0.0175071864167264 ion binding 0.00554326948461673 guanyl-nucleotide exchange factor activity 0.00263301972619241 NADH dehydrogenase (ubiquinone) activity 0.0309707540076524 flavin adenine dinucleotide binding 0.0108954554562625 electron transfer activity voltage-gated ion channel activity 0.0203117696110609 voltage-gated calcium channel activity involved in positive regulation of presynaptic cytosolic calcium levels 0.0145986780765393 ubiquitin-like modifier activating enzyme activity 0.00974673163076518 transmembrane receptor protein serine/threonine kinase activity 0.0143942200141092 transforming growth factor beta receptor activity, type 0.00422559493115674 spermine:oxygen oxidoreductase (spermidine-forming) activity 0.0175220740770618 solute:proton antiporter activity 0.0350786868787837 small molecule binding 0.013898772308817 signaling receptor activator activity 0.019211729034885 riboflavin transmembrane transporter activity 0.00921761403395423 polyamine oxidase activity 0.0220819986001925 phosphatase activator activity 0.0340658011898242 peptidase activator activity 0.00422559493115674 norspermine:oxygen oxidoreductase activity 0.00422559493115674 N1-acetylspermine:oxygen oxidoreductase (3-acetamidopropanal-forming) activity 0.00422559493115674 N1-acetylspermidine:oxygen oxidoreductase (3-acetamidopropanal-forming) activity 0.0339337040685974 ionotropic glutamate receptor binding 0.0370453749215416 quanvl nucleotide binding 0.00377484049634302 glycine-tRNA ligase activity 0.00504163952258754 glycerol kinase activity 0.0200483522935589 folic acid binding 0.00911092352785795 ethanol binding 0.0237298967477823 dipeptidase activity 0.0148059232597885 dimethylglycine dehydrogenase activity calcium-independent protein kinase C activity 0.00911092352785795 calcium-dependent protein kinase C activity 0.0215441919564352 0.00528937695178148 BMP receptor activity 0.00974673163076518 BMP binding 0.00812198803532114 bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) activity 0.00565458694960487 Atg8 activating enzyme activity Atg12 activating enzyme activity 0.00565458694960487 0.0280219981921447 ammonium transmembrane transporter activity 0.0472566631304238 actin monomer binding 0.0447991388980873 1-phosphatidylinositol binding 0.0146257994914612 early endosome 0.0255123079804608 organelle 0.0385527288691505 lamellipodium 0.0294539516678126 external side of plasma membrane 0.0103029735867807 adherens junction 0.029235944430786 WASH complex 0.0170558006577591 uropod 0.0216314932581692 spermatoproteasome complex 0.030201637024793 proteasome complex 0.0490870652312004 presynaptic cytosol 0.0143853951340217 plant-type cell wall 0.0426349359737887 nucleosome MMXD complex 0.0350084597695118 immunological synapse 0.00528937695178148 HFE-transferrin receptor complex 0.0091979546267608 fungal-type cell wall 0.0277394173333058 flotillin complex 0.0323182534612337 dopaminergic synapse 0.0175064031244791 **CIA** complex 0.0225253076623475 cell-cell contact zone 0.00921761403395423 apoplas retina development in camera-type eye 0.0126081088579642 0.0322605276408956 positive regulation of neuron projection development 7.14626546270518e-05 positive regulation of mucus secretion 0.0136267357849581 positive regulation of GTPase activity positive regulation of epithelial cell migration 0.00559661385999873 nitrogen compound metabolic process 0.0176263611419219 0.0011445692947202 neural crest cell development 0.0276945134827111 nervous system process 0.000512721640645256 eve morphogenesis 0.00191969934452142 electron transport chain cellular response to nerve growth factor stimulus 0.00636895694398089 0.0282304903594218 viral process ventricular trabecula myocardium morphogenesis 0.022580629226894 0.0427717193090034 ventricular septum morphogenesis 0.0243797283367982 ventricular compact myocardium morphogenesis 0.0387732401298491 triglyceride metabolic process 0.00528937695178148 tricuspid valve morphogenesis transmembrane receptor protein serine/threonine kinase signaling pathway 0.0336291730746741 0.00911092352785795 TRAM-dependent toll-like receptor 4 signaling pathway 0.00422559493115674 thermospermine catabolic process 0.024185742070638 tetrahydrofolate interconversion 0.00565458694960487 suppression by virus of host autophagy 0.0328416771855385 sterol transpor 0.00422559493115674 spermine catabolic process 0.00422559493115674 spermidine catabolic process 0.0243264313914578 spermatogenesis, exchange of chromosomal proteins 0.0307526576900487 sorocarp development 0.0110511743719755 somatic muscle development 0.0345786071368907 sensory processing 0.0292850128345418 sensory perception of touch 0.0162898858131305 sensory perception of chemical stimulus 0.019211729034885 riboflavin transport 0.0495696205512648 response to UV 0.0282313217057335 response to salt 0.00877061110338495 response to methamphetamine hydrochloride response to fluoride 0.0103854890598208 regulation of Rho protein signal transduction 0.0295069066276025 regulation of receptor internalization 0.0380195413532669 0.0139660922558379 regulation of protein serine/threonine kinase activity 0.0229687594926099 regulation of peptidyl-tyrosine phosphorylation 0.00930041630621834 regulation of neurotransmitter uptake 0.0256142466194413 regulation of lateral mesodermal cell fate specification 0.022135443472799 regulation of hemopoiesis 0.0103943112885653 regulation of cellular senescence regulation of cell junction assembly 0.0112375364627894 ontology 0.0436908884898867 regulation of cell development 0.00740772919760068 Rap protein signal transduction BP 0.0244195327622303 pyramidal neuron development proteoglycan biosynthetic process 0.0340801843356912 CC 0.0474967675517345 protein monoubiquitination 0.024796911967536 protein maturation by iron-sulfur cluster transfer MF 0.0199428248541833 protein localization to membrane raft 0.0238110376110023 protein localization to endosome 0.0213252332482076 protein lipidation protein kinase C signaling 0.0281527299608775 proteasomal ubiquitin-independent protein catabolic process 0.0164375671391085 positive regulation of wound healing positive regulation of vascular smooth muscle cell proliferation 0.0384404991151804 0.046221738032613 0.00528937695178148 positive regulation of transforming growth factor beta2 production positive regulation of toll-like receptor 3 signaling pathway 0.00932811945282608 0.0477559813553117 positive regulation of synaptic transmission, GABAergic 0.00902975966646492 positive regulation of synaptic transmission, dopaminergic 0.0277457059519351 positive regulation of SMAD protein signal transduction 0.0198978865976898 positive regulation of skeletal muscle tissue development 0.0334334776164589 positive regulation of Rho protein signal transduction 0.0247586835211774 positive regulation of protein serine/threonine kinase activity 0.0416910040750223 positive regulation of pri-miRNA transcription by RNA polymerase I 0.0164115491476105 positive regulation of positive chemotaxis 0.00766824434265085 positive regulation of phosphate metabolic process 0.0435663201598523 positive regulation of pathway-restricted SMAD protein phosphorylation 0.0132012006949089 positive regulation of myoblast fusion 0.00911092352785795 positive regulation of lipid catabolic process 0.00941640385787171 positive regulation of heterotypic cell-cell adhesion 0.0109973599842523 positive regulation of extrinsic apoptotic signaling pathway via death domain receptors 0.0180366831051611 positive regulation of chondrocyte differentiation positive regulation of cellular glucuronidation 0.0350305976439402 positive regulation of cell-substrate adhesion 0.0202970379390774 positive regulation of cell-cell adhesion mediated by cadhering 0.00995466249158722 positive regulation of cell junction assembly 0.0194420680706162 positive regulation of cell adhesion molecule production 0.00528937695178148 positive regulation of cardiac ventricle development 0.00510659111748354 positive regulation of AMPA glutamate receptor clustering 0.0107714406850367 positive regulation by symbiont of host autophagy 0.00528433077891416 plasma membrane raft assembly 0.0401566382436185 pituitary gland development 0.0143625014285401 pharyngeal arch artery morphogenesis 0.00528937695178148 paraxial mesoderm structural organization 0.0290988138638099 oviposition 0.00528937695178148 ovarian cumulus expansion neural plate mediolateral regionalization 0.00528937695178148 0.018529139036507 nerve growth factor signaling pathway 0.00565458694960487 negative stranded viral RNA replication 0.00565458694960487 negative regulation of sphingolipid biosynthetic process 0.0128567755420075 negative regulation of sodium ion transmembrane transporter activity negative regulation of smooth muscle cell migration 0.0199358963488429 0.0127068260865469 negative regulation of response to drug negative regulation of release of sequestered calcium ion into cytosol 0.0127068260865469 0.0344943978007203 negative regulation of oxidative stress-induced neuron death 0.0153439692977812 negative regulation of muscle cell differentiation 0.0260928685694574 negative regulation of mitochondrial membrane potential 0.00565458694960487 negative regulation of mitochondrial DNA replication 0.0127068260865469 negative regulation of mitochondrial calcium ion concentration negative regulation of inward rectifier potassium channel activity 0.00915109055167422 0.00565458694960487 negative regulation of histone H4–K16 acetylation 0.00974673163076518 negative regulation of chondrocyte proliferation 0.0169536878861784 muscle attachmen 0.0104549422346041 Mullerian duct regression 0.0152578082109687 mitral valve morphogenesis 0.0238909217864333 mesendoderm development 0.0135696569826712 marginal zone B cell differentiation 0.0222489106658009 macrophage activation involved in immune response 0.0230254427138125 lipopolysaccharide-mediated signaling pathway 0.00366977801489268 lateral root morphogenesis 0.0218011352498467 insulin-like growth factor receptor signaling pathway 0.0102516309563114 induction of synaptic vesicle exocytosis by positive regulation of presynaptic cytosolic calcium ion concentration 0.0235310246727933 hindlimb morphogenesis heart formation 0.00377484049634302 glycyl-tRNA aminoacylation 0.0188518041524188 glycine metabolic process 0.00504163952258754 glycerol-3-phosphate biosynthetic process glycerol metabolic process 0.00528937695178148 fibrous ring of heart morphogenesis 0.0141844807266093 Fc-gamma receptor signaling pathway involved in phagocytosis 0.0365265137392964 extracellular matrix disassembly 0.0200762010930417 estrogen biosynthetic process 0.00510659111748354 establishment of natural killer cell polarity 0.0210798374371218 establishment of endothelial barrie 0.010266755158384 endosome to plasma membrane protein transport 0.0182511387793764 endochondral bone morphogenesis 0.0106832523838366 endocardial cushion formation 0.0191879899017756 ectoderm developmen 0.0228174820335812 dsRNA transport 0.00989889630397959 dorsal aorta morphogenesis 0.00909038181802042 diadenosine tetraphosphate biosynthetic process 0.0127068260865469 dense core granule exocytosis 0.0213529015303508 dauer larval development 0.0232693112959128 0.0110253321033741 chaperone-mediated autophagy 0.0267047212661226 cerebellar Purkinje cell layer developmen 0.0155104612930288 central nervous system neuron axonogenesis 0.0114066580899907 cellular sphingolipid homeostasis cellular response to reactive oxygen species 0.0323525003223095 0.032553671043143 cellular response to prostaglandin E stimulus 0.043272832404156 cellular response to platelet-derived growth factor stimulus -0.00965016805643528 cellular response to morphine 0.0186656813215698 cellular response to hyperoxia cellular response to exogenous dsRNA 0.0251183037385812 0.0433049514227488 cartilage condensation 0.0297165963330392 cardiac right ventricle morphogenesis 0.0435359092494429 calcium ion import BMP signaling pathway involved in heart development 0.00950287104719153 0.0260482257794153 B cell homeostasis 0.0244457489642103 autophagy of mitochondrion 0.00967974670545373 atrioventricular node cell development 0.0319838847505113 anterior head development 0.0196014822213557 ammonium transmembrane transport 0.00565458694960487 amino acid homeostasis