type I pneumocyte differe proximal/distal pattern formation involved positive regulation of meiotic cell c Notch signaling pathway involved in arterial end negative regulation of transcription from RNA polymerase II promoter involved in smooth negative regulation of synaptic assembly negative regulation of postness. anatomical structure development hemangiobl GABAergic neuron differen epithelial cell proliferation involved chondrocyte intercalation involved in growth cerebral cortex GABAerg cerebellar Purkinje cell lave anatomical structure formation involved in morpho translation elongation facto low-density lipoprotein p insulin-like growth factor re binding anaphase-promoting comp 3-phosphoinositide-dependent protein kinase b pore formation in membrane of another organism membrane depolarization positive regulation of glycoprotein biosynthetic process glucose 6-phosphate metabolic process biological regulation carbohydrate derivative metabolic process carbohydrate metabolic process leukotriene biosynthetic process sulfide:quinope oxidoreductase activity carboxylic acid metabolic process oxidoreductase activity, acting on a su hydroxymethylglutaryl-CoA reductase hydrolyzing N-gl catalytic activity glutamate-5-semialdehyde deh gamma-glutamylcycloti ethanolaminephosph 8-methylthiopropyl glucosinol cell cycle process positive regulation of macrophage derived foam cell differentiation l cell differentiation cell motility cellular amino acid metabolic process site of polarized growth cellular anatomical entity neuron projection maintenance l cellular component organization or biogenesis hemolysis in another organism l cellular process cytolysis l cvtolvsis mitotic spindle assembly l cytoskeleton organization cellular detoxification of cadmium ion t detoxification RNA polymerase II intronic transcription regulatory region sequence—specific BNA binding the RNA polymerase II cis—regulatory region sequence—specific BNA binding the sequence of the sequenc **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 **DNA** repair **DNA replication DNA**-templated transcription low-density lipoprotein particle complement component C1 complex extracellular region heat shock protein binding leukocyte migration involved in inflar complement activation, immune system process positive regulation of protein insertion into mitochondrial outer membraneintracellular protein transport lipid bindina **Number of Genes** N-acylphosp lipid metabolic process 100 microtubule-based movement transformation of host cell by virus I modulation by symbiont of host process ubiquitin-protein, transferase activator activity molecular function regulator activity acetylcholine receptor activity 1 molecular transducer activity positive regulation of mRNA polyadenylation I mRNA metabolic process plasma lipoprotein particle clearance amyloid-beta clearance multicellular organismal process Adjusted p-value muscle system process 0.04 0.03 sensory perception of tastenervous system process 0.02 regulation of protein 0.01 nitrogen compound metabolic process NuA3b histone acc organelle peroxisome fission peroxisome organization acetylcholine-gated channel complex plasma membrane activation of phospholipase D activity I positive regulation of phospholipase activity programmed cell death negative regulation of hydrogen peroxide-mediated programmed cell death I protein binding anaphase-promoting complex-dependent catabolic process l protein catabolic process protein containing complex negative regulation of chaperone-mediated protein folding I protein folding protein localization to mitotic spindle pole body positive regulation of protein localization to nucleolus protein localization zymogen activation protein maturation regulation of myosin-light-chain-phosphatase activity-protein adenylylation-histone acetylation protein modification process protein-containing complex assembly regulation of biological process positive regulation of protein—containing complex ulsassellition of cell cycle phase transition hegative regulation of cell division hegative regulation of cell division. regulation of cellular process positive regulation of cholesterol storage positive regulation of macromolecule metabolic process negative regulation of interleukin—10 production negative regulation of gene expression. regulation of lipid storage regulation of macromolecule metabolic process regulation of hydrogen peroxide metabolic process l regulation of reactive oxygen negative regulation of transporter activity I regulation of transport reproduction regulation of meiotic nuclear division positive regulation of meiotic cell cycle multicellular organismal reproductive process male meiosis reproductive process response to nitrogen compound response to food-negative regulation of appetite-chemotaxis to folateresponse to nutrient levels negative regulation of cellular response to transforming growth response to stimulus response to stress regulatory RNA binding RNA binding transmembrane receptor protein tyrosine phosphatase signaling pa regulation of vascular endothelial growth factor regulation of vascular endothelial growth factor regulation of adenylate cyclase—activating G protein—coupled receptor regulation of acetylcholine secretion regulation of acetylcholine secretion. signaling negative regula negative regulation of gl negative regulation of G protein activation of transmembrane recepto abscisic a sulfide oxidation, using sulfide S-adengsylmethion sulfur compound metabolic process telomere organization transmembrane transport transport dehydroasco transporter activity negative regulation of regulated secretory vesicle-mediated transport vitamin B6 metabolic process l vitamin metabolic process CC

**Ontology Category**