0.0164145840912634 0.0177815710433178 transmembrane transporter ac RNA polymerase II cis-regulatory region sequence-specific DNA bin gated channel ac FAD bin 0.00275188243191773 0.000219917336383188 ubiquitin-protein transferase activator Hsp90 protein l 0.00907364333129377 extracellular ligand-gated monoatomic ion channel ac acetylcholine-gated monoatomic cation-selective channel ac sulfide quinone oxidoreductase a sugar transmembrane transporter a oxidoreductase activity, acting on the CH-CH group of d MAP kinase kinase a 0.0048581925052706 8.82293232856132e-05 0.0132643105841583 0.00636050058930757 0.00437836182575443 hydrolase activity, hydrolyzing in Hsp70 protein binding fructose transmembrane transporter activity dehydroascorbic acid transmembrane transporter activity acetylcholine receptor activity 1-acylglycerol-3-phosphate O-acyltransferase activity trehalose transmembrane transporter activity trehalose transmembrane transporter activity translation elongation factor binding TORC2 complex binding RNA-3'-phosphate cyclase activity activity transmembrane transporter activity translation elongation factor binding RNA-3'-phosphate cyclase activity transmembrane transcription regulatory region sequence-specific DNA binding regulatory RNA binding protein adenylytransferase activity activity activity transferase activity activi 0.0275852290562625 0.0012951456322559 0.001/29514953/2599 0.003728242888608 0.0126983456794979 0.00741485332222667 0.00410560664722527 0.0374033185348288 0.00989190504256872 0.0285371838828164 0.0196744468317107 0.0399672284771285 0.0456131889086253 0.0196864287363995 PTB domain binding protein adenylyltransterase activity proline dehydrogenase activity phosphatidic acid transfer activity phosphatidic acid transfer activity phosphatidic acid transfer activity phosphatidic acid transfer activity oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor methionine–tRNA ligase activity methionine adenosyltransferase activity methionine adenosyltransferase activity 0.0406189592015332 0.0268704835388554 0.0268/04835388554 0.0402924726226616 0.0296330263162711 0.0420052294021302 0.0317197040093465 0.0274384954498306 0.040676843724965 0.0160713676079029 0.0100713070073023 0.0477888396818788 0.0098919122808378 0.0196864287362803 0.0293845038548549 0.0484951015733041 hydroxymethylglutaryl–CoA reductase (NADPH) a hexokinase ac guanylate cyclase activator ac glutamate–5–semialdenyde denydrogenase ac glutamate 5–kinase ac 0.0196864284914942 glucokinase ac gamma-glutamylcyclotransferase ac 0.0200448915754808 0.0382561441227617 0.0219100540318735 diaminephosphotransterase active epoxide hydrolase active epoxide hydrolase active epoxide hydrolase active Description of the provide hydrolase activity Description of the provide hydrolase activity C-4 methylsterol oxidase activity butyryl-CoA dehydrogenase activity anaphase-promoting complex binding adenylate cyclase activator activity activity 0.00954512042795304 0.0284327407224135 0.028432/40/224135 0.00927985046646266 0.0248086594575899 0.0483884689925619 0.0196864287360016 0.0478877943956186 acetyltransferase activator activity 8-methylthiopropyl glucosinolate, S-oxygenase activity 5'-nucleotidase activity 4-methylthiopropyl glucosinolate S-oxygenase activity 3-phosphoinositide-dependent protein kinase binding 3-oxo-5-alpha-steroid 4-dehydrogenase activity endoplasmic reticulum membrane cell cortex SCF ubiquitin ligase complex low-density lipoprotein particle dopaminergic synapse cholinergic synapse anaphase-promoting complex acetylcholine-gated channel complex -8-methylthiopropyl glucośinolate S 0.00821748014254507 0.0426362494131657 0.00821748014254507 0.00156759028320274 0.0482650647029973 5.57709495012803e-05 0.000875420772098635 0.0164055230884816 0.0111331165895799 acetylcholine—gated channel complex - Volk - Volk - Volk - Slx1—Slx4 complex - Slx1—Slx4 complex - Site of polarized growth - radial spoke head - pole plasm - po 0.0196864287362778 0.0196822631293605 0.0378955690240113 0.034467661587426 myosin filament
MWP complex MWP complex muscle myosin complex methionine adenosyltransferase complex insulin receptor complex insulin receptor complex extrinsic component of postsynaptic specialization membrane extrinsic component of neuronal dense core vesicle membrane complement component C1 complex cell sufface receptor signaling pathway negative regulation of gene expression anatomical structure morphogenesis vesicle - mediated transport positive regulation of macromolecule metabolic process endocvtosis -0.0479055913647316 0.0364477375839159 0.00989191228083781 0.0434684683862228 0.0258390472628767 0.030995803613596 positive regulation of macromolecule metabolic process endocytosis - response to hypoxia - response to abiotic stimulus anatomical structure formation involved in morphogenesis - response to abiotic stimulus anatomical structure formation involved in morphogenesis - response to heat response to heat - response to heat - response to heat - regulation of protein metabolic process - positive regulation of transcription of nucleolar large rRNA by RNA polymerase I - negative regulation of Notch signaling pathway - response to involve a positive regulation of Notch signaling pathway - insulin receptor signaling pathway - inorganic cation transper pathway - glutathione biosynthetic process - embryonic heart left/right asymmetry - detection of stimulus - cholesterol transport - cholesterol transport - behavioral response to nicotine -0.0309157370110513 0.0364271467163921 0.02619251423703 0.0195641352534222 0.0466107307883671 7.39297936648336e-05 0.00357081241986138 0.0383607687400617 0.00485679550531705 0.028276426982798 0.028276426982798 0.00518600795066683 0.0137073683127 0.0186071730869273 0.0075465061730759 0.00113754585209442 behavioral response to nicotine amyloid-beta clearance zymogen activation telencephalon development 0.0008570325936332 0.000368606073346319 0.0254616389921634 0.0451922824198265 0.000553698859821245 0.000531341628752261 telencephalon development
synaptic transmission involved in micturition
sulfide oxidation, using sulfide: quinone oxidoreductase
steroid metabolic process
sexual reproduction
sensory perception of taste
response to food
regulation of dendrite morphogenesis
regulation of circadian rhythm
proximal/distal pattern formation 0.0416811415693858 0.0322882093749414 0.0322882093749414 0.0157695777856981 0.0320222743915681 0.014677870829473 0.04657412247376 0.0143263626405517 provintal distance protein tetramerization protein heteramerization protein homotrimerization protein heterooligomerization protein heterooligomerization positive regulation of macrophage derived foam cell differentiation positive regulation of cholesterol storage plasma lipoprotein particle clearance phosphatic acid higsynthetic process 0.0387775843690959 0.00840694065744634 0.00131854998796812 0.000573346009011435 0.000915768464923764 0.000921664764561451 0.0124322680951348 0.0115696258034541 0.0275219667999293 0.00843509088783757 0.0259445336382974 0.00497894197640997 0.0370768821971032 0.0149056724050818 ontology 0.0365426126477855 BP 0.0068783421666728 0.0012951456322559 0.00388446269612418 0.003728242888608 CC denydroascorbic acid transport cytolysis cerebellum development cellular detoxification of cadmium ion anaphase–promoting complex–dependent catabolic process vitamin B6 metabolic process vesicle docking type I pneumocyte differentiation trehalose transport 0.0228357125718001 MF 0.0388446587274326 0.000633146889904759 0.00517713860304313 0.00562655588113441 0.0474955374821043 0.0286110081510558 0.0374033185348288 0.0293829711181447 0.0293029711161447 0.0293010942378449 0.0430115495587162 0.0196864287363032 0.0293671939599571 transmembrane receptor protein tyrosine phosphatase signa transition between fast a transformation of hos trachea formation
telomeric D-loop disassembly
t-circle formation
subpallium development
stem vascular tissue pattern formation
spermine acetylation
specification of proximal tubule identity
skin epidermis development 0.0444861711247874 0.0444621069462164 0.0146251283702518 0.0293829711181447 0.00804417813101266 0.00804417813101266 0.00555591376904829 0.0291822319734934 0.0272802349630597 0.0196864287362778 response to vanadate(3-)
response to resveratrol
response to melanocyte-stimulating hormone
regulation of vascular endothelial growth factor signaling pathway
regulation of the force of skeletal muscle contraction
regulation of slow-twitch skeletal muscle fiber contraction
regulation of myosin-light-chain-phosphatase activity
regulation of myosin-light-chain-phosphatase activity
regulation of medite huclear division
regulation of myosin-light-chain-phosphatase activity
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regulation of themale gonad development
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regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway
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regulation of synapse maturation positive regulation of synapse maturation positive regulation of RNA biosynthetic process positive regulation of respiratory burst positive regulation of protein localization to nucleolus positive regulation of protein localization to nucleolus positive regulation of protein insertion into mitochondrial outer membrane positive regulation of menotaxis to cAMP positive regulation of mRNA polyadenylation positive regulation of menotic cell cycle process involved in occyte maturation positive regulation of medicic cell cycle process involved in occyte maturation positive regulation of immature I cell proliferation in thymus positive regulation of glycoprotein biosynthetic process positive regulation of glycoprotein biosynthetic process positive regulation of cell cycle process positive regulation of fatty acid oxidation positive regulation of cell cycle phase transition positive regulation of cell cycle phase transition positive regulation of amacrine cell 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glucose 6-phosphate metabolic proces dominis developmer 0.020646524870784 0.00989191196127756 0.0124913478855628 GABAergic neuron differentiation in basal dangli 0.00864539435300204 epithelial cell proliferation in cell alian in dandia darigitation fatty acid derivative biosynthetic process epithelial cell proliferation involved in lung morphogenesis endothelial tip cell fate specification embryonic liver development embryonic liver development cytokinesis cotyledon vascular tissue pattern formation complement activation, classical pathway citrulline biosynthetic process chondrocyte intercalation involved in growth plate cartilage morphogenesis cerebral cortex GABAergic interneuron fate commitment cerebellar Purkinje cell layer structural organization cerebellar molecular layer formation cerebellar response to sodium arsenite cellular response to sodium arsenite cellular response to diamide cellular response to diamide cellular response to camping hormone carbohydrate transmembrane transport blastoderm segmentation anterograde neuronal dense core vesicle transport activation of transmembrane receptor protein tyrosine kinase activity abscisic acid—activated signaling pathway abscisic acid transport telepasing pathway telepasing pathway abscisic acid transport telepasing pathway telepasing pathway appects acid transport telepasing pathway telepas 0.00989191228073119 0.0196864287363995 0.0279402109269492 0.0313418902649525 0.0293829711181447 0.0162961395704561 0.0389855651710524 0.0300371445180775 0.0290480203781593 0.0190454888586518 0.0180469364818167 0.0052322327546541 0.0363258253786083 0.0196864287363995 0.0196864287363995 0.0385331845515077 0.0289577272090603 0.00989191228043569 0.00989190504256872 0.0484951015725381 0.0365243219880626 0.0238571793428137 0.0217917605459172 0.0196864287359961 0.0196864287363995 0.018269417411713 0.0186437447321638 0.0196848807568753 0.0293833368795402