cluster1 cluster2 cluster3 cluster4 cluster5 cluster6 cluster7 mRNA cis splicing, via spliceosome (GO:0045292)
mitotic sister chromatid cohesion (GO:0007064)
floor plate morphogenesis (GO:0033505)
floor plate formation (GO:0021508)
ventral midline development (GO:0033504)
neural plate development (GO:0001840)
embrane disruption in other organism (GO:0051673) neural plate development membrane disruption in other organism medial fin morphogenesis hindbrain development anterior/posterior pattern specification rostrocaudal neural tube patterning neural tube patterning midbrain-hindbrain boundary development forebrain development diencephalon development diencephalon development neural precursor cell proliferation spinal cord motor neuron differentiation metencephalon development metencephalon development cerebellum development cell population proliferation Notch signaling pathway GO:0009952 30.0030900 GO:0022037 GO:0021549 Notch signaling pathway regulation of axonogenesis neuron fate commitment cranial nerve development morphogenesis of embryonic epithelium central nervous system neuron development central nervous system neuron differentiation ventral spinal cord development cell differentiation in spinal cord peripheral nervous system neuron axonogenesis pancreatic A cell differentiation peripheral nervous system neuron axonogenesis pancreatic A cell differentiation peripheral nervous system neuron development peripheral nervous system neuron differentiation enteroendocrine cell differentiation glandular epithelial cell differentiation endocrine pancreas development. glandular epithelial cell differentiation (
endocrine pancreas development (
central nervous system neuron axonogenesis (
central nervous system projection neuron axonogenesis (
endoplasmic reticulum to Golgi vesicle—mediated transport (
protein folding (
positive regulation of supramolecular fiber organization (
positive regulation of cytoskeleton organization (
positive regulation of cellular component biogenesis (
regulation of protein metabolic process (O:0006457 positive regulation of cellular component biogenesis (
regulation of protein metabolic process (
regulation of cellular protein metabolic process (
regulation of protein modification process (
organelle organization (
positive regulation of protein metabolic process (
positive regulation of cellular protein metabolic process (
cellular macromolecule metabolic process (
macromolecule metabolic process (
protein modification process (protein modification process cellular protein modification process macromolecule modification of protein phosphorylation (protein phosphorylation of protein phosphorylation of protein phosphorylation of localization of locali GO:0043412 GO:0006468 macromolecule modification GO:0006796 GO:0006793 GO:0071704 GO:0044238 metabolic process organonitrogen compound metabolic process organonitrogen compound metabolic process organic cyclic compound biosynthetic process organic cyclic compound biosynthetic process of the pr aromatic compound biosynthetic process organic substance biosynthetic process cellular biosynthetic process biosynthetic process carbohydrate derivative metabolic process organonitrogen compound biosynthetic process cellular nitrogen compound biosynthetic process organic substance catabolic process GO:1901566 GO:0044271 catabolic process (GO:0044271)
catabolic process (GO:009056)
cellular catabolic process (GO:004248)
lipid catabolic process (GO:0016042)
Unclassified (UNCLASSIFIED)
establishment of localization (GO:0051234)
transport (GO:0051234)
organic code organic substance transport cellular macromolecule localization cellular protein localization cellular localization (intracellular protein transport (intracellular transport (establishment of protein localization protein localization macromolecule localization (peptide transport protein transport) GO:0015833 amide transport (nitrogen compound transport (vesicle–mediated transport (regulation of protein polymerization (GO:0032271)
regulation of actin filament polymerization (GO:0032271)
regulation of actin filament length (GO:0030832)
of actin polymerization or depolymerization (GO:0008064) regulation of actin poly regulation of actin polymerization or depolymerization is regulation of protein complex assembly of actin filament organization of regulation of actin filament—based process of regulation of actin cytoskeleton organization of regulation of supramolecular fiber organization of regulation of cellular component biogenesis of the process membrane fusion (organelle fusion (vesicle organization (vesicle organization (
cellular response to topologically incorrect protein (
response to topologically incorrect protein (
response to endoplasmic reticulum stress (
positive regulation of protein polymerization (
positive regulation of protein complex assembly (
positive regulation of actin filament polymerization (
Ras protein signal transduction (
small GTPase mediated signal transduction (
Rho protein signal transduction (
protein localization to endoplasmic reticulum (
sensory organ morphogenesis (ein localization to endoplasmic reticulum (
sensory organ morphogenesis (
eye morphogenesis (
retina development in camera—type eye (
sensory system development (
sensory organ development (
visual system development (
eye development (
camera—type eye development (
axon development (axon development cell morphogenesis involved in neuron differentiation cell projection morphogenesis neuron projection morphogenesis plasma membrane bounded cell projection morphogenesis GO:0048858 GO:0048812 axonogenesis cell part morphogenesis cell morphogenesis involved in differentiation neuron development neuron projection development GO:0048666 cell morphogenesis camera–type eye morphogenesis generation of neurons GO:0048699 neurogenesis nervous system development néuron differentiation plasma membrane bounded cell projection organization cell projection organization neuron projection organization (
neuron projection guidance (
axon guidance (
microtubule cytoskeleton organization (
epithelial tube morphogenesis (
regulation of cell morphogenesis (
pattern specification process (
regionalization (
epithelial tube formation (GO:0097485 GO:0007411 GO:0060562 regulation of neuron differentiation of regulation of neuron projection development regulation of cell differentiation of regulation of cell differentiation of cell different regulation of cell development regulation of neurogenesis regulation of nervous system development head development brain development central nervous system development GO:0007420 regulation of nitrogen compound metabolic process (
regulation of nitrogen compound metabolic process (
regulation of primary metabolic process (
regulation of cellular metabolic process (
regulation of metabolic process (GO:0031323 positive regulation of nitrogen compound metabolic process positive regulation of macromolecule metabolic process positive regulation of cellular metabolic process positive regulation of cellular metabolic process of positive regulation of metabolic process of positive regulation of cellular process of positive regulation of biological process of negative regulation of cellular process of negative regulation of biological process of negative regulation of cellular metabolic process of negative regulation of metabolic process of negative regulation of metabolic process of negative regulation of cellular metabolic process of negative regulation of cellular metabolic process of negative regulation of metabolic process of negative regulation negative regulation negative regulation negative regulation negative regulation nega GO:0009893 GO:0048522 GO:0048518 GO:0048523 negative regulation of cellular metabolic process (
negative regulation of metabolic process (
negative regulation of RNA biosynthetic process (
negative regulation of RNA biosynthetic process (
negative regulation of transcription, DNA-templated (
negative regulation of nucleic acid-templated transcription (
negative regulation of RNA metabolic process (
negative regulation of cellular biosynthetic process (
regulation of cellular macromolecule biosynthetic process (
regulation of cellular macromolecule biosynthetic process (negative regulation of cellular macromolecule biosynthetic process (
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positive regulation of RNA metabolic process (
positive regulation of RNA biosynthetic process (
regulation of nucleobase—containing compound metabolic process (
regulation of nucleobase—containing compound metabolic process (
regulation of RNA me negative regulation of cellular macromolecule biosynthetic process negative regulation of macromolecule biosynthetic process GO:0010629 GO:0010557 (GO:0006357) (GO:0045944) positive regulation of neuron differentiation positive regulation of nervous system development endocrine system development epithelial cell differentiation (
cell fate commitment (
columnar/cuboidal epithelial cell differentiation (
peripheral nervous system development (regulation of cell cycle process (
negative regulation of cell cycle process (
tissue morphogenesis (
morphogenesis of an epithelium (embryonic organ development (
embryonic organ morphogenesis (
embryonic morphogenesis (
tube development (
embryo development (embryo development (
epithelium development (
regulation of cellular component organization (
regulation of organelle organization (
tissue development (
animal organ morphogenesis (
anatomical structure formation involved in morphogenesis (
transmembrane receptor protein serine/threonine kinase signaling pathway (
determination of bilateral symmetry (
specification of symmetry (
determination of left/right symmetry (
cellular response to growth factor stimulus (
response to growth factor (
circulatory system development (
tube morphogenesis () GO:0060429 GO:0051128 GO:0009888 GO:0071363 GO:0070848 circulatory system development (
tube morphogenesis (
localization of cell (
cell motility (
cell migration (
developmental growth (
growth (
mesenchyme development (
cell-cell signaling by wnt (
Wnt signaling pathway (
cell surface receptor signaling pathway involved in cell-cell signaling (
mesoderm development (GO:0048870 GO:0016477 GO:0040007 GO:0060485 GO:0198738 GO:0016055 gnaling pathway involved in cell-cell signaling (
mesoderm development (
skeletal system development (
ameboidal-type cell migration (
regulation of phosphorus metabolic process (
regulation of phosphate metabolic process (
regulation of phosphorylation (
regulation of protein phosphorylation (
positive regulation of phosphorylation (
regulation of protein kinase activity (
actin cytoskeleton organization (
actin filament-based process (GO:0001667) GO:0051174) GO:0019220) GO:0019225 GO:0042325 GO:0001932 GO:0042327 GO:0045859 actin filament–based process (regulation of cellular process regulation of biological process regulation of biological process (regulation of biological process) GO:0030029 GO:0050794 regulation of biological process (
biological regulation of biological regulation or biologenesis (
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regulation of signal transduction or regulation of signaling or regulation of cell communication organism development of development organism development of system development organism development organis GO:0016043) GO:0048583) GO:0009966) multicellular organism development (
system development (
animal organ development (
multicellular organismal process (
cell surface receptor signaling pathway (
regulation of transferase activity (
regulation of kinase activity (
anatomical structure morphogenesis (
locomotion (
byement of cell or subcellular component (GO:0048737 GO:0048513 movement of cell or subcellular component (
cytoskeleton organization (
transmembrane receptor protein tyrosine kinase signaling pathway (
enzyme linked receptor protein signaling pathway (
regulation of multicellular organismal development (
regulation of developmental process (
cellular developmental process (
cell development (GO:0050793 GO:0048869 cell differentiation cell development (regulation of multicellular organismal process cellular component morphogenesis (negative regulation of signaling negative regulation of cell communication negative regulation of signal transduction regulation of anatomical structure morphogenesis (negulation of transmembrane receptor protein serine/threonine kinase signaling pathway positive regulation of kinase activity dorsal/ventral pattern formation regulation of megative regulation of bMP signaling pathway negative regulation of nervous system development negative regulation of neurogenesis negative regulation of developmental process negative regulation of developmental process mitotic DNA integrity checkpoint pigmentation (protein acetylation) go_term GO:0007093 mitotic cell cycle checkpoint (
pigmentation (
chromatin remodeling (
appendage morphogenesis (
fin morphogenesis (
regulation of cellular response to growth factor stimulus (
appendage development (
fin development (
retinal ganglion cell axon guidance (
digestive system development (
digestive tract development (GO:0033333 GO:0031290 digestive system development (GO:003123)
digestive tract development (GO:0048565)
pectoral fin development (GO:0033339)
neural crest cell development (GO:0014032)
mesenchymal cell development (GO:0014031) stem cell development stem cell differentiation neural crest cell differentiation stem cell differentiation (
neural crest cell differentiation (
mesenchymal cell differentiation (
negative regulation of cell cycle (
regulation of canonical What signaling pathway (
regulation of What signaling pathway (
negative regulation of cell cycle Gazinization (
negative regulation of organelle organization (
regulation of cell cycle Gazinization (
regulation of cell cycle Gazinization (
mitotic sister chromatid segregation (
mitotic cell cycle gazinization (
mitotic chromosome condensation (
mitotic chromosome condensation (
negative regulation of cell cycle phase transition (
negative regulation of cell cycle phase transition (
negative regulation of DNA metabolic process (
negative regulation of DNA recombination (
positive regulation of gene expression, epigenetic (
negative regulation of chromatin organization (
negative regulation of chromatin silencing (
negative regulation of chromatin silencing (
regulation of chromatin silencing (
chromosome condensation (
regulation of DNA recombination (
regulation of DNA recombination (
regulation of bNA recombination (
regulation of chromatin silencing (
chromosome condensation (
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chromosome condensation (
regulation of gene silencing (
chromosome condensation (
regulation of gene silencing (
chromosome condensation (
regulation of gene silencing (
chromosome condensation (
regulation of chromatin silencing (
chromoso regulation of DNA recombination (
regulation of gene silencing (
chordate embryonic development (
embryo development ending in birth or egg hatching (
gland development (
cell division (
somite development (
embryonic skeletal system morphogenesis (
embryonic cranial skeleton morphogenesis (
embryonic skeletal system development (
skeletal system morphogenesis (
cranial skeletal system development (
embryonic viscerocranium morphogenesis (embryonic viscerocranium morphogenesis convergent extension involved in gastrulation GO:0048703 inner ear development ear development cell migration involved in heart development heart formation vasculogenesis animal organ formation of cell migration to the midline involved in heart development of mesoderm formation of blood vessel morphogenesis of blood vessel development of b GO:0048514 angiogenesis cardiovascular system development vasculature development GO:0001525 GO:0072358 vasculature developments in mesoderm morphogenesis (response to BMP (BMP signaling pathway (cellular response to BMP stimulus (convergent extension (gastrulation (gastrulation cell migration involved in gastrulation cell migration involved in ğastrulation (
endoderm development (
gastrulation with mouth forming second (
formation of primary germ layer (
embryonic heart tube morphogenesis (
heart looping (
determination of heart left/right asymmetry (
embryonic heart tube development (
heart morphogenesis (
heart development (
cardiac muscle cell development (
cardiac cell development (
cardiac muscle tissue development (cardiac muscle tissue development cardiac muscle cell differentiation cardiac muscle cell differentiation (
cardiocyte differentiation (
skeletal muscle organ development (
muscle organ development (
negative regulation of intracellular signal transduction (
muscle tissue development (
striated muscle tissue development (
actomyosin structure organization (
non-canonical Wnt signaling pathway (
myofibril assembly (
cellular component assembly involved in morphogenesis (
striated muscle cell development (
striated muscle cell development (
striated muscle cell differentiation (
muscle structure development (
regulation of embryonic development (
myotube differentiation (
myotube myotube differentiation (
nucleic acid metabolic process (
RNA metabolic process (
RNA processing (
cellular nitrogen compound metabolic process) gene expression
heterocycle metabolic process
cellular aromatic compound metabolic process organic cyclic compound metabolic process nucleobase—containing compound metabolic process regulation of cell cycle (
DNA metabolic process (
DNA metabolic process (
regulation of mitotic cell cycle (
cellular response to DNA damage stimulus (
mitotic cell cycle process (
mitotic cell cycle cell cycle agent silencing) regulation of gene expression, epigenetic cell cycle process cell cycle negative regulation of mitotic cell cycle spindle organization (G0:0007051)
mitotic spindle organization (G0:0007052)
microtubule cytoskeleton organization involved in mitosis (G0:1902850)
regulation of DNA metabolic process (G0:0051052)
chromosome organization (G0:0051276) GO:0043484 GO:0031497 nucleosome assembly of DNA packaging of DNA complex assembly of DNA complex assembly of DNA conformation change of the protein of cell cycle phase transition of sister chromatid cohesion of cells of the protein of th sister chromatid conesion (
sister chromatid segregation (
meiotic cell cycle process (
meiotic cell cycle process (
meiotic cell cycle GO:0008380 chromosome segregation nuclear division mRNA metabolic process mRNA processing secretion secretion by cell regulation of neurotransmitter levels regulation of neurotransmitter lévels (
exocytosis (
cell-cell signaling)
regulation of regulated secretory pathway (
regulation of exocytosis (
cell-cell adhesion via plasma-membrane adhesion molecules (
homophilic cell adhesion via plasma membrane adhesion molecules (
cell-cell adhesion (
regulated exocytosis (
regulation of calcium ion-dependent exocytosis (
synaptic transmission, glutamatergic (
regulation of secretion by cell (
regulation of secretion (regulation of secretion signal release from synapse neurotransmitter secretion synaptic vesicle exocytosis (
signal release (
synaptic vesicle cycle (
vesicle–mediated transport in synapse (
neurotransmitter transport (
applications) calcium-ion regulated exocytosis gamma-aminobutyric acid signaling pathway biological adhesion regulation of vesicle—mediated transport export from cell lens development in camera—type eye sensory perception of light stimulus visual perception visual perception (
nervous system process (
regulation of trans—synaptic signaling (
modulation of chemical synaptic transmission (
regulation of ion transmembrane transport (
regulation of transmembrane transport (
regulation of ion transport (
regulation of ion transport (
anterograde trans—synaptic signaling (
chemical synaptic transmission (
trans—synaptic signaling (
synaptic signaling (synaptic signaling G protein–coupled receptor signaling pathway Golgi vesicle transport endosomal transport organelle membrane fusion vesicle fusion organelle membrane fusion (
vesicle fusion (
mitochondrial gene expression (
dicarboxylic acid metabolic process (
nucleoside triphosphate biosynthetic process (
mitochondrial translation (
nucleoside triphosphate metabolic process (
Mitochondrial respiratory chain complex I sasembly (
NADH dehydrogenase complex assembly (
Mitochondrial electron transport, NADH to ubiquinone (
respiratory chain complex III assembly (
mitochondrial electron transport, ubiquinol to cytochrome c
mitochondrial respiratory chain complex III assembly (
aerobic electron transport chain (
mitochondrial electron transport, cytochrome c to oxygen (
ATP synthesis coupled proton transport (
energy coupled proton transport, down electrochemical gradient (
ATP biosynthetic process (
lipid oxidation (
fatty acid oxidation (
fatty acid oxidation (
purine ribonucleoside triphosphate biosynthetic process (
purine nucleoside triphosphate metabolic process (
purine ribonucleoside triphosphate metabolic process (
purine ribonucleoside triphosphate metabolic process (
proton transmembrane transport (
respiratory chain complex IV assembly (
) GO:0140053 proton transmembrane transport (respiratory chain complex IV assembly cytochrome complex assembly cellular respiration (aerobic respiration) aerobic respiration (GO:0009060)
ATP synthesis coupled electron transport (GO:0042773)
oxidative phosphorylation (GO:0006119)
mitochondrial ATP synthesis coupled electron transport (GO:0042775)
respiratory electron transport chain (GO:0022904)
electron transport chain (GO:0022900)
mitochondrial respiratory chain complex assembly (GO:0033108)
alpha–amino acid catabolic process (GO:1901606)
cellular amino acid catabolic process (GO:0009063) glutathione metabolic process negative regulation of endopeptidase activity ribonucleoside triphosphate biosynthetic process ribonucleoside triphosphate metabolic process regulation of endopeptidase activity regulation of peptidase activity
ATP metabolic process cellular lipid catabolic process monocarboxylic acid catabolic process fatty acid catabolic process mitochondrial transport carbohydrate catabolic process nucleotide metabolic process nucleotide metabolic process nucleoside phosphate metabolic process nucleobase–containing small molecule metabolic process organophosphate metabolic process small molecule biosynthetic process GO:0006753 GO:004428; purine ribonucleotide metabolic process purine nucleotide metabolic process purine–containing compound metabolic process ribose phosphate metabolic process ribonucleotide metabolic process negative regulation of proteolysis negative regulation of peptidase activity alpha–amino acid metabolic process GO:0010466 GO:1901605 purine ribonucleotide biosynthetic process purine nucleotide biosynthetic process purine–containing compound biosynthetic process GO:0006164 ribose phosphate biosynthetic process ribonucleotide biosynthetic process carboxylic acid catabolic process GO:0009260 organic acid catabolic process small molecule catabolic process nucleoside phosphate biosynthetic process nucleotide biosynthetic process organophosphate biosynthetic process GO:000916 cofactor biosynthetic process coenzyme metabolic process negative regulation of hydrolase activity mitochondrial transmembrane transport cellular amino acid metabolic process 3O:199054: monocarboxylic acid metabolic process O:000663 fatty acid metabolic process mitochondrion organization purine ribonucleoside diphosphate metabolic process purine nucleoside diphosphate metabolic process ribonucleoside diphosphate metabolic process ADP metabolic process ATP generation from ADP O:0046031 glycolytic process nucleotide phosphorylation nucleoside diphosphate phosphorylation 0.0006096protein localization to mitochondrion of protein localization to mitochondrion of protein targeting to mitochondrion of protein localization to mitochondrion of pyruvate metabolic process of nucleoside diphosphate metabolic process of management of protein localization to mitochondrion of pyruvate metabolic process of nucleoside diphosphate metabolic process of monopological process of the pro monosaccharide metabolic process regulation of small molecule metabolic process cellular lipid metabolic process lipid metabolic process sulfur compound metabolic process oxidation-reduction process generation of precursor metabolites and energy oxoacid metabolic process organic acid metabolic process carboxylic acid metabolic process small molecule metabolic process cofactor metabolic process O:0051186 drug metabolic process transmembrane transport ion transport ion transmembrane transport amide biosynthetic process cellular amide metabolic process GO:0043604 carbohydrate metabolic process energy derivation by oxidation of organic compounds cellular modified amino acid metabolic process lipid modification O:0030258 peptide biosynthetic process translation peptide metabolic process GO:0006412 GO:0006518 protein autophosphorylation (GO:0046777 3 1 2 3 2 2 3 0 0 0 3 0 3 abs_log2_fold_enrichment