0.0499805619160778 nucleotidyltransferase activity transmembrane receptor protein tyrosine kinase activity
RS domain binding 0.0497769053903803 0.0492684981103214 0.0489983991744069 snRNA binding 0.0476101930326073 sequence-specific mRNA binding 0.0475821399477862 damaged DNA binding ubiquitin-like protein ligase binding 0.0463798351321831 0.0445767804653733 carbonate dehydratase activity 0.0435326440190507 D1 dopamine receptor binding glycosaminoglycan binding glycosaminoglycan binding ubiquitin protein ligase binding ribonucleoprotein complex binding protein phosphatase 2A binding phosphatidylinositol–3,5–bisphosphate binding benarin binding 0.0435259953097331 0.042947277083506 0.0420256711641263 0.0401096325873669 0.0398751060969015 0.0395859340179941 heparin binding phosphatidylinositol–3,4,5–trisphosphate binding phosphatidylinositol 3–kinase activity protein domain specific binding phosphatidylinositol 3–kinase binding 0.0381269860748478 0.0378216281319102 0.03640779420289 0.0363584077679192 0.0363318069110707 adenyl ribonucleotide binding 0.0362236605612431 methylation-dépendent protein binding 0.0362236605612431 methylated histone binding 0.0352614925921977 PDZ domain binding 0.0349203614779591 DNA-directed DNA polymerase activity adenyl nucleotide binding RNA binding 0.0344900587311062 0.0338051586204536 0.0319886350481366 spectrin binding 0.0310608914286979 microtubule binding 0.0296132725484199 tubulin binding 0.02764548388011 purine ribonucleotide binding 0.0268145850166943 amyloid-beta binding 0.0261972486450708 phospholipase activity DNA polymerase activity ribonucleotide binding 0.0249731520787215 0.0249071841165023 0.0240352159718027 histone H3K4 demethylase activity 0.0240280748894511 insulin recéptor binding 0.0239128619072054 sphingolipid binding nitric-oxide synthase regulator activity 0.0218762671423571 phosphatase binding 0.020549745421396 anion binding sodium ion binding ATP binding 0.0193907919382463 0.0191160312326965 0.016083057560865 phospholipid binding 0.0159260017324369 protein kinase A catalytic subunit binding 0.0149431808611917 nitric-oxide synthase binding 0.0143771931050889 purine nucleotide binding mRNA binding phosphatidylinositol bisphosphate kinase activity carbohydrate derivative binding small GTPase binding 0.0134377432249035 0.0127399745234059 0.011086935888262 0.0105287047441589 0.0103668597441283 phosphatidylinositol-4,5-bisphosphate binding 0.0099927585944768 GTPase binding purine ribonucleoside triphosphate binding phosphatidylinositol–4,5–bisphosphate 3–kinase activity 0.00999028687326069 0.0082257979505237 0.0074133791001849 ribosome binding kinase binding 0.0062225189026089 0.00522891806512705 protein phosphatase binding protein kinase binding phosphatidylinositol–3–phosphate binding 0.00483306427121726 0.00448166472354174 0.0038866398926299 phosphatidylinositol phosphate binding 0.00247393417673424 protein-containing complex binding enzyme binding phosphatidylinositol–3,4-bisphosphate binding phosphatidylinositol binding phosphatidylinositol bisphosphate binding 0.000915220571817692 0.000841572713574213 0.000580081427768547 0.0494230370743731 condensed chromosome 0.0487487811066811 cAMP-dependent protein kinase complex 0.0486510412800762 ciliary pocket membrane 0.0486510412800762 ciliary pocket nucleus meiotic spindle 0.0478407082145316 0.045564988596627 post-mRNA release spliceosomal complex nuclear envelope lumen 0.0441920230375768 0.0404560360749662 0.0404514067740119 smooth endoplasmic reticulum 0.0400327986832219 germinal vesicle Wnt signalosome 0.0400224769715197 • dosage compensation complex endocytic vesicle 0.0380207596612284 0.0372553186973854 neuron projection cytoplasm 0.0329016452028013 0.0324224383395531 Golgi-associated vesicle 0.0311826123163377 extrinsic component of organelle membrane 0.0306047111086199 chromocenter female germ cell nucleus 0.0295782625826748 catalytic step 1 spliceosome 0.0287167123075116 mitotic spindle midzone 0.0240773258053299 Golgi-associated vesicle membrane chromosome, centromeric region 0.0232803040600674 0.0224804725836204 type Ib terminal bouton 0.0203409812040211 early endosome membrane 0.020147508073284 endoplasmic reticulum 0.0199851456260683 filamentous actin 0.0196410698845349 sodium:potassium-exchanging ATPase complex 0.0179543388484825 translation preinitiation complex cytoplasmic region eukaryotic translation initiation factor 2 complex 0.0169738274014799 0.0169640150164889 0.0158997429307778 dendrite terminus 0.0144937749759538 sex chromosome 0.0140197235173218 endocytic vesicle lumen 0.0130600570973158 endosome membrane 0.0127876142396554axonal growth cone 0.00731127707493191 cell cortex 0.00616146673031289 endocytic vesicle membrane 0.00496649514734296 multi-eIF complex 0.00330087959603733 endoplasmic reticulum lumen 0.0022876685937756 dendritic growth cone endoplasmic reticulum exit site 0.00199966589731562 endoplasmic reticulum-Golgi intermediate compartment 0.0019611857213189 nuclear speck nuclear body regulation of fibroblast migration 0.000923534830678297 0.0499824439288477 0.0499800507539083 microtubule polymerization 0.0499350865788688 membranous septum morphogenesis oocyte microtubule cytoskeleton organization 0.0496786178041006 regulation of actomyosin contractile ring contraction 0.0496685307803725 viral process muscle cell proliferation forebrain generation of neurons olfactory bulb interneuron differentiation 0.0496639395447238 0.0495114420548184 0.049483633890072 0.04945616956834 negative regulation of protein–containing complex assembly positive regulation of fatty acid oxidation 0.049242976014852 regulation of cytokine activity regulation of cell cycle G1/S phase transition 0.0489697708850237rhabdomere development 0.0487317130661224 regulation of growth steroid hormone secretion 0.0485712267147535 0.0485712267147535 progesterone secretion positive regulation of phosphatidylinositol 3–kinase activity 0.048448684421482 0.048448684421482 positive regulation of lipid kinase activity negative regulation of morphogenesis negative regulation of ossification positive regulation of gene expression bud elongation involved in lung branching anesthesia–resistant memory 0.048430152227876 0.0484292265357452 0.0483431949564926 0.0482978191862096 0.0482706573335655 0.0481996773095014 olfactory placode morphogenesis 0.0481996773095014 olfactory placode development lagging strand elongation 0.0480700250406286 substrate-dependent cerebral cortex tangential migration substantia nigra development regulation of parathyroid hormone secretion regulation of mitotic cell cycle DNA replication regulation of branching involved in salivary gland morphogenesis by mesenchymal—epithelial signaling 0.0480700250406286 0.0480700250406286 0.0480700250406286 0.0480700250406286 0.0480700250406286 regulation of branching involved in salivary gland morphogenesis regulation of bile acid metabolic process 0.0480700250406286 regulation of bile acid biosynthetic process postnatal olfactory bulb interneuron migration positive regulation of parathyroid hormone secretion positive regulation of mitotic cell cycle DNA replication positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway olfactory nerve morphogenesis 0.04807002504062860.0480700250406286 0.0480700250406286 0.0480700250406286 0.0480700250406286 olfactory nerve formation motogenic signaling involved in postnatal olfactory bulb interneuron migration fibroblast growth factor receptor apoptotic signaling pathway 0.0480700250406286 endodermal cell fate determination cerebral cortex tangential migration using cell–cell interactions
cerebral cortex tangential migration
alveolar secondary septum development
photoreceptor cell fate commitment 0.0480700250406286 0.0480700250406286 0.0480700250406286 0.0478727654627298 0.0476222564339418 stem cell proliferation 0.0471028064824624 regulation of polysaccharide biosynthetic process regulation of physactrianide phosphilietic process regulation of glycogen metabolic process regulation of mitotic cell cycle chorionic trophoblast cell differentiation steroid hormone mediated signaling pathway protein kinase B signaling positive regulation of multicellular organismal process 0.0470900955629374 0.0469078666987727 0.0468785464090691 0.0467202014978118 0.0466421071427686 0.0462287108085679 0.0462121655146794 regulation of mesoderm development 0.0461207483267558 instar larval development cellular component maintenance positive regulation of lipid metabolic process positive regulation of cell growth positive regulation of axon extension 0.0459594829140914 0.0459048432451268 0.0456082321710432 0.0451549905660956 0.04509865957375 regulation of leukocyte migration 0.0450606786157007 ventral cord development 0.0448718216390028 multicellular organism growth 0.0445136972907091 positive regulation of cell population proliferation mitotic cytokinesis checkpoint signaling positive regulation of response to external stimulus Wnt protein secretion 0.0444487842202196 0.044398357656715 0.0442879333943138 0.0442642422296403 0.0442325676926484 protein localization to microtubule cytoskeleton 0.0440752224521544 regulation of cardiac muscle cell proliferation wing disc pattern formation determination of pancreatic left/right asymmetry
ribonucleoside bisphosphate biosynthetic process
purine nucleoside bisphosphate biosynthetic process
nucleoside bisphosphate biosynthetic process
regulation of mRNA splicing, via spliceosome
vascular endothelial growth factor receptor signaling pathway 0.0438979818544791 0.0435453577173898 0.0435453577173898 0.0435453577173898 0.0428576598586145 0.0427266082450668 0.0427111790502602 vasculogenesis 0.0426389887458776 cell fate determination 0.0426341036734476 regulation of RNA splicing larval chitin-based cuticle development cuticle development involved in chitin-based cuticle molting cycle peripheral nervous system development polysaccharide catabolic process 0.0426002241440587 0.0426002241440587 0.0423478767560941 0.0421368088546238 0.0421368088546238 cellular polysaccharide catabolic process regulation of calcium ion transmembrane transport embryonic placenta morphogenesis positive regulation of cell division. 0.0416926591353138 0.041234140148059 0.041135321799797 0.0411072785083274 0.0408367351328202 0.0407365154660428 mRNA splice site selection 0.0406549025215634 regulation of lipid biosynthetic process 0.0404477698575607 regulation of cellular response to insulin stimulus 0.0402956454212962 positive regulation of protein localization to plasma membrane 0.0402909387505217 ossification mitotic cell cycle, embryonic ATF6-mediated unfolded protein response 0.0401001445828455 0.0400484818795562 fin regeneration 0.040045441755006 negative regulation of lipid catabolic process iňsulin receptor signaling pathway 0.0397578216550428 cellular response to steroid hormone stimulus 0.0394397821769041 lateral mesoderm development 0.0392877818558189 ER overload response protein–containing complex localization membrane invagination 0.039195131082456 0.0391764612493792 regulation of cellular component organization 0.0389125394028141 positive regulation of mitotic nuclear division 0.0389103792106677 extraembryonic membrane development regulation of calcium—mediated signaling cell fate commitment involved in formation of primary germ layer regulation of calcium ion transport histone monoubiquitination regulation of cell size 0.0386976126019707 0.038642782959164 0.0385261489890574 0.0380876931096627 0.0375145167665602 glucan metabolic process 0.0375145167665602 cellular glucan metabolic process response to endogenous stimulus positive regulation of nuclear cell cycle DNA replication positive regulation of nuclear division regulation of morphogenesis of an epithelium mesoderm formation regulation of polygopathodida metabolic process 0.0372841276665809 0.0372039391996368 0.0371225667761356 0.0367812796252145 0.036453132941674 0.0364326916142215 regulation of polysaccharide metabolic process 0.0360838445727302 negative regulation of telomere maintenance via telomerase 0.0359128796535278 endoplasmic reticulum to Golgi vesicle-mediated transport positive regulation of cellular metabolic process 0.0358251772033576 beta-catenin destruction complex disassembly positive regulation of RNA binding cardiac muscle tissue growth 0.0354668878316519 0.0352570483435211 0.0351904394841265 regulation of cellular component size 0.0351228333444857 regulation of cell division 0.035027733845848 single fertilization 0.0350148717049707 morphogenesis of a branching epithelium regulation of oviposition
ventricular septum morphogenesis
regulation of actin filament polymerization
inner ear receptor cell development 0.0349277993570377 0.0346102261198105 0.0345526721461867 0.0343510575035498 epithelial tube branching involved in lung morphogenesis positive regulation of chemotaxis 0.0342633025683432 0.0342370865143986 0.0337238963592828 regulation of anatomical structure morphogenesis 0.0337180191764167 vesicle budding from membrane regulation of mRNA binding pericardial nephrocyte differentiation nephrocyte differentiation energy reserve metabolic process 0.0335552915225532 0.0335436151773349 0.0335436151773349 0.0334105547106563 0.0332677470571698 olfactory bulb interneuron development 0.0332082603515263 regulation of cardiac muscle contraction middle ear morphogenesis 0.0331199053438311 epicardial cell to mesenchymal cell transition 0.0330953422444497 establishment of imaginal disc-derived wing hair orientation negative regulation of protein serine/threonine kinase activity regulation of mesodermal cell fate specification regulation of mesodermal cell differentiation 0.0326160608662074 0.0325977771492471 0.0325977771492471 0.0325977771492471 regulation of mesoderm formation 0.0323845233530482 RNA splicing 0.0323704237919571 sister chromatid segregation response to cholesterol regulation of phosphate transport establishment of chromosome localization biological process involved in interspecies interaction between organisms 0.0321098551381509 0.0317767392124491 0.0315582365865194 0.0312593630320621 0.0310935571728811 positive regulation of protein metabolic process 0.0308589990404902 positive regulation of mitotic cell cycle 0.0308556687351062 signal transduction by p53 class mediator 0.0305404366159248 metaphase plate congression 0.0304792596462994molting cycle biological process involved in symbiotic interaction regulation of amyloid precursor protein catabolic process midbrain dopaminergic neuron differentiation positive regulation of synaptic assembly at neuromuscular junction 0.0304523636032703 0.0303009904487529 0.0300375745900149 0.030010484426856 0.0297790514422251 positive régulation of DNA replication dendritic spine organization 0.029750050007348 positive regulation of growth 0.0297317911948767 positive regulation of epithelial cell proliferation 0.029111 regulation of multicellular organismal development regulation of embryonic development regulation of developmental growth 0.0290062308995645 0.0288052617915757 ontology 0.0286927647431571 regulation of cell differentiation cellular carbohydrate catabolic process 0.0286874153703044 positive regulation of macromolecule biosynthetic process 0.0286524479990663 0.0285619645746973 negative regulation of response to endoplasmic reticulum stress 0.0285248239400806 regulation of photoreceptor cell differentiation positive regulation of organelle organization photoreceptor cell morphogenesis CC 0.0281901115756658 0.0281180705034007 MF 0.0280166098932844 regulation of extracellular matrix organization 0.0278766654830216 neuronal stem cell division neuroblast division 0.0277554151035038 vesicle cytoskeletal trafficking 0.0276879799262312 regulation of GTPase activity posterior lateral line system development mechanosensory lateral line system development positive regulation of cell morphogenesis involved in differentiation 0.027651504946042 0.027651504946042 0.0276319391575792 0.0275656821895966 osteoblast differentiation 0.0274377890173607 regulation of animal organ morphogenesis 0.0273939341700438 regulation of steroid biosynthetic process regulation of cytokinetic process positive regulation of immune system process cell morphogenesis involved in neuron differentiation negative regulation of cellular component organization alternative mRNA splicing, via spliceosome substrate-dependent cell migration sleep. regulation of steroid biosynthetic process 0.0272263621021673 0.0271404207795312 0.0269574872100312 0.0267089756548303 0.0265602982600785 0.0263631536965635 0.0260960114357245 forebrain neuroblast division 0.026016241647386 glucan catabolic process 0.0259485707102562 stem cell division hair cell differentiation 0.0257421583456752 0.0256510285175188 gliogenesis digestive tract morphogenesis 0.0255748932367813 0.0254746005328478 epidermis morphogenesis 0.0252847429142398 otic vesicle development 0.0251286318499384 regulation of organelle assembly 0.0250415225735726 receptor-mediated endocytosis 0.0250270297225934 positive regulation of developmental growth head segmentation regulation of monooxygenase activity spliceosomal complex assembly histone H3–K4 demethylation 0.0249275634880253 0.0246287550137475 0.0245518941532197 0.0240352159718027 regulation of glucose metabolic process 0.0235497276561616 maintenance of cell number response to hormone cell morphogenesis involved in differentiation negative regulation of protein polymerization vesicle transport along actin filament actin filament—based transport 0.0235386967581304 0.0233614503285686 0.0232485711868029 0.023050184527942 0.023050184527942 0.0225523148259689 regulation of aspartic-type peptidase activity 0.0225523148259689 regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process 0.022488932168842 regulation of protein polymerization 0.0224715481176744 regulation of protein localization to endosome regulation of protein localization to early endosome positive regulation of protein localization to endosome 0.0224715481176744 0.0224715481176744 0.0224715481176744 positive regulation of protein localization to early endosome 0.0221717488724135 rhodopsin biosynthetic process mitotic metaphase plate congression neural tube patterning 0.0218794687301873central nervous system myelination 0.0218794687301873 axon ensheathment in central nervous system chondrocyte proliferation regulation of fatty acid beta-oxidation 0.021824086914597 0.0218169276218311 0.0217926171995866 cardiocyte differentiation 0.0217749602923271 molting cycle, chitin-based cuticle 0.0217364779019058 actin filament network formation 0.0216941815909966 voluntary musculoskeletal movement positive regulation of translation
positive regulation of retinal cell programmed cell death
positive regulation of compound eye retinal cell programmed cell death
regulation of stem cell population maintenance 0.0216679114746736 0.0215709395077976 0.0215709395077976 0.0215619382710436 0.0215373831103153 regulation of respiratory gaseous exchange by nervous system process 0.0214510896893857 placenta blood vessel development 0.0214050516594688 response to iron(II) ion astral microtubule nucleation regulation of actin cytoskeleton organization 0.0212513071265981 0.0212404743622206 rostrocaudal neural tube patterning organ induction lymphocyte costimulation 0.0211480544784611 0.0211227381416595 0.0211100513713561 regulation of ossification 0.0210103747217834 positive regulation of cell cycle phase transition negative regulation of cell cycle phase transition negative regulation of synaptic transmission, glutamatergic regulation of protein ADP-ribosylation regulation of mitotic cell cycle phase transition regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway anterior/posterior lineage restriction, imaginal disc regulation of extracellular matrix disassembly 0.0210055281093239 0.0209975229724951 0.0208952985521539 0.0208516575690286 0.0207916629699324 0.0207665840242972 0.0206267416644645 protein polymerization 0.0206045160717776 response to peptide hormone positive regulation of locomotion nucleus localization positive regulation of developmental process stem cell population maintenance regulation of endodermal cell fate specification 0.0205436402315019 0.0205139077687333 0.020172012567186 0.0201482689091094 0.0201482689091094 regulation of endodermal cell differentiation 0.0201482689091094 negative regulation of endodermal cell fate specification 0.0201482689091094 negative regulation of endodermal cell differentiation 0.0199623260660047 labyrinthine layer morphogenesis 0.0199004582555883 mammary gland duct morphogenesis sodium ion export across plasma membrane regulation of calcium:sodium antiporter activity 0.0196410698845349 0.0196410698845349 0.0196410698845349 intracellular potassium ion homeostasis 0.0194948276579268 cardioblast differentiation 0.019326714146642 telencephalon development posterior lateral line development 0.0189047970224518 regulation of centrosome cycle neuroblast fate specification regulation of actin filament organization formation of primary germ layer C-terminal protein lipidation 0.0188500899755075 0.0186193614595119 0.0186113857247073 0.0185147417631483 0.0184905931623378 positive regulation of actin filament depolymerization regulation of triglyceride catabolic process 0.0182122985973295 response to fructose 0.0180706449008855 otic vesicle formation symmetric cell division positive regulation of stem cell population maintenance 0.0179705561122608 0.0177704178359937 0.0176946449782445 positive regulation of neuromuscular junction development 0.0175199856344089 positive regulation of axonogenesis mitotic sister chromatid segregation 0.0173242795725099 anterior head segmentation 0.0170564846368684 ureteric bud development regulation of organ growth
ER-nucleus signaling pathway
endodermal digestive tract morphogenesis
endodermal cell differentiation 0.0170424389939725 0.0170174835220491 0.0169134330122129 0.0168841928922035 0.0168641918301439 regulation of actin filament-based process regulation of oskar mRNA translation 0.0167755896877891 establishment or maintenance of microtubule cytoskeleton polarity regulation of mRNA processing 0.0165289151588149 0.0165205691709172 stem cell fate commitment dendritic spine morphogenesis positive regulation of mRNA binding 0.0164760405515224 0.0163487453898721 regulation of amyloid-beta formation 0.0163032703776877 response to insulin-like growth factor stimulus wing disc anterior/posterior pattern formation positive regulation of cellular biosynthetic process 0.0161863722994246 positive regulation of neuron projection development chorion development stem cell differentiation 0.0159400804537678 0.0158499089597944 0.0158473819931297 0.0158316417104596 extrinsic apoptotic signaling pathway 0.0157829316151925 nucleocytoplasmic transport 0.0157641238314236 positive regulation of eye photoreceptor cell development positive regulation of eye photoreceptor cell development positive regulation of compound eye photoreceptor development negative regulation of calcineurin—NFAT signaling cascade negative regulation of calcineurin—mediated signaling morphogenesis of an epithelial bud negative regulation of osteoblast differentiation tangential migration from the subventricular zone to the olfactory bulb 0.0157641238314236 0.0157598897567724 0.0157598897567724 0.015724035726883 0.0154609213093159 0.0154208393885678 0.0153833565955684 DNA strand elongation negative chemotaxis 0.0151895158351812 nucleobase-containing compound transport positive regulation of G1/S transition of mitotic cell cycle limbic system development positive regulation of biosynthetic process midbrain development 0.0151361734146067 0.0150929478007559 0.015080738502839 0.015069399218821 0.0150299716154429 negative regulation of triglyceride metabolic process 0.0150099658756967 negative regulation of cytokinesis positive regulation of amide metabolic process regulation of mitotic spindle organization
endodermal cell fate commitment
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positive regulation of mitochondrial translation 0.0143656982091537 0.014348149296214 0.0141676122327274 0.0140821127679856 0.0139157268838706 cell communication by electrical coupling 0.0138815776009428 RNA splicing, via transesterification reactions 0.0138405521663633 phosphatidylinositol 3-kinase signaling 0.0134999791894862 negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway regulation of eye photoreceptor cell development regulation of compound eye photoreceptor development synaptic target inhibition regulation of striated muscle contraction positive regulation of cell cycle G1/S phase transition 0.0134720586975 0.0134720586975 0.013417142359291 0.0133115776699089 0.0132765999733934 0.0131189274431337 spindle elongation 0.0130808775358235 dorsal/ventral pattern formation cerebral cortex development branching involved in labyrinthine layer morphogenesis striated muscle cell proliferation cardiac muscle cell proliferation 0.01307617304793660.0130671368397722 0.0129505667127899 0.0129505667127899 somatic stem cell division 0.0129348271190234 0.0128175147449713 regulation of heterochromatin formation 0.0127255554619846 negative regulation of cell fate specification 0.0125425787884781 mammary gland epithelium development 0.0118573834069654 lateral sprouting from an epithelium 0.0117727593378019 cellular response to cholesterol pronuclear migration bicarbonate transport 0.0117702613476625 0.0117329092361364 0.0116489182003662 positive regulation of neurogenesis mRNA export from nucleus positive regulation of cell differentiation 0.0116208489406542 0.0115871011484012 0.0115553927889694 anterior/posterior pattern specification, imaginal disc neuroepithelial cell differentiation inner ear auditory receptor cell differentiation regulation of gastrulation positive regulation of heart contraction positive regulation of photoreceptor cell differentiation motile cilium assembly hormone—mediated signaling pathway. 0.0114850802175571 0.0112395756629113 0.0111709823874018 0.0111653120633961 0.0110985068320587 0.0110905992017283 0.0110610502134857 hormone—mediated signaling pathway positive regulation of blood circulation cerebral cortex cell migration regulation of cellular component biogenesis cellular response to DNA damage stimulus regulation of centrosome duplication 0.0108402587865751 0.010710618544407 0.0106316166142945 0.0106128862918789 0.0104471630008631 0.0103817623336876 regulation of neurogenesis 0.0102977157577966 cellular response to hormone stimulus mesonephros development mesonephric tubule development mesonephric epithelium development midbrain-hindbrain boundary development 0.0102619493579503 0.0102619493579503 0.0102619493579503 0.0101391995557963 0.0100920535060632 DNA strand elongation involved in DNA replication 0.0100822992741414 positive regulation of organ growth 0.00991023566153279 regulation of cell development 0.00979452300723179 dopaminergic neuron differentiation neuron projection organization cell fate specification regulation of nitric-oxide synthase activity labyrinthine layer development positive regulation of cell cycle process 0.0097135240419008 0.00970587590711304 0.009607788408238 0.00955053428263797 0.00936017564804109 0.00922367497442194 oligodendrocyte development 0.00895684502882464 positive regulation of cellular response to insulin stimulus ribonucleoprotein complex localization regulation of osteoblast differentiation.

RNA splicing, via transesterification reactions with bulged adenosine as nucleophile mRNA splicing, via spliceosome regulation of telomere maintenance via telomerase 0.00877462280702959 0.00864771439629323 0.00856946253195652 0.00856946253195652 0.00856909092435762 0.008189896855213 telencephalon cell migration 0.008189896855213 forebrain cell migration virion assembly endoderm formation RNA localization negative regulation of gastrulation regulation of G2/M transition of mitotic cell cycle 0.00796385601439868 0.00792291415773788 0.00773550244120047 0.00768381573343469 0.00761111612821232 negative regulation of organelle organization 0.00753385791700492 endoderm development 0.00751885157738935 regulation of cell cycle phase transition regulation of cell cycle G2/M phase transition 0.00751742573790054 0.00747430668954443 regulation of calcium ion transmembrane transporter activity 0.00738831629692475 regulation of presynapse assembly establishment of RNA localization 0.00737745642309586 0.0072274119549953 mRNA processing 0.00720679511922297 phosphatidylinositol-mediated signaling 0.00704865887594859 in utero embryonic development 0.00702935522399328 negative regulation of cell fate commitment 0.00699060283029682 asymmetric protein localization involved in cell fate determination 0.00698936346371194negative regulation of triglyceride catabolic process mammary gland epithelial cell differentiation 0.00681026331520905 establishment or maintenance of cytoskeleton polarity 0.0067173733778893 0.00645407719495807 positive regulation of cellular component organization 0.00642184092711255 nuclear transport 0.00624008196517106 rhodopsin metabolic process 0.00606708517409678 auditory receptor cell development 0.00584407309839885 negative regulation of embryonic development 0.00573883900621506 protein localization to microtubule 0.00567916322803324 inositol lipid-mediated signaling 0.00540444268949195 establishment of organelle localization 0.00539540230953521 abscission 0.00525520041520055 regulation of organelle organization 0.00517832034888049 positive regulation of neuron differentiation cell communication by electrical coupling involved in cardiac conduction

central nervous system segmentation

brain segmentation

positive regulation of cell development 0.00497760262542934 0.00465712746291843 0.00465712746291843 0.00441196666238342 0.00436109297213609 protein export from nucleus 0.00428620108641911 mRNA transport 0.00425763868899499 regulation of nervous system development 0.00420641382371444 RNA export from nucleus 0.0041051252875803 regulation of neuron differentiation 0.00393497300562104 rhabdomere morphogenesis ocellus photoreceptor cell differentiation ocellus photoreceptor cell development 0.00393497300562104 0.00393497300562104 0.00393497300562104 ocellus morphogenesis 0.00393497300562104 anterior region determination 0.00391303273957604 labyrinthine layer blood vessel development RNA transport 0.00389205877616995 nucleic acid transport 0.00322547152593905 regulation of cell cycle process 0.00288530049634692 somatic stem cell population maintenance p38MAPK cascade 0.00287707618978244 0.00280926095081005 embryonic digestive tract development 0.00276498055570412 pallium development 0.00275272351703679 regulation of spindle organization 0.00262168973733776 nuclear export 0.00247730752482387 negative regulation of cell division 0.00224979446451587 regulation of protein kinase B signaling oligodendrocyte differentiation positive regulation of protein kinase B signaling 0.00198795148615802 0.00196184904155195 0.00187548206752056 regulation of cytoskeleton organization 0.00184857188830176 positive regulation of nervous system development 0.00158394553474101 regulation of mitotic spindle assembly 0.00130080359038527 cell fate commitment stem cell fate specification retinal pigment epithelium development mitotic spindle elongation regulation of spindle assembly 0.00125800220020677 0.000858627032965355 0.000672673611076188 0.000537513563200386 0.000422562144011524 embryonic digestive tract morphogenesis 0.000364164537578898 regulation of microtubule cytoskeleton organization 3.37725420748105e-05 regulation of microtubule-based process 300 Number of Differentially Expressed Genes in GO Term