 | His-Purkinje system development | 1 | 6 | 0.02991 |
| GO:0003321 | positive regulation of blood pressure by epinephrine-norepinephrine | 1 | 6 | 0.02991 |
| GO:0006972 | hyperosmotic response | 1 | 6 | 0.02991 |
| GO:0032471 | negative regulation of endoplasmic reticulum calcium ion concentration | 1 | 6 | 0.02991 |
| GO:0032908 | regulation of transforming growth factor beta1 production | 1 | 6 | 0.02991 |
| GO:0034145 | positive regulation of toll-like receptor 4 signaling pathway | 1 | 6 | 0.02991 |
| GO:0042033 | chemokine biosynthetic process | 1 | 6 | 0.02991 |
| GO:0042535 | positive regulation of tumor necrosis factor biosynthetic process | 1 | 6 | 0.02991 |
| GO:0042754 | negative regulation of circadian rhythm | 1 | 6 | 0.02991 |
| GO:0043116 | negative regulation of vascular permeability | 1 | 6 | 0.02991 |
| GO:0043649 | dicarboxylic acid catabolic process | 1 | 6 | 0.02991 |
| GO:0045019 | negative regulation of nitric oxide biosynthetic process | 1 | 6 | 0.02991 |
| GO:0045073 | regulation of chemokine biosynthetic process | 1 | 6 | 0.02991 |
| GO:0048711 | positive regulation of astrocyte differentiation | 1 | 6 | 0.02991 |
| GO:0050755 | chemokine metabolic process | 1 | 6 | 0.02991 |
| GO:0051152 | positive regulation of smooth muscle cell differentiation | 1 | 6 | 0.02991 |
| GO:0060339 | negative regulation of type I interferon-mediated signaling pathway | 1 | 6 | 0.02991 |
| GO:0061309 | cardiac neural crest cell development involved in outflow tract morphogenesis | 1 | 6 | 0.02991 |
| GO:0061643 | chemorepulsion of axon | 1 | 6 | 0.02991 |
| GO:0071493 | cellular response to UV-B | 1 | 6 | 0.02991 |
| GO:0071635 | negative regulation of transforming growth factor beta production | 1 | 6 | 0.02991 |
| GO:0071688 | striated muscle myosin thick filament assembly | 1 | 6 | 0.02991 |
| GO:0090647 | modulation of age-related behavioral decline | 1 | 6 | 0.02991 |
| GO:0097264 | self proteolysis | 1 | 6 | 0.02991 |
| GO:1900119 | positive regulation of execution phase of apoptosis | 1 | 6 | 0.02991 |
| GO:1900165 | negative regulation of interleukin-6 secretion | 1 | 6 | 0.02991 |
| GO:1900364 | negative regulation of mRNA polyadenylation | 1 | 6 | 0.02991 |
| GO:1902177 | positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway | 1 | 6 | 0.02991 |
| GO:1902713 | regulation of interferon-gamma secretion | 1 | 6 | 0.02991 |
| GO:1903140 | regulation of establishment of endothelial barrier | 1 | 6 | 0.02991 |
| GO:1903980 | positive regulation of microglial cell activation | 1 | 6 | 0.02991 |
| GO:1904406 | negative regulation of nitric oxide metabolic process | 1 | 6 | 0.02991 |
| GO:2000316 | regulation of T-helper 17 type immune response | 1 | 6 | 0.02991 |
| GO:2000319 | regulation of T-helper 17 cell differentiation | 1 | 6 | 0.02991 |
| GO:2001135 | regulation of endocytic recycling | 1 | 6 | 0.02991 |
| GO:0048864 | stem cell development | 4 | 232 | 0.03019 |
| GO:0050803 | regulation of synapse structure or activity | 4 | 232 | 0.03019 |
| GO:0009966 | regulation of signal transduction | 22 | 2880 | 0.03037 |
| GO:0002718 | regulation of cytokine production involved in immune response | 2 | 54 | 0.03049 |
| GO:0051897 | positive regulation of protein kinase B signaling | 2 | 54 | 0.03049 |
| GO:0072006 | nephron development | 3 | 134 | 0.03051 |
| GO:0031325 | positive regulation of cellular metabolic process | 21 | 2719 | 0.03086 |
| GO:0065009 | regulation of molecular function | 22 | 2888 | 0.03121 |
| GO:0014855 | striated muscle cell proliferation | 2 | 55 | 0.03154 |
| GO:0045685 | regulation of glial cell differentiation | 2 | 55 | 0.03154 |
| GO:0097285 | cell-type specific apoptotic process | 5 | 348 | 0.03184 |
| GO:0048844 | artery morphogenesis | 2 | 56 | 0.0326 |
| GO:0051702 | interaction with symbiont | 2 | 56 | 0.0326 |
| GO:0007568 | aging | 3 | 138 | 0.03287 |
| GO:0048762 | mesenchymal cell differentiation | 4 | 240 | 0.03358 |
| GO:0055006 | cardiac cell development | 2 | 57 | 0.03368 |
| GO:0010594 | regulation of endothelial cell migration | 3 | 140 | 0.03409 |
| GO:0001944 | vasculature development | 7 | 606 | 0.03415 |
| GO:0045087 | innate immune response | 5 | 356 | 0.0346 |
| GO:0006616 | SRP-dependent cotranslational protein targeting to membrane, translocation | 1 | 7 | 0.03481 |
| GO:0006620 | posttranslational protein targeting to membrane | 1 | 7 | 0.03481 |
| GO:0010898 | positive regulation of triglyceride catabolic process | 1 | 7 | 0.03481 |
| GO:0010960 | magnesium ion homeostasis | 1 | 7 | 0.03481 |
| GO:0014820 | tonic smooth muscle contraction | 1 | 7 | 0.03481 |
| GO:0019054 | modulation by virus of host process | 1 | 7 | 0.03481 |
| GO:0019344 | cysteine biosynthetic process | 1 | 7 | 0.03481 |
| GO:0031033 | myosin filament organization | 1 | 7 | 0.03481 |
| GO:0031034 | myosin filament assembly | 1 | 7 | 0.03481 |
| GO:0032691 | negative regulation of interleukin-1 beta production | 1 | 7 | 0.03481 |
| GO:0032780 | negative regulation of ATPase activity | 1 | 7 | 0.03481 |
| GO:0033033 | negative regulation of myeloid cell apoptotic process | 1 | 7 | 0.03481 |
| GO:0046628 | positive regulation of insulin receptor signaling pathway | 1 | 7 | 0.03481 |
| GO:0047484 | regulation of response to osmotic stress | 1 | 7 | 0.03481 |
| GO:0048541 | Peyer's patch development | 1 | 7 | 0.03481 |
| GO:0051004 | regulation of lipoprotein lipase activity | 1 | 7 | 0.03481 |
| GO:0051561 | positive regulation of mitochondrial calcium ion concentration | 1 | 7 | 0.03481 |
| GO:0060605 | tube lumen cavitation | 1 | 7 | 0.03481 |
| GO:0060900 | embryonic camera-type eye formation | 1 | 7 | 0.03481 |
| GO:0060907 | positive regulation of macrophage cytokine production | 1 | 7 | 0.03481 |
| GO:0071236 | cellular response to antibiotic | 1 | 7 | 0.03481 |
| GO:0071285 | cellular response to lithium ion | 1 | 7 | 0.03481 |
| GO:0071476 | cellular hypotonic response | 1 | 7 | 0.03481 |
| GO:1900363 | regulation of mRNA polyadenylation | 1 | 7 | 0.03481 |
| GO:1901550 | regulation of endothelial cell development | 1 | 7 | 0.03481 |
| GO:1902725 | negative regulation of satellite cell differentiation | 1 | 7 | 0.03481 |
| GO:1903978 | regulation of microglial cell activation | 1 | 7 | 0.03481 |
| GO:1904467 | regulation of tumor necrosis factor secretion | 1 | 7 | 0.03481 |
| GO:1990000 | amyloid fibril formation | 1 | 7 | 0.03481 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 4 | 243 | 0.0349 |
| GO:0016032 | viral process | 4 | 243 | 0.0349 |
| GO:0048667 | cell morphogenesis involved in neuron differentiation | 6 | 481 | 0.03535 |
| GO:2000145 | regulation of cell motility | 8 | 746 | 0.03546 |
| GO:0045787 | positive regulation of cell cycle | 4 | 245 | 0.0358 |
| GO:0048709 | oligodendrocyte differentiation | 2 | 59 | 0.03587 |
| GO:0050793 | regulation of developmental process | 18 | 2270 | 0.03595 |
| GO:0048167 | regulation of synaptic plasticity | 3 | 143 | 0.03596 |
| GO:0031175 | neuron projection development | 9 | 888 | 0.036 |
| GO:0031346 | positive regulation of cell projection organization | 4 | 247 | 0.03671 |
| GO:0061448 | connective tissue development | 4 | 247 | 0.03671 |
| GO:0001817 | regulation of cytokine production | 6 | 486 | 0.03689 |
| GO:0000910 | cytokinesis | 3 | 145 | 0.03723 |
| GO:0030278 | regulation of ossification | 3 | 145 | 0.03723 |
| GO:0031668 | cellular response to extracellular stimulus | 3 | 145 | 0.03723 |
| GO:0048514 | blood vessel morphogenesis | 6 | 488 | 0.03751 |
| GO:0032269 | negative regulation of cellular protein metabolic process | 9 | 895 | 0.03755 |
| GO:0001822 | kidney development | 4 | 249 | 0.03764 |
| GO:0043112 | receptor metabolic process | 3 | 146 | 0.03788 |
| GO:0090257 | regulation of muscle system process | 3 | 146 | 0.03788 |
| GO:0048666 | neuron development | 10 | 1041 | 0.03796 |
| GO:0001755 | neural crest cell migration | 2 | 61 | 0.03812 |
| GO:0007632 | visual behavior | 2 | 61 | 0.03812 |
| GO:0046849 | bone remodeling | 2 | 61 | 0.03812 |
| GO:0003007 | heart morphogenesis | 4 | 252 | 0.03905 |
| GO:0033138 | positive regulation of peptidyl-serine phosphorylation | 2 | 62 | 0.03926 |
| GO:0051149 | positive regulation of muscle cell differentiation | 2 | 62 | 0.03926 |
| GO:0071346 | cellular response to interferon-gamma | 2 | 62 | 0.03926 |
| GO:0001993 | regulation of systemic arterial blood pressure by norepinephrine-epinephrine | 1 | 8 | 0.03969 |
| GO:0002138 | retinoic acid biosynthetic process | 1 | 8 | 0.03969 |
| GO:0002374 | cytokine secretion involved in immune response | 1 | 8 | 0.03969 |
| GO:0002739 | regulation of cytokine secretion involved in immune response | 1 | 8 | 0.03969 |
| GO:0006878 | cellular copper ion homeostasis | 1 | 8 | 0.03969 |
| GO:0010889 | regulation of sequestering of triglyceride | 1 | 8 | 0.03969 |
| GO:0010896 | regulation of triglyceride catabolic process | 1 | 8 | 0.03969 |
| GO:0016102 | diterpenoid biosynthetic process | 1 | 8 | 0.03969 |
| GO:0030730 | sequestering of triglyceride | 1 | 8 | 0.03969 |
| GO:0031125 | rRNA 3'-end processing | 1 | 8 | 0.03969 |
| GO:0032793 | positive regulation of CREB transcription factor activity | 1 | 8 | 0.03969 |
| GO:0032802 | low-density lipoprotein particle receptor catabolic process | 1 | 8 | 0.03969 |
| GO:0032803 | regulation of low-density lipoprotein particle receptor catabolic process | 1 | 8 | 0.03969 |
| GO:0040015 | negative regulation of multicellular organism growth | 1 | 8 | 0.03969 |
| GO:0045623 | negative regulation of T-helper cell differentiation | 1 | 8 | 0.03969 |
| GO:0048664 | neuron fate determination | 1 | 8 | 0.03969 |
| GO:0048934 | peripheral nervous system neuron differentiation | 1 | 8 | 0.03969 |
| GO:0048935 | peripheral nervous system neuron development | 1 | 8 | 0.03969 |
| GO:0051124 | synaptic growth at neuromuscular junction | 1 | 8 | 0.03969 |
| GO:0060013 | righting reflex | 1 | 8 | 0.03969 |
| GO:0061307 | cardiac neural crest cell differentiation involved in heart development | 1 | 8 | 0.03969 |
| GO:0061308 | cardiac neural crest cell development involved in heart development | 1 | 8 | 0.03969 |
| GO:0071472 | cellular response to salt stress | 1 | 8 | 0.03969 |
| GO:0071636 | positive regulation of transforming growth factor beta production | 1 | 8 | 0.03969 |
| GO:0090026 | positive regulation of monocyte chemotaxis | 1 | 8 | 0.03969 |
| GO:1900016 | negative regulation of cytokine production involved in inflammatory response | 1 | 8 | 0.03969 |
| GO:1901388 | regulation of transforming growth factor beta activation | 1 | 8 | 0.03969 |
| GO:1901741 | positive regulation of myoblast fusion | 1 | 8 | 0.03969 |
| GO:1902004 | positive regulation of beta-amyloid formation | 1 | 8 | 0.03969 |
| GO:1903209 | positive regulation of oxidative stress-induced cell death | 1 | 8 | 0.03969 |
| GO:1903799 | negative regulation of production of miRNAs involved in gene silencing by miRNA | 1 | 8 | 0.03969 |
| GO:1903817 | negative regulation of voltage-gated potassium channel activity | 1 | 8 | 0.03969 |
| GO:1990774 | tumor necrosis factor secretion | 1 | 8 | 0.03969 |
| GO:2000628 | regulation of miRNA metabolic process | 1 | 8 | 0.03969 |
| GO:2001015 | negative regulation of skeletal muscle cell differentiation | 1 | 8 | 0.03969 |
| GO:1901184 | regulation of ERBB signaling pathway | 2 | 63 | 0.04042 |
| GO:0051260 | protein homooligomerization | 4 | 255 | 0.0405 |
| GO:0051402 | neuron apoptotic process | 3 | 150 | 0.04051 |
| GO:0048878 | chemical homeostasis | 9 | 908 | 0.04055 |
| GO:0050709 | negative regulation of protein secretion | 2 | 64 | 0.04158 |
| GO:0007165 | signal transduction | 40 | 6160 | 0.04173 |
| GO:0008361 | regulation of cell size | 3 | 152 | 0.04187 |
| GO:0010721 | negative regulation of cell development | 4 | 258 | 0.04197 |
| GO:0001667 | ameboidal-type cell migration | 5 | 377 | 0.04253 |
| GO:0019915 | lipid storage | 2 | 65 | 0.04277 |
| GO:0045639 | positive regulation of myeloid cell differentiation | 2 | 65 | 0.04277 |
| GO:0045778 | positive regulation of ossification | 2 | 65 | 0.04277 |
| GO:0051701 | interaction with host | 2 | 65 | 0.04277 |
| GO:2000177 | regulation of neural precursor cell proliferation | 2 | 65 | 0.04277 |
| GO:0045665 | negative regulation of neuron differentiation | 3 | 155 | 0.04394 |
| GO:0045069 | regulation of viral genome replication | 2 | 66 | 0.04396 |
| GO:1902106 | negative regulation of leukocyte differentiation | 2 | 66 | 0.04396 |
| GO:0051336 | regulation of hydrolase activity | 11 | 1218 | 0.04403 |
| GO:0001774 | microglial cell activation | 1 | 9 | 0.04454 |
| GO:0002251 | organ or tissue specific immune response | 1 | 9 | 0.04454 |
| GO:0002385 | mucosal immune response | 1 | 9 | 0.04454 |
| GO:0010587 | miRNA catabolic process | 1 | 9 | 0.04454 |
| GO:0014029 | neural crest formation | 1 | 9 | 0.04454 |
| GO:0030240 | skeletal muscle thin filament assembly | 1 | 9 | 0.04454 |
| GO:0043353 | enucleate erythrocyte differentiation | 1 | 9 | 0.04454 |
| GO:0044068 | modulation by symbiont of host cellular process | 1 | 9 | 0.04454 |
| GO:0045408 | regulation of interleukin-6 biosynthetic process | 1 | 9 | 0.04454 |
| GO:0045475 | locomotor rhythm | 1 | 9 | 0.04454 |
| GO:0045634 | regulation of melanocyte differentiation | 1 | 9 | 0.04454 |
| GO:0050932 | regulation of pigment cell differentiation | 1 | 9 | 0.04454 |
| GO:0060330 | regulation of response to interferon-gamma | 1 | 9 | 0.04454 |
| GO:0060334 | regulation of interferon-gamma-mediated signaling pathway | 1 | 9 | 0.04454 |
| GO:0060340 | positive regulation of type I interferon-mediated signaling pathway | 1 | 9 | 0.04454 |
| GO:0072530 | purine-containing compound transmembrane transport | 1 | 9 | 0.04454 |
| GO:0072538 | T-helper 17 type immune response | 1 | 9 | 0.04454 |
| GO:0072539 | T-helper 17 cell differentiation | 1 | 9 | 0.04454 |
| GO:0072643 | interferon-gamma secretion | 1 | 9 | 0.04454 |
| GO:1900078 | positive regulation of cellular response to insulin stimulus | 1 | 9 | 0.04454 |
| GO:1901739 | regulation of myoblast fusion | 1 | 9 | 0.04454 |
| GO:1903427 | negative regulation of reactive oxygen species biosynthetic process | 1 | 9 | 0.04454 |
| GO:2000811 | negative regulation of anoikis | 1 | 9 | 0.04454 |
| GO:2001028 | positive regulation of endothelial cell chemotaxis | 1 | 9 | 0.04454 |
| GO:0001818 | negative regulation of cytokine production | 3 | 156 | 0.04464 |
| GO:0051716 | cellular response to stimulus | 47 | 7492 | 0.04487 |
| GO:0010469 | regulation of receptor activity | 5 | 383 | 0.04498 |
| GO:0072001 | renal system development | 4 | 264 | 0.04501 |
| GO:0002698 | negative regulation of immune effector process | 2 | 67 | 0.04517 |
| GO:0048663 | neuron fate commitment | 2 | 67 | 0.04517 |
| GO:0060415 | muscle tissue morphogenesis | 2 | 67 | 0.04517 |
| GO:0070555 | response to interleukin-1 | 2 | 67 | 0.04517 |
| GO:0072676 | lymphocyte migration | 2 | 67 | 0.04517 |
| GO:0048534 | hematopoietic or lymphoid organ development | 8 | 784 | 0.04526 |
| GO:0010770 | positive regulation of cell morphogenesis involved in differentiation | 3 | 157 | 0.04535 |
| GO:0048638 | regulation of developmental growth | 4 | 265 | 0.04553 |
| GO:0016192 | vesicle-mediated transport | 12 | 1378 | 0.04565 |
| GO:0072657 | protein localization to membrane | 5 | 385 | 0.04582 |
| GO:0016358 | dendrite development | 3 | 158 | 0.04606 |
| GO:0048839 | inner ear development | 3 | 158 | 0.04606 |
| GO:0060537 | muscle tissue development | 5 | 388 | 0.04709 |
| GO:0051270 | regulation of cellular component movement | 8 | 792 | 0.04753 |
| GO:0002367 | cytokine production involved in immune response | 2 | 69 | 0.04762 |
| GO:1901222 | regulation of NIK/NF-kappaB signaling | 2 | 69 | 0.04762 |
| GO:1903706 | regulation of hemopoiesis | 4 | 269 | 0.04764 |
| GO:0044764 | multi-organism cellular process | 4 | 270 | 0.04817 |
| GO:0001837 | epithelial to mesenchymal transition | 3 | 161 | 0.04824 |
| GO:0044767 | single-organism developmental process | 36 | 5496 | 0.0487 |
| GO:0009416 | response to light stimulus | 4 | 271 | 0.04871 |
| GO:0045596 | negative regulation of cell differentiation | 6 | 521 | 0.04883 |
| GO:0031124 | mRNA 3'-end processing | 2 | 70 | 0.04886 |
| GO:0051817 | modification of morphology or physiology of other organism involved in symbiotic interaction | 2 | 70 | 0.04886 |
| GO:0009615 | response to virus | 3 | 162 | 0.04897 |
| GO:0050877 | neurological system process | 8 | 797 | 0.04899 |
| GO:0002230 | positive regulation of defense response to virus by host | 1 | 10 | 0.04936 |
| GO:0006654 | phosphatidic acid biosynthetic process | 1 | 10 | 0.04936 |
| GO:0006971 | hypotonic response | 1 | 10 | 0.04936 |
| GO:0016322 | neuron remodeling | 1 | 10 | 0.04936 |
| GO:0018065 | protein-cofactor linkage | 1 | 10 | 0.04936 |
| GO:0031441 | negative regulation of mRNA 3'-end processing | 1 | 10 | 0.04936 |
| GO:0032692 | negative regulation of interleukin-1 production | 1 | 10 | 0.04936 |
| GO:0033690 | positive regulation of osteoblast proliferation | 1 | 10 | 0.04936 |
| GO:0042226 | interleukin-6 biosynthetic process | 1 | 10 | 0.04936 |
| GO:0042533 | tumor necrosis factor biosynthetic process | 1 | 10 | 0.04936 |
| GO:0042534 | regulation of tumor necrosis factor biosynthetic process | 1 | 10 | 0.04936 |
| GO:0042762 | regulation of sulfur metabolic process | 1 | 10 | 0.04936 |
| GO:0043371 | negative regulation of CD4-positive, alpha-beta T cell differentiation | 1 | 10 | 0.04936 |
| GO:0044406 | adhesion of symbiont to host | 1 | 10 | 0.04936 |
| GO:0045603 | positive regulation of endothelial cell differentiation | 1 | 10 | 0.04936 |
| GO:0045651 | positive regulation of macrophage differentiation | 1 | 10 | 0.04936 |
| GO:0045876 | positive regulation of sister chromatid cohesion | 1 | 10 | 0.04936 |
| GO:0048537 | mucosal-associated lymphoid tissue development | 1 | 10 | 0.04936 |
| GO:0048714 | positive regulation of oligodendrocyte differentiation | 1 | 10 | 0.04936 |
| GO:0048739 | cardiac muscle fiber development | 1 | 10 | 0.04936 |
| GO:0061158 | 3'-UTR-mediated mRNA destabilization | 1 | 10 | 0.04936 |
| GO:0070886 | positive regulation of calcineurin-NFAT signaling cascade | 1 | 10 | 0.04936 |
| GO:0071243 | cellular response to arsenic-containing substance | 1 | 10 | 0.04936 |
| GO:0090085 | regulation of protein deubiquitination | 1 | 10 | 0.04936 |
| GO:1902993 | positive regulation of amyloid precursor protein catabolic process | 1 | 10 | 0.04936 |
| GO:2000209 | regulation of anoikis | 1 | 10 | 0.04936 |