Supplementary table GO enrichment of DEGs.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ONTOLOGY | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | Count |
| BP | GO:0001655 | urogenital system development | 27/504 | 330/18670 | 3.46337E-07 | 3.46337E-07 | 0.000944994 | 27 |
| MF | GO:0048018 | receptor ligand activity | 35/510 | 482/17697 | 5.63897E-07 | 5.63897E-07 | 0.000370985 | 35 |
| BP | GO:0060485 | mesenchyme development | 24/504 | 278/18670 | 5.95438E-07 | 5.95438E-07 | 0.000944994 | 24 |
| BP | GO:0010038 | response to metal ion | 28/504 | 364/18670 | 7.33451E-07 | 7.33451E-07 | 0.000944994 | 28 |
| BP | GO:0048762 | mesenchymal cell differentiation | 20/504 | 219/18670 | 2.18399E-06 | 2.18399E-06 | 0.002110424 | 20 |
| BP | GO:0001823 | mesonephros development | 13/504 | 102/18670 | 3.62499E-06 | 3.62499E-06 | 0.002802308 | 13 |
| BP | GO:0072073 | kidney epithelium development | 15/504 | 140/18670 | 5.92487E-06 | 5.92487E-06 | 0.003816866 | 15 |
| BP | GO:0001822 | kidney development | 22/504 | 278/18670 | 7.22293E-06 | 7.22293E-06 | 0.003988362 | 22 |
| CC | GO:0043034 | costamere | 6/534 | 19/19717 | 7.70891E-06 | 7.70891E-06 | 0.003456837 | 6 |
| BP | GO:0071526 | semaphorin-plexin signaling pathway | 8/504 | 40/18670 | 9.58896E-06 | 9.58896E-06 | 0.004183375 | 8 |
| BP | GO:0001657 | ureteric bud development | 12/504 | 97/18670 | 1.16786E-05 | 1.16786E-05 | 0.004183375 | 12 |
| BP | GO:0051592 | response to calcium ion | 15/504 | 148/18670 | 1.16924E-05 | 1.16924E-05 | 0.004183375 | 15 |
| BP | GO:0072163 | mesonephric epithelium development | 12/504 | 98/18670 | 1.29876E-05 | 1.29876E-05 | 0.004183375 | 12 |
| BP | GO:0072164 | mesonephric tubule development | 12/504 | 98/18670 | 1.29876E-05 | 1.29876E-05 | 0.004183375 | 12 |
| BP | GO:0072001 | renal system development | 22/504 | 293/18670 | 1.65127E-05 | 1.65127E-05 | 0.004909678 | 22 |
| BP | GO:0001755 | neural crest cell migration | 9/504 | 57/18670 | 2.01441E-05 | 2.01441E-05 | 0.005375963 | 9 |
| BP | GO:0048732 | gland development | 28/504 | 434/18670 | 2.08626E-05 | 2.08626E-05 | 0.005375963 | 28 |
| BP | GO:0050919 | negative chemotaxis | 8/504 | 46/18670 | 2.82259E-05 | 2.82259E-05 | 0.006818791 | 8 |
| BP | GO:0045778 | positive regulation of ossification | 11/504 | 90/18670 | 3.02228E-05 | 3.02228E-05 | 0.006871711 | 11 |
| BP | GO:0060993 | kidney morphogenesis | 11/504 | 94/18670 | 4.55239E-05 | 4.55239E-05 | 0.009287781 | 11 |
| BP | GO:0072028 | nephron morphogenesis | 10/504 | 78/18670 | 4.56548E-05 | 4.56548E-05 | 0.009287781 | 10 |
| BP | GO:0045669 | positive regulation of osteoblast differentiation | 9/504 | 64/18670 | 5.21725E-05 | 5.21725E-05 | 0.010083023 | 9 |
| BP | GO:0071248 | cellular response to metal ion | 16/504 | 190/18670 | 6.04145E-05 | 6.04145E-05 | 0.010656232 | 16 |
| BP | GO:0014032 | neural crest cell development | 10/504 | 81/18670 | 6.34092E-05 | 6.34092E-05 | 0.010656232 | 10 |
| BP | GO:0110110 | positive regulation of animal organ morphogenesis | 10/504 | 81/18670 | 6.34092E-05 | 6.34092E-05 | 0.010656232 | 10 |
| BP | GO:0007409 | axonogenesis | 28/504 | 468/18670 | 7.86612E-05 | 7.86612E-05 | 0.012668591 | 28 |
| BP | GO:0071241 | cellular response to inorganic substance | 17/504 | 217/18670 | 8.84825E-05 | 8.84825E-05 | 0.013680321 | 17 |
| BP | GO:0014031 | mesenchymal cell development | 10/504 | 85/18670 | 9.59517E-05 | 9.59517E-05 | 0.013736244 | 10 |
| BP | GO:0048864 | stem cell development | 10/504 | 85/18670 | 9.59517E-05 | 9.59517E-05 | 0.013736244 | 10 |
| MF | GO:0045499 | chemorepellent activity | 6/510 | 27/17697 | 9.82928E-05 | 9.82928E-05 | 0.032333155 | 6 |
| BP | GO:0007218 | neuropeptide signaling pathway | 11/504 | 104/18670 | 0.000115474 | 0.000115474 | 0.015490161 | 11 |
| BP | GO:0030900 | forebrain development | 24/504 | 381/18670 | 0.000116218 | 0.000116218 | 0.015490161 | 24 |
| BP | GO:0072006 | nephron development | 13/504 | 142/18670 | 0.00012678 | 0.00012678 | 0.016334625 | 13 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 25/534 | 406/19717 | 0.000128137 | 0.000128137 | 0.028729684 | 25 |
| BP | GO:0051961 | negative regulation of nervous system development | 21/504 | 315/18670 | 0.000141166 | 0.000141166 | 0.01760146 | 21 |
| BP | GO:0014033 | neural crest cell differentiation | 10/504 | 90/18670 | 0.000155577 | 0.000155577 | 0.018332596 | 10 |
| BP | GO:0007612 | learning | 13/504 | 145/18670 | 0.000156516 | 0.000156516 | 0.018332596 | 13 |
| BP | GO:0050768 | negative regulation of neurogenesis | 20/504 | 295/18670 | 0.000161637 | 0.000161637 | 0.018375619 | 20 |
| MF | GO:0001047 | core promoter binding | 8/510 | 55/17697 | 0.000166592 | 0.000166592 | 0.03653326 | 8 |
| BP | GO:0050890 | cognition | 20/504 | 296/18670 | 0.000169103 | 0.000169103 | 0.018392174 | 20 |
| BP | GO:0001101 | response to acid chemical | 22/504 | 343/18670 | 0.000171686 | 0.000171686 | 0.018392174 | 22 |
| BP | GO:0072009 | nephron epithelium development | 11/504 | 109/18670 | 0.000176058 | 0.000176058 | 0.018392174 | 11 |
| BP | GO:1900745 | positive regulation of p38MAPK cascade | 6/504 | 32/18670 | 0.00018732 | 0.00018732 | 0.018817681 | 6 |
| BP | GO:0097529 | myeloid leukocyte migration | 16/504 | 210/18670 | 0.000195078 | 0.000195078 | 0.018817681 | 16 |
| BP | GO:0048485 | sympathetic nervous system development | 5/504 | 21/18670 | 0.000199867 | 0.000199867 | 0.018817681 | 5 |
| BP | GO:0072088 | nephron epithelium morphogenesis | 9/504 | 76/18670 | 0.00020278 | 0.00020278 | 0.018817681 | 9 |
| BP | GO:0072080 | nephron tubule development | 10/504 | 93/18670 | 0.000204473 | 0.000204473 | 0.018817681 | 10 |
| BP | GO:0007611 | learning or memory | 18/504 | 256/18670 | 0.000217484 | 0.000217484 | 0.01954963 | 18 |
| BP | GO:0010975 | regulation of neuron projection development | 28/504 | 499/18670 | 0.000230013 | 0.000230013 | 0.020205954 | 28 |
| BP | GO:0061326 | renal tubule development | 10/504 | 95/18670 | 0.000243765 | 0.000243765 | 0.020802263 | 10 |
| BP | GO:0001890 | placenta development | 13/504 | 152/18670 | 0.000250075 | 0.000250075 | 0.020802263 | 13 |
| BP | GO:0021516 | dorsal spinal cord development | 5/504 | 22/18670 | 0.000252947 | 0.000252947 | 0.020802263 | 5 |
| MF | GO:0001046 | core promoter sequence-specific DNA binding | 7/510 | 45/17697 | 0.000278142 | 0.000278142 | 0.045746986 | 7 |
| CC | GO:0043204 | perikaryon | 12/534 | 134/19717 | 0.000290195 | 0.000290195 | 0.038452361 | 12 |
| BP | GO:0002685 | regulation of leukocyte migration | 15/504 | 196/18670 | 0.000292024 | 0.000292024 | 0.023515598 | 15 |
| BP | GO:0002088 | lens development in camera-type eye | 9/504 | 80/18670 | 0.000300137 | 0.000300137 | 0.023675691 | 9 |
| BP | GO:0060675 | ureteric bud morphogenesis | 8/504 | 65/18670 | 0.000348802 | 0.000348802 | 0.026964239 | 8 |
| CC | GO:0044449 | contractile fiber part | 16/534 | 221/19717 | 0.000361678 | 0.000361678 | 0.038452361 | 16 |
| BP | GO:0031098 | stress-activated protein kinase signaling cascade | 20/504 | 315/18670 | 0.000381529 | 0.000381529 | 0.028087046 | 20 |
| BP | GO:0072171 | mesonephric tubule morphogenesis | 8/504 | 66/18670 | 0.000387692 | 0.000387692 | 0.028087046 | 8 |
| BP | GO:0071277 | cellular response to calcium ion | 9/504 | 83/18670 | 0.000396159 | 0.000396159 | 0.028087046 | 9 |
| BP | GO:0045665 | negative regulation of neuron differentiation | 16/504 | 225/18670 | 0.00042348 | 0.00042348 | 0.028087046 | 16 |
| BP | GO:0021527 | spinal cord association neuron differentiation | 4/504 | 14/18670 | 0.000423482 | 0.000423482 | 0.028087046 | 4 |
| BP | GO:0030278 | regulation of ossification | 15/504 | 203/18670 | 0.000424573 | 0.000424573 | 0.028087046 | 15 |
| MF | GO:0030215 | semaphorin receptor binding | 5/510 | 23/17697 | 0.000426496 | 0.000426496 | 0.047528779 | 5 |
| BP | GO:0001558 | regulation of cell growth | 24/504 | 416/18670 | 0.000426723 | 0.000426723 | 0.028087046 | 24 |
| BP | GO:0048846 | axon extension involved in axon guidance | 6/504 | 37/18670 | 0.000428725 | 0.000428725 | 0.028087046 | 6 |
| BP | GO:1902284 | neuron projection extension involved in neuron projection guidance | 6/504 | 37/18670 | 0.000428725 | 0.000428725 | 0.028087046 | 6 |
| CC | GO:0005667 | transcription factor complex | 22/534 | 365/19717 | 0.000428753 | 0.000428753 | 0.038452361 | 22 |
| MF | GO:0001228 | DNA-binding transcription activator activity, RNA polymerase II-specific | 26/510 | 439/17697 | 0.000447601 | 0.000447601 | 0.047528779 | 26 |
| BP | GO:0097530 | granulocyte migration | 12/504 | 141/18670 | 0.000448029 | 0.000448029 | 0.028862469 | 12 |
| BP | GO:0050770 | regulation of axonogenesis | 14/504 | 183/18670 | 0.000462168 | 0.000462168 | 0.028874907 | 14 |
| BP | GO:0010721 | negative regulation of cell development | 21/504 | 344/18670 | 0.000463162 | 0.000463162 | 0.028874907 | 21 |
| BP | GO:0071230 | cellular response to amino acid stimulus | 8/504 | 68/18670 | 0.000476059 | 0.000476059 | 0.029207818 | 8 |
| MF | GO:0001664 | G protein-coupled receptor binding | 19/510 | 280/17697 | 0.000515717 | 0.000515717 | 0.047528779 | 19 |
| CC | GO:0043025 | neuronal cell body | 27/534 | 497/19717 | 0.000520079 | 0.000520079 | 0.038869067 | 27 |
| BP | GO:0050900 | leukocyte migration | 27/504 | 499/18670 | 0.000520715 | 0.000520715 | 0.030880463 | 27 |
| BP | GO:0043062 | extracellular structure organization | 24/504 | 422/18670 | 0.000523358 | 0.000523358 | 0.030880463 | 24 |
| BP | GO:0038066 | p38MAPK cascade | 7/504 | 53/18670 | 0.000527289 | 0.000527289 | 0.030880463 | 7 |
| BP | GO:2000027 | regulation of animal organ morphogenesis | 17/504 | 253/18670 | 0.000543563 | 0.000543563 | 0.031023662 | 17 |
| BP | GO:0001503 | ossification | 23/504 | 398/18670 | 0.000545787 | 0.000545787 | 0.031023662 | 23 |
| BP | GO:0001892 | embryonic placenta development | 9/504 | 87/18670 | 0.00056223 | 0.00056223 | 0.031029642 | 9 |
| BP | GO:2000826 | regulation of heart morphogenesis | 6/504 | 39/18670 | 0.000574874 | 0.000574874 | 0.031029642 | 6 |
| BP | GO:0048596 | embryonic camera-type eye morphogenesis | 5/504 | 26/18670 | 0.000578003 | 0.000578003 | 0.031029642 | 5 |
| BP | GO:0048843 | negative regulation of axon extension involved in axon guidance | 5/504 | 26/18670 | 0.000578003 | 0.000578003 | 0.031029642 | 5 |
| BP | GO:0045667 | regulation of osteoblast differentiation | 11/504 | 126/18670 | 0.000618894 | 0.000618894 | 0.032769725 | 11 |
| BP | GO:0048568 | embryonic organ development | 24/504 | 428/18670 | 0.000638619 | 0.000638619 | 0.033357157 | 24 |
| MF | GO:0050839 | cell adhesion molecule binding | 28/510 | 499/17697 | 0.000642616 | 0.000642616 | 0.047528779 | 28 |
| BP | GO:0048863 | stem cell differentiation | 17/504 | 257/18670 | 0.000648806 | 0.000648806 | 0.033437401 | 17 |
| MF | GO:0005518 | collagen binding | 8/510 | 67/17697 | 0.000660122 | 0.000660122 | 0.047528779 | 8 |
| BP | GO:0071470 | cellular response to osmotic stress | 6/504 | 40/18670 | 0.000661098 | 0.000661098 | 0.033622607 | 6 |
| CC | GO:0043292 | contractile fiber | 16/534 | 234/19717 | 0.00067603 | 0.00067603 | 0.040661377 | 16 |
| BP | GO:0002687 | positive regulation of leukocyte migration | 11/504 | 128/18670 | 0.000706481 | 0.000706481 | 0.034880063 | 11 |
| BP | GO:0071214 | cellular response to abiotic stimulus | 20/504 | 331/18670 | 0.000712895 | 0.000712895 | 0.034880063 | 20 |
| BP | GO:0104004 | cellular response to environmental stimulus | 20/504 | 331/18670 | 0.000712895 | 0.000712895 | 0.034880063 | 20 |
| MF | GO:0044548 | S100 protein binding | 4/510 | 15/17697 | 0.000722437 | 0.000722437 | 0.047528779 | 4 |
| BP | GO:0022604 | regulation of cell morphogenesis | 26/504 | 484/18670 | 0.000730415 | 0.000730415 | 0.034885698 | 26 |
| BP | GO:0033631 | cell-cell adhesion mediated by integrin | 4/504 | 16/18670 | 0.000737623 | 0.000737623 | 0.034885698 | 4 |
| BP | GO:0090183 | regulation of kidney development | 7/504 | 56/18670 | 0.000740086 | 0.000740086 | 0.034885698 | 7 |
| CC | GO:0033267 | axon part | 22/534 | 382/19717 | 0.000786525 | 0.000786525 | 0.040661377 | 22 |
| BP | GO:0061387 | regulation of extent of cell growth | 10/504 | 110/18670 | 0.000790278 | 0.000790278 | 0.036802798 | 10 |
| BP | GO:0051403 | stress-activated MAPK cascade | 18/504 | 286/18670 | 0.000813996 | 0.000813996 | 0.037126466 | 18 |
| CC | GO:0150034 | distal axon | 18/534 | 285/19717 | 0.000816091 | 0.000816091 | 0.040661377 | 18 |
| BP | GO:0030324 | lung development | 13/504 | 172/18670 | 0.000816812 | 0.000816812 | 0.037126466 | 13 |
| BP | GO:1902668 | negative regulation of axon guidance | 5/504 | 28/18670 | 0.000826044 | 0.000826044 | 0.037126466 | 5 |
| BP | GO:0072078 | nephron tubule morphogenesis | 8/504 | 74/18670 | 0.00084318 | 0.00084318 | 0.037461054 | 8 |
| BP | GO:0050807 | regulation of synapse organization | 15/504 | 218/18670 | 0.000889509 | 0.000889509 | 0.039070311 | 15 |
| BP | GO:0048593 | camera-type eye morphogenesis | 10/504 | 112/18670 | 0.00090922 | 0.00090922 | 0.039199094 | 10 |
| BP | GO:0042476 | odontogenesis | 11/504 | 132/18670 | 0.000912724 | 0.000912724 | 0.039199094 | 11 |
| CC | GO:0030018 | Z disc | 11/534 | 132/19717 | 0.000939741 | 0.000939741 | 0.042139964 | 11 |
| BP | GO:0043010 | camera-type eye development | 19/504 | 314/18670 | 0.000943861 | 0.000943861 | 0.040090899 | 19 |
| BP | GO:0030323 | respiratory tube development | 13/504 | 176/18670 | 0.001010338 | 0.001010338 | 0.042213647 | 13 |
| BP | GO:0001658 | branching involved in ureteric bud morphogenesis | 7/504 | 59/18670 | 0.00101568 | 0.00101568 | 0.042213647 | 7 |
| BP | GO:0010977 | negative regulation of neuron projection development | 12/504 | 155/18670 | 0.001040041 | 0.001040041 | 0.042766303 | 12 |
| BP | GO:0010463 | mesenchymal cell proliferation | 6/504 | 44/18670 | 0.001110113 | 0.001110113 | 0.045167131 | 6 |
| BP | GO:0030595 | leukocyte chemotaxis | 15/504 | 224/18670 | 0.001170061 | 0.001170061 | 0.047110352 | 15 |
| BP | GO:0061333 | renal tubule morphogenesis | 8/504 | 78/18670 | 0.001194446 | 0.001194446 | 0.047463162 | 8 |
| CC | GO:0016327 | apicolateral plasma membrane | 4/534 | 18/19717 | 0.001203199 | 0.001203199 | 0.049049072 | 4 |
| BP | GO:0045666 | positive regulation of neuron differentiation | 21/504 | 371/18670 | 0.0012144 | 0.0012144 | 0.047463162 | 21 |
| BP | GO:0001649 | osteoblast differentiation | 15/504 | 225/18670 | 0.001223388 | 0.001223388 | 0.047463162 | 15 |
| BP | GO:0051591 | response to cAMP | 9/504 | 97/18670 | 0.001236313 | 0.001236313 | 0.047463162 | 9 |
| BP | GO:0032233 | positive regulation of actin filament bundle assembly | 7/504 | 61/18670 | 0.001240221 | 0.001240221 | 0.047463162 | 7 |
| BP | GO:0060562 | epithelial tube morphogenesis | 19/504 | 322/18670 | 0.001267326 | 0.001267326 | 0.048024967 | 19 |
| BP | GO:0003151 | outflow tract morphogenesis | 8/504 | 79/18670 | 0.001298296 | 0.001298296 | 0.048360947 | 8 |
| BP | GO:0010565 | regulation of cellular ketone metabolic process | 13/504 | 181/18670 | 0.001304828 | 0.001304828 | 0.048360947 | 13 |
| BP | GO:0032103 | positive regulation of response to external stimulus | 19/504 | 323/18670 | 0.001313727 | 0.001313727 | 0.048360947 | 19 |
| BP | GO:0050803 | regulation of synapse structure or activity | 15/504 | 227/18670 | 0.001336195 | 0.001336195 | 0.048724023 | 15 |
| CC | GO:0044306 | neuron projection terminus | 11/534 | 138/19717 | 0.001351656 | 0.001351656 | 0.050509236 | 11 |
| BP | GO:0007015 | actin filament organization | 22/504 | 400/18670 | 0.001356035 | 0.001356035 | 0.048985359 | 22 |
| BP | GO:0050679 | positive regulation of epithelial cell proliferation | 14/504 | 206/18670 | 0.001467324 | 0.001467324 | 0.052326112 | 14 |
| BP | GO:0001837 | epithelial to mesenchymal transition | 11/504 | 140/18670 | 0.001475591 | 0.001475591 | 0.052326112 | 11 |
| CC | GO:0043679 | axon terminus | 10/534 | 119/19717 | 0.001485335 | 0.001485335 | 0.051235053 | 10 |
| BP | GO:1902903 | regulation of supramolecular fiber organization | 20/504 | 352/18670 | 0.001504194 | 0.001504194 | 0.052647671 | 20 |
| BP | GO:0022612 | gland morphogenesis | 10/504 | 120/18670 | 0.001540989 | 0.001540989 | 0.052647671 | 10 |
| BP | GO:0045987 | positive regulation of smooth muscle contraction | 5/504 | 32/18670 | 0.001548921 | 0.001548921 | 0.052647671 | 5 |
| BP | GO:0048841 | regulation of axon extension involved in axon guidance | 5/504 | 32/18670 | 0.001548921 | 0.001548921 | 0.052647671 | 5 |
| BP | GO:0070169 | positive regulation of biomineral tissue development | 6/504 | 47/18670 | 0.001577467 | 0.001577467 | 0.052647671 | 6 |
| BP | GO:1900744 | regulation of p38MAPK cascade | 6/504 | 47/18670 | 0.001577467 | 0.001577467 | 0.052647671 | 6 |
| BP | GO:0016049 | cell growth | 25/504 | 484/18670 | 0.001580004 | 0.001580004 | 0.052647671 | 25 |
| BP | GO:0031589 | cell-substrate adhesion | 20/504 | 354/18670 | 0.001608563 | 0.001608563 | 0.053076972 | 20 |
| BP | GO:0060326 | cell chemotaxis | 18/504 | 304/18670 | 0.001620351 | 0.001620351 | 0.053076972 | 18 |
| CC | GO:0090575 | RNA polymerase II transcription factor complex | 12/534 | 163/19717 | 0.001652575 | 0.001652575 | 0.052932094 | 12 |
| BP | GO:0071229 | cellular response to acid chemical | 14/504 | 209/18670 | 0.001681241 | 0.001681241 | 0.05460872 | 14 |
| BP | GO:0050673 | epithelial cell proliferation | 23/504 | 434/18670 | 0.001727769 | 0.001727769 | 0.055247122 | 23 |
| BP | GO:0050808 | synapse organization | 22/504 | 408/18670 | 0.001739754 | 0.001739754 | 0.055247122 | 22 |
| BP | GO:0001667 | ameboidal-type cell migration | 24/504 | 461/18670 | 0.001753641 | 0.001753641 | 0.055247122 | 24 |
| BP | GO:0009612 | response to mechanical stimulus | 14/504 | 210/18670 | 0.001758068 | 0.001758068 | 0.055247122 | 14 |
| CC | GO:0031674 | I band | 11/534 | 143/19717 | 0.001798864 | 0.001798864 | 0.053776575 | 11 |
| BP | GO:0060039 | pericardium development | 4/504 | 20/18670 | 0.001802543 | 0.001802543 | 0.056187926 | 4 |
| BP | GO:0060560 | developmental growth involved in morphogenesis | 15/504 | 235/18670 | 0.001878705 | 0.001878705 | 0.057716537 | 15 |
| BP | GO:0003007 | heart morphogenesis | 16/504 | 259/18670 | 0.001881446 | 0.001881446 | 0.057716537 | 16 |
| BP | GO:0110053 | regulation of actin filament organization | 16/504 | 261/18670 | 0.002033782 | 0.002033782 | 0.060881355 | 16 |
| BP | GO:1990253 | cellular response to leucine starvation | 3/504 | 10/18670 | 0.002036821 | 0.002036821 | 0.060881355 | 3 |
| BP | GO:0031128 | developmental induction | 5/504 | 34/18670 | 0.002047616 | 0.002047616 | 0.060881355 | 5 |
| BP | GO:0048048 | embryonic eye morphogenesis | 5/504 | 34/18670 | 0.002047616 | 0.002047616 | 0.060881355 | 5 |
| BP | GO:0043405 | regulation of MAP kinase activity | 19/504 | 337/18670 | 0.002131517 | 0.002131517 | 0.062892165 | 19 |
| BP | GO:0072111 | cell proliferation involved in kidney development | 4/504 | 21/18670 | 0.002179643 | 0.002179643 | 0.062914977 | 4 |
| BP | GO:1900273 | positive regulation of long-term synaptic potentiation | 4/504 | 21/18670 | 0.002179643 | 0.002179643 | 0.062914977 | 4 |
| BP | GO:0014009 | glial cell proliferation | 6/504 | 50/18670 | 0.002181121 | 0.002181121 | 0.062914977 | 6 |
| BP | GO:0071496 | cellular response to external stimulus | 19/504 | 339/18670 | 0.002277575 | 0.002277575 | 0.064758331 | 19 |
| BP | GO:0008643 | carbohydrate transport | 11/504 | 148/18670 | 0.002295696 | 0.002295696 | 0.064758331 | 11 |
| BP | GO:0021510 | spinal cord development | 9/504 | 106/18670 | 0.002297077 | 0.002297077 | 0.064758331 | 9 |
| BP | GO:0007219 | Notch signaling pathway | 13/504 | 193/18670 | 0.002312042 | 0.002312042 | 0.064758331 | 13 |
| MF | GO:0001158 | enhancer sequence-specific DNA binding | 10/510 | 119/17697 | 0.002330136 | 0.002330136 | 0.131439646 | 10 |
| BP | GO:0031667 | response to nutrient levels | 25/504 | 499/18670 | 0.002379508 | 0.002379508 | 0.065414412 | 25 |
| BP | GO:0050920 | regulation of chemotaxis | 14/504 | 217/18670 | 0.002381707 | 0.002381707 | 0.065414412 | 14 |
| BP | GO:0048146 | positive regulation of fibroblast proliferation | 6/504 | 51/18670 | 0.002416625 | 0.002416625 | 0.065414412 | 6 |
| BP | GO:0048592 | eye morphogenesis | 11/504 | 149/18670 | 0.002420084 | 0.002420084 | 0.065414412 | 11 |
| BP | GO:2000058 | regulation of ubiquitin-dependent protein catabolic process | 11/504 | 149/18670 | 0.002420084 | 0.002420084 | 0.065414412 | 11 |
| CC | GO:0044420 | extracellular matrix component | 6/534 | 51/19717 | 0.002458545 | 0.002458545 | 0.068903972 | 6 |
| BP | GO:0032874 | positive regulation of stress-activated MAPK cascade | 12/504 | 172/18670 | 0.002515775 | 0.002515775 | 0.067340431 | 12 |
| BP | GO:0030198 | extracellular matrix organization | 20/504 | 368/18670 | 0.002526183 | 0.002526183 | 0.067340431 | 20 |
| BP | GO:0007265 | Ras protein signal transduction | 23/504 | 448/18670 | 0.002582661 | 0.002582661 | 0.068235306 | 23 |
| BP | GO:0072330 | monocarboxylic acid biosynthetic process | 19/504 | 343/18670 | 0.00259506 | 0.00259506 | 0.068235306 | 19 |
| BP | GO:0070304 | positive regulation of stress-activated protein kinase signaling cascade | 12/504 | 173/18670 | 0.002639038 | 0.002639038 | 0.068922804 | 12 |
| BP | GO:0055088 | lipid homeostasis | 11/504 | 151/18670 | 0.002685227 | 0.002685227 | 0.069658452 | 11 |
| MF | GO:0000979 | RNA polymerase II core promoter sequence-specific DNA binding | 5/510 | 34/17697 | 0.002717839 | 0.002717839 | 0.131439646 | 5 |
| MF | GO:0005201 | extracellular matrix structural constituent | 12/510 | 163/17697 | 0.002741195 | 0.002741195 | 0.131439646 | 12 |
| BP | GO:0000185 | activation of MAPKKK activity | 3/504 | 11/18670 | 0.002744786 | 0.002744786 | 0.069798172 | 3 |
| BP | GO:0061307 | cardiac neural crest cell differentiation involved in heart development | 3/504 | 11/18670 | 0.002744786 | 0.002744786 | 0.069798172 | 3 |
| BP | GO:0061308 | cardiac neural crest cell development involved in heart development | 3/504 | 11/18670 | 0.002744786 | 0.002744786 | 0.069798172 | 3 |
| BP | GO:0060395 | SMAD protein signal transduction | 7/504 | 70/18670 | 0.002769434 | 0.002769434 | 0.069964645 | 7 |
| MF | GO:0005179 | hormone activity | 10/510 | 122/17697 | 0.002797036 | 0.002797036 | 0.131439646 | 10 |
| BP | GO:0045927 | positive regulation of growth | 16/504 | 270/18670 | 0.0028528 | 0.0028528 | 0.071602757 | 16 |
| BP | GO:0060541 | respiratory system development | 13/504 | 198/18670 | 0.002887646 | 0.002887646 | 0.072009749 | 13 |
| BP | GO:0060563 | neuroepithelial cell differentiation | 6/504 | 53/18670 | 0.002944377 | 0.002944377 | 0.072953799 | 6 |
| BP | GO:0010717 | regulation of epithelial to mesenchymal transition | 8/504 | 90/18670 | 0.002983884 | 0.002983884 | 0.07297861 | 8 |
| BP | GO:0003156 | regulation of animal organ formation | 5/504 | 37/18670 | 0.00300202 | 0.00300202 | 0.07297861 | 5 |
| BP | GO:0031076 | embryonic camera-type eye development | 5/504 | 37/18670 | 0.00300202 | 0.00300202 | 0.07297861 | 5 |
| BP | GO:0045598 | regulation of fat cell differentiation | 10/504 | 132/18670 | 0.003114874 | 0.003114874 | 0.075248791 | 10 |
| BP | GO:0042180 | cellular ketone metabolic process | 15/504 | 248/18670 | 0.003145297 | 0.003145297 | 0.075511795 | 15 |
| BP | GO:0006636 | unsaturated fatty acid biosynthetic process | 6/504 | 54/18670 | 0.003238431 | 0.003238431 | 0.077267831 | 6 |
| CC | GO:0030016 | myofibril | 14/534 | 224/19717 | 0.003281806 | 0.003281806 | 0.081805408 | 14 |
| MF | GO:0015250 | water channel activity | 3/510 | 11/17697 | 0.003303043 | 0.003303043 | 0.144870297 | 3 |
| CC | GO:0044798 | nuclear transcription factor complex | 13/534 | 201/19717 | 0.003387556 | 0.003387556 | 0.081805408 | 13 |
| BP | GO:0048608 | reproductive structure development | 22/504 | 431/18670 | 0.003395046 | 0.003395046 | 0.077888177 | 22 |
| BP | GO:0050678 | regulation of epithelial cell proliferation | 20/504 | 378/18670 | 0.003423125 | 0.003423125 | 0.077888177 | 20 |
| BP | GO:0007259 | JAK-STAT cascade | 11/504 | 156/18670 | 0.003451652 | 0.003451652 | 0.077888177 | 11 |
| BP | GO:0030856 | regulation of epithelial cell differentiation | 11/504 | 156/18670 | 0.003451652 | 0.003451652 | 0.077888177 | 11 |
| BP | GO:0046683 | response to organophosphorus | 10/504 | 134/18670 | 0.003471072 | 0.003471072 | 0.077888177 | 10 |
| BP | GO:0008361 | regulation of cell size | 12/504 | 179/18670 | 0.003485829 | 0.003485829 | 0.077888177 | 12 |
| BP | GO:0051090 | regulation of DNA-binding transcription factor activity | 22/504 | 432/18670 | 0.003489858 | 0.003489858 | 0.077888177 | 22 |
| BP | GO:0010769 | regulation of cell morphogenesis involved in differentiation | 17/504 | 301/18670 | 0.003506906 | 0.003506906 | 0.077888177 | 17 |
| BP | GO:0043200 | response to amino acid | 9/504 | 113/18670 | 0.003541552 | 0.003541552 | 0.077888177 | 9 |
| BP | GO:0003207 | cardiac chamber formation | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0019755 | one-carbon compound transport | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0030950 | establishment or maintenance of actin cytoskeleton polarity | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0046541 | saliva secretion | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0060394 | negative regulation of pathway-restricted SMAD protein phosphorylation | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0071472 | cellular response to salt stress | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| BP | GO:0098962 | regulation of postsynaptic neurotransmitter receptor activity | 3/504 | 12/18670 | 0.003586844 | 0.003586844 | 0.077888177 | 3 |
| CC | GO:0005911 | cell-cell junction | 23/534 | 459/19717 | 0.003648079 | 0.003648079 | 0.081805408 | 23 |
| CC | GO:0097060 | synaptic membrane | 22/534 | 432/19717 | 0.003648598 | 0.003648598 | 0.081805408 | 22 |
| BP | GO:0001889 | liver development | 10/504 | 135/18670 | 0.003660906 | 0.003660906 | 0.079052324 | 10 |
| BP | GO:0061458 | reproductive system development | 22/504 | 434/18670 | 0.003686154 | 0.003686154 | 0.079155302 | 22 |
| MF | GO:0005126 | cytokine receptor binding | 17/510 | 286/17697 | 0.004014121 | 0.004014121 | 0.165054322 | 17 |
| BP | GO:0021536 | diencephalon development | 7/504 | 75/18670 | 0.004087786 | 0.004087786 | 0.086815207 | 7 |
| BP | GO:0032482 | Rab protein signal transduction | 7/504 | 75/18670 | 0.004087786 | 0.004087786 | 0.086815207 | 7 |
| CC | GO:0098793 | presynapse | 24/534 | 491/19717 | 0.004117282 | 0.004117282 | 0.087917905 | 24 |
| BP | GO:0001666 | response to hypoxia | 19/504 | 359/18670 | 0.004260448 | 0.004260448 | 0.089607602 | 19 |
| BP | GO:0061008 | hepaticobiliary system development | 10/504 | 138/18670 | 0.004280205 | 0.004280205 | 0.089607602 | 10 |
| BP | GO:0032147 | activation of protein kinase activity | 18/504 | 333/18670 | 0.004288817 | 0.004288817 | 0.089607602 | 18 |
| MF | GO:0005372 | water transmembrane transporter activity | 3/510 | 12/17697 | 0.004310507 | 0.004310507 | 0.166815269 | 3 |
| BP | GO:0060411 | cardiac septum morphogenesis | 7/504 | 76/18670 | 0.004400369 | 0.004400369 | 0.091443991 | 7 |
| BP | GO:0030516 | regulation of axon extension | 8/504 | 96/18670 | 0.004439216 | 0.004439216 | 0.091757957 | 8 |
| BP | GO:0001886 | endothelial cell morphogenesis | 3/504 | 13/18670 | 0.00457018 | 0.00457018 | 0.093465333 | 3 |
| BP | GO:0043568 | positive regulation of insulin-like growth factor receptor signaling pathway | 3/504 | 13/18670 | 0.00457018 | 0.00457018 | 0.093465333 | 3 |
| BP | GO:0001654 | eye development | 19/504 | 362/18670 | 0.004654663 | 0.004654663 | 0.094692084 | 19 |
| BP | GO:0030099 | myeloid cell differentiation | 21/504 | 416/18670 | 0.004711281 | 0.004711281 | 0.094869268 | 21 |
| BP | GO:1990266 | neutrophil migration | 9/504 | 118/18670 | 0.004715962 | 0.004715962 | 0.094869268 | 9 |
| BP | GO:0046330 | positive regulation of JNK cascade | 10/504 | 140/18670 | 0.004737004 | 0.004737004 | 0.094869268 | 10 |
| BP | GO:0043567 | regulation of insulin-like growth factor receptor signaling pathway | 4/504 | 26/18670 | 0.004894908 | 0.004894908 | 0.097026194 | 4 |
| BP | GO:0060706 | cell differentiation involved in embryonic placenta development | 4/504 | 26/18670 | 0.004894908 | 0.004894908 | 0.097026194 | 4 |
| BP | GO:0006633 | fatty acid biosynthetic process | 11/504 | 164/18670 | 0.005033392 | 0.005033392 | 0.099156006 | 11 |
| BP | GO:0007389 | pattern specification process | 22/504 | 446/18670 | 0.005067987 | 0.005067987 | 0.099156006 | 22 |
| BP | GO:0008306 | associative learning | 7/504 | 78/18670 | 0.005079315 | 0.005079315 | 0.099156006 | 7 |
| BP | GO:0050769 | positive regulation of neurogenesis | 23/504 | 474/18670 | 0.005128023 | 0.005128023 | 0.099603809 | 23 |
| BP | GO:0031345 | negative regulation of cell projection organization | 12/504 | 188/18670 | 0.005154385 | 0.005154385 | 0.099615271 | 12 |
| MF | GO:0035326 | enhancer binding | 10/510 | 133/17697 | 0.005182567 | 0.005182567 | 0.189421296 | 10 |
| BP | GO:0150063 | visual system development | 19/504 | 366/18670 | 0.005226644 | 0.005226644 | 0.100203089 | 19 |
| BP | GO:0030517 | negative regulation of axon extension | 5/504 | 42/18670 | 0.005247749 | 0.005247749 | 0.100203089 | 5 |
| BP | GO:0072089 | stem cell proliferation | 9/504 | 120/18670 | 0.005262572 | 0.005262572 | 0.100203089 | 9 |
| BP | GO:0097696 | STAT cascade | 11/504 | 166/18670 | 0.005506865 | 0.005506865 | 0.104340605 | 11 |
| BP | GO:0048675 | axon extension | 9/504 | 121/18670 | 0.005553648 | 0.005553648 | 0.104713713 | 9 |
| BP | GO:0042063 | gliogenesis | 16/504 | 290/18670 | 0.005672678 | 0.005672678 | 0.106438809 | 16 |
| BP | GO:0006979 | response to oxidative stress | 22/504 | 451/18670 | 0.005758624 | 0.005758624 | 0.106787251 | 22 |
| BP | GO:0032956 | regulation of actin cytoskeleton organization | 18/504 | 343/18670 | 0.005797635 | 0.005797635 | 0.106787251 | 18 |
| BP | GO:0001935 | endothelial cell proliferation | 12/504 | 191/18670 | 0.005833904 | 0.005833904 | 0.106787251 | 12 |
| BP | GO:0032535 | regulation of cellular component size | 19/504 | 370/18670 | 0.005855185 | 0.005855185 | 0.106787251 | 19 |
| BP | GO:0036293 | response to decreased oxygen levels | 19/504 | 370/18670 | 0.005855185 | 0.005855185 | 0.106787251 | 19 |
| BP | GO:0032434 | regulation of proteasomal ubiquitin-dependent protein catabolic process | 9/504 | 122/18670 | 0.005857013 | 0.005857013 | 0.106787251 | 9 |
| BP | GO:0048880 | sensory system development | 19/504 | 371/18670 | 0.006021627 | 0.006021627 | 0.109273115 | 19 |
| BP | GO:0048839 | inner ear development | 12/504 | 192/18670 | 0.006075558 | 0.006075558 | 0.109736586 | 12 |
| BP | GO:0071621 | granulocyte chemotaxis | 9/504 | 123/18670 | 0.006173003 | 0.006173003 | 0.11097805 | 9 |
| BP | GO:0033238 | regulation of cellular amine metabolic process | 7/504 | 81/18670 | 0.006241472 | 0.006241472 | 0.11107067 | 7 |
| BP | GO:0055123 | digestive system development | 10/504 | 146/18670 | 0.006340425 | 0.006340425 | 0.11107067 | 10 |
| BP | GO:0038084 | vascular endothelial growth factor signaling pathway | 5/504 | 44/18670 | 0.006411641 | 0.006411641 | 0.11107067 | 5 |
| BP | GO:1902667 | regulation of axon guidance | 5/504 | 44/18670 | 0.006411641 | 0.006411641 | 0.11107067 | 5 |
| BP | GO:0001516 | prostaglandin biosynthetic process | 4/504 | 28/18670 | 0.006425456 | 0.006425456 | 0.11107067 | 4 |
| BP | GO:0046457 | prostanoid biosynthetic process | 4/504 | 28/18670 | 0.006425456 | 0.006425456 | 0.11107067 | 4 |
| BP | GO:0060512 | prostate gland morphogenesis | 4/504 | 28/18670 | 0.006425456 | 0.006425456 | 0.11107067 | 4 |
| BP | GO:0085029 | extracellular matrix assembly | 4/504 | 28/18670 | 0.006425456 | 0.006425456 | 0.11107067 | 4 |
| BP | GO:0006521 | regulation of cellular amino acid metabolic process | 6/504 | 62/18670 | 0.006436775 | 0.006436775 | 0.11107067 | 6 |
| BP | GO:0048638 | regulation of developmental growth | 18/504 | 347/18670 | 0.006511366 | 0.006511366 | 0.111858409 | 18 |
| BP | GO:0061351 | neural precursor cell proliferation | 10/504 | 147/18670 | 0.006644358 | 0.006644358 | 0.11363802 | 10 |
| BP | GO:0009952 | anterior/posterior pattern specification | 13/504 | 219/18670 | 0.006712653 | 0.006712653 | 0.113798997 | 13 |
| BP | GO:0043583 | ear development | 13/504 | 219/18670 | 0.006712653 | 0.006712653 | 0.113798997 | 13 |
| BP | GO:0007178 | transmembrane receptor protein serine/threonine kinase signaling pathway | 18/504 | 349/18670 | 0.006894134 | 0.006894134 | 0.115574285 | 18 |
| BP | GO:0060253 | negative regulation of glial cell proliferation | 3/504 | 15/18670 | 0.006985069 | 0.006985069 | 0.115574285 | 3 |
| BP | GO:0060841 | venous blood vessel development | 3/504 | 15/18670 | 0.006985069 | 0.006985069 | 0.115574285 | 3 |
| BP | GO:0070365 | hepatocyte differentiation | 3/504 | 15/18670 | 0.006985069 | 0.006985069 | 0.115574285 | 3 |
| BP | GO:0071474 | cellular hyperosmotic response | 3/504 | 15/18670 | 0.006985069 | 0.006985069 | 0.115574285 | 3 |
| BP | GO:0014014 | negative regulation of gliogenesis | 5/504 | 45/18670 | 0.007056578 | 0.007056578 | 0.115574285 | 5 |
| BP | GO:0048483 | autonomic nervous system development | 5/504 | 45/18670 | 0.007056578 | 0.007056578 | 0.115574285 | 5 |
| BP | GO:1900271 | regulation of long-term synaptic potentiation | 5/504 | 45/18670 | 0.007056578 | 0.007056578 | 0.115574285 | 5 |
| BP | GO:0006970 | response to osmotic stress | 7/504 | 83/18670 | 0.00711934 | 0.00711934 | 0.115622361 | 7 |
| BP | GO:0042509 | regulation of tyrosine phosphorylation of STAT protein | 7/504 | 83/18670 | 0.00711934 | 0.00711934 | 0.115622361 | 7 |
| BP | GO:1903829 | positive regulation of cellular protein localization | 17/504 | 324/18670 | 0.007226099 | 0.007226099 | 0.116865157 | 17 |
| BP | GO:0045600 | positive regulation of fat cell differentiation | 6/504 | 64/18670 | 0.007505385 | 0.007505385 | 0.120726055 | 6 |
| BP | GO:0018105 | peptidyl-serine phosphorylation | 16/504 | 299/18670 | 0.007527296 | 0.007527296 | 0.120726055 | 16 |
| BP | GO:0051963 | regulation of synapse assembly | 8/504 | 106/18670 | 0.008006267 | 0.008006267 | 0.127797942 | 8 |
| BP | GO:0006940 | regulation of smooth muscle contraction | 6/504 | 65/18670 | 0.008085124 | 0.008085124 | 0.127797942 | 6 |
| BP | GO:0050772 | positive regulation of axonogenesis | 7/504 | 85/18670 | 0.008085519 | 0.008085519 | 0.127797942 | 7 |
| BP | GO:0099177 | regulation of trans-synaptic signaling | 21/504 | 437/18670 | 0.008100482 | 0.008100482 | 0.127797942 | 21 |
| BP | GO:0071480 | cellular response to gamma radiation | 4/504 | 30/18670 | 0.008243726 | 0.008243726 | 0.12952915 | 4 |
| BP | GO:0003206 | cardiac chamber morphogenesis | 9/504 | 129/18670 | 0.008353067 | 0.008353067 | 0.130715802 | 9 |
| BP | GO:0030952 | establishment or maintenance of cytoskeleton polarity | 3/504 | 16/18670 | 0.008426788 | 0.008426788 | 0.130810252 | 3 |
| BP | GO:0061548 | ganglion development | 3/504 | 16/18670 | 0.008426788 | 0.008426788 | 0.130810252 | 3 |
| BP | GO:0021537 | telencephalon development | 14/504 | 251/18670 | 0.008513953 | 0.008513953 | 0.131634672 | 14 |
| BP | GO:0007260 | tyrosine phosphorylation of STAT protein | 7/504 | 86/18670 | 0.008603286 | 0.008603286 | 0.13248591 | 7 |
| BP | GO:0051017 | actin filament bundle assembly | 10/504 | 153/18670 | 0.008712298 | 0.008712298 | 0.133632247 | 10 |
| BP | GO:0032526 | response to retinoic acid | 8/504 | 108/18670 | 0.008922906 | 0.008922906 | 0.136321654 | 8 |
| BP | GO:0002690 | positive regulation of leukocyte chemotaxis | 7/504 | 87/18670 | 0.009145 | 0.009145 | 0.138664568 | 7 |
| BP | GO:0030850 | prostate gland development | 5/504 | 48/18670 | 0.009260844 | 0.009260844 | 0.138664568 | 5 |
| BP | GO:0045933 | positive regulation of muscle contraction | 5/504 | 48/18670 | 0.009260844 | 0.009260844 | 0.138664568 | 5 |
| BP | GO:0010719 | negative regulation of epithelial to mesenchymal transition | 4/504 | 31/18670 | 0.009267068 | 0.009267068 | 0.138664568 | 4 |
| BP | GO:1902895 | positive regulation of pri-miRNA transcription by RNA polymerase II | 4/504 | 31/18670 | 0.009267068 | 0.009267068 | 0.138664568 | 4 |
| BP | GO:0007266 | Rho protein signal transduction | 12/504 | 203/18670 | 0.009291508 | 0.009291508 | 0.138664568 | 12 |
| BP | GO:1902905 | positive regulation of supramolecular fiber organization | 12/504 | 204/18670 | 0.009639255 | 0.009639255 | 0.143300984 | 12 |
| BP | GO:0006939 | smooth muscle contraction | 8/504 | 110/18670 | 0.009915734 | 0.009915734 | 0.144661997 | 8 |
| BP | GO:0035924 | cellular response to vascular endothelial growth factor stimulus | 6/504 | 68/18670 | 0.010016925 | 0.010016925 | 0.144661997 | 6 |
| BP | GO:0051965 | positive regulation of synapse assembly | 6/504 | 68/18670 | 0.010016925 | 0.010016925 | 0.144661997 | 6 |
| BP | GO:0090596 | sensory organ morphogenesis | 14/504 | 256/18670 | 0.010020267 | 0.010020267 | 0.144661997 | 14 |
| BP | GO:0010224 | response to UV-B | 3/504 | 17/18670 | 0.010030214 | 0.010030214 | 0.144661997 | 3 |
| BP | GO:0021514 | ventral spinal cord interneuron differentiation | 3/504 | 17/18670 | 0.010030214 | 0.010030214 | 0.144661997 | 3 |
| BP | GO:0048521 | negative regulation of behavior | 3/504 | 17/18670 | 0.010030214 | 0.010030214 | 0.144661997 | 3 |
| BP | GO:1905331 | negative regulation of morphogenesis of an epithelium | 3/504 | 17/18670 | 0.010030214 | 0.010030214 | 0.144661997 | 3 |
| BP | GO:0030509 | BMP signaling pathway | 10/504 | 157/18670 | 0.010343538 | 0.010343538 | 0.148075909 | 10 |
| BP | GO:0061572 | actin filament bundle organization | 10/504 | 157/18670 | 0.010343538 | 0.010343538 | 0.148075909 | 10 |
| BP | GO:0048565 | digestive tract development | 9/504 | 134/18670 | 0.01057969 | 0.01057969 | 0.150683143 | 9 |
| BP | GO:0021700 | developmental maturation | 15/504 | 284/18670 | 0.010603629 | 0.010603629 | 0.150683143 | 15 |
| BP | GO:0043406 | positive regulation of MAP kinase activity | 14/504 | 258/18670 | 0.010678332 | 0.010678332 | 0.151188875 | 14 |
| BP | GO:0050771 | negative regulation of axonogenesis | 6/504 | 69/18670 | 0.010728013 | 0.010728013 | 0.151337937 | 6 |
| BP | GO:0003279 | cardiac septum development | 8/504 | 112/18670 | 0.010988376 | 0.010988376 | 0.153969409 | 8 |
| BP | GO:0070482 | response to oxygen levels | 19/504 | 394/18670 | 0.011049363 | 0.011049363 | 0.153969409 | 19 |
| BP | GO:0050921 | positive regulation of chemotaxis | 9/504 | 135/18670 | 0.011073889 | 0.011073889 | 0.153969409 | 9 |
| BP | GO:0060359 | response to ammonium ion | 9/504 | 135/18670 | 0.011073889 | 0.011073889 | 0.153969409 | 9 |
| BP | GO:0048588 | developmental cell growth | 13/504 | 234/18670 | 0.011344071 | 0.011344071 | 0.157160646 | 13 |
| BP | GO:0048639 | positive regulation of developmental growth | 11/504 | 184/18670 | 0.011524399 | 0.011524399 | 0.159088691 | 11 |
| BP | GO:0072574 | hepatocyte proliferation | 3/504 | 18/18670 | 0.011798621 | 0.011798621 | 0.16171906 | 3 |
| BP | GO:0072575 | epithelial cell proliferation involved in liver morphogenesis | 3/504 | 18/18670 | 0.011798621 | 0.011798621 | 0.16171906 | 3 |
| BP | GO:0051496 | positive regulation of stress fiber assembly | 5/504 | 51/18670 | 0.011898475 | 0.011898475 | 0.16245315 | 5 |
| BP | GO:0048562 | embryonic organ morphogenesis | 15/504 | 288/18670 | 0.011936236 | 0.011936236 | 0.16245315 | 15 |
| BP | GO:0046425 | regulation of JAK-STAT cascade | 9/504 | 137/18670 | 0.012113936 | 0.012113936 | 0.164130853 | 9 |
| BP | GO:0002688 | regulation of leukocyte chemotaxis | 8/504 | 114/18670 | 0.012144432 | 0.012144432 | 0.164130853 | 8 |
| BP | GO:0042531 | positive regulation of tyrosine phosphorylation of STAT protein | 6/504 | 71/18670 | 0.012256127 | 0.012256127 | 0.165063266 | 6 |
| BP | GO:0034330 | cell junction organization | 15/504 | 290/18670 | 0.012649923 | 0.012649923 | 0.168308745 | 15 |
| BP | GO:0048871 | multicellular organismal homeostasis | 22/504 | 485/18670 | 0.012792846 | 0.012792846 | 0.168308745 | 22 |
| BP | GO:0003382 | epithelial cell morphogenesis | 4/504 | 34/18670 | 0.012821149 | 0.012821149 | 0.168308745 | 4 |
| BP | GO:0048566 | embryonic digestive tract development | 4/504 | 34/18670 | 0.012821149 | 0.012821149 | 0.168308745 | 4 |
| BP | GO:0070884 | regulation of calcineurin-NFAT signaling cascade | 4/504 | 34/18670 | 0.012821149 | 0.012821149 | 0.168308745 | 4 |
| BP | GO:0106056 | regulation of calcineurin-mediated signaling | 4/504 | 34/18670 | 0.012821149 | 0.012821149 | 0.168308745 | 4 |
| BP | GO:0072132 | mesenchyme morphogenesis | 5/504 | 52/18670 | 0.012880148 | 0.012880148 | 0.168308745 | 5 |
| BP | GO:0048167 | regulation of synaptic plasticity | 11/504 | 187/18670 | 0.012887699 | 0.012887699 | 0.168308745 | 11 |
| BP | GO:0032092 | positive regulation of protein binding | 7/504 | 93/18670 | 0.012932547 | 0.012932547 | 0.168308745 | 7 |
| BP | GO:0033273 | response to vitamin | 7/504 | 93/18670 | 0.012932547 | 0.012932547 | 0.168308745 | 7 |
| BP | GO:0051098 | regulation of binding | 18/504 | 373/18670 | 0.013074644 | 0.013074644 | 0.169022423 | 18 |
| BP | GO:0035019 | somatic stem cell population maintenance | 6/504 | 72/18670 | 0.013074842 | 0.013074842 | 0.169022423 | 6 |
| BP | GO:0031214 | biomineral tissue development | 10/504 | 163/18670 | 0.013213264 | 0.013213264 | 0.169829537 | 10 |
| BP | GO:0007586 | digestion | 9/504 | 139/18670 | 0.013225151 | 0.013225151 | 0.169829537 | 9 |
| BP | GO:0007254 | JNK cascade | 12/504 | 214/18670 | 0.013699066 | 0.013699066 | 0.171805839 | 12 |
| BP | GO:0002313 | mature B cell differentiation involved in immune response | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0006833 | water transport | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0015669 | gas transport | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0060004 | reflex | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0060973 | cell migration involved in heart development | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0072576 | liver morphogenesis | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:2000696 | regulation of epithelial cell differentiation involved in kidney development | 3/504 | 19/18670 | 0.013734642 | 0.013734642 | 0.171805839 | 3 |
| BP | GO:0060251 | regulation of glial cell proliferation | 4/504 | 35/18670 | 0.014173986 | 0.014173986 | 0.176656662 | 4 |
| BP | GO:0042593 | glucose homeostasis | 13/504 | 241/18670 | 0.014213837 | 0.014213837 | 0.176656662 | 13 |
| BP | GO:0046394 | carboxylic acid biosynthetic process | 21/504 | 462/18670 | 0.014478437 | 0.014478437 | 0.178753105 | 21 |
| BP | GO:0031668 | cellular response to extracellular stimulus | 14/504 | 268/18670 | 0.014491058 | 0.014491058 | 0.178753105 | 14 |
| BP | GO:0018209 | peptidyl-serine modification | 16/504 | 322/18670 | 0.014521256 | 0.014521256 | 0.178753105 | 16 |
| BP | GO:0033500 | carbohydrate homeostasis | 13/504 | 242/18670 | 0.014665485 | 0.014665485 | 0.179955424 | 13 |
| BP | GO:0016053 | organic acid biosynthetic process | 21/504 | 463/18670 | 0.014798704 | 0.014798704 | 0.181015463 | 21 |
| BP | GO:0042594 | response to starvation | 11/504 | 191/18670 | 0.014891766 | 0.014891766 | 0.181579159 | 11 |
| BP | GO:0021515 | cell differentiation in spinal cord | 5/504 | 54/18670 | 0.015004583 | 0.015004583 | 0.181807712 | 5 |
| BP | GO:0043392 | negative regulation of DNA binding | 5/504 | 54/18670 | 0.015004583 | 0.015004583 | 0.181807712 | 5 |
| BP | GO:0003002 | regionalization | 17/504 | 351/18670 | 0.015095575 | 0.015095575 | 0.182312762 | 17 |
| BP | GO:0043393 | regulation of protein binding | 12/504 | 217/18670 | 0.015140598 | 0.015140598 | 0.182312762 | 12 |
| BP | GO:0032755 | positive regulation of interleukin-6 production | 7/504 | 96/18670 | 0.015198735 | 0.015198735 | 0.182444446 | 7 |
| BP | GO:0050804 | modulation of chemical synaptic transmission | 20/504 | 436/18670 | 0.015330685 | 0.015330685 | 0.183311481 | 20 |
| BP | GO:0045165 | cell fate commitment | 14/504 | 270/18670 | 0.015365815 | 0.015365815 | 0.183311481 | 14 |
| BP | GO:0050731 | positive regulation of peptidyl-tyrosine phosphorylation | 11/504 | 192/18670 | 0.015427557 | 0.015427557 | 0.183481752 | 11 |
| BP | GO:0045655 | regulation of monocyte differentiation | 3/504 | 20/18670 | 0.015840306 | 0.015840306 | 0.185781787 | 3 |
| BP | GO:1900017 | positive regulation of cytokine production involved in inflammatory response | 3/504 | 20/18670 | 0.015840306 | 0.015840306 | 0.185781787 | 3 |
| BP | GO:0042176 | regulation of protein catabolic process | 18/504 | 381/18670 | 0.01590388 | 0.01590388 | 0.185781787 | 18 |
| BP | GO:0010771 | negative regulation of cell morphogenesis involved in differentiation | 7/504 | 97/18670 | 0.016013194 | 0.016013194 | 0.185781787 | 7 |
| BP | GO:0030316 | osteoclast differentiation | 7/504 | 97/18670 | 0.016013194 | 0.016013194 | 0.185781787 | 7 |
| BP | GO:0032231 | regulation of actin filament bundle assembly | 7/504 | 97/18670 | 0.016013194 | 0.016013194 | 0.185781787 | 7 |
| BP | GO:0050806 | positive regulation of synaptic transmission | 10/504 | 168/18670 | 0.016030189 | 0.016030189 | 0.185781787 | 10 |
| BP | GO:1990138 | neuron projection extension | 10/504 | 168/18670 | 0.016030189 | 0.016030189 | 0.185781787 | 10 |
| BP | GO:0042304 | regulation of fatty acid biosynthetic process | 5/504 | 55/18670 | 0.016149659 | 0.016149659 | 0.185781787 | 5 |
| BP | GO:0048016 | inositol phosphate-mediated signaling | 5/504 | 55/18670 | 0.016149659 | 0.016149659 | 0.185781787 | 5 |
| BP | GO:2000242 | negative regulation of reproductive process | 5/504 | 55/18670 | 0.016149659 | 0.016149659 | 0.185781787 | 5 |
| BP | GO:0030307 | positive regulation of cell growth | 10/504 | 169/18670 | 0.01664327 | 0.01664327 | 0.190756657 | 10 |
| BP | GO:0031346 | positive regulation of cell projection organization | 18/504 | 383/18670 | 0.016680818 | 0.016680818 | 0.190756657 | 18 |
| BP | GO:0030038 | contractile actin filament bundle assembly | 7/504 | 98/18670 | 0.016858123 | 0.016858123 | 0.191088215 | 7 |
| BP | GO:0043149 | stress fiber assembly | 7/504 | 98/18670 | 0.016858123 | 0.016858123 | 0.191088215 | 7 |
| BP | GO:0050848 | regulation of calcium-mediated signaling | 7/504 | 98/18670 | 0.016858123 | 0.016858123 | 0.191088215 | 7 |
| BP | GO:0032941 | secretion by tissue | 4/504 | 37/18670 | 0.017142668 | 0.017142668 | 0.192618959 | 4 |
| BP | GO:0033280 | response to vitamin D | 4/504 | 37/18670 | 0.017142668 | 0.017142668 | 0.192618959 | 4 |
| BP | GO:0071276 | cellular response to cadmium ion | 4/504 | 37/18670 | 0.017142668 | 0.017142668 | 0.192618959 | 4 |
| BP | GO:0071772 | response to BMP | 10/504 | 170/18670 | 0.017273546 | 0.017273546 | 0.192967631 | 10 |
| BP | GO:0071773 | cellular response to BMP stimulus | 10/504 | 170/18670 | 0.017273546 | 0.017273546 | 0.192967631 | 10 |
| BP | GO:0010332 | response to gamma radiation | 5/504 | 56/18670 | 0.017351442 | 0.017351442 | 0.193279218 | 5 |
| BP | GO:1904892 | regulation of STAT cascade | 9/504 | 146/18670 | 0.017714277 | 0.017714277 | 0.19599474 | 9 |
| BP | GO:0001708 | cell fate specification | 7/504 | 99/18670 | 0.01773407 | 0.01773407 | 0.19599474 | 7 |
| BP | GO:0048678 | response to axon injury | 6/504 | 77/18670 | 0.017747345 | 0.017747345 | 0.19599474 | 6 |
| BP | GO:0003205 | cardiac chamber development | 10/504 | 171/18670 | 0.017921283 | 0.017921283 | 0.196968625 | 10 |
| BP | GO:0009713 | catechol-containing compound biosynthetic process | 3/504 | 21/18670 | 0.018117083 | 0.018117083 | 0.196968625 | 3 |
| BP | GO:0042423 | catecholamine biosynthetic process | 3/504 | 21/18670 | 0.018117083 | 0.018117083 | 0.196968625 | 3 |
| BP | GO:0048245 | eosinophil chemotaxis | 3/504 | 21/18670 | 0.018117083 | 0.018117083 | 0.196968625 | 3 |
| BP | GO:2000738 | positive regulation of stem cell differentiation | 3/504 | 21/18670 | 0.018117083 | 0.018117083 | 0.196968625 | 3 |
| BP | GO:0071560 | cellular response to transforming growth factor beta stimulus | 13/504 | 249/18670 | 0.018141282 | 0.018141282 | 0.196968625 | 13 |
| BP | GO:0045444 | fat cell differentiation | 12/504 | 223/18670 | 0.018365468 | 0.018365468 | 0.198844161 | 12 |
| BP | GO:0021543 | pallium development | 10/504 | 172/18670 | 0.018586748 | 0.018586748 | 0.19977588 | 10 |
| BP | GO:0022600 | digestive system process | 7/504 | 100/18670 | 0.018641575 | 0.018641575 | 0.19977588 | 7 |
| BP | GO:0032970 | regulation of actin filament-based process | 18/504 | 388/18670 | 0.018752553 | 0.018752553 | 0.19977588 | 18 |
| BP | GO:0048009 | insulin-like growth factor receptor signaling pathway | 4/504 | 38/18670 | 0.018761632 | 0.018761632 | 0.19977588 | 4 |
| BP | GO:0071867 | response to monoamine | 4/504 | 38/18670 | 0.018761632 | 0.018761632 | 0.19977588 | 4 |
| BP | GO:0071869 | response to catecholamine | 4/504 | 38/18670 | 0.018761632 | 0.018761632 | 0.19977588 | 4 |