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| Table 1 hsa-mir-4551 targets prediction results | | |
| targets ID | taegets | name |
| ENSG00000115966 | ATF2 | activating transcription factor 2(ATF2) |
| ENSG00000100422 | CERK | ceramide kinase(CERK) |
| ENSG00000139990 | DCAF5 | DDB1 and CUL4 associated factor 5(DCAF5) |
| ENSG00000165046 | LETM2 | leucine zipper and EF-hand containing transmembrane protein 2(LETM2) |
| ENSG00000161921 | CXCL16 | C-X-C motif chemokine ligand 16(CXCL16) |
| ENSG00000166436 | TRIM66 | tripartite motif containing 66(TRIM66) |
| ENSG00000109189 | USP46 | ubiquitin specific peptidase 46(USP46) |
| ENSG00000104142 | VPS18 | VPS18, CORVET/HOPS core subunit(VPS18) |
| ENSG00000182831 | C16orf72 | chromosome 16 open reading frame 72(C16orf72) |
| ENSG00000166971 | AKTIP | AKT interacting protein(AKTIP) |
| ENSG00000143867 | OSR1 | odd-skipped related transciption factor 1(OSR1) |
| ENSG00000165699 | TSC1 | tuberous sclerosis 1(TSC1) |
| ENSG00000240972 | MIF | macrophage migration inhibitory factor (glycosylation-inhibiting factor)(MIF) |
| ENSG00000164924 | YWHAZ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta(YWHAZ) |
| ENSG00000120549 | KIAA1217 | KIAA1217(KIAA1217) |
| ENSG00000129933 | MAU2 | MAU2 sister chromatid cohesion factor(MAU2) |
| ENSG00000139154 | AEBP2 | AE binding protein 2(AEBP2) |
| ENSG00000196405 | EVL | Enah/Vasp-like(EVL) |
| ENSG00000126464 | PRR12 | proline rich 12(PRR12) |
| ENSG00000162591 | MEGF6 | multiple EGF like domains 6(MEGF6) |
| ENSG00000197226 | TBC1D9B | TBC1 domain family member 9B(TBC1D9B) |
| ENSG00000108671 | PSMD11 | proteasome 26S subunit, non-ATPase 11(PSMD11) |
| ENSG00000055070 | SZRD1 | SUZ RNA binding domain containing 1(SZRD1) |
| ENSG00000085563 | ABCB1 | ATP binding cassette subfamily B member 1(ABCB1) |
| ENSG00000135932 | CAB39 | calcium binding protein 39(CAB39) |
| ENSG00000187398 | LUZP2 | leucine zipper protein 2(LUZP2) |
| ENSG00000163637 | PRICKLE2 | prickle planar cell polarity protein 2(PRICKLE2) |
| ENSG00000111859 | NEDD9 | neural precursor cell expressed, developmentally down-regulated 9(NEDD9) |
| ENSG00000211689 | TARP | TCR gamma alternate reading frame protein(TARP) |
| ENSG00000140092 | FBLN5 | fibulin 5(FBLN5) |
| ENSG00000155657 | TTN | titin(TTN) |
| ENSG00000148468 | FAM171A1 | family with sequence similarity 171 member A1(FAM171A1) |
| ENSG00000111249 | CUX2 | cut like homeobox 2(CUX2) |
| ENSG00000146373 | RNF217 | ring finger protein 217(RNF217) |
| ENSG00000113532 | ST8SIA4 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4(ST8SIA4) |
| ENSG00000267534 | S1PR2 | sphingosine-1-phosphate receptor 2(S1PR2) |
| ENSG00000116604 | MEF2D | myocyte enhancer factor 2D(MEF2D) |
| ENSG00000129355 | CDKN2D | cyclin dependent kinase inhibitor 2D(CDKN2D) |
| ENSG00000184058 | TBX1 | T-box 1(TBX1) |
| ENSG00000147883 | CDKN2B | cyclin dependent kinase inhibitor 2B(CDKN2B) |
| ENSG00000198814 | GK | glycerol kinase(GK) |
| ENSG00000105974 | CAV1 | caveolin 1(CAV1) |
| ENSG00000091317 | CMTM6 | CKLF like MARVEL transmembrane domain containing 6(CMTM6) |
| ENSG00000140650 | PMM2 | phosphomannomutase 2(PMM2) |
| ENSG00000172071 | EIF2AK3 | eukaryotic translation initiation factor 2 alpha kinase 3(EIF2AK3) |
| ENSG00000179134 | SAMD4B | sterile alpha motif domain containing 4B(SAMD4B) |
| ENSG00000183826 | BTBD9 | BTB domain containing 9(BTBD9) |
| ENSG00000165355 | FBXO33 | F-box protein 33(FBXO33) |
| ENSG00000176624 | MEX3C | mex-3 RNA binding family member C(MEX3C) |
| ENSG00000204264 | PSMB8 | proteasome subunit beta 8(PSMB8) |
| ENSG00000143614 | GATAD2B | GATA zinc finger domain containing 2B(GATAD2B) |
| ENSG00000130717 | UCK1 | uridine-cytidine kinase 1(UCK1) |
| ENSG00000101558 | VAPA | VAMP associated protein A(VAPA) |
| ENSG00000158966 | CACHD1 | cache domain containing 1(CACHD1) |
| ENSG00000144566 | RAB5A | RAB5A, member RAS oncogene family(RAB5A) |

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| Table 2 GO enrichment results | | | |
| Ontology | GO ID | GO term | P-value |
| BP | GO:2000286 | receptor internalization involved in canonical Wnt signaling pathway | 0.00002 |
| BP | GO:0016310 | phosphorylation | 0.00002 |
| BP | GO:0045859 | regulation of protein kinase activity | 0.00017 |
| BP | GO:0002062 | chondrocyte differentiation | 0.00022 |
| BP | GO:0001932 | regulation of protein phosphorylation | 0.00024 |
| BP | GO:0009887 | animal organ morphogenesis | 0.00025 |
| BP | GO:0006464 | cellular protein modification process | 0.00030 |
| BP | GO:0036211 | protein modification process | 0.00030 |
| BP | GO:0043549 | regulation of kinase activity | 0.00033 |
| BP | GO:0006468 | protein phosphorylation | 0.00037 |
| BP | GO:0006796 | phosphate-containing compound metabolic process | 0.00042 |
| BP | GO:0006793 | phosphorus metabolic process | 0.00047 |
| BP | GO:0060537 | muscle tissue development | 0.00053 |
| BP | GO:0042325 | regulation of phosphorylation | 0.00056 |
| BP | GO:0061448 | connective tissue development | 0.00057 |
| BP | GO:0043412 | macromolecule modification | 0.00063 |
| BP | GO:0010629 | negative regulation of gene expression | 0.00069 |
| BP | GO:0051338 | regulation of transferase activity | 0.00072 |
| BP | GO:0051179 | localization | 0.00084 |
| BP | GO:2001242 | regulation of intrinsic apoptotic signaling pathway | 0.00088 |
| BP | GO:0032413 | negative regulation of ion transmembrane transporter activity | 0.00094 |
| BP | GO:1905114 | cell surface receptor signaling pathway involved in cell-cell signaling | 0.00098 |
| BP | GO:0009628 | response to abiotic stimulus | 0.00103 |
| BP | GO:0042474 | middle ear morphogenesis | 0.00105 |
| BP | GO:0065009 | regulation of molecular function | 0.00106 |
| BP | GO:0016192 | vesicle-mediated transport | 0.00115 |
| BP | GO:0045055 | regulated exocytosis | 0.00127 |
| BP | GO:0031323 | regulation of cellular metabolic process | 0.00132 |
| BP | GO:0006970 | response to osmotic stress | 0.00137 |
| BP | GO:0032410 | negative regulation of transporter activity | 0.00137 |
| BP | GO:0043488 | regulation of mRNA stability | 0.00137 |
| BP | GO:1904063 | negative regulation of cation transmembrane transport | 0.00141 |
| BP | GO:0044093 | positive regulation of molecular function | 0.00156 |
| BP | GO:0031329 | regulation of cellular catabolic process | 0.00160 |
| BP | GO:0045786 | negative regulation of cell cycle | 0.00161 |
| BP | GO:0044070 | regulation of anion transport | 0.00164 |
| BP | GO:0019220 | regulation of phosphate metabolic process | 0.00164 |
| BP | GO:0051174 | regulation of phosphorus metabolic process | 0.00166 |
| BP | GO:0048729 | tissue morphogenesis | 0.00167 |
| BP | GO:0043487 | regulation of RNA stability | 0.00167 |
| BP | GO:0099003 | vesicle-mediated transport in synapse | 0.00167 |
| BP | GO:0006810 | transport | 0.00168 |
| BP | GO:0009888 | tissue development | 0.00169 |
| BP | GO:0071900 | regulation of protein serine/threonine kinase activity | 0.00175 |
| BP | GO:0031645 | negative regulation of neurological system process | 0.00177 |
| BP | GO:0097186 | amelogenesis | 0.00177 |
| BP | GO:1903959 | regulation of anion transmembrane transport | 0.00177 |
| BP | GO:1903047 | mitotic cell cycle process | 0.00181 |
| BP | GO:0001501 | skeletal system development | 0.00182 |
| BP | GO:0051216 | cartilage development | 0.00182 |
| BP | GO:0090630 | activation of GTPase activity | 0.00190 |
| BP | GO:0034766 | negative regulation of ion transmembrane transport | 0.00200 |
| BP | GO:0061013 | regulation of mRNA catabolic process | 0.00201 |
| BP | GO:0031399 | regulation of protein modification process | 0.00218 |
| BP | GO:1901017 | negative regulation of potassium ion transmembrane transporter activity | 0.00221 |
| BP | GO:0045930 | negative regulation of mitotic cell cycle | 0.00225 |
| BP | GO:0050678 | regulation of epithelial cell proliferation | 0.00228 |
| BP | GO:0007049 | cell cycle | 0.00229 |
| BP | GO:0031146 | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | 0.00229 |
| BP | GO:0051234 | establishment of localization | 0.00232 |
| BP | GO:0010800 | positive regulation of peptidyl-threonine phosphorylation | 0.00236 |
| BP | GO:0008039 | synaptic target recognition | 0.00240 |
| BP | GO:0060734 | regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation | 0.00240 |
| BP | GO:0061078 | positive regulation of prostaglandin secretion involved in immune response | 0.00240 |
| BP | GO:0072165 | anterior mesonephric tubule development | 0.00240 |
| BP | GO:0072167 | specification of mesonephric tubule identity | 0.00240 |
| BP | GO:0072168 | specification of anterior mesonephric tubule identity | 0.00240 |
| BP | GO:0072169 | specification of posterior mesonephric tubule identity | 0.00240 |
| BP | GO:0072184 | renal vesicle progenitor cell differentiation | 0.00240 |
| BP | GO:0072258 | metanephric interstitial fibroblast differentiation | 0.00240 |
| BP | GO:0072259 | metanephric interstitial fibroblast development | 0.00240 |
| BP | GO:0090323 | prostaglandin secretion involved in immune response | 0.00240 |
| BP | GO:1900085 | negative regulation of peptidyl-tyrosine autophosphorylation | 0.00240 |
| BP | GO:0010605 | negative regulation of macromolecule metabolic process | 0.00249 |
| BP | GO:0050793 | regulation of developmental process | 0.00260 |
| BP | GO:0098693 | regulation of synaptic vesicle cycle | 0.00267 |
| BP | GO:1900027 | regulation of ruffle assembly | 0.00268 |
| BP | GO:0022402 | cell cycle process | 0.00274 |
| BP | GO:0032526 | response to retinoic acid | 0.00280 |
| BP | GO:0006887 | exocytosis | 0.00281 |
| BP | GO:0007507 | heart development | 0.00285 |
| BP | GO:0010737 | protein kinase A signaling | 0.00285 |
| BP | GO:0045736 | negative regulation of cyclin-dependent protein serine/threonine kinase activity | 0.00285 |
| BP | GO:1901380 | negative regulation of potassium ion transmembrane transport | 0.00285 |
| BP | GO:1902230 | negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage | 0.00285 |
| BP | GO:0031623 | receptor internalization | 0.00294 |
| BP | GO:0014706 | striated muscle tissue development | 0.00299 |
| BP | GO:1904030 | negative regulation of cyclin-dependent protein kinase activity | 0.00302 |
| BP | GO:0010948 | negative regulation of cell cycle process | 0.00315 |
| BP | GO:0009894 | regulation of catabolic process | 0.00344 |
| BP | GO:0007050 | cell cycle arrest | 0.00349 |
| BP | GO:0060071 | Wnt signaling pathway, planar cell polarity pathway | 0.00353 |
| BP | GO:0071453 | cellular response to oxygen levels | 0.00354 |
| BP | GO:0008104 | protein localization | 0.00356 |
| BP | GO:1901890 | positive regulation of cell junction assembly | 0.00357 |
| BP | GO:0032412 | regulation of ion transmembrane transporter activity | 0.00359 |
| BP | GO:0090175 | regulation of establishment of planar polarity | 0.00369 |
| BP | GO:0044267 | cellular protein metabolic process | 0.00373 |
| BP | GO:0034763 | negative regulation of transmembrane transport | 0.00377 |
| BP | GO:0048706 | embryonic skeletal system development | 0.00377 |
| BP | GO:0042476 | odontogenesis | 0.00385 |
| BP | GO:0032879 | regulation of localization | 0.00395 |
| BP | GO:0045022 | early endosome to late endosome transport | 0.00396 |
| BP | GO:0022898 | regulation of transmembrane transporter activity | 0.00399 |
| BP | GO:2000113 | negative regulation of cellular macromolecule biosynthetic process | 0.00400 |
| BP | GO:2001233 | regulation of apoptotic signaling pathway | 0.00407 |
| BP | GO:0050673 | epithelial cell proliferation | 0.00411 |
| BP | GO:0051259 | protein complex oligomerization | 0.00418 |
| BP | GO:0033036 | macromolecule localization | 0.00434 |
| BP | GO:0043267 | negative regulation of potassium ion transport | 0.00437 |
| BP | GO:0000278 | mitotic cell cycle | 0.00443 |
| BP | GO:1901991 | negative regulation of mitotic cell cycle phase transition | 0.00449 |
| BP | GO:0098927 | vesicle-mediated transport between endosomal compartments | 0.00459 |
| BP | GO:1902229 | regulation of intrinsic apoptotic signaling pathway in response to DNA damage | 0.00459 |
| BP | GO:0048863 | stem cell differentiation | 0.00460 |
| BP | GO:2000027 | regulation of animal organ morphogenesis | 0.00466 |
| BP | GO:0051641 | cellular localization | 0.00468 |
| BP | GO:0010256 | endomembrane system organization | 0.00473 |
| BP | GO:0021644 | vagus nerve morphogenesis | 0.00480 |
| BP | GO:0032915 | positive regulation of transforming growth factor beta2 production | 0.00480 |
| BP | GO:0035981 | tongue muscle cell differentiation | 0.00480 |
| BP | GO:0048389 | intermediate mesoderm development | 0.00480 |
| BP | GO:0061227 | pattern specification involved in mesonephros development | 0.00480 |
| BP | GO:0072071 | kidney interstitial fibroblast differentiation | 0.00480 |
| BP | GO:0072098 | anterior/posterior pattern specification involved in kidney development | 0.00480 |
| BP | GO:0072141 | renal interstitial fibroblast development | 0.00480 |
| BP | GO:0072166 | posterior mesonephric tubule development | 0.00480 |
| BP | GO:0072183 | negative regulation of nephron tubule epithelial cell differentiation | 0.00480 |
| BP | GO:0072185 | metanephric cap development | 0.00480 |
| BP | GO:0072186 | metanephric cap morphogenesis | 0.00480 |
| BP | GO:0072208 | metanephric smooth muscle tissue development | 0.00480 |
| BP | GO:0086098 | angiotensin-activated signaling pathway involved in heart process | 0.00480 |
| BP | GO:0090094 | metanephric cap mesenchymal cell proliferation involved in metanephros development | 0.00480 |
| BP | GO:0099040 | ceramide translocation | 0.00480 |
| BP | GO:1905407 | regulation of creatine transmembrane transporter activity | 0.00480 |
| BP | GO:1905408 | negative regulation of creatine transmembrane transporter activity | 0.00480 |
| BP | GO:2001035 | regulation of tongue muscle cell differentiation | 0.00480 |
| BP | GO:2001037 | positive regulation of tongue muscle cell differentiation | 0.00480 |
| BP | GO:0031644 | regulation of neurological system process | 0.00483 |
| BP | GO:0032409 | regulation of transporter activity | 0.00484 |
| BP | GO:0016043 | cellular component organization | 0.00488 |
| BP | GO:0000086 | G2/M transition of mitotic cell cycle | 0.00496 |
| BP | GO:0001736 | establishment of planar polarity | 0.00502 |
| BP | GO:0007164 | establishment of tissue polarity | 0.00502 |
| BP | GO:0010608 | posttranscriptional regulation of gene expression | 0.00508 |
| BP | GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process | 0.00509 |
| BP | GO:0050804 | modulation of chemical synaptic transmission | 0.00523 |
| BP | GO:0009892 | negative regulation of metabolic process | 0.00528 |
| BP | GO:0099177 | regulation of trans-synaptic signaling | 0.00528 |
| BP | GO:0010463 | mesenchymal cell proliferation | 0.00548 |
| BP | GO:0098815 | modulation of excitatory postsynaptic potential | 0.00548 |
| BP | GO:0071901 | negative regulation of protein serine/threonine kinase activity | 0.00562 |
| BP | GO:1901988 | negative regulation of cell cycle phase transition | 0.00566 |
| BP | GO:0018105 | peptidyl-serine phosphorylation | 0.00586 |
| BP | GO:0010558 | negative regulation of macromolecule biosynthetic process | 0.00587 |
| BP | GO:0002063 | chondrocyte development | 0.00595 |
| BP | GO:0010799 | regulation of peptidyl-threonine phosphorylation | 0.00595 |
| BP | GO:0030534 | adult behavior | 0.00604 |
| BP | GO:0044839 | cell cycle G2/M phase transition | 0.00613 |
| BP | GO:0006511 | ubiquitin-dependent protein catabolic process | 0.00625 |
| BP | GO:0048468 | cell development | 0.00627 |
| BP | GO:0032268 | regulation of cellular protein metabolic process | 0.00630 |
| BP | GO:0034613 | cellular protein localization | 0.00642 |
| BP | GO:0097178 | ruffle assembly | 0.00645 |
| BP | GO:2000026 | regulation of multicellular organismal development | 0.00647 |
| BP | GO:0030100 | regulation of endocytosis | 0.00649 |
| BP | GO:0019941 | modification-dependent protein catabolic process | 0.00651 |
| BP | GO:0060341 | regulation of cellular localization | 0.00654 |
| BP | GO:0044237 | cellular metabolic process | 0.00657 |
| BP | GO:0051246 | regulation of protein metabolic process | 0.00658 |
| BP | GO:0009653 | anatomical structure morphogenesis | 0.00662 |
| BP | GO:0097193 | intrinsic apoptotic signaling pathway | 0.00671 |
| BP | GO:0001738 | morphogenesis of a polarized epithelium | 0.00671 |
| BP | GO:0070727 | cellular macromolecule localization | 0.00672 |
| BP | GO:0048522 | positive regulation of cellular process | 0.00681 |
| BP | GO:0019222 | regulation of metabolic process | 0.00690 |
| BP | GO:1903793 | positive regulation of anion transport | 0.00696 |
| BP | GO:0043632 | modification-dependent macromolecule catabolic process | 0.00701 |
| BP | GO:0090263 | positive regulation of canonical Wnt signaling pathway | 0.00707 |
| BP | GO:0006407 | rRNA export from nucleus | 0.00720 |
| BP | GO:0019065 | receptor-mediated endocytosis of virus by host cell | 0.00720 |
| BP | GO:0021564 | vagus nerve development | 0.00720 |
| BP | GO:0033484 | nitric oxide homeostasis | 0.00720 |
| BP | GO:0036022 | limb joint morphogenesis | 0.00720 |
| BP | GO:0036023 | embryonic skeletal limb joint morphogenesis | 0.00720 |
| BP | GO:0044211 | CTP salvage | 0.00720 |
| BP | GO:0048769 | sarcomerogenesis | 0.00720 |
| BP | GO:0072190 | ureter urothelium development | 0.00720 |
| BP | GO:0072194 | kidney smooth muscle tissue development | 0.00720 |
| BP | GO:0075509 | endocytosis involved in viral entry into host cell | 0.00720 |
| BP | GO:0110024 | positive regulation of cardiac muscle myoblast proliferation | 0.00720 |
| BP | GO:1902811 | positive regulation of skeletal muscle fiber differentiation | 0.00720 |
| BP | GO:1903598 | positive regulation of gap junction assembly | 0.00720 |
| BP | GO:1990737 | response to manganese-induced endoplasmic reticulum stress | 0.00720 |
| BP | GO:0030856 | regulation of epithelial cell differentiation | 0.00731 |
| BP | GO:0071840 | cellular component organization or biogenesis | 0.00733 |
| BP | GO:0072359 | circulatory system development | 0.00745 |
| BP | GO:0030857 | negative regulation of epithelial cell differentiation | 0.00748 |
| BP | GO:0031214 | biomineral tissue development | 0.00755 |
| BP | GO:0043271 | negative regulation of ion transport | 0.00755 |
| BP | GO:0018209 | peptidyl-serine modification | 0.00756 |
| BP | GO:0007033 | vacuole organization | 0.00768 |
| BP | GO:0050680 | negative regulation of epithelial cell proliferation | 0.00768 |
| BP | GO:0031327 | negative regulation of cellular biosynthetic process | 0.00773 |
| BP | GO:0051017 | actin filament bundle assembly | 0.00780 |
| BP | GO:0051049 | regulation of transport | 0.00792 |
| BP | GO:0035567 | non-canonical Wnt signaling pathway | 0.00793 |
| BP | GO:0051496 | positive regulation of stress fiber assembly | 0.00803 |
| BP | GO:0010498 | proteasomal protein catabolic process | 0.00814 |
| BP | GO:0061572 | actin filament bundle organization | 0.00832 |
| BP | GO:0007519 | skeletal muscle tissue development | 0.00845 |
| BP | GO:0009890 | negative regulation of biosynthetic process | 0.00845 |
| BP | GO:0022603 | regulation of anatomical structure morphogenesis | 0.00847 |
| BP | GO:0051172 | negative regulation of nitrogen compound metabolic process | 0.00856 |
| BP | GO:0051649 | establishment of localization in cell | 0.00886 |
| BP | GO:0008333 | endosome to lysosome transport | 0.00888 |
| BP | GO:0051128 | regulation of cellular component organization | 0.00910 |
| BP | GO:0007040 | lysosome organization | 0.00917 |
| BP | GO:0046847 | filopodium assembly | 0.00917 |
| BP | GO:0080171 | lytic vacuole organization | 0.00917 |
| BP | GO:0022607 | cellular component assembly | 0.00920 |
| BP | GO:0006665 | sphingolipid metabolic process | 0.00941 |
| BP | GO:0031529 | ruffle organization | 0.00947 |
| BP | GO:0032890 | regulation of organic acid transport | 0.00947 |
| BP | GO:0002901 | mature B cell apoptotic process | 0.00959 |
| BP | GO:0002905 | regulation of mature B cell apoptotic process | 0.00959 |
| BP | GO:0002906 | negative regulation of mature B cell apoptotic process | 0.00959 |
| BP | GO:0003415 | chondrocyte hypertrophy | 0.00959 |
| BP | GO:0009298 | GDP-mannose biosynthetic process | 0.00959 |
| BP | GO:0032057 | negative regulation of translational initiation in response to stress | 0.00959 |
| BP | GO:0035995 | detection of muscle stretch | 0.00959 |
| BP | GO:0044860 | protein localization to plasma membrane raft | 0.00959 |
| BP | GO:0046167 | glycerol-3-phosphate biosynthetic process | 0.00959 |
| BP | GO:0070836 | caveola assembly | 0.00959 |
| BP | GO:0072131 | kidney mesenchyme morphogenesis | 0.00959 |
| BP | GO:0072133 | metanephric mesenchyme morphogenesis | 0.00959 |
| BP | GO:0072180 | mesonephric duct morphogenesis | 0.00959 |
| BP | GO:0072268 | pattern specification involved in metanephros development | 0.00959 |
| BP | GO:0090168 | Golgi reassembly | 0.00959 |
| BP | GO:0099039 | sphingolipid translocation | 0.00959 |
| BP | GO:1901529 | positive regulation of anion channel activity | 0.00959 |
| BP | GO:1902809 | regulation of skeletal muscle fiber differentiation | 0.00959 |
| BP | GO:1903596 | regulation of gap junction assembly | 0.00959 |
| BP | GO:1903609 | negative regulation of inward rectifier potassium channel activity | 0.00959 |
| BP | GO:0010646 | regulation of cell communication | 0.00964 |
| BP | GO:0060538 | skeletal muscle organ development | 0.00969 |
| BP | GO:0009967 | positive regulation of signal transduction | 0.00976 |
| BP | GO:0016050 | vesicle organization | 0.00986 |
| BP | GO:0120032 | regulation of plasma membrane bounded cell projection assembly | 0.00998 |
| BP | GO:0061024 | membrane organization | 0.01014 |
| BP | GO:0016055 | Wnt signaling pathway | 0.01022 |
| BP | GO:0060491 | regulation of cell projection assembly | 0.01027 |
| BP | GO:1901564 | organonitrogen compound metabolic process | 0.01031 |
| BP | GO:0065008 | regulation of biological quality | 0.01036 |
| BP | GO:0198738 | cell-cell signaling by wnt | 0.01037 |
| BP | GO:0051099 | positive regulation of binding | 0.01057 |
| BP | GO:0051171 | regulation of nitrogen compound metabolic process | 0.01062 |
| BP | GO:0044265 | cellular macromolecule catabolic process | 0.01074 |
| BP | GO:0060070 | canonical Wnt signaling pathway | 0.01075 |
| BP | GO:0023051 | regulation of signaling | 0.01089 |
| BP | GO:0032233 | positive regulation of actin filament bundle assembly | 0.01101 |
| BP | GO:0048869 | cellular developmental process | 0.01105 |
| BP | GO:0001101 | response to acid chemical | 0.01105 |
| BP | GO:1903311 | regulation of mRNA metabolic process | 0.01105 |
| BP | GO:0060255 | regulation of macromolecule metabolic process | 0.01113 |
| BP | GO:1901016 | regulation of potassium ion transmembrane transporter activity | 0.01134 |
| BP | GO:0030177 | positive regulation of Wnt signaling pathway | 0.01135 |
| BP | GO:0051603 | proteolysis involved in cellular protein catabolic process | 0.01150 |
| BP | GO:0030029 | actin filament-based process | 0.01170 |
| BP | GO:0010565 | regulation of cellular ketone metabolic process | 0.01182 |
| BP | GO:0060627 | regulation of vesicle-mediated transport | 0.01187 |
| BP | GO:0010138 | pyrimidine ribonucleotide salvage | 0.01197 |
| BP | GO:0044206 | UMP salvage | 0.01197 |
| BP | GO:0048550 | negative regulation of pinocytosis | 0.01197 |
| BP | GO:0072047 | proximal/distal pattern formation involved in nephron development | 0.01197 |
| BP | GO:0072081 | specification of nephron tubule identity | 0.01197 |
| BP | GO:0072162 | metanephric mesenchymal cell differentiation | 0.01197 |
| BP | GO:1900028 | negative regulation of ruffle assembly | 0.01197 |
| BP | GO:1901552 | positive regulation of endothelial cell development | 0.01197 |
| BP | GO:1903142 | positive regulation of establishment of endothelial barrier | 0.01197 |
| BP | GO:2000697 | negative regulation of epithelial cell differentiation involved in kidney development | 0.01197 |
| BP | GO:0043312 | neutrophil degranulation | 0.01221 |
| BP | GO:0023014 | signal transduction by protein phosphorylation | 0.01231 |
| BP | GO:0099504 | synaptic vesicle cycle | 0.01231 |
| BP | GO:0036465 | synaptic vesicle recycling | 0.01232 |
| BP | GO:1902110 | positive regulation of mitochondrial membrane permeability involved in apoptotic process | 0.01232 |
| BP | GO:0042127 | regulation of cell proliferation | 0.01236 |
| BP | GO:0046903 | secretion | 0.01244 |
| BP | GO:0090090 | negative regulation of canonical Wnt signaling pathway | 0.01248 |
| BP | GO:0035914 | skeletal muscle cell differentiation | 0.01266 |
| BP | GO:0002009 | morphogenesis of an epithelium | 0.01272 |
| BP | GO:0002283 | neutrophil activation involved in immune response | 0.01272 |
| BP | GO:0018193 | peptidyl-amino acid modification | 0.01283 |
| BP | GO:0008219 | cell death | 0.01300 |
| BP | GO:1902686 | mitochondrial outer membrane permeabilization involved in programmed cell death | 0.01300 |
| BP | GO:0001505 | regulation of neurotransmitter levels | 0.01302 |
| BP | GO:0002366 | leukocyte activation involved in immune response | 0.01303 |
| BP | GO:0031032 | actomyosin structure organization | 0.01315 |
| BP | GO:0019058 | viral life cycle | 0.01325 |
| BP | GO:0002263 | cell activation involved in immune response | 0.01332 |
| BP | GO:0043112 | receptor metabolic process | 0.01333 |
| BP | GO:1905330 | regulation of morphogenesis of an epithelium | 0.01333 |
| BP | GO:0002446 | neutrophil mediated immunity | 0.01343 |
| BP | GO:0035794 | positive regulation of mitochondrial membrane permeability | 0.01370 |
| BP | GO:0044260 | cellular macromolecule metabolic process | 0.01376 |
| BP | GO:0051726 | regulation of cell cycle | 0.01378 |
| BP | GO:0042119 | neutrophil activation | 0.01379 |
| BP | GO:0044248 | cellular catabolic process | 0.01385 |
| BP | GO:0031324 | negative regulation of cellular metabolic process | 0.01388 |
| BP | GO:0071300 | cellular response to retinoic acid | 0.01405 |
| BP | GO:0018108 | peptidyl-tyrosine phosphorylation | 0.01408 |
| BP | GO:0010035 | response to inorganic substance | 0.01416 |
| BP | GO:0003057 | regulation of the force of heart contraction by chemical signal | 0.01434 |
| BP | GO:0032262 | pyrimidine nucleotide salvage | 0.01434 |
| BP | GO:0036492 | eiF2alpha phosphorylation in response to endoplasmic reticulum stress | 0.01434 |
| BP | GO:0044789 | modulation by host of viral release from host cell | 0.01434 |
| BP | GO:0044791 | positive regulation by host of viral release from host cell | 0.01434 |
| BP | GO:0051029 | rRNA transport | 0.01434 |
| BP | GO:0051036 | regulation of endosome size | 0.01434 |
| BP | GO:0071921 | cohesin loading | 0.01434 |
| BP | GO:0072143 | mesangial cell development | 0.01434 |
| BP | GO:0098528 | skeletal muscle fiber differentiation | 0.01434 |
| BP | GO:0110021 | cardiac muscle myoblast proliferation | 0.01434 |
| BP | GO:0110022 | regulation of cardiac muscle myoblast proliferation | 0.01434 |
| BP | GO:1900084 | regulation of peptidyl-tyrosine autophosphorylation | 0.01434 |
| BP | GO:0001934 | positive regulation of protein phosphorylation | 0.01440 |
| BP | GO:1902108 | regulation of mitochondrial membrane permeability involved in apoptotic process | 0.01441 |
| BP | GO:0018212 | peptidyl-tyrosine modification | 0.01445 |
| BP | GO:0043687 | post-translational protein modification | 0.01445 |
| BP | GO:0036230 | granulocyte activation | 0.01464 |
| BP | GO:0006687 | glycosphingolipid metabolic process | 0.01477 |
| BP | GO:1905710 | positive regulation of membrane permeability | 0.01477 |
| BP | GO:0080090 | regulation of primary metabolic process | 0.01480 |
| BP | GO:0051260 | protein homooligomerization | 0.01482 |
| BP | GO:0050790 | regulation of catalytic activity | 0.01495 |
| BP | GO:0030154 | cell differentiation | 0.01495 |
| BP | GO:0036293 | response to decreased oxygen levels | 0.01507 |
| BP | GO:0080135 | regulation of cellular response to stress | 0.01526 |
| BP | GO:0044257 | cellular protein catabolic process | 0.01550 |
| BP | GO:0003151 | outflow tract morphogenesis | 0.01551 |
| BP | GO:2000300 | regulation of synaptic vesicle exocytosis | 0.01551 |
| BP | GO:0009893 | positive regulation of metabolic process | 0.01551 |
| BP | GO:0048523 | negative regulation of cellular process | 0.01598 |
| BP | GO:0006521 | regulation of cellular amino acid metabolic process | 0.01664 |
| BP | GO:0017148 | negative regulation of translation | 0.01665 |
| BP | GO:0019563 | glycerol catabolic process | 0.01672 |
| BP | GO:0031642 | negative regulation of myelination | 0.01672 |
| BP | GO:0032055 | negative regulation of translation in response to stress | 0.01672 |
| BP | GO:0036491 | regulation of translation initiation in response to endoplasmic reticulum stress | 0.01672 |
| BP | GO:0044829 | positive regulation by host of viral genome replication | 0.01672 |
| BP | GO:0048752 | semicircular canal morphogenesis | 0.01672 |
| BP | GO:0060017 | parathyroid gland development | 0.01672 |
| BP | GO:0071455 | cellular response to hyperoxia | 0.01672 |
| BP | GO:0072007 | mesangial cell differentiation | 0.01672 |
| BP | GO:0090238 | positive regulation of arachidonic acid secretion | 0.01672 |
| BP | GO:0150093 | amyloid-beta clearance by transcytosis | 0.01672 |
| BP | GO:1901979 | regulation of inward rectifier potassium channel activity | 0.01672 |
| BP | GO:1903071 | positive regulation of ER-associated ubiquitin-dependent protein catabolic process | 0.01672 |
| BP | GO:2000535 | regulation of entry of bacterium into host cell | 0.01672 |
| BP | GO:0006898 | receptor-mediated endocytosis | 0.01690 |
| BP | GO:0007610 | behavior | 0.01695 |
| BP | GO:0033554 | cellular response to stress | 0.01696 |
| BP | GO:0008344 | adult locomotory behavior | 0.01703 |
| BP | GO:0051093 | negative regulation of developmental process | 0.01704 |
| BP | GO:0010604 | positive regulation of macromolecule metabolic process | 0.01713 |
| BP | GO:0007032 | endosome organization | 0.01742 |
| BP | GO:0060415 | muscle tissue morphogenesis | 0.01742 |
| BP | GO:1902803 | regulation of synaptic vesicle transport | 0.01742 |
| BP | GO:0044085 | cellular component biogenesis | 0.01742 |
| BP | GO:0043299 | leukocyte degranulation | 0.01748 |
| BP | GO:0044772 | mitotic cell cycle phase transition | 0.01759 |
| BP | GO:0060429 | epithelium development | 0.01763 |
| BP | GO:0030178 | negative regulation of Wnt signaling pathway | 0.01765 |
| BP | GO:0042886 | amide transport | 0.01769 |
| BP | GO:0008283 | cell proliferation | 0.01780 |
| BP | GO:0010647 | positive regulation of cell communication | 0.01791 |
| BP | GO:0000122 | negative regulation of transcription by RNA polymerase II | 0.01792 |
| BP | GO:0006643 | membrane lipid metabolic process | 0.01805 |
| BP | GO:0046902 | regulation of mitochondrial membrane permeability | 0.01821 |
| BP | GO:0070482 | response to oxygen levels | 0.01829 |
| BP | GO:0002275 | myeloid cell activation involved in immune response | 0.01835 |
| BP | GO:0042327 | positive regulation of phosphorylation | 0.01837 |
| BP | GO:0023056 | positive regulation of signaling | 0.01838 |
| BP | GO:0071705 | nitrogen compound transport | 0.01843 |
| BP | GO:0060548 | negative regulation of cell death | 0.01901 |
| BP | GO:0048518 | positive regulation of biological process | 0.01907 |
| BP | GO:0019405 | alditol catabolic process | 0.01908 |
| BP | GO:0031666 | positive regulation of lipopolysaccharide-mediated signaling pathway | 0.01908 |
| BP | GO:0032906 | transforming growth factor beta2 production | 0.01908 |
| BP | GO:0032909 | regulation of transforming growth factor beta2 production | 0.01908 |
| BP | GO:0034085 | establishment of sister chromatid cohesion | 0.01908 |
| BP | GO:0043587 | tongue morphogenesis | 0.01908 |
| BP | GO:0048102 | autophagic cell death | 0.01908 |
| BP | GO:0051683 | establishment of Golgi localization | 0.01908 |
| BP | GO:0060056 | mammary gland involution | 0.01908 |
| BP | GO:0060355 | positive regulation of cell adhesion molecule production | 0.01908 |
| BP | GO:0071476 | cellular hypotonic response | 0.01908 |
| BP | GO:0072161 | mesenchymal cell differentiation involved in kidney development | 0.01908 |
| BP | GO:0072239 | metanephric glomerulus vasculature development | 0.01908 |
| BP | GO:0098909 | regulation of cardiac muscle cell action potential involved in regulation of contraction | 0.01908 |
| BP | GO:1903361 | protein localization to basolateral plasma membrane | 0.01908 |
| BP | GO:1903961 | positive regulation of anion transmembrane transport | 0.01908 |
| BP | GO:1904238 | pericyte cell differentiation | 0.01908 |
| BP | GO:2000288 | positive regulation of myoblast proliferation | 0.01908 |
| BP | GO:2001012 | mesenchymal cell differentiation involved in renal system development | 0.01908 |
| BP | GO:2001016 | positive regulation of skeletal muscle cell differentiation | 0.01908 |
| BP | GO:0002444 | myeloid leukocyte mediated immunity | 0.01914 |
| BP | GO:0007517 | muscle organ development | 0.01931 |
| BP | GO:0042475 | odontogenesis of dentin-containing tooth | 0.01983 |
| BP | GO:1902036 | regulation of hematopoietic stem cell differentiation | 0.01983 |
| BP | GO:0032270 | positive regulation of cellular protein metabolic process | 0.01986 |
| BP | GO:0007015 | actin filament organization | 0.01991 |
| BP | GO:0097190 | apoptotic signaling pathway | 0.01996 |
| BP | GO:0010033 | response to organic substance | 0.02015 |
| BP | GO:0006402 | mRNA catabolic process | 0.02021 |
| BP | GO:0048644 | muscle organ morphogenesis | 0.02024 |
| BP | GO:0031669 | cellular response to nutrient levels | 0.02039 |
| BP | GO:0034249 | negative regulation of cellular amide metabolic process | 0.02039 |
| BP | GO:0045595 | regulation of cell differentiation | 0.02060 |
| BP | GO:0045444 | fat cell differentiation | 0.02062 |
| BP | GO:0032436 | positive regulation of proteasomal ubiquitin-dependent protein catabolic process | 0.02066 |
| BP | GO:0051492 | regulation of stress fiber assembly | 0.02066 |
| BP | GO:0036294 | cellular response to decreased oxygen levels | 0.02084 |
| BP | GO:0048705 | skeletal system morphogenesis | 0.02106 |
| BP | GO:0060021 | roof of mouth development | 0.02108 |
| BP | GO:0006072 | glycerol-3-phosphate metabolic process | 0.02144 |
| BP | GO:0010359 | regulation of anion channel activity | 0.02144 |
| BP | GO:0010760 | negative regulation of macrophage chemotaxis | 0.02144 |
| BP | GO:0019673 | GDP-mannose metabolic process | 0.02144 |
| BP | GO:0036490 | regulation of translation in response to endoplasmic reticulum stress | 0.02144 |
| BP | GO:0042473 | outer ear morphogenesis | 0.02144 |
| BP | GO:0042748 | circadian sleep/wake cycle, non-REM sleep | 0.02144 |
| BP | GO:0043379 | memory T cell differentiation | 0.02144 |
| BP | GO:0044828 | negative regulation by host of viral genome replication | 0.02144 |
| BP | GO:0048149 | behavioral response to ethanol | 0.02144 |
| BP | GO:0048793 | pronephros development | 0.02144 |
| BP | GO:0060013 | righting reflex | 0.02144 |
| BP | GO:0060023 | soft palate development | 0.02144 |
| BP | GO:0060586 | multicellular organismal iron ion homeostasis | 0.02144 |
| BP | GO:0060872 | semicircular canal development | 0.02144 |
| BP | GO:0060982 | coronary artery morphogenesis | 0.02144 |
| BP | GO:0061004 | pattern specification involved in kidney development | 0.02144 |
| BP | GO:0070417 | cellular response to cold | 0.02144 |
| BP | GO:0072048 | renal system pattern specification | 0.02144 |
| BP | GO:0072172 | mesonephric tubule formation | 0.02144 |
| BP | GO:0072177 | mesonephric duct development | 0.02144 |
| BP | GO:0090237 | regulation of arachidonic acid secretion | 0.02144 |
| BP | GO:0090527 | actin filament reorganization | 0.02144 |
| BP | GO:0090649 | response to oxygen-glucose deprivation | 0.02144 |
| BP | GO:0090650 | cellular response to oxygen-glucose deprivation | 0.02144 |
| BP | GO:0090715 | immunological memory formation process | 0.02144 |
| BP | GO:1901844 | regulation of cell communication by electrical coupling involved in cardiac conduction | 0.02144 |
| BP | GO:1903069 | regulation of ER-associated ubiquitin-dependent protein catabolic process | 0.02144 |
| BP | GO:1901379 | regulation of potassium ion transmembrane transport | 0.02151 |
| BP | GO:1900407 | regulation of cellular response to oxidative stress | 0.02194 |
| BP | GO:0006469 | negative regulation of protein kinase activity | 0.02197 |
| BP | GO:0044255 | cellular lipid metabolic process | 0.02212 |
| BP | GO:0016567 | protein ubiquitination | 0.02234 |
| BP | GO:2001021 | negative regulation of response to DNA damage stimulus | 0.02237 |
| BP | GO:0019538 | protein metabolic process | 0.02252 |
| BP | GO:0044770 | cell cycle phase transition | 0.02278 |
| BP | GO:0048704 | embryonic skeletal system morphogenesis | 0.02281 |
| BP | GO:0061097 | regulation of protein tyrosine kinase activity | 0.02281 |
| BP | GO:0061418 | regulation of transcription from RNA polymerase II promoter in response to hypoxia | 0.02281 |
| BP | GO:0090559 | regulation of membrane permeability | 0.02281 |
| BP | GO:1901700 | response to oxygen-containing compound | 0.02295 |
| BP | GO:0006813 | potassium ion transport | 0.02313 |
| BP | GO:1905897 | regulation of response to endoplasmic reticulum stress | 0.02325 |
| BP | GO:0032092 | positive regulation of protein binding | 0.02369 |
| BP | GO:0003376 | sphingosine-1-phosphate receptor signaling pathway | 0.02379 |
| BP | GO:0006013 | mannose metabolic process | 0.02379 |
| BP | GO:0006222 | UMP biosynthetic process | 0.02379 |
| BP | GO:0006971 | hypotonic response | 0.02379 |
| BP | GO:0007614 | short-term memory | 0.02379 |
| BP | GO:0008343 | adult feeding behavior | 0.02379 |
| BP | GO:0009173 | pyrimidine ribonucleoside monophosphate metabolic process | 0.02379 |
| BP | GO:0009174 | pyrimidine ribonucleoside monophosphate biosynthetic process | 0.02379 |
| BP | GO:0009414 | response to water deprivation | 0.02379 |
| BP | GO:0010998 | regulation of translational initiation by eIF2 alpha phosphorylation | 0.02379 |
| BP | GO:0033483 | gas homeostasis | 0.02379 |
| BP | GO:0042428 | serotonin metabolic process | 0.02379 |
| BP | GO:0045792 | negative regulation of cell size | 0.02379 |
| BP | GO:0046049 | UMP metabolic process | 0.02379 |
| BP | GO:0052646 | alditol phosphate metabolic process | 0.02379 |
| BP | GO:0072203 | cell proliferation involved in metanephros development | 0.02379 |
| BP | GO:1903789 | regulation of amino acid transmembrane transport | 0.02379 |
| BP | GO:2001054 | negative regulation of mesenchymal cell apoptotic process | 0.02379 |
| BP | GO:2001225 | regulation of chloride transport | 0.02379 |
| BP | GO:0031532 | actin cytoskeleton reorganization | 0.02414 |
| BP | GO:0060218 | hematopoietic stem cell differentiation | 0.02414 |
| BP | GO:0051701 | interaction with host | 0.02457 |
| BP | GO:0000079 | regulation of cyclin-dependent protein serine/threonine kinase activity | 0.02459 |
| BP | GO:0031145 | anaphase-promoting complex-dependent catabolic process | 0.02459 |
| BP | GO:0120035 | regulation of plasma membrane bounded cell projection organization | 0.02463 |
| BP | GO:0071702 | organic substance transport | 0.02476 |
| BP | GO:0010562 | positive regulation of phosphorus metabolic process | 0.02478 |
| BP | GO:0045937 | positive regulation of phosphate metabolic process | 0.02478 |
| BP | GO:0007267 | cell-cell signaling | 0.02482 |
| BP | GO:0061061 | muscle structure development | 0.02490 |
| BP | GO:0030036 | actin cytoskeleton organization | 0.02544 |
| BP | GO:0033238 | regulation of cellular amine metabolic process | 0.02550 |
| BP | GO:0110020 | regulation of actomyosin structure organization | 0.02550 |
| BP | GO:1901532 | regulation of hematopoietic progenitor cell differentiation | 0.02550 |
| BP | GO:1901888 | regulation of cell junction assembly | 0.02550 |
| BP | GO:0032269 | negative regulation of cellular protein metabolic process | 0.02558 |
| BP | GO:0006401 | RNA catabolic process | 0.02579 |
| BP | GO:0003007 | heart morphogenesis | 0.02581 |
| BP | GO:0070647 | protein modification by small protein conjugation or removal | 0.02598 |
| BP | GO:0031344 | regulation of cell projection organization | 0.02600 |
| BP | GO:0002903 | negative regulation of B cell apoptotic process | 0.02614 |
| BP | GO:0016264 | gap junction assembly | 0.02614 |
| BP | GO:0032308 | positive regulation of prostaglandin secretion | 0.02614 |
| BP | GO:0034141 | positive regulation of toll-like receptor 3 signaling pathway | 0.02614 |
| BP | GO:0035542 | regulation of SNARE complex assembly | 0.02614 |
| BP | GO:0035627 | ceramide transport | 0.02614 |
| BP | GO:0043097 | pyrimidine nucleoside salvage | 0.02614 |
| BP | GO:0044854 | plasma membrane raft assembly | 0.02614 |
| BP | GO:0048548 | regulation of pinocytosis | 0.02614 |
| BP | GO:0060272 | embryonic skeletal joint morphogenesis | 0.02614 |
| BP | GO:0072584 | caveolin-mediated endocytosis | 0.02614 |
| BP | GO:0099149 | regulation of postsynaptic neurotransmitter receptor internalization | 0.02614 |
| BP | GO:1902882 | regulation of response to oxidative stress | 0.02642 |
| BP | GO:1904029 | regulation of cyclin-dependent protein kinase activity | 0.02642 |
| BP | GO:0032231 | regulation of actin filament bundle assembly | 0.02689 |
| BP | GO:0046928 | regulation of neurotransmitter secretion | 0.02689 |
| BP | GO:0042180 | cellular ketone metabolic process | 0.02733 |
| BP | GO:0050730 | regulation of peptidyl-tyrosine phosphorylation | 0.02733 |
| BP | GO:0035239 | tube morphogenesis | 0.02733 |
| BP | GO:0006996 | organelle organization | 0.02735 |
| BP | GO:0030038 | contractile actin filament bundle assembly | 0.02736 |
| BP | GO:0043149 | stress fiber assembly | 0.02736 |
| BP | GO:2000060 | positive regulation of ubiquitin-dependent protein catabolic process | 0.02736 |
| BP | GO:2001243 | negative regulation of intrinsic apoptotic signaling pathway | 0.02736 |
| BP | GO:0033673 | negative regulation of kinase activity | 0.02759 |
| BP | GO:0006641 | triglyceride metabolic process | 0.02784 |
| BP | GO:0006672 | ceramide metabolic process | 0.02784 |
| BP | GO:0043085 | positive regulation of catalytic activity | 0.02786 |
| BP | GO:0031668 | cellular response to extracellular stimulus | 0.02811 |
| BP | GO:0043266 | regulation of potassium ion transport | 0.02831 |
| BP | GO:0060079 | excitatory postsynaptic potential | 0.02831 |
| BP | GO:0006983 | ER overload response | 0.02849 |
| BP | GO:0008655 | pyrimidine-containing compound salvage | 0.02849 |
| BP | GO:0010649 | regulation of cell communication by electrical coupling | 0.02849 |
| BP | GO:0010739 | positive regulation of protein kinase A signaling | 0.02849 |
| BP | GO:0032306 | regulation of prostaglandin secretion | 0.02849 |
| BP | GO:0034086 | maintenance of sister chromatid cohesion | 0.02849 |
| BP | GO:0034088 | maintenance of mitotic sister chromatid cohesion | 0.02849 |
| BP | GO:0042532 | negative regulation of tyrosine phosphorylation of STAT protein | 0.02849 |
| BP | GO:0044793 | negative regulation by host of viral process | 0.02849 |
| BP | GO:0048251 | elastic fiber assembly | 0.02849 |
| BP | GO:0048703 | embryonic viscerocranium morphogenesis | 0.02849 |
| BP | GO:0051956 | negative regulation of amino acid transport | 0.02849 |
| BP | GO:0060353 | regulation of cell adhesion molecule production | 0.02849 |
| BP | GO:0090394 | negative regulation of excitatory postsynaptic potential | 0.02849 |
| BP | GO:0090520 | sphingolipid mediated signaling pathway | 0.02849 |
| BP | GO:1903044 | protein localization to membrane raft | 0.02849 |
| BP | GO:2000650 | negative regulation of sodium ion transmembrane transporter activity | 0.02849 |
| BP | GO:2001053 | regulation of mesenchymal cell apoptotic process | 0.02849 |
| BP | GO:0048731 | system development | 0.02868 |
| BP | GO:0051247 | positive regulation of protein metabolic process | 0.02906 |
| BP | GO:0097435 | supramolecular fiber organization | 0.02920 |
| BP | GO:0009057 | macromolecule catabolic process | 0.02952 |
| BP | GO:0044249 | cellular biosynthetic process | 0.02987 |
| BP | GO:0033138 | positive regulation of peptidyl-serine phosphorylation | 0.03026 |
| BP | GO:0006807 | nitrogen compound metabolic process | 0.03039 |
| BP | GO:1901990 | regulation of mitotic cell cycle phase transition | 0.03043 |
| BP | GO:0048646 | anatomical structure formation involved in morphogenesis | 0.03063 |
| BP | GO:0010972 | negative regulation of G2/M transition of mitotic cell cycle | 0.03075 |
| BP | GO:0030148 | sphingolipid biosynthetic process | 0.03075 |
| BP | GO:0030241 | skeletal muscle myosin thick filament assembly | 0.03082 |
| BP | GO:0031953 | negative regulation of protein autophosphorylation | 0.03082 |
| BP | GO:0034139 | regulation of toll-like receptor 3 signaling pathway | 0.03082 |
| BP | GO:0044857 | plasma membrane raft organization | 0.03082 |
| BP | GO:0047484 | regulation of response to osmotic stress | 0.03082 |
| BP | GO:0051001 | negative regulation of nitric-oxide synthase activity | 0.03082 |
| BP | GO:0071688 | striated muscle myosin thick filament assembly | 0.03082 |
| BP | GO:0072178 | nephric duct morphogenesis | 0.03082 |
| BP | GO:0090713 | immunological memory process | 0.03082 |
| BP | GO:0097152 | mesenchymal cell apoptotic process | 0.03082 |
| BP | GO:0098903 | regulation of membrane repolarization during action potential | 0.03082 |
| BP | GO:1901160 | primary amino compound metabolic process | 0.03082 |
| BP | GO:1902306 | negative regulation of sodium ion transmembrane transport | 0.03082 |
| BP | GO:1903960 | negative regulation of anion transmembrane transport | 0.03082 |
| BP | GO:2000543 | positive regulation of gastrulation | 0.03082 |
| BP | GO:0034765 | regulation of ion transmembrane transport | 0.03102 |
| BP | GO:0007041 | lysosomal transport | 0.03125 |
| BP | GO:0017158 | regulation of calcium ion-dependent exocytosis | 0.03125 |
| BP | GO:0043269 | regulation of ion transport | 0.03135 |
| BP | GO:0006915 | apoptotic process | 0.03167 |
| BP | GO:0030282 | bone mineralization | 0.03175 |
| BP | GO:0043270 | positive regulation of ion transport | 0.03192 |
| BP | GO:0008630 | intrinsic apoptotic signaling pathway in response to DNA damage | 0.03225 |
| BP | GO:0099565 | chemical synaptic transmission, postsynaptic | 0.03225 |
| BP | GO:0032446 | protein modification by small protein conjugation | 0.03234 |
| BP | GO:0043066 | negative regulation of apoptotic process | 0.03247 |
| BP | GO:0007268 | chemical synaptic transmission | 0.03312 |
| BP | GO:0098916 | anterograde trans-synaptic signaling | 0.03312 |
| BP | GO:0009056 | catabolic process | 0.03316 |
| BP | GO:0006241 | CTP biosynthetic process | 0.03316 |
| BP | GO:0031034 | myosin filament assembly | 0.03316 |
| BP | GO:0036295 | cellular response to increased oxygen levels | 0.03316 |
| BP | GO:0038166 | angiotensin-activated signaling pathway | 0.03316 |
| BP | GO:0043558 | regulation of translational initiation in response to stress | 0.03316 |
| BP | GO:0046036 | CTP metabolic process | 0.03316 |
| BP | GO:0048308 | organelle inheritance | 0.03316 |
| BP | GO:0048313 | Golgi inheritance | 0.03316 |
| BP | GO:0051645 | Golgi localization | 0.03316 |
| BP | GO:0060352 | cell adhesion molecule production | 0.03316 |
| BP | GO:0071287 | cellular response to manganese ion | 0.03316 |
| BP | GO:0072182 | regulation of nephron tubule epithelial cell differentiation | 0.03316 |
| BP | GO:0072498 | embryonic skeletal joint development | 0.03316 |
| BP | GO:0090128 | regulation of synapse maturation | 0.03316 |
| BP | GO:1905522 | negative regulation of macrophage migration | 0.03316 |
| BP | GO:0007346 | regulation of mitotic cell cycle | 0.03328 |
| BP | GO:0031667 | response to nutrient levels | 0.03344 |
| BP | GO:0048519 | negative regulation of biological process | 0.03374 |
| BP | GO:0010811 | positive regulation of cell-substrate adhesion | 0.03378 |
| BP | GO:0070498 | interleukin-1-mediated signaling pathway | 0.03378 |
| BP | GO:0042221 | response to chemical | 0.03378 |
| BP | GO:0052547 | regulation of peptidase activity | 0.03385 |
| BP | GO:0007166 | cell surface receptor signaling pathway | 0.03409 |
| BP | GO:0044087 | regulation of cellular component biogenesis | 0.03427 |
| BP | GO:0070252 | actin-mediated cell contraction | 0.03430 |
| BP | GO:0051248 | negative regulation of protein metabolic process | 0.03431 |
| BP | GO:0045892 | negative regulation of transcription, DNA-templated | 0.03443 |
| BP | GO:0015031 | protein transport | 0.03458 |
| BP | GO:0080134 | regulation of response to stress | 0.03470 |
| BP | GO:0099537 | trans-synaptic signaling | 0.03478 |
| BP | GO:0018107 | peptidyl-threonine phosphorylation | 0.03482 |
| BP | GO:0031325 | positive regulation of cellular metabolic process | 0.03484 |
| BP | GO:0016049 | cell growth | 0.03490 |
| BP | GO:1901576 | organic substance biosynthetic process | 0.03495 |
| BP | GO:0006664 | glycolipid metabolic process | 0.03534 |
| BP | GO:0016079 | synaptic vesicle exocytosis | 0.03534 |
| BP | GO:0035556 | intracellular signal transduction | 0.03534 |
| BP | GO:0001574 | ganglioside biosynthetic process | 0.03548 |
| BP | GO:0007512 | adult heart development | 0.03548 |
| BP | GO:0009209 | pyrimidine ribonucleoside triphosphate biosynthetic process | 0.03548 |
| BP | GO:0030240 | skeletal muscle thin filament assembly | 0.03548 |
| BP | GO:0031033 | myosin filament organization | 0.03548 |
| BP | GO:0032310 | prostaglandin secretion | 0.03548 |
| BP | GO:0035635 | entry of bacterium into host cell | 0.03548 |
| BP | GO:0043248 | proteasome assembly | 0.03548 |
| BP | GO:0044794 | positive regulation by host of viral process | 0.03548 |
| BP | GO:0072075 | metanephric mesenchyme development | 0.03548 |
| BP | GO:2000343 | positive regulation of chemokine (C-X-C motif) ligand 2 production | 0.03548 |
| BP | GO:0051239 | regulation of multicellular organismal process | 0.03567 |
| BP | GO:0051348 | negative regulation of transferase activity | 0.03568 |
| BP | GO:0099536 | synaptic signaling | 0.03580 |
| BP | GO:0031401 | positive regulation of protein modification process | 0.03581 |
| BP | GO:0007613 | memory | 0.03586 |
| BP | GO:1901800 | positive regulation of proteasomal protein catabolic process | 0.03586 |
| BP | GO:1903509 | liposaccharide metabolic process | 0.03586 |
| BP | GO:0010941 | regulation of cell death | 0.03625 |
| BP | GO:0043069 | negative regulation of programmed cell death | 0.03629 |
| BP | GO:0017015 | regulation of transforming growth factor beta receptor signaling pathway | 0.03639 |
| BP | GO:0030163 | protein catabolic process | 0.03643 |
| BP | GO:1902750 | negative regulation of cell cycle G2/M phase transition | 0.03692 |
| BP | GO:0042471 | ear morphogenesis | 0.03746 |
| BP | GO:1903844 | regulation of cellular response to transforming growth factor beta stimulus | 0.03746 |
| BP | GO:0060828 | regulation of canonical Wnt signaling pathway | 0.03749 |
| BP | GO:0000165 | MAPK cascade | 0.03762 |
| BP | GO:0002274 | myeloid leukocyte activation | 0.03772 |
| BP | GO:0051146 | striated muscle cell differentiation | 0.03780 |
| BP | GO:0001765 | membrane raft assembly | 0.03780 |
| BP | GO:0006491 | N-glycan processing | 0.03780 |
| BP | GO:0009130 | pyrimidine nucleoside monophosphate biosynthetic process | 0.03780 |
| BP | GO:0009208 | pyrimidine ribonucleoside triphosphate metabolic process | 0.03780 |
| BP | GO:0043173 | nucleotide salvage | 0.03780 |
| BP | GO:0043174 | nucleoside salvage | 0.03780 |
| BP | GO:0043518 | negative regulation of DNA damage response, signal transduction by p53 class mediator | 0.03780 |
| BP | GO:0072160 | nephron tubule epithelial cell differentiation | 0.03780 |
| BP | GO:0072189 | ureter development | 0.03780 |
| BP | GO:0072224 | metanephric glomerulus development | 0.03780 |
| BP | GO:1902188 | positive regulation of viral release from host cell | 0.03780 |
| BP | GO:1901987 | regulation of cell cycle phase transition | 0.03794 |
| BP | GO:0015833 | peptide transport | 0.03859 |
| BP | GO:0090066 | regulation of anatomical structure size | 0.03906 |
| BP | GO:0001838 | embryonic epithelial tube formation | 0.03908 |
| BP | GO:0018210 | peptidyl-threonine modification | 0.03908 |
| BP | GO:0008610 | lipid biosynthetic process | 0.03915 |
| BP | GO:0042552 | myelination | 0.03962 |
| BP | GO:0002902 | regulation of B cell apoptotic process | 0.04012 |
| BP | GO:0007076 | mitotic chromosome condensation | 0.04012 |
| BP | GO:0007379 | segment specification | 0.04012 |
| BP | GO:0009129 | pyrimidine nucleoside monophosphate metabolic process | 0.04012 |
| BP | GO:0009415 | response to water | 0.04012 |
| BP | GO:0021783 | preganglionic parasympathetic fiber development | 0.04012 |
| BP | GO:0032305 | positive regulation of icosanoid secretion | 0.04012 |
| BP | GO:0033033 | negative regulation of myeloid cell apoptotic process | 0.04012 |
| BP | GO:0072176 | nephric duct development | 0.04012 |
| BP | GO:0086103 | G protein-coupled receptor signaling pathway involved in heart process | 0.04012 |
| BP | GO:0090185 | negative regulation of kidney development | 0.04012 |
| BP | GO:2000121 | regulation of removal of superoxide radicals | 0.04012 |
| BP | GO:2000811 | negative regulation of anoikis | 0.04012 |
| BP | GO:0035270 | endocrine system development | 0.04017 |
| BP | GO:0009058 | biosynthetic process | 0.04050 |
| BP | GO:0009991 | response to extracellular stimulus | 0.04066 |
| BP | GO:0007272 | ensheathment of neurons | 0.04072 |
| BP | GO:0008366 | axon ensheathment | 0.04072 |
| BP | GO:2000134 | negative regulation of G1/S transition of mitotic cell cycle | 0.04072 |
| BP | GO:0001568 | blood vessel development | 0.04081 |
| BP | GO:0016579 | protein deubiquitination | 0.04125 |
| BP | GO:0008152 | metabolic process | 0.04164 |
| BP | GO:1903507 | negative regulation of nucleic acid-templated transcription | 0.04170 |
| BP | GO:0046907 | intracellular transport | 0.04177 |
| BP | GO:0002223 | stimulatory C-type lectin receptor signaling pathway | 0.04184 |
| BP | GO:0019079 | viral genome replication | 0.04184 |
| BP | GO:1902679 | negative regulation of RNA biosynthetic process | 0.04198 |
| BP | GO:0070887 | cellular response to chemical stimulus | 0.04237 |
| BP | GO:0008637 | apoptotic mitochondrial changes | 0.04240 |
| BP | GO:0010766 | negative regulation of sodium ion transport | 0.04243 |
| BP | GO:0014866 | skeletal myofibril assembly | 0.04243 |
| BP | GO:0015732 | prostaglandin transport | 0.04243 |
| BP | GO:0032780 | negative regulation of ATPase activity | 0.04243 |
| BP | GO:0060977 | coronary vasculature morphogenesis | 0.04243 |
| BP | GO:0070166 | enamel mineralization | 0.04243 |
| BP | GO:0071428 | rRNA-containing ribonucleoprotein complex export from nucleus | 0.04243 |
| BP | GO:0098884 | postsynaptic neurotransmitter receptor internalization | 0.04243 |
| BP | GO:0140239 | postsynaptic endocytosis | 0.04243 |
| BP | GO:1900242 | regulation of synaptic vesicle endocytosis | 0.04243 |
| BP | GO:1901550 | regulation of endothelial cell development | 0.04243 |
| BP | GO:1902166 | negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 0.04243 |
| BP | GO:1903140 | regulation of establishment of endothelial barrier | 0.04243 |
| BP | GO:0008284 | positive regulation of cell proliferation | 0.04261 |
| BP | GO:0009966 | regulation of signal transduction | 0.04289 |
| BP | GO:0006639 | acylglycerol metabolic process | 0.04296 |
| BP | GO:0055007 | cardiac muscle cell differentiation | 0.04296 |
| BP | GO:2000736 | regulation of stem cell differentiation | 0.04296 |
| BP | GO:0006638 | neutral lipid metabolic process | 0.04353 |
| BP | GO:0072175 | epithelial tube formation | 0.04353 |
| BP | GO:0051050 | positive regulation of transport | 0.04359 |
| BP | GO:1902807 | negative regulation of cell cycle G1/S phase transition | 0.04410 |
| BP | GO:0007275 | multicellular organism development | 0.04438 |
| BP | GO:0009148 | pyrimidine nucleoside triphosphate biosynthetic process | 0.04474 |
| BP | GO:0035493 | SNARE complex assembly | 0.04474 |
| BP | GO:0035994 | response to muscle stretch | 0.04474 |
| BP | GO:0042693 | muscle cell fate commitment | 0.04474 |
| BP | GO:0044827 | modulation by host of viral genome replication | 0.04474 |
| BP | GO:0045947 | negative regulation of translational initiation | 0.04474 |
| BP | GO:0048486 | parasympathetic nervous system development | 0.04474 |
| BP | GO:0060546 | negative regulation of necroptotic process | 0.04474 |
| BP | GO:0061003 | positive regulation of dendritic spine morphogenesis | 0.04474 |
| BP | GO:0072074 | kidney mesenchyme development | 0.04474 |
| BP | GO:0072079 | nephron tubule formation | 0.04474 |
| BP | GO:2000193 | positive regulation of fatty acid transport | 0.04474 |
| BP | GO:2000341 | regulation of chemokine (C-X-C motif) ligand 2 production | 0.04474 |
| BP | GO:0002220 | innate immune response activating cell surface receptor signaling pathway | 0.04524 |
| BP | GO:0007498 | mesoderm development | 0.04524 |
| BP | GO:0032434 | regulation of proteasomal ubiquitin-dependent protein catabolic process | 0.04524 |
| BP | GO:0015672 | monovalent inorganic cation transport | 0.04544 |
| BP | GO:0045860 | positive regulation of protein kinase activity | 0.04569 |
| BP | GO:0060048 | cardiac muscle contraction | 0.04582 |
| BP | GO:1903052 | positive regulation of proteolysis involved in cellular protein catabolic process | 0.04582 |
| BP | GO:0002479 | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 0.04640 |
| BP | GO:0070646 | protein modification by small protein removal | 0.04690 |
| BP | GO:0032303 | regulation of icosanoid secretion | 0.04703 |
| BP | GO:0032769 | negative regulation of monooxygenase activity | 0.04703 |
| BP | GO:0043586 | tongue development | 0.04703 |
| BP | GO:0045019 | negative regulation of nitric oxide biosynthetic process | 0.04703 |
| BP | GO:0048739 | cardiac muscle fiber development | 0.04703 |
| BP | GO:0048745 | smooth muscle tissue development | 0.04703 |
| BP | GO:0072234 | metanephric nephron tubule development | 0.04703 |
| BP | GO:0098911 | regulation of ventricular cardiac muscle cell action potential | 0.04703 |
| BP | GO:1903204 | negative regulation of oxidative stress-induced neuron death | 0.04703 |
| BP | GO:1904406 | negative regulation of nitric oxide metabolic process | 0.04703 |
| BP | GO:2000696 | regulation of epithelial cell differentiation involved in kidney development | 0.04703 |
| BP | GO:0008285 | negative regulation of cell proliferation | 0.04723 |
| BP | GO:0045184 | establishment of protein localization | 0.04733 |
| BP | GO:0001944 | vasculature development | 0.04764 |
| BP | GO:0012501 | programmed cell death | 0.04803 |
| BP | GO:0006950 | response to stress | 0.04808 |
| BP | GO:0030048 | actin filament-based movement | 0.04816 |
| BP | GO:0051291 | protein heterooligomerization | 0.04816 |
| BP | GO:0009968 | negative regulation of signal transduction | 0.04866 |
| BP | GO:0007569 | cell aging | 0.04875 |
| BP | GO:0042590 | antigen processing and presentation of exogenous peptide antigen via MHC class I | 0.04875 |
| BP | GO:0051588 | regulation of neurotransmitter transport | 0.04875 |
| BP | GO:0002689 | negative regulation of leukocyte chemotaxis | 0.04933 |
| BP | GO:0006907 | pinocytosis | 0.04933 |
| BP | GO:0010042 | response to manganese ion | 0.04933 |
| BP | GO:0032891 | negative regulation of organic acid transport | 0.04933 |
| BP | GO:0036499 | PERK-mediated unfolded protein response | 0.04933 |
| BP | GO:0043555 | regulation of translation in response to stress | 0.04933 |
| BP | GO:0045603 | positive regulation of endothelial cell differentiation | 0.04933 |
| BP | GO:0046132 | pyrimidine ribonucleoside biosynthetic process | 0.04933 |
| BP | GO:0050802 | circadian sleep/wake cycle, sleep | 0.04933 |
| BP | GO:0050951 | sensory perception of temperature stimulus | 0.04933 |
| BP | GO:0055093 | response to hyperoxia | 0.04933 |
| BP | GO:0071636 | positive regulation of transforming growth factor beta production | 0.04933 |
| BP | GO:0072087 | renal vesicle development | 0.04933 |
| BP | GO:0072111 | cell proliferation involved in kidney development | 0.04933 |
| BP | GO:0072567 | chemokine (C-X-C motif) ligand 2 production | 0.04933 |
| BP | GO:0097503 | sialylation | 0.04933 |
| BP | GO:1902165 | regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 0.04933 |
| BP | GO:1903817 | negative regulation of voltage-gated potassium channel activity | 0.04933 |
| BP | GO:1904294 | positive regulation of ERAD pathway | 0.04933 |
| BP | GO:0033135 | regulation of peptidyl-serine phosphorylation | 0.04934 |
| BP | GO:0043618 | regulation of transcription from RNA polymerase II promoter in response to stress | 0.04934 |
| BP | GO:0072358 | cardiovascular system development | 0.04951 |
| BP | GO:0034097 | response to cytokine | 0.04960 |
| BP | GO:0071310 | cellular response to organic substance | 0.04980 |
| BP | GO:0007006 | mitochondrial membrane organization | 0.04994 |
| BP | GO:0070972 | protein localization to endoplasmic reticulum | 0.04994 |
| CC | GO:0030897 | HOPS complex | 0.00050 |
| CC | GO:0032116 | SMC loading complex | 0.00479 |
| CC | GO:0033596 | TSC1-TSC2 complex | 0.00479 |
| CC | GO:0090694 | Scc2-Scc4 cohesin loading complex | 0.00479 |
| CC | GO:0097129 | cyclin D2-CDK4 complex | 0.00479 |
| CC | GO:1904813 | ficolin-1-rich granule lumen | 0.00481 |
| CC | GO:0098559 | cytoplasmic side of early endosome membrane | 0.00718 |
| CC | GO:0035577 | azurophil granule membrane | 0.00885 |
| CC | GO:0071953 | elastic fiber | 0.00957 |
| CC | GO:0098842 | postsynaptic early endosome | 0.00957 |
| CC | GO:1902494 | catalytic complex | 0.01027 |
| CC | GO:0010009 | cytoplasmic side of endosome membrane | 0.01194 |
| CC | GO:0033263 | CORVET complex | 0.01194 |
| CC | GO:0070695 | FHF complex | 0.01194 |
| CC | GO:0030027 | lamellipodium | 0.01244 |
| CC | GO:0031901 | early endosome membrane | 0.01295 |
| CC | GO:1990234 | transferase complex | 0.01567 |
| CC | GO:0005811 | lipid droplet | 0.01584 |
| CC | GO:0099023 | tethering complex | 0.01584 |
| CC | GO:0099503 | secretory vesicle | 0.01603 |
| CC | GO:0101002 | ficolin-1-rich granule | 0.01640 |
| CC | GO:0000502 | proteasome complex | 0.01815 |
| CC | GO:0005769 | early endosome | 0.01825 |
| CC | GO:1905369 | endopeptidase complex | 0.01855 |
| CC | GO:0031252 | cell leading edge | 0.01882 |
| CC | GO:0008541 | proteasome regulatory particle, lid subcomplex | 0.01904 |
| CC | GO:0005925 | focal adhesion | 0.02283 |
| CC | GO:0005924 | cell-substrate adherens junction | 0.02333 |
| CC | GO:0034098 | VCP-NPL4-UFD1 AAA ATPase complex | 0.02375 |
| CC | GO:0030055 | cell-substrate junction | 0.02400 |
| CC | GO:0030141 | secretory granule | 0.02507 |
| CC | GO:0005829 | cytosol | 0.02523 |
| CC | GO:1902554 | serine/threonine protein kinase complex | 0.02543 |
| CC | GO:0030123 | AP-3 adaptor complex | 0.02609 |
| CC | GO:0005884 | actin filament | 0.02823 |
| CC | GO:0032009 | early phagosome | 0.02843 |
| CC | GO:1905368 | peptidase complex | 0.02871 |
| CC | GO:0042470 | melanosome | 0.03266 |
| CC | GO:0048770 | pigment granule | 0.03266 |
| CC | GO:0098845 | postsynaptic endosome | 0.03309 |
| CC | GO:1902911 | protein kinase complex | 0.03523 |
| CC | GO:0098993 | anchored component of synaptic vesicle membrane | 0.03541 |
| CC | GO:0015629 | actin cytoskeleton | 0.03652 |
| CC | GO:0000151 | ubiquitin ligase complex | 0.03737 |
| CC | GO:0016581 | NuRD complex | 0.03773 |
| CC | GO:0090545 | CHD-type complex | 0.03773 |
| CC | GO:0035098 | ESC/E(Z) complex | 0.04004 |
| CC | GO:0005938 | cell cortex | 0.04177 |
| CC | GO:0031982 | vesicle | 0.04195 |
| CC | GO:1990111 | spermatoproteasome complex | 0.04464 |
| CC | GO:0101031 | chaperone complex | 0.04923 |
| MF | GO:0016301 | kinase activity | 0.00030 |
| MF | GO:0097493 | structural molecule activity conferring elasticity | 0.00033 |
| MF | GO:0004861 | cyclin-dependent protein serine/threonine kinase inhibitor activity | 0.00046 |
| MF | GO:0019900 | kinase binding | 0.00049 |
| MF | GO:0016772 | transferase activity, transferring phosphorus-containing groups | 0.00104 |
| MF | GO:0019901 | protein kinase binding | 0.00127 |
| MF | GO:0070320 | inward rectifier potassium channel inhibitor activity | 0.00248 |
| MF | GO:0099038 | ceramide-translocating ATPase activity | 0.00248 |
| MF | GO:0102773 | dihydroceramide kinase activity | 0.00248 |
| MF | GO:0030291 | protein serine/threonine kinase inhibitor activity | 0.00320 |
| MF | GO:0019899 | enzyme binding | 0.00413 |
| MF | GO:0001729 | ceramide kinase activity | 0.00495 |
| MF | GO:0004615 | phosphomannomutase activity | 0.00495 |
| MF | GO:0033149 | FFAT motif binding | 0.00495 |
| MF | GO:0090555 | phosphatidylethanolamine-translocating ATPase activity | 0.00495 |
| MF | GO:0051879 | Hsp90 protein binding | 0.00556 |
| MF | GO:0016538 | cyclin-dependent protein serine/threonine kinase regulator activity | 0.00630 |
| MF | GO:1904121 | phosphatidylethanolamine transporter activity | 0.00741 |
| MF | GO:0016740 | transferase activity | 0.00803 |
| MF | GO:0004370 | glycerol kinase activity | 0.00987 |
| MF | GO:0004694 | eukaryotic translation initiation factor 2alpha kinase activity | 0.00987 |
| MF | GO:0004849 | uridine kinase activity | 0.00987 |
| MF | GO:0050178 | phenylpyruvate tautomerase activity | 0.00987 |
| MF | GO:0090554 | phosphatidylcholine-translocating ATPase activity | 0.00987 |
| MF | GO:0000978 | RNA polymerase II proximal promoter sequence-specific DNA binding | 0.01072 |
| MF | GO:0045182 | translation regulator activity | 0.01165 |
| MF | GO:0000987 | proximal promoter sequence-specific DNA binding | 0.01188 |
| MF | GO:0004860 | protein kinase inhibitor activity | 0.01199 |
| MF | GO:0001727 | lipid kinase activity | 0.01232 |
| MF | GO:0003828 | alpha-N-acetylneuraminate alpha-2,8-sialyltransferase activity | 0.01232 |
| MF | GO:0004167 | dopachrome isomerase activity | 0.01232 |
| MF | GO:0016862 | intramolecular oxidoreductase activity, interconverting keto- and enol-groups | 0.01232 |
| MF | GO:0003690 | double-stranded DNA binding | 0.01293 |
| MF | GO:0019210 | kinase inhibitor activity | 0.01375 |
| MF | GO:0019887 | protein kinase regulator activity | 0.01387 |
| MF | GO:0042030 | ATPase inhibitor activity | 0.01477 |
| MF | GO:0000977 | RNA polymerase II regulatory region sequence-specific DNA binding | 0.01495 |
| MF | GO:0001012 | RNA polymerase II regulatory region DNA binding | 0.01554 |
| MF | GO:0033613 | activating transcription factor binding | 0.01679 |
| MF | GO:0031433 | telethonin binding | 0.01721 |
| MF | GO:0005113 | patched binding | 0.01964 |
| MF | GO:0008140 | cAMP response element binding protein binding | 0.01964 |
| MF | GO:0035620 | ceramide transporter activity | 0.01964 |
| MF | GO:0038036 | sphingosine-1-phosphate receptor activity | 0.01964 |
| MF | GO:0019207 | kinase regulator activity | 0.02018 |
| MF | GO:0000976 | transcription regulatory region sequence-specific DNA binding | 0.02050 |
| MF | GO:0019870 | potassium channel inhibitor activity | 0.02207 |
| MF | GO:0030023 | extracellular matrix constituent conferring elasticity | 0.02207 |
| MF | GO:0005522 | profilin binding | 0.02449 |
| MF | GO:0008525 | phosphatidylcholine transporter activity | 0.02449 |
| MF | GO:0019206 | nucleoside kinase activity | 0.02449 |
| MF | GO:1990837 | sequence-specific double-stranded DNA binding | 0.02548 |
| MF | GO:0043565 | sequence-specific DNA binding | 0.02638 |
| MF | GO:0016868 | intramolecular transferase activity, phosphotransferases | 0.02691 |
| MF | GO:0033691 | sialic acid binding | 0.02691 |
| MF | GO:0000980 | RNA polymerase II distal enhancer sequence-specific DNA binding | 0.02790 |
| MF | GO:0005515 | protein binding | 0.02796 |
| MF | GO:0046624 | sphingolipid transporter activity | 0.02932 |
| MF | GO:0005041 | low-density lipoprotein particle receptor activity | 0.03172 |
| MF | GO:0005488 | binding | 0.03177 |
| MF | GO:0045125 | bioactive lipid receptor activity | 0.03412 |
| MF | GO:0044212 | transcription regulatory region DNA binding | 0.03640 |
| MF | GO:0032794 | GTPase activating protein binding | 0.03651 |
| MF | GO:0050998 | nitric-oxide synthase binding | 0.03651 |
| MF | GO:0001067 | regulatory region nucleic acid binding | 0.03670 |
| MF | GO:0047485 | protein N-terminus binding | 0.03783 |
| MF | GO:0030228 | lipoprotein particle receptor activity | 0.03890 |
| MF | GO:0044325 | ion channel binding | 0.04064 |
| MF | GO:0050839 | cell adhesion molecule binding | 0.04064 |
| MF | GO:0035497 | cAMP response element binding | 0.04128 |
| MF | GO:0051371 | muscle alpha-actinin binding | 0.04128 |
| MF | GO:0001158 | enhancer sequence-specific DNA binding | 0.04178 |
| MF | GO:0016773 | phosphotransferase activity, alcohol group as acceptor | 0.04264 |
| MF | GO:0005178 | integrin binding | 0.04470 |
| MF | GO:0003951 | NAD+ kinase activity | 0.04603 |
| MF | GO:0016863 | intramolecular oxidoreductase activity, transposing C=C bonds | 0.04603 |
| MF | GO:0046982 | protein heterodimerization activity | 0.04710 |
| MF | GO:0031072 | heat shock protein binding | 0.04768 |

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| Table 3 KEGG enrichment results | | | | |
| classification A | classification B | KEGG ID | pathway | P-value |
| Cellular Processes | Cell growth and death | ko04110 | Cell cycle | 0.0048218 |
| Human Diseases | Infectious diseases | ko05169 | Epstein-Barr virus infection | 0.008727 |
| Genetic Information Processing | Folding, sorting and degradation | ko03050 | Proteasome | 0.0127135 |
| Organismal Systems | Aging | ko04211 | Longevity regulating pathway - mammal | 0.0322073 |
| Human Diseases | Cancers | ko05203 | Viral carcinogenesis | 0.0323794 |
| Organismal Systems | Endocrine system | ko04928 | Parathyroid hormone synthesis, secretion and action | 0.0392567 |
| Environmental Information Processing | Signal transduction | ko04152 | AMPK signaling pathway | 0.0468405 |
| Metabolism | Amino acid metabolism | ko00360 | Phenylalanine metabolism | 0.0475716 |
| Cellular Processes | Transport and catabolism | ko04140 | Autophagy - animal | 0.0494805 |