0.00389061022818778 identical protein binding 0.00237080333896606 oxidoreductase activit enzyme bindin 0.0412608951922469 0.0388740821308744 transmembrane transporter activity 0.0434683580370703 monoatomic ion channel activit 0.0103030620925672 0.000622984264899625 0.00558148062744229 Wnt-protein binding
scavenger receptor activity
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
monooxygenase activity
gated channel activity
extracellular ligand-gated monoatomic ion channel activity
acetylcholine-gated monoatomic cation-selective channel activity 0.0311245859544493 0.0386259532299781 0.00338839815081505 0.0147967820084615 0.000696844792199898 potassium channel activity PDZ domain binding Notch binding 0.0111003608543911 Notch binding glucose binding cargo receptor activity amyloid-beta binding amyloid-beta binding ubiquitin-protein transferase activator activity sulfide:quinone oxidoreductase activity sugar transmembrane transporter activity peroxidase activity low-density lipoprotein particle binding hydrolase activity, hydrolyzing N-glycosyl compounds hydro-lyase activity Hsp70 protein binding fructose transmembrane transporter activity dehydroascorbic acid transmembrane transporter activity carbonate dehydratase activity acetylcholine receptor activity 0.00044215279115198 0.0105899056924084 0.00878454420546901 0.000122855383628445 0.00179536908202071 0.0365549444467711 0.00887587319588475 0.00602269336880398 0.00824618034097862 0.037723964323968 0.00514783625879853 0.0173495621448187 0.0101694407200872 carbonate denydratase activity
acetylcholine receptor activity
1-acylglycerol-3-phosphate O-acyltransferase activity
trehalose transmembrane transporter activity
TORC2 complex binding
soluble NSF attachment protein activity
RNA-3'-phosphate cyclase activity
PTB domain binding 0.00569274296779405 0.0439844846613518 0.0334766162712787 0.0229559413478774 0.0229666373353994 protein—lysine 6—oxidase activity
protein adenylyltransferase activity
proline dehydrogenase activity
proline dehydrogenase activity
phosphatidic acid transfer activity
peptide—methionine (R)—S—oxide reductase activity
methionine—tRNA ligase activity
methionine adenosyltransferase activity
maleylactoracetate isomerase activity 0.0478991355460979 0.0316281019699764 0.0355908071078228 0.0373334540185163 0.0322853902673352 0.0112931350925219 maleylacetoacetate isomerase activity maieyiacetoacetate isomerase activity lipoic acid binding leukotriene—A4 hydrolase activity isovaleryl—CoA dehydrogenase activity intracellular cAMP—activated cation channel activity insulin—like growth factor II binding insulin—like growth factor I binding insulin—receptor activity hydroxymethylglutaryl—CoA reductase (NADPH) activity hexokinase activity 0.0476554537985995 0.0115497559628749 0.0190228779324628 0.0336572539670426 0.0115497559628806 0.0342521667689241 hydroxymethylglutaryl—CoA reductase (NADPH) activity—hexokinase activity—guanylate cyclase activator activity—glutamate—5—semialdehyde dehydrogenase activity—glutamate—5—semialdehyde dehydrogenase activity—glutamate—5—kinase activity—glutamate—5—kinase activity—glutamate—5—kinase activity—glutamate—5—kinase activity—fructokinase activity—fructokinase activity—fructokinase activity—epoxide hydrolase activity—epoxide hydrolase activity—deoxyhypusine synthase activity—blutamate—5—beautivity—blutamate—5—beautivity—blutamate—5—beautivity—blutamate—5—blutamate—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10—clipation—10— 0.033697633569746 0.0229666373350423 0.0115497559628806 0.0229666371167756 0.0236955062570451 0.0456287339377715 0.0260136179903327 0.0486961416436164 0.0111523631348858 0.0112396683413607 0.033389470021204 0.0109979130089141 0.0294237226082197 0.0229666373350423 0.00988785860401975 0.0499481217804692 0.00988785860401975 0.0229666373352904 0.0155185138135018 0.014935537121844 cell cortex mitochondrial inner membrane mitochondrial inner membrane collagen trimer zymogen granule membrane low—density lipoprotein particle dopaminergic synapse dendrite membrane cholinergic synapse dendrite membrane cholinergic synapse anaphase—promoting complex acetylcholine—gated channel complex yolk t—UTP complex origin recognition complex origin recognition complex NuA3b histone acetyltransferase complex NuA3a histone acetyltransferase complex myosin filament methionine adenosyltransferase complex insulin receptor complex HCN channel complex extrinsic component of neuronal dense core vesicle membrane complement component C1 complex cellular response to stimulus response to organic substance ubiquitin—dependent protein catabolic process response to chemical endocytosis cellular metabolic process 0.0445031113422567 0.0377337793256958 0.0191554546158032 8.10025605513606e-05 0.0337475991398095 0.022347563116948 0.0152340803349093 0.0310940764537128 0.0229666373352904 0.0229629187864362 0.0111948735982219 0.029203629739992 0.0342521667689778 0.0429134992302429 0.0115497559628806 0.0115497559625873 0.0342521667690327 0.0102234491120564 0.00119643104572315 0.0474371791938756 0.0171057510972721 0.0386044480295424 0.0190011266067345 endocytosis cellular metabolic process 0.0356362141963034 response to abiotic stimulus protein homooligomerization immune response circulatory system development biosynthetic process 0.0160161361382244 0.00678676910505613 0.0486121464639188 0.00304496223353882 0.0100306423600093 0.0433975361581972 anatomical structure formation involved in morphogenesis telencephalon development T cell activation small GTPase mediated signal transduction 0.0073568673150568 small GTPase mediated signal transduction response to heat positive regulation of transcription of nucleolar large rRNA by RNA polymerase I negative regulation of Whit signaling pathway negative regulation of Notch signaling pathway negative regulation of interleukin–6 production negative regulation of interleukin–1 beta production insulin receptor signaling pathway inorganic cation transmembrane transport glutathione biosynthetic process glucose homeostasis fatty acid biosynthetic process detection of stimulus cholesterol transport behavioral response to nicotine amyloid–beta clearance zymogen activation 0.029909655259579 0.000117904188600034 0.005721895989786 0.0497442192170099 0.0305625913658707 0.00768085214178988 0.0424951109650674 0.00808871692219506 0.0119453911288843 0.0117679821653812 0.0018126723634944 0.00137247318104499 0.000596718174025154 synaptic transmission involved in micturition sulfide oxidation, using sulfide:quinone oxidoreductase 0.000761040636194444 0.000736449050580426 sulfide oxidation, using sulfide:quinone oxidoreductase sexual reproduction sensory perception of taste response to food regulation of neurotransmitter levels regulation of dendrite morphogenesis regulation of dendrite development protein homotrimerization protein heterooligomerization positive regulation of protein—containing complex assembly positive regulation of macrophage derived foam cell differentiation positive regulation of cysteine—type endopeptidase activity involved in apoptotic process positive regulation of cholesterol storage plasma lipoprotein particle clearance phosphatidic acid biosynthetic process phagocytosis, engulfment organic substance biosynthetic process neural crest cell development negative regulation of synaptic assembly at neuromuscular junction negative regulation of Rho protein signal transduction male meiosis I
lipoprotein transport sexual reproduction 0.0216702838367105 0.0430792954477486 0.0160359882828399 0.00482473206761534 0.0194128054040418 0.00181125023939877 0.0256054459917605 ontology 0.0234998395285588 0.000817850780246193 0.0201882522863375 BP 0.00130074801829515 0.00130725812755424 CC 0.0170149263347109 0.0158636282776482 MF 0.0225394835387069 0.0152780100195911 0.0116629994307635 0.0251162149630146 male meiosis I lipoprotein transport leukotriene biosynthetic process intracellular sulfide Ion homeostasis hydrogen sulfide metabolic process hormone transport hemolysis in another organism glucose transmembrane transport fructose transmembrane transport floor plate development determination of pancreatic left/right asymmetry dehydroascorbic acid transport cytolysis -0.020157008743591 0.0072032902929703 0.0019323766333977 0.000122855383628445 0.000355014474287034 0.0404980037831308 0.0178711073303841 0.0094144489223816 0.00546805798461738 0.0195830980865275 0.0216070469747016 0.00514783625879853 cellular response to cGMP cellular detoxification of cadmium ion aromatic amino acid metabolic process anaphase–promoting complex–dependent catabolic process vitamin B6 metabolic process type I pneumocyte differentiation 0.0313446388538641 0.00129855527177574 0.000888062991825653 0.00454082340465492 0.0071561574980328 0.00680983046892266 0.0335463448059129 0.0439844846613518 tréhalose transport transmembrane receptor protein tyrosine phosphatase signaling pathway transformation of host cell by virus 0.0229666373353134 transformation of nost cell by virus
subpallium development
stem vascular tissue pattern formation
spinal cord dorsal/ventral patterning
specification of proximal tubule identity
skin epidermis development
skeletal muscle satellite cell migration
retrograde neuronal dense core vesicle transport
response to vanadate(3-) 0.017402256626572 0.0342508008192321 0.0328270519000906 0.0067231624133327 0.0321799209541582 0.0229666373353994 0.0229666373352904 0.0425440073272276 response to cisplatin response to cisplatin response to cisplatin 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 meiotic huclear division regulation of meiotic huclear division regulation of mast cell activation regulation of hydrogen peroxide metabolic process regulation of female gonad development regulation of DNA endoreduplication regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway regulation of acetylcholine secretion, neurotransmission proximal/distal pattern formation involved in pronephric nephron development protein transport along microtubule protein adenylylation repair 0.0229666373351096 response to cisplati 0.0115497559628807 0.0115497559628807 0.016587579151257 0.0444705494362364 0.0439909626523382 0.0115497559628806 0.0115497559625191 0.0111970381607342 proximal/distal pattern formation involved in pronephtic negron development protein transport along protein development protein transport along protein development protein transport along protein protein protein protein development protein pr 0.0181552500908598 0.0395265973233223 0.0457442374996403 0.033705073826439 0.0342521667683323 0.0453503548581889 0.045350354858273 0.044995680733273 0.0229666373353994 0.0229666373352904 0.011549755962832 0.0326790301436438 0.010989853537055 0.0220348114491686 0.0114902302154512 0.0267600726665717 0.0224211433090642 0.0229666373352904 0.043887963041448 0.00632519051308714 0.0251209964967312 0.0339243608918212 0.0147817033109804 0.0225373371891025 0.0202514926993385 0.0192960829979212 0.0335993861987089 0.0114888205842957 0.0342521667689241 0.0067231624133327 0.0229652554867501 0.0444902911887469 0.03375868640257 0.0229666373352904 0.00632519051308714 0.0449180054406315 0.024119042272662 0.0465647378494879 0.0373334540185163 0.0412093458341877 0.0339780240165061 0.0340999966438231 0.0229652554867501 0.0115497559628807 0.02446866982266 0.0115497556771351 0.0150207806295476 0.0461184120628116 0.0395841157488203 0.0291347233129894 tatty acid derivative biosynthetic process endothelial tip cell fate specification embryonic liver development cytokinin transport craniofacial suture morphogenesis cotyledon vascular tissue pattern formation complement activation, classical pathway citrulline biosynthetic process chemotaxis to folate cerebral cortex GABAergic interneuron fate commitment cerebellar Purkinje cell layer structural organization cerebellar molecular layer formation cerebellar molecular layer formation cerebellar cortex development cellular response to gonadotropin—releasing hormone cellular response to chemical stress cellular defense response cardiolipin acyl—chain remodeling carbohydrate transmembrane transport blastoderm segmentation asexual reproduction antigen transcytosis by M cells in mucosal—associated lymphoid tissue 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 0.0229666373353994 0.0328459750501034 0.0342508008192321 0.0308587213388804 0.0454064993024048 0.0357872366328537 0.0339523035799845 0.0223881791994001 0.0213444187339061 0.00632519051308714 0.0426112266696636 0.0229666373353994 0.0115497559625191 0.0299776982366045 0.0228649985878184 0.0428759207707715 0.0285231364654222 0.0261615987439031 0.0229666373350101 0.0429538299902953 0.0229666373353994 0.0216563652209227 0.0220258673002985 0.0229652554867501 0.0342511267797388