
type I pneumocyte differentiation
trachea formation
telencephalon development
subpallium development
stem vascular tissue pattern formation
specification of proximal tubule identity
skin epidermis development
rostrocaudal neural tube patterning
regulation of female gonad development
regulation of dendrite morphogenesis
proximal/distal pattern formation involved in pronephric nephron development
proximal/distal pattern formation
positive regulation of synapse maturation
positive regulation of skeletal muscle tissue growth
positive regulation of meiotic cell cycle process involved in oocyte maturation
positive regulation of megakaryocyte differentiation
positive regulation of immature T cell proliferation in thymus
positive regulation of amacrine cell differentiation
phloem or xylem histogenesis
oocyte dorsal/ventral axis specification
notochord cell differentiation
Notch signaling pathway involved in arterial endothelial cell fate commitment
neural nucleus development
neural crest cell development
negative regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
negative regulation of synaptic assembly at neuromuscular junction
negative regulation of post−embryonic development
negative regulation of cardiac muscle cell differentiation
manchette disassembly
male sex determination
hemangioblast cell differentiation
glomus development
GABAergic neuron differentiation in basal ganglia
forebrain neuron differentiation
floor plate development
epithelial cell proliferation involved in lung morphogenesis
endothelial tip cell fate specification
embryonic liver development
embryonic heart tube morphogenesis
determination of heart left/right asymmetry
cotyledon vascular tissue pattern formation
chondrocyte intercalation involved in growth plate cartilage morphogenesis
cerebral cortex GABAergic interneuron fate commitment
cerebellum development
cerebellar Purkinje cell layer structural organization
cerebellar molecular layer formation
cerebellar cortex development
blastoderm segmentation
anatomical structure morphogenesis
anatomical structure formation involved in morphogenesis
translation elongation factor binding
TORC2 complex binding
PTB domain binding
low−density lipoprotein particle binding
insulin−like growth factor receptor binding
insulin binding
glucose binding
FAD binding
anaphase−promoting complex binding
amyloid−beta binding
3−phosphoinositide−dependent protein kinase binding
pore formation in membrane of another organism
membrane depolarization
positive regulation of glycoprotein biosynthetic process
glucose 6−phosphate metabolic process
positive regulation of glycogen biosynthetic process
negative regulation of glycogen biosynthetic process
leukotriene biosynthetic process
sulfide:quinone oxidoreductase activity
SCF ubiquitin ligase complex
RNA−3'−phosphate cyclase activity
protein adenylyltransferase activity
proline dehydrogenase activity
positive regulation of lipase activity
peptide−methionine (R)−S−oxide reductase activity
oxidoreductase activity, acting on the CH−CH group of donors
oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor
oxidoreductase activity
methionine−tRNA ligase activity
methionine adenosyltransferase complex
methionine adenosyltransferase activity
MAP kinase kinase activity
leukotriene−A4 hydrolase activity
isovaleryl−CoA dehydrogenase activity
insulin receptor activity
hydroxymethylglutaryl−CoA reductase (NADPH) activity
hydrolase activity, hydrolyzing N−glycosyl compounds
hexokinase activity
glutamate−5−semialdehyde dehydrogenase activity
glutamate 5−kinase activity
glucokinase activity
gamma−glutamylcyclotransferase activity
fructokinase activity
ethanolaminephosphotransferase activity
epoxide hydrolase activity
diamine N−acetyltransferase activity
carbonate dehydratase activity
C−4 methylsterol oxidase activity
butyryl−CoA dehydrogenase activity
8−methylthiopropyl glucosinolate S−oxygenase activity
5'−nucleotidase activity
4−methylthiopropyl glucosinolate S−oxygenase activity
3−oxo−5−alpha−steroid 4−dehydrogenase activity
1−acylglycerol−3−phosphate O−acyltransferase activity
cytokinesis
positive regulation of macrophage derived foam cell differentiation
skeletal muscle satellite cell migration
regulation of fibroblast migration
hematopoietic stem cell migration
proline catabolic process
ornithine biosynthetic process
methionyl−tRNA aminoacylation
methionine catabolic process
citrulline biosynthetic process
4−hydroxyproline catabolic process
yolk
site of polarized growth
pole plasm
myosin filament
cell cortex
neuron projection maintenance
hemolysis in another organism
cytolysis
mitotic spindle assembly
cellular detoxification of cadmium ion
RNA polymerase II intronic transcription regulatory region sequence−specific DNA binding
RNA polymerase II cis−regulatory region sequence−specific DNA binding
negative regulation of double−strand break repair via nonhomologous end joining
DNA double−strand break processing involved in repair via single−strand annealing
regulation of DNA endoreduplication
positive regulation of transcription of nucleolar large rRNA by RNA polymerase I
positive regulation of transcription from RNA polymerase II promoter in response to heat stress
low−density lipoprotein particle
complement component C1 complex
catalysis of the reaction: 2 L−glutamate + NAD+ = 2−oxoglutarate + L−glutamine + H+ + NADH
glutamate dehydrogenase [NAD(P)+] activity
catalysis of the formation of L−glutamine and 2−oxoglutarate from L−glutamate
catalysis of the reaction: ATP + L−glutamate + NH4+ = ADP + H+ + L−glutamine + phosphate
the directed movement of glutamine, 2−amino−4−carbamoylbutanoic acid
Hsp90 protein binding
Hsp70 protein binding
regulation of mast cell activation
leukocyte migration involved in inflammatory response
complement activation, classical pathway
positive regulation of protein insertion into mitochondrial outer membrane
lipoic acid binding
steroid metabolic process
positive regulation of fatty acid oxidation
phosphatidic acid biosynthetic process
N−acylphosphatidylethanolamine metabolic process
green leaf volatile biosynthetic process
fatty acid derivative biosynthetic process
cardiolipin acyl−chain remodeling
retrograde neuronal dense core vesicle transport
protein transport along microtubule
maintenance of ciliary planar beating movement pattern
anterograde neuronal dense core vesicle transport
transformation of host cell by virus
ubiquitin−protein transferase activator activity
guanylate cyclase activator activity
adenylate cyclase activator activity
acetyltransferase activator activity
acetylcholine receptor activity
positive regulation of mRNA polyadenylation
plasma lipoprotein particle clearance
amyloid−beta clearance
transition between fast and slow fiber
regulation of the force of skeletal muscle contraction
regulation of slow−twitch skeletal muscle fiber contraction
muscle filament sliding
sensory perception of taste
spermine acetylation
spermidine acetylation
regulation of protein metabolic process
putrescine acetylation
protein repair
positive regulation of RNA biosynthetic process
nor−spermidine metabolic process
t−UTP complex
Slx1−Slx4 complex
radial spoke head
origin recognition complex
nuclear outer membrane
NuA3b histone acetyltransferase complex
NuA3a histone acetyltransferase complex
muscle myosin complex
integral component of postsynaptic specialization membrane
extrinsic component of postsynaptic specialization membrane
extrinsic component of neuronal dense core vesicle membrane
endoplasmic reticulum membrane
anaphase−promoting complex
peroxisome fission
insulin receptor complex
acetylcholine−gated channel complex
activation of phospholipase D activity
negative regulation of hydrogen peroxide−mediated programmed cell death
insulin−like growth factor II binding
insulin−like growth factor I binding
identical protein binding
D5 dopamine receptor binding
anaphase−promoting complex−dependent catabolic process
MWP complex
negative regulation of chaperone−mediated protein folding
protein localization to mitotic spindle pole body
positive regulation of protein localization to nucleolus
zymogen activation
regulation of myosin−light−chain−phosphatase activity
protein adenylylation
histone acetylation
radial spoke assembly
protein tetramerization
protein homotrimerization
protein heterooligomerization
regulation of circadian rhythm
positive regulation of respiratory burst
negative regulation of feeding behavior
dopaminergic synapse
cholinergic synapse
regulation of Golgi inheritance
positive regulation of protein−containing complex disassembly
positive regulation of cell cycle phase transition
negative regulation of cell division
positive regulation of cholesterol storage
positive regulation of macromolecule metabolic process
negative regulation of interleukin−10 production
negative regulation of gene expression
regulation of hydrogen peroxide metabolic process
negative regulation of transporter activity
sexual reproduction
asexual reproduction
regulation of meiotic nuclear division
positive regulation of meiotic cell cycle
multicellular organismal reproductive process
male meiosis I
response to melanocyte−stimulating hormone
cellular response to gonadotropin−releasing hormone
cellular response to diamide
cellular response to cGMP
response to food
negative regulation of appetite
chemotaxis to folate
response to vanadate(3−)
response to resveratrol
response to abiotic stimulus
positive regulation of positive chemotaxis to cAMP
negative regulation of cellular response to transforming growth factor beta stimulus
detection of stimulus
cellular response to sodium arsenite
cellular detoxification of sulfide
behavioral response to nicotine
response to hypoxia
response to heat
regulatory RNA binding
transmembrane receptor protein tyrosine phosphatase signaling pathway
synaptic transmission involved in micturition
regulation of vascular endothelial growth factor signaling pathway
regulation of adenylate cyclase−activating G protein−coupled receptor signaling pathway
regulation of acetylcholine secretion, neurotransmission
positive regulation of TORC2 signaling
positive regulation of testosterone secretion
positive regulation of synaptic plasticity
positive regulation of chemorepellent activity
polyphosphate−mediated signaling
negative regulation of Wnt signaling pathway
negative regulation of Notch signaling pathway
negative regulation of insulin receptor signaling pathway
negative regulation of glucocorticoid secretion
negative regulation of glucocorticoid receptor signaling pathway
negative regulation of glucagon secretion
negative regulation of G protein−coupled receptor signaling pathway
insulin receptor signaling pathway
cell surface receptor signaling pathway
activation of transmembrane receptor protein tyrosine kinase activity
abscisic acid−activated signaling pathway
sulfide oxidation, using sulfide:quinone oxidoreductase
S−adenosylmethionine biosynthetic process
hydrogen sulfide metabolic process
glutathione biosynthetic process
glucosinolate biosynthetic process
telomeric D−loop disassembly
t−circle formation
inorganic cation transmembrane transport
glucose transmembrane transport
fructose transmembrane transport
carbohydrate transmembrane transport
vesicle−mediated transport
trehalose transport
transpiration
metal ion transport
lipoprotein transport
intercellular transport
hormone transport
dehydroascorbic acid transport
cytokinin transport
cholesterol transport
cargo receptor activity
abscisic acid transport
trehalose transmembrane transporter activity
transmembrane transporter activity
sugar transmembrane transporter activity
phosphatidic acid transfer activity
gated channel activity
fructose transmembrane transporter activity
extracellular ligand−gated ion channel activity
dehydroascorbic acid transmembrane transporter activity
D−glucose transmembrane transporter activity
acetylcholine−gated cation−selective channel activity
vesicle docking
phagocytosis, engulfment
negative regulation of regulated secretory pathway
endocytosis
vitamin B6 metabolic process
BP
CC
MF
Ontology Category
anatomical structure development
binding
biological process involved in interspecies interaction between organisms
biological regulation
carbohydrate derivative metabolic process
carbohydrate metabolic process
carboxylic acid metabolic process
catalytic activity
cell cycle process
cell differentiation
cell motility
cellular amino acid metabolic process
cellular anatomical entity
cellular component organization or biogenesis
cellular process
cytolysis
cytoskeleton organization
detoxification
DNA binding
DNA repair
DNA replication
DNA−templated transcription
extracellular region
glutamate synthase (NADH) activity
glutamate synthase activity
glutamine synthetase activity
glutamine transport
heat shock protein binding
immune system process
intracellular protein transport
lipid binding
lipid metabolic process
microtubule−based movement
modulation by symbiont of host process
molecular function regulator activity
molecular transducer activity
mRNA metabolic process
multicellular organismal process
muscle system process
nervous system process
nitrogen compound metabolic process
organelle
peroxisome organization
plasma membrane
positive regulation of phospholipase activity
programmed cell death
protein binding
protein catabolic process
protein containing complex
protein folding
protein localization
protein maturation
protein modification process
protein−containing complex assembly
regulation of biological process
regulation of cellular process
regulation of lipid storage
regulation of macromolecule metabolic process
regulation of reactive oxygen
regulation of transport
reproduction
reproductive process
response to nitrogen compound
response to nutrient levels
response to stimulus
response to stress
RNA binding
signaling
sulfur compound metabolic process
telomere organization
transmembrane transport
transport
transporter activity
vesicle−mediated transport
vitamin metabolic process
Adjusted p−value
0.04
0.03
0.02
0.01
Number of Genes
100
200
300
400
500