0.0164145840912669 0.00491715407751183 0.0177815710435756 transmembrane transporter activity

RNA polymerase II cis–regulatory region sequence–specific DNA bindin
gated channel activity

FAD bindin 0.00188459241942239 0.00275188243189706 0.000219917336385679 ubiquitin-protein transferase activator a 0.00907364333127041 0.00027197183555405 extracellular ligand-gated ion channel ad 0.0462619877296831 acetylcholine-gated cation-selective channel a sulfide:quinone oxidoreductase a 0.00485819250537245 0.00129514563228159 sugar transmembrane transporter activity oxidoreductase activity, acting on the CH–CH group of donor MAP kinase kinase activity 0.0459427654326638 0.0132643105841775 hydrolase activity, hydrolyzing N-glycosy, HSp/O protein binding I HSp/O protein binding I fructose transmembrane transporter activity of dehydroascorbic acid transmembrane transporter activity acetylcholine receptor activity trehalose transmembrane transporter activity translation elongation factor bind translation elongation factor bind RNA-3'-phosphate cyclase activity acetylcholine regulatory RNA by activity region sequence-specific DNA bir regulatory RNA by a factor bind regulator bind regulator bind regulator by a factor bind regulator bin low-density lipoprotein r hydrolase activity, hydrolyzing N-glyco 0.027585229056267 0.00129514563228159 0.00372824288866177 0.003/2824288661/7 0.0126983456795568 0.00741485332235475 0.0041050606472462 0.0374033185354154 0.00989190504257365 0.0285371838830197 0.0196744468317401 RNA polymerase II intronic transcription regulatory region sequence—specific regulatory 0.0399672284773274 0.0402924726226483 0.0296330263163055 peptide-methionine (R)-S-oxide reductase activit oxidoreductase activity, acting on a sulfur group of donors, disulfide as accepto methionine-tRNA ligase activit 0.02743849544959 0.0406768437250163 0.00989191228070898 0.0160713676077876 0.0477888396815131 0.00989191228071346 0.0196864287360688 0.0293845038545243 hydroxymethylglutaryl–CoA reductase (NADPH) 0.0287622397719321 0.024816869947206 0.0196864287358718 0.00989191228071346 0.0196864284913715 0.0200448915756612 0.0382561441227437 guanylate cyclase activator aci glutamate–5–semialdenyde dehydrogenase aci glutamate 5–kinase aci gamma-glutamylcyclotransferase a 0.0219100540320316 ethanolaminephosphotransferase activity
epoxide hydrolase activity
epoxide hydrolase activity
diamine N-acetyltransferase activity
D5 dopamine receptor binding
D-glucose transmembrane transporter activity
C-4 methylsterol oxidase activity
butyryl-CoA dehydrogenase activity
anaphase-promoting complex binding
adenylate cyclase activator activity
acetyltransferase activator activity
8-methylthiopropyl glucosinolate S-oxygenase activity 0.00930573807123737 0.00927985046659682 0.024808659457558 0.0196864287358718 0.0478877943954999 0.00821748014256852 0.0426362494135709 acetyltransferase activator activity acetyltransferase activator activity 4—methylthiopropyl glucosinolate S—oxygenase 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 corriex—SCF ubiquitin ligase complex—low—density lipoprotein particle—integral component of postsynaptic specialization membrane—dopaminergic synapse—cholinergic synapse—anaphase—promoting complex—acetylcholine—gated channel complex—acetylcholine—gated channel complex—site of polarized growth—radial spoke head—pole plasm—origin recognition complex—nuclear outer membrane—NuA3b histone acetyltransferase complex—NuA3a histone acetyltransferase complex—myosin filament—myosin filament—muscle myosin comblex—muscle myosin comblex—myosin comblex—myosin comblex—muscle myosin comblex—myosin comb 0.00821748014256852 0.019686428736067 0.0128189021408885 0.00156759028319025 0.048265064703014 5.57709495013346e-05 0.0373957474146012 0.000875420772104194 0.0164055230887518 0.0111331165894898 0.017133110305408 0.022919522450641 0.019686428736067 0.0196822631292974 0.0162521564267641 0.01956721181861 0.0480134391772181 0.0378955690242564 0.0344676615875843 0.0094950320224315 0.0247558250737053 0.0293845038545664 myosin MWP 0.00987305295208217 MWP complex - muscle myosin complex - muscle myosin complex - methionine adenosyltransferase comblex - insulin receptor complex - extrinsic component of postsynaptic specialization membrane - extrinsic component of neuronal dense core vesicle membrane - complement component C1 complex - cell surface receptor signaling pathway - negative regulation of gene expression - anatomical structure morphogenesis - vesicle-mediated transport - positive regulation of macromolecule metabolic process - endocytosis - endocytosis - endocytosis -0.0479055913645547 0.0364477375838055 0.00989191228071346 0.0434684683862555 0.0293845038546097 0.00852221580095591 0.0151936092889696 0.0353349066189089 response to hypoxia response to hypoxia anatomical structure formation involved in morphogenesis response to heat positive regulation of protein metabolic process positive regulation of transcription of nucleolar large rRNA by RNA polymerase I negative regulation of Notch signaling pathway metal ion transport insulin receptor signaling pathway insulin receptor signaling pathway inorganic cation transmembrane transport glutathione biosynthetic process embryonic heart tube morphogenesis determination of heart left/right asymmetry detection of stimulus 0.0334839646529328 0.0309157370109802 0.0364271467163858 0.026192514236789 0.019564135253302 0.0466107307886047 7.392979366379386-05 0.00357081241988245 0.0035/081241986243 0.0383607687397971 0.00485679550530388 0.0282764269823515 0.00518600795073671 0.0137073683125209 0.0186071730867459 determination of heart tube in principles is sometry detection of stimulus cholesterol transport cholesterol transport behavioral response to nicotine amyloid—beta clearance zymogen activation telencephalon development synaptic transmission involved in micturition sulfide oxidation, using sulfide quinone oxidoreductase steroid metabolic process 0.0075465061729562 0.0011375458521072 0.045192282419687 $\begin{array}{c} 0.000553698859832341 \\ 0.000531341628760512 \end{array}$ sensory perception of taste sensory perception of taste response to food regulation of dendrite morphogenesis regulation of circadian rhythm proximal/distal pattern formation 0.0146778708294691 0.0465741224734921 0.0143263626404671 proximal/distal pattern formation protein terramerization protein homotrimerization protein homotrimerization protein heterooligomerization protein heterooligomerization protein heterooligomerization protein heterooligomerization protein heterooligomerization positive regulation of cholesterol storage plasma lipoprotein particle clearance phosphatidic acid biosynthetic process phagocytosis, engulment -0.000915768464937145 0.00092166476457564 0.0124322680950877 0.016528629090905 .0259445336381882 0.00497894197635177 0.0370768821971442 0.0149056724051427 ontology 0.0365426126479421 0.0129923802675074 hemolysis in another organisi glucose transmembrane transpo fructose transmembrane transpo floor plate developmen dehydroascorbic acid transpo 0.0129923802675074 0.00687834216674249 0.00129514563228159 0.00388446269611257 0.00372824288866177 0.0228357125718428 BP CC cerebellum development
cellular sulfide ion homedstasis
cellular detoxification of cadmium ion
anaphase–promoting complex–dependent catabolic process vitamin B6 metabolic process type I preums MF 0.0388446587274848 0.036446034774646 8.82293232852957e-05 0.000633146889905548 0.00517713860304065 0.00562655588108858 0.0474955374823379 vesicle dockin type I pneumocyte differentiatio trehalose transpo 0.0286110081509217 0.0374033185354154 0.0293829711180187 0.0293010942375539 0.043011549558502 0.0196864287360851 transmembrane receptor protein tyrosine phosphatase signaling pathway transition between fast and slow fiber transformation of host cell by virus telomeric D—loop disassemibly - t—circle formation - subpallium development - stem vascular tissue pattern formation - spermine acetylation - skin epidermis development - restroaval neural tube patterning - restroaval neural tube patterning - restroaval neural tube patterning - restroaval neural neuronal dense core vesicle transport - response to vanadate(3 -) - regulation of stopalition of report contraction - regulation of myosin—light—chain—phosphatase activity - regulation of myosin—light—chain—phosphatase activity - regulation of myosin—chain—phosphatase activity - regulation of myosin—chain phosphatase activity - regulation of folio of polio inheritance - regulation of folio of polio inheritance - regulation of female gonad development - regulation of polio representation - regulation of spoke assembly - regulation of polio representation - regulation of polio representation - regulation of polio representation - regulation of polio represen 0.0293671939600009 0.0444861711242688 telomeric D-loop disassemb 0.0444621069459076 0.00804417813102461 0.00804417813102461 0.00555591376900245 0.0291822319734111 0.0458363603293876 0.019686428736067 0.0362689775763034 0.0468158278288107 0.0375309393831313 0.0196793118384323 0.0477644978061453 0.00989191228071346 0.0293640113566224 0.0338259233799253 0.00804417813102461 proximal/distal pattern formation involved in pronephric nephron developmen protein transport along microtubule. 0.0153479755161932 0.0334552162955449 0.0380933466468941 0.00987305295208217 protein localization to mitotic spindle pole body protein regulation of transcription from RNA polymerase II promoter in response to heat stress positive regulation of tresponse to heat stress positive regulation of synaptic plasticity positive regulation of synaptic process positive regulation of protein formation of RNA biosynthetic process positive regulation of protein fositive regulation of protein fositive regulation of protein fositive regulation of protein fositive chemotaxis to cAMP positive regulation of positive regulation of membrane of positive regulation of membrane positive regulation of membrane of positive regulation of positive re 0.0293833293643246 0.0223879615466221 0.029384503854058 0.029072445475496 0.03892245936720230.03892245936726910.038524361677234 0.00988215132334453 0.01968428736153 0.019686428736153 0.019686428736067 0.0277866796827265 0.00927129937686849 0.0186889627733987 0.0368219552442053 0.00982534160407854 0.0228584397532106 0.0190803935033292 0.027280234963215 0.019686428736067 0.0374238998746193 0.0193712670149508 0.0193712670149508 0.0293845038539425 0.00989190504257365 0.0052322327546083 0.0211670087285688 polyphosphate—mediated signaling phloem or xylem histogenesis peroxisome fission ornithine biosynthetic process ocyte dorsal/ventral axis specification. Notch signaling pathway involved in arterial endothelial cell fate commitment nor—spermidine metabolic process neuron projection maintenance in endothelial cell fate commitment nor—spermidine metabolic process neuron projection maintenance neural nucleus development negative regulation of transporter activity negative regulation of transporter activity negative regulation of transporter activity negative regulation of programmed cell death negative regulation of interleukin—10 production negative regulation of procure of interleukin—10 production negative regulation of procure process negative regulation of procure process negative regulation of glucocorticoid secretory and negative regulation of glucocorticoid secretory negative regulation of celloprocess negative regulation of glucocorticoid secretory negative regulation of celloprocess negative regulation of celloproces 0.0290166646235 0.0495222503943324 0.0293845038545443 0.00804417813102461 0.0478428376233673 0.00982376513612284 0.0293845038545243 0.00555591376900245 0.00989191228042947 0.0196848807568714 0.00969370419306043 0.0484675742941491 0.0095736165024729 0.019686428736067 0.019686421569279 0.0185761747663942 0.0482773493210665 0.0462/7349321006 0.0203953831973171 0.031719704009117 0.0177210678441604 0.0347850305594989 0.01956721181861 0.0463484061207106 0.01956721181861 0.0124913478855452 glucosinolate bio glucose 6-phosphate n 0.0393366859797255 GABAergic neuron differentiation i forebrain neuron fatty acid derivative piosyr al cell proliferation involved in the control of the control fatty acid derivative biosynthetic process epithelial cell proliferation involved in lung morphogenesis endothelial tip cell fate specification embryonic liver development embryonic liver development cytokinin transport cytokinin transport cytokinin transport cytokinin transport cotyledon vascular tissue pattern formation complement activation, classical pathway citrulline biosynthetic process chondrocyte intercalation involved in growth plate cartilage morphogenesis chemotaxis to folate cartely GABAergic interneuron fate commitment 0.019686428736153 0.019606426.736153 0.0279402109267783 0.0313418902650954 0.0293829711180187 0.0162961395702926 0.0389855651708125 0.0300371445181523 0.029048144316132 0.029048020378076 0.0190454888587736 0.0180469364818349 0.0052322327546083 0.036325825378219 0.019686428736153 ndrocyte intercalation involved in growth plate cartilage morphogenesis chemotaxis to folate cerebral cortex GABAergic interneuron fate commitment cerebellar Purkinje cell layer structural organization cerebellar molecular layer formation cerebellar cortex development cellular response to socium arsenite cellular response to socium arsenite cellular response to diamide cellular response to diamide cellular response to GMP cardiolipin acyl-chain remodeling carbohydrate transmembrane transport blastoderm segmentation ascenda reproduction anterograde neuronal dense core vesicle transport activation of transmembrane receptor protein tyrosine kinase activity abscisic acid-activated signaling pathway abscisic acid transport 4-hydroxyproline catabolic process 0.0385331845515041 0.0289577272093807 0.029871/2093807 0.00989191228042947 0.00989190504257365 0.0484951015721996 0.0365243219880466 0.0238571793429505 0.0217917605459538 0.0196864287358469 0.0196864287361531 0.0182694174119522 0.0186437447324465 0.0196848807568714 0.0293833368794043