0.0184355808572816 0.0110176326401252 protein kinase activit protein tyrosine kinase activit 0.00238701738761054 0.0219096764805773 DNA-binding transcription factor activity 0.0455529538595306 0.00125668870800072 0.0432985946080581 protease bindir 0.00440672878071888 ephrin receptor activit epnrin receptor activity cyclin binding
ATPase-coupled glutathione S-conjugate transmembrane transporter activity
ATPase-coupled bile acid transmembrane transporter activity

s-3' DNA helicase activity

water transmembrane transporter activity

tRNA (guanine-N1-)—methyltransferase activity

transmembrane-ephrin receptor activity

splicing factor binding

site-specific endodeoxyribonuclease activity, specific for altered base

single-stranded DNA exodeoxyribonuclease activity

proton channel activity

protein serine/threonine kinase inhibitor activity

protein histidine kinase activity

pre-mRNA 3'-splice site binding

POZ domain binding

phosphotransferase activity, for other substituted phosphate groups

oxidoreductase activity, acting on the CH-NH group of donors, oxygen as acceptor

NAD transmembrane transporter activity

metalloendopeptidase activity involved in amyloid procursor protein catabolic process

MDM2/MDM4 family protein binding

mannosyl-oligosaccharide 1,2-alpha-mannosidase activity 0.00657919187359873 0.0196751041458776 0.0145739287544335 0.00728688821680111 0.0155125428729559 0.00703971355787972 0.0349460341844175 0.0461508909140878 0.0072868882168011 0.0376134619264375 0.0119974575638328 0.0254968045744847 0.0484510224685062 0.0225106875723368 0.0257813275251445 0.0462336206589409 0.0276293859124408 mannosyl-oligosaccharide 1,2-alpha-mannosidase activi intermediate filament bindir 0.0203925544446221 intermediate inament biliding inorganic anion exchanger activity histone kinase activity GPI-linked ephrin receptor activity ethanolaminephosphotransferase activity ethanolamine kinase activity DH domain binding properties and exidence activity and properties and exidence activity. 0.0148605075845783 0.0148363922543972 0.00703971355787972 0.0279692066342407 0.0226212701383911 0.00703971355787972 D–amino–acid oxidase activiti ceramide kinase activiti 0.0104418285599995 0.014554174612943 carnitine transmembrane transporter activity bis(5'-adenosyl)-triphosphatase activity bicarbonate transmembrane transporter activity BH3 domain binding 0.0379283007290595 0.0154055329692062 0.00799025393237928 BH3 domain bindin beta–N–acetylhexosaminidase activit axon guidance receptor activit Arp2/3 complex bindin amide transmembrane transporter activit 0.0443511585502299 0.0415841922873536 0.035973485184473 0.032596491417025 active borate transmembrane transporter activity
active borate transmembrane transporter activity
[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity
(1->3)-beta-D-glucan binding
extracellular region
cellular_component
mitotic spindle 0.00728688821680111 0.0306974565708427 0.0438769750138629 0.0385863799278903 U2-type precatalytic spliceosome
U12-type spliceosomal complex
sperm flagellum
catalytic step 2 spliceosome
adherens junction 0.0236720156766533 0.0373107007228678 0.00691923011680517 0.0344298638291066 0.0348263186055714 0.0370604928859387 0.0108435275277804 U2AF U11/U12 SRNP transcription factor TFIIH holo complex SCAR complex RSF complex 0.0301988852503203 0.0418998281839541 0.0251304005409184 postsynapse of neuromuscular junction 0.00799268677291317 polar microtubule pericentric peterochromatii 0.0289819085482283 0.0277168456364087 0.0225084929872222 oligosaccharyltransferase I complex NURF complex nucleotide-excision repair factor 3 complex Ndc80 complex MMXD complex 0.0154940467669304 0.0387308364282555 0.0458367662571056 gamma DNA polymerase complex filopodium tip cyclin B1–CDK1 complex 0.0339259486602825 0.0230250888664129 0.038909638636085 Bcl-2 family protein complex 0.00799025393237928 0.0142243350316216 90S preribosome 0.0437098474950234 protein phosphorylation positive regulation of transcription by RNA polymerase I 0.00984472015569677 0.044572701166897 0.00255351344478696 peptidyl–serine phosphorylation organonitrogen compound metabolic process 0.0201228294304294 0.0268259401168962 0.0154189902118123 lung developmen 0.012369884030407 eye development cytoskeleton organization xenobiotic transport 0.00162306739677301 0.00807915159394764 0.0161511853175427 transmembrane receptor protein tyrosine kinase signaling pathway spliceosomal complex assembly spindle assembly response to other organism 0.0442557166176234 0.00414603655138272 0.0112044403097432 0.0490139666218234 response to other organism response to hydrogen peroxide response to ethylene regulation of mitochondrial membrane potential regulation of MAPK cascade regulation of locomotion regulation of circadian rhythm regulation of cell shape positive regulation of cell shape positive regulation of DNA binding phosphatidylethanolamine biosynthetic process negative regulation of Rho protein signal transduction negative regulation of cell size mitotic spindle organization mitochondrial DNA repair microtubule—based process leukotriene transport 0.024208775341709 0.0030256678459801 0.00586521989546382 0.0225141267108767 0.00818620812720756 0.0314231573620754 0.0231324117823088 0.00533652530085463 0.0027764437330647 0.000504795751142201 0.0191361230155771 0.0282611581905789 0.00297075626344045 0.0375977957063033 0.0183719878463854 leukotriene transport lamellipodium assembly integrin-mediated signaling pathway hemostasis 0.00825425612800284 0.0152151155751101 0.0281615252975034 0.00844607709820293 hematopoietic stem cell differentiation export across plasma membrane embryonic organ development embryonic cleavage dendritic spine development chromosome segregation blood coagulation viral genome integration into host DNA UTP biosynthetic process urate metabolic process trophectodermal cellular morphogenesis trophectodermal cellular morphogenesis transcription—coupled nucleotide—excision repair transcription—from RNA polymerase I promoter synaptic vesicle recycling via endosome suppression by virus of host apoptotic process stress fiber assembly stem cell division semicorporum synaptic vesicle recycling via endosome suppression by virus of host apoptotic process hematopoietic stem cell differențiation 0.0199757874121045 0.00248495268687397 0.00308191068881419 0.0194088468311825 0.0185964844058123 0.0444898087236311 0.0340662890435339 0.0324573817722939 0.00898414269261878 0.0466468575522396 0.0154940467669304 0.00799025393237928 0.0393498397851327 stem cell division
sperm chromatin decondensation
sperm chromatin condensation
Spemann organizer formation
somatic muscle development
skeletal muscle satellite cell activation 0.0349653612734732 0.0142243350316216 ontology 0.0387218701323366 0.0397522372282473 BP skeletal muscle development skeletal muscle satellite cell activation segmentation segmentation secondary palate development retinal cone cell differentiation regulation of Schwann cell differentiation regulation of protein serine/threonine kinase activity regulation of mitochondrial membrane permeability regulation of mesenchymal stem cell differentiation regulation of long—term synaptic depression regulation of precursor metabolites and energy regulation of cell—cell adhesion mediated by cadherin regulation of sell junction assembly regulation of BMP signaling pathway receptor recycling Rac protein signal transduction purine ribonucleoside catabolic process protein sulfation pronuclear migration pronuclear fusion posterior compartment specification 0.0222533644299361 0.0382621480969235 CC 0.0297553932714629 0.0157883863432047 0.00751111841110237 0.0495322794234576 MF 0.0241675940035822 0.0159739125134064 0.0387210049950039 0.0393286277581981 0.00806866902781406 0.0412058061697962 0.0453531980067041 0.0150948260795648 0.0221360777606588 protein sulfation pronuclear migration pronuclear fusion pronuclear fusion pronuclear fusion positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway positive regulation of T cell chemotaxis positive regulation of synaptic vesicle exocytosis positive regulation of synaptic vesicle clustering positive regulation of mitor exocution of synaptic vesicle clustering positive regulation of myelination positive regulation of myelination positive regulation of mitor exocmbination positive regulation of mitor exocmbination positive regulation of mitor exocmbination positive regulation of positive regulation of positive regulation of positive regulation of glial cell migration positive regulation of cell fate commitment positive regulation of ATP biosynthetic process positive regulation of ATP biosynthetic process positive regulation of ATP biosynthetic process positive regulation of proximal/distal axis polarity specification of proximal/distal axis polarity specification of anterior/posterior axis polarity specification of anterior/posterior axis polarity specification of proximal/distal axis polarity specification of anterior/posterior axis polarity specification of proximal/distal axis polarity specification of proximal/distal axis polarity specification of proximal/distal axis polarity specification of anterior/posterior axis polarity specification of a 0.0218742171727446 0.0183914296912158 0.030657230645663 0.038323937242078 0.00799025393237928 0.00703971355787972 0.0224950908843746 0.0170248874093238 0.041588767856955 0.00799268677291317 0.00806866902781406 0.00749363400788836 0.0350170463092641 0.0257148036458605 0.0239705542091933 0.00858915968024239 0.00799268677291317 0.0151343996797564 0.0225015586540645 0.0154940467669304 nuclear protein quality control by the ubiquitin-proteasome system NIK/NF-kappaB signaling neural plate anterior/posterior regionalization neural crest cell fate specification neural crest cell fate specification neural crest cell fate specification neural crest cell differentiation neural crest cell differentiation negative regulation of telomeric DNA binding negative regulation of skeletal muscle satellite cell proliferation negative regulation of satellite cell differentiation negative regulation of satellite cell differentiation negative regulation of Protein serine/threonine kinase activity negative regulation of protein serine/threonine kinase activity negative regulation of protein modification process negative regulation of protein localization to plasma membrane negative regulation of protein localization to plasma membrane negative regulation of neuron projection arborization negative regulation of neuron projection arborization negative regulation of meworane permeability negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage negative regulation of execution phase of apoptosis negative regulation of execution phase of apoptosis negative regulation of execution phase of apoptosis negative regulation of cell fate commitment negative regulation of cell fate specification negative regulation of call fate specification negative regulation of barbed—end actin filament capping negative regulation of anolikis natural killer cell differentiation monovalent inordanic cation homeostasis 0.0142243350316216 'nuclear speck organizatio 0.0351615415347207 0.0378782522355285 0.0286105203199798 0.0183914296912158 0.0379252496923067 0.0394708486529668 0.00703971355787972 0.0380896698350908 0.0383781429004035 0.0489405434162084 0.0492504967468605 0.0146586042806588 0.0144607335348635 0.0200015494645691 0.0380896698350908 0.00799025393237928 0.0146586042806588 0.00749363400788836 0.0149649766701725 0.0319839712242341 0.046188919885552 0.0398784789486617 0.00799268677291317 myoblast fate specification monovalent inorganic cation homeostasis 0.0386005921559404 0.0352663337754716 monocyte aggregation monocyte activation modification of postsynaptic actin cytoskeletor 0.0370758378582017 modification of postsynapic actin cytoskeleton mitotic telomere maintenance via semi-conservative replication mitotic recombination mitochondrial tRNA methylation mitochondrial NAD transmembrane transport metanephric nephron tubule development mesodermal cell fate determination 0.0267713108667484 0.0318205756863262 0.0266435613668449 0.0118078684783453 0.0152913578646753 mesodermal cell fate determination mesoderm migration involved in gastrulation annose trimming involved in glycoprotein ERAD pathway lymphocyte proliferation lymph gland plasmatocyte differentiation lymph gland crystal cell differentiation lung goblet cell differentiation larval visceral muscle development lamellipodium morphogenesis intestinal epithelial cell development immunological synapse formation GTP biosynthetic process gonadal mesoderm development Golgi disassembly glial cell growth fluid transport fibroblast apoptotic process 0.0178880939687352 0.049264267496067 0.00799268677291317 0.015449775316174 0.0079926867729131 0.0132960849623607 0.0326897657238612 0.0334214015191227 0.0356358502188503 0.0420427458353451 0.00799268677291317 0.0251532536849449 fibroblast apoptotic process fasciculation of sensory neuron axon establishment of integrated proviral latency establishment of animal organ orientation erythrocyte maturation endodermal cell fate determination 0.0165489837917571 0.0149649766701725 0.0352962000974303 0.0154833794880869 0.0432068279792919 endocardial cushion development embryonic axis specification ectodermal placode formation ecdysone receptor-mediated signaling pathway double-strand break repair via single-strand annealing dorsal spinal cord development DNA replication, removal of RNA primer DNA replication, Okazaki fragment processing DNA methylation-dependent heterochromatin assembly endocardial cushion developmen 0.0383520505165248 0.0142243350316216 0.0408940983198114 0.0337216313420898 0.0386720186159824 0.00713870788509267 detection of yeast 2-amino acid metabolic process 0.0104418285599995 D-amino acid catabolic process CTP biosynthetic process cranial nerve development 0.04394085071011 0.0291104262566803 constitutive protein ectodomain proteolysis central nervous system projection neuron axonogenesis central nervous system myelin formation 0.0370592118135427 0.0175175399207071 cellular response to thapsigargin cellular response to prolactin cellular response to erythropoietin 0.016046900887153 cellular response to erythropoietin cellular response to astaxanthin cellular response to alkaloid cellular response to alkaloid cellular rypotonic response cellular cation homeostasis cell-cell signaling by wnt cell recognition carnitine transmembrane transport cardioblast differentiation canonical Wnt signaling pathway involved in neural crest cell differentiation canonical Wnt signaling pathway involved in cardiac muscle cell fate commitment borate transport -0.00799025393237928 0.016381357830755 0.0357600724214338 0.0350918231824967 0.0220479805099014 0.0297435997389012 0.0479512302431487 0.0419118972663396 0.00728688821680111 borate transpor bicarbonate transport
bicarbonate transport
barbed–end actin filament uncapping
anterior compartment pattern formation
aerobic electron transport chain
actin filament network formation 0.0154055329692062 0.0265483093111087 0.0183914296912158 0.0118078684783453 0.0493856067645771