Top 10 significantly over–represented GO terms for OB series for dPSI cutoff of 0.15 and any sig qvalue 0.01 encompassing 915 genes MF regulation of organelle organization -cytoskeleton organization -RNA splicing cell adhesion molecule binding cell-substrate junction cytoskeletal protein binding focal adhesion actin cytoskeleton organization actin filament–based process positive regulation of cellular component organization SH3 domain binding cell–substrate adherens junction + cadherin binding · adherens junction actin binding positive regulation of organelle organization regulation of RNA splicing anchoring junction + protein domain specific binding -14–3–3 protein binding supramolecular fiber organization -cell cycle process -mitotic cell cycle cell junction peroxisome proliferator activated receptor binding actin cytoskeleton transcription coregulator activity microtubule cytoskeleton + regulation of cell-substrate adhesion regulation of cell-substrate adheśion cell cycle phase transition of cellular response to DNA damage stimulus regulation of cell cycle regulation of mitotic cell cycle intrinsic apoptotic signaling pathway regulation of mRNA splicing, via spliceosome regulation of intrinsic apoptotic signaling pathway cell cycle G2/M phase transition regulation of cellular component biogenesis mitotic cell cycle process negative regulation of mitotic cell cycle processing mitotic cell cycle phase transition mitotic cell cycle phase transition transcription factor binding lamellipodium integrin binding nuclear body microtubule binding nucleoplasm part protein-containing complex binding cell leading edge protease binding -Golgi subcompartment chromatin binding · protein-lysine 6-oxidase activity cell cortex retinoic acid receptor binding supramolecular polymer protein serine/threonine kinase activity supramolecular complex platelet-derived growth factor binding RNA processing mitotic cell cycle phase transition RNA splicing, via transesterification reactions with bulged adenosine as nu... mRNA splicing, via spliceosome regulation of integrin—mediated signaling pathway apoptotic signaling pathway negative regulation of peptidyl—cysteine S—nitrosylation regulation of cell cycle phase transition RNA splicing, via transesterification reactions positive regulation of apoptotic signaling pathway positive regulation of chromosome segregation regulation of mRNA processing integrin—mediated signaling pathway organelle disassembly mRNA processing circulatory system development histone deacetylation negative regulation of cell cycle supramolecular fiber 5-formyltetrahydrofolate cyclo-ligase activity Golgi apparatus part histone deacetylase binding -Golgi membrane transferase activity, transferring phosphorus-containing groups nuclear speck cell cortex part hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds FANCM-MHF complex tRNA-specific adenosine deaminase activity CCAAT-binding factor complex transcription coactivator activity deacetylase activity microtubule pre-mRNA binding nucleolus nuclear hormone receptor binding perinuclear region of cytoplasm clathrin binding circulatory system development histone deacetylation negative regulation of cell cycle organelle assembly regulation of cell matrix adhesion tetrahydrofolate interconversion microtubule—based process protein—containing complex localization—positive regulation of chromosome organization—positive regulation of organelle organization—positive regulation of organelle organization—positive regulation of cell cycle process—ribonucleoprotein complex export from nucleus—regulation of cell cycle process—ribonucleoprotein complex localization—positive regulation of programmed cell death—G2/M transition of mitotic cell cycle—mitochondrion organization—regulation of cell cycle G2/M phase transition—regulation of mitochondrion organization—regulation of integrin—mediated signaling pathway—negative regulation of cell cycle phase transition—actin filament organization—mRNA—containing ribonucleoprotein complex export from nucleus—cardiovascular system development—cell—substrate adhesion—regulation of mitotic cell cycle phase transition—regulation of chromosome organization—regulation of chromo costamere - I proteoglycan binding plasma membrane bounded cell projection part calmodulin binding cell projection part structural molecule activity -SAP kinase activity interstitial matrix ribonuclease inhibitor activity 1 invadopodium membrane phosphothreonine residue bindina synapse -JUN kinase activity collagen type I trimer cyclo-ligase activity microtubule organizing center alkylglycerophosphoethanolamine phosphodiesterase activity retinoid X receptor binding MKS complex uridylyltransferase activity midbody phosphotransferase activity, alcohol group as acceptor trans-Golgi network repressing transcription factor binding microtubule end calcium-transporting ATPase activity ruffle adenosine deaminase activity structural constituent of cytoskeleton microtubule plus-end nucleosomal DNA binding spindle extracellular matrix structural constituent cortical actin cytoskeleton extracellular matrix structural constituent conferring tensile strength · actin filament methylenetetrahydrofolate dehydrogenase (NADP+) activity polymeric cytoskeletal fiber catalytic step 2 spliceosome protein kinase activity spliceosomal complex profilin binding spectrin regulation of chromosome organization hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in c... chromosomal region plasma membrane bounded cell projection assembly RNA export from nucleus histone deacetylase complex transcription corepressor activity 1 ciliary transition zone regulation of apoptotic signaling pathway -negative regulation of cellular component organization -protein export from nucleus isopeptidase activity nuclear transcription factor complex inositol hexakisphosphate kinase activity Golgi-associated vesicle membrane inositol hexakisphosphate 5-kinase activity H3 histone acetyltransferase activity endoplasmic reticulum exit site double-stranded RNA adenosine deaminase activity extracellular matrix organization cytoplasmic region protein deacylation alternative mRNA splicing, via splice sosome microtubule minus-end binding collagen type VI trimer alternative mRNA splicing, via spliceosome nuclear export nuclear export G2 DNA damage checkpoint positive regulation of cellular component biogenesis negative regulation of cell cycle process positive regulation of mitochondrion organization negative regulation of nuclear cell cycle DNA replication cell projection assembly protein deacetylation cellular response to ketone chloride ion binding collagen beaded filament protein tyrosine/serine/threonine phosphatase activity centrosome -GTPase binding ribonucleoprotein complex cysteine-type endopeptidase activity involved in apoptotic process glycosaminoglycan binding cortical cytoskeleton phosphatase binding 1 RNA polymerase II transcription factor complex hormone receptor binding axon initial segment Ral GTPase binding positive regulation of intrinsic apoptotic signaling pathway mRNA metabolic process extracellular matrix component nitric-oxide synthase binding polyubiquitin modification-dependent protein binding contractile fiber nucleobase–containing compound transport cell division I Notch binding centriole symbiont process -symbiont process -macromolecule deacylation -cellular component morphogenesis -peptidyl-serine modification -cilium assembly enhancer sequence–specific DNA binding protein C–terminus binding beta-catenin-TCF complex elastic fiber · RNA polymerase II transcription factor binding actin cap protein phosphatase binding phosphatidylinositol–3,4,5–trisphosphate binding cilium assembly positive regulation of cell-substrate adhesion microtubule cytoskeleton organization positive regulation of cell projection organization cell-substrate junction assembly regulation of substrate adhesion-dependent cell spreading positive regulation of cell death DNA-dependent DNA replication
regulation of organile assembly chromosome, telomeric region collagen trimer kinase binding - 1 ubiquitin-like protein binding complex of collagen trimers hydrolase activity, acting on acid anhydrides, in phosphorus-containing anh. myofibril hydrolase activity, acting on acid anhydrides - oxidoreductase activity, acting on the CH–NH2 group of donors, oxygen as ac... nucleolar part regulation of organelle assembly cell-matrix adhesion npBAF complex · microtubule plus-end binding cell-matrix adhesion peptidyl-serine phosphorylation viral process mitotic cell cycle checkpoint peptidyl-amino acid modification peptidyl-lysine oxidation negative regulation of pancreatic juice secretion establishment of RNA localization establishment of RNA localization fibrillar collagen trimer glucocorticoid receptor binding banded collagen fibril dopamine receptor binding nuclear receptor transcription coactivator activity ciliary basal body vascular endothelial growth factor-activated receptor activity SWI/SNF superfamily-type complex type 1 angiotensin receptor binding fibrillar center thioredoxin-disulfide reductase activity lamellipodium organization DNA integrity checkpoint synapse part syndecan binding sodium channel inhibitor activity integral component of mitochondrial membrane nuclear transport organelle localization positive regulation of histone deacetylation negative regulation of sodium ion transport clathrin light chain binding spectrin binding paranode region of axon zinc ion binding nuclear inclusion body cell aging pancreatic juice secretion cilium organization DNA damage checkpoint chromatin organization carbohydrate derivative transmembrane transporter activity Fanconi anaemia nuclear complex -NAD binding eukaryotic translation initiation factor 4F complex lamin binding intrinsic component of mitochondrial membrane transition metal ion binding regulation of protein complex assembly one-carbon metabolic process thyroid hormone receptor binding actin filament bundle miRNA binding cellular protein—containing complex assembly protein localization to cell periphery regulation of actin cytoskeleton organization regulation of alternative mRNA splicing, via spliceosome tetrahydrofolate metabolic process -1 neuron projection histone deacetylase activity - pyrophosphatase activity -9+0 non-motile cilium non-motile cilium protein kinase binding Ras GTPase binding -Golgi-associated vesicle nucleosome disassembly-negative regulation of DNA-dependent DNA replication-ciliary basal body-plasma membrane docking-intracellular protein transportubiquitin-specific protease binding glutamatergic synapse nucleotide diphosphatase activity integral component of organelle membrane protein deacetylase activity establishment or maintenance of cell polarity regulation of small GTPase mediated signal transduction contractile fiber part deaminase activity microtubule organizing center part primary miRNA binding septin ring mRNA transport non-membrane spanning protein tyrosine phosphatase activity negative regulation of sodium ion transmembrane transporter activity negative regulation of sodium ion transmembrane transporter activity hepatocyte apoptotic process regulation of protein binding regulation of pancreatic juice secretion positive regulation of oxidative stress—induced intrinsic apoptotic signali... regulation of G2/M transition of mitotic cell cycle cellular response to oxidative stress interspecies interaction between organisms regulation of histone deacetylation regulation of androgen receptor signaling pathway nucleocytoplasmic transport negative regulation of organelle assembly RNA transport nucleic acid transport septin complex · nitric-oxide synthase regulator activity photoreceptor outer segment membrane -N6-methyladenosine-containing RNA binding DEAD/H-box RNA helicase binding A band cAMP response element binding protein binding catalytic complex + angiotensin receptor binding protein serine/threonine/tyrosine kinase activity membrane coat nucleobase-containing compound transmembrane transporter activity endonuclease activity, active with either ribo- or deoxyribonucleic acids a... coated membrane · androgen receptor binding actin-based cell projection -RNA polymerase II distal enhancer sequence–specific DNA binding intrinsic component of organelle membrane · endoribonuclease activity, producing 5'-phosphomonoesters nucleic acid transport regulation of focal adhesion assembly regulation of cell–substrate junction assembly histone modification coated vesicle I band protein methyltransferase activity actomyosin copper ion binding negative regulation of mitotic cell cycle phase transition cell morphogenesis double-stranded RNA binding microtubule bundle regulation of cellular amino acid biosynthetic process negative regulation of protein localization to chromosome, telomeric region negative regulation of mitotic cell cycle DNA replication guanyl-nucleotide exchange factor activity ATPase complex chromatin DNA binding septin cytoskeleton enhancer binding negative regulation of cell–substrate adhesion mitochondrion disassembly autophagy of mitochondrion covalent chromatin modification protein–DNA complex disassembly nBAF complex -RNA polymerase binding COPII vesicle coat -Ras guanyl-nucleotide exchange factor activity glial cell projection rDNA binding pre-mRNA intronic binding integral component of Golgi membrane potassium channel inhibitor activity chromatin disassembly protein nitrosylation peptidyl-cysteine S-nitrosylation peptidyl-cysteine S-nitrosylation negative regulation of substrate adhesion-dependent cell spreading negative regulation of sodium ion transmembrane transport protein polymerization regulation of cell adhesion cytoplasmic translation regulation of autophagy of mitochondrion Golgi to plasma membrane protein transport collagen fibril organization cell cycle DNA replication cell cycle DNA replication response to oxidative stress negative regulation of cell cycle G2/M phase transition regulation of cellular response to stress extracellular structure organization positive regulation of protein deacetylation negative regulation of neural precursor cell proliferation regulation of anatomical structure morphogenesis endocytosis en endosome phosphatidylinositol–4,5–bisphosphate 5–phosphatase activity D1 dopamine receptor binding growth cone -PML body cysteine-type endopeptidase activity involved in apoptotic signaling pathway oxidoreductase activity, acting on the CH-NH2 group of donors Z disc · stress fiber nucleotide transmembrane transporter activity enzyme activator activity main axon · enzyme regulator activity contractile actin filament bundle transcription factor activity, direct ligand regulated sequence-specific DN... invadopodium nuclear receptor activity mitochondrial membrane ubiquitin binding · vesicle coat hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in I. mitochondrial envelope small GTPase binding -Rab GTPase binding mitochondrial outer membrane steroid hormone receptor binding · axon · nucleoside-triphosphatase activity regulation of anatomical structure morphogenesis endocytosis and pantothenate metabolic process L—serine biosynthetic process activation of protein kinase B activity protein oxidation regulation of chromosome segregation post—Golgi vesicle—mediated transport—blood vessel morphogenesis regulation of cilium assembly actin polymerization or depolymerization response to copper ion intrinsic apoptotic signaling pathway in response to DNA damage cellular response to prostaglandin stimulus—cell migration—bone development site of polarized growth · ligase activity, forming carbon-nitrogen bonds cytoplasmic ubiquitin ligase complex -Cajal body -K63-linked polyubiquitin modification-dependent protein binding oxidoreductase activity, acting on CH or CH2 groups transcriptional repressor complex -G-rich strand telomeric DNA binding podosome · cyclic nucleotide-dependent protein kinase activity photoreceptor cell cilium -BH domain binding intrinsic component of Golgi membrane flavin adenine dinucleotide binding sarcomere electron transfer activity sarcolemma · protein homodimerization activity N-methyltransferase activity cell cortex region · RNA polymerase II repressing transcription factor binding presynaptic active zone membrane regulatory RNA binding cell migration bone development membrane assembly regulation of cell morphogenesis tissue migration neural precursor cell proliferation production of miRNAs involved in gene silencing by miRNA protein localization to plasma membrane regulation of actin filament-based process ameboidal-type cell migration tube development regulation of adherens junction organization centriolar satellite single-stranded RNA binding filopodium protein kinase activator activity regulatory region nucleic acid binding GTPase activator activity axon part · postsynaptic density, intracellular component -R-SMAD binding filopodium tip catalytic activity, acting on a glycoprotein double-stranded DNA binding replication fork ciliary part protein-arginine N-methyltransferase activity regulation of adherens junction organization ribonucleoprotein complex disassembly positive regulation of mitochondrial fission neuronal stem cell division kinetochore cardiolipin binding arginine N-methyltransferase activity brush border organelle outer membrane aldehyde-lyase activity · vesicle-mediated transport to the plasma membrane telomeric DNA binding RNA N6-methyladenosine methyltransferase complex heparin binding regulation of cell morphogenesis involved in differentiation regulation of sister chromatid segregation regulation of sister chromatid segregation focal adhesion assembly cell–substrate adherens junction assembly adenosine to inosine editing DNA replication paranodal junction sequence-specific double-stranded DNA binding mRNA editing complex vinculin binding leading edge membrane structural molecule activity conferring elasticity single-stranded telomeric DNA binding sex chromosome sequence-specific mRNA binding outer membrane regulation of cell projection organization heart development organelle fission tube morphogenesis regulation of cellular protein localization negative regulation of intrinsic apoptotic signaling pathway regulation of mitotic sister chromatid segregation phosphatidylinositol phosphate 5-phosphatase activity intrinsic component of presynaptic active zone membrane oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acce. exon-exon junction complex actin-dependent ATPase activity apicolateral plasma membrane catalytic activity, acting on DNÁ cytosolic part phosphotransferase activity, phosphate group as acceptor PDZ domain binding mitochondrial part epithelial cell migration cargo loading into vesicle G1/S transition of mitotic cell cycle response to water transferase activity, transferring pentosyl groups ER to Golgi transport vesicle membrane transcription regulatory region DNA binding neuromuscular junction translation initiation factor activity retromer complex lamellipodium morphogenesis -protein localization to membrane -cell part morphogenesis histone methyltransferase activity integral component of mitochondrial outer membrane extracellular matrix binding nuclear localization sequ transcription regulatory region sequence-specific DNA binding -BORC complex regulation of autophagy GTPase regulator activity regulation of release of cytochrome c from mitochondria -nuclear DNA replication mitotic spindle kinase activator activity basement membrane nuclear DNA replication - epithelium migration - regulation of blood pressure - negative regulation of extrinsic apoptotic signaling pathway via death doma... - cellular response to cadmium ion regulation of plasma membrane bounded cell projection organization regulation of supramolecular fiber organization peripheral nervous system axon ensheathment myelination in peripheral nervous system positive regulation of plasma membrane bounded cell projection assembly signal transduction by trans-phosphorylation response to flavonoid regulation of transcription from RNA polymerase II promoter in response to ... regulation of telomeric loop disassembly regulation of peroxisome organization neuroblast division in subventricular zone melanocyte proliferation receptor activator activity transcription factor complex phosphatidylinositol-4,5-bisphosphate phosphatase activity postsynaptic specialization mvosin II bindina neuron to neuron synapse adenylate cyclase binding helicase activity ubiquitin ligase complex phosphatidylinositol phosphate binding SWI/SNF complex hyaluronic acid binding postsynaptic specialization, intracellular component fibronectin binding intrinsic component of mitochondrial outer membrane · RNA helicase activity -COPII-coated ER to Golgi transport vesicle phospholipid binding sequence-specific single stranded DNA binding COP9 signalosome -MAP kinase activity basolateral plasma membrane -DNA-(apurinic or apyrimidinic site) endonuclease activity development involved in symbiotic interaction negative regulation of cellular protein localization production of small RNA involved in gene silencing by RNA dsRNA processing X chromosome sequence-specific DNA binding unconventional myosin complex ribosome binding -ER ubiquitin ligase complex phosphatidylinositol—3,4—bisphosphate binding organophosphate ester transmembrane transporter activity AP-3 adaptor complex aging -regulation of protein polymerization -cell morphogenesis involved in differentiation -regulation of circadian rhythm calmodulin-dependent protein kinase activity cell-cell junction modification-dependent protein binding U2-type precatalytic spliceosome cell morphogenesis involved in differentiation regulation of circadian rhythm serine family amino acid biosynthetic process regulation of cathrin-dependent endocytosis positive regulation of mitotic sister chromatid segregation kinetochore assembly cellular response to prostaglandin E stimulus postsynaptic signal transduction postsynapse to nucleus signaling pathway positive regulation of synaptic vesicle exocytosis actin filament reorganization cellular amide metabolic process regulation of plasma membrane bounded cell projection assembly regulation of cellular component size positive regulation of catalytic activity Golgi to plasma membrane transport regulation of DNA-dependent DNA replication response to inorganic substance regulation of cell—matrix adhesion membrane bioding regulation of cell projection assembly regulation of sodium ion transmembrane transport negative regulation of protein binding methyltransferase activity endoplasmic reticulum part cell adhesion mediator activity transport vesicle + ligase activity, forming carbon-oxygen bonds precatalytic spliceosome kinesin binding chromatin core promoter sequence-specific DNA binding aminoacyl-tRNA ligase activity membrane raft -RNA polymerase II regulatory region DNA binding membrane microdomain protein kinase regulator activity postsynapse cytokine binding · T-tubule -S100 protein binding clathrin-coated pit purine ribonucleotide transmembrane transporter activity phosphatidylglycerol binding postsynaptic density oligosaccharide binding recycling endosome -NAD-dependent histone deacetylase activity cluster of actin-based cell projections intronic transcription regulatory region sequence-specific DNA binding endoplasmic reticulum lumen intronic transcription regulatory region DNA binding vesicle membrane adenine nucleotide transmembrane transporter activity filamentous actin protein-containing complex scaffold activity peptidyl-prolyl cis-trans isomerase activity asymmetric synapse negative regulation of protein binding muscle structure development protein dimerization activity regulation of protein localization to cell periphery folic acid-containing compound metabolic process regulation of intrinsic apoptotic signaling pathway in response to DNA damage fibroblast migration cellular response to growth factor stimulus positive regulation of cell-matrix adhesion vesicle budding from membrane positive regulation of protein polymerization substrate adhesion-dependent cell spreading positive regulation of sister chromatid cohesion folic acid-containing compound biosynthetic process asymmetric stem cell division Golgi vesicle transport regulation of cell junction assembly mitotic DNA integrity checkpoint negative regulation of cellular component movement Schmidt-Lanterman incisure · calcium-dependent protein binding M band purine nucleotide transmembrane transporter activity
NAD-dependent protein deacetylase activity collagen-containing extracellular matrix condensed chromosome kinetochore death receptor binding translation factor activity, RNA binding presynaptic active zone mitochondrial inner membrane protein serine/threonine kinase activator activity RNA polymerase II regulatory region sequence-specific DNA binding cell projection membrane nucleoside-triphosphatase regulator activity chromosome, centromeric region · Rho guanyl-nucleotide exchange factor activity membrane region cholesterol binding coated vesicle membrane · transferase activity, transferring one-carbon groups cilium protein serine/threonine kinase inhibitor activity proteasome binding photoreceptor outer segment endodeoxyribonuclease activity, producing 5'-phosphomonoesters negative regulation of cellular component movement regulation of histone modification SAGA-type complex structural constituent of ribosome transport vesicle membrane negative regulation of cell migration regulation of sodium ion transmembrane transporter activity Schwann cell development GTPase activity nuclear matrix -ATPase activity meiotic spindle · actin filament binding nucleobase–containing small molecule interconversion mitotic G2/M transition checkpoint regulation of cell cycle G1/S phase transition mitotic G2 DNA damage checkpoint folic acid metabolic process coloress inaction accombly protein kinase A binding photoreceptor connecting cilium promoter-specific chromatin binding protein acetyltransferase complex protein tyrosine phosphatase activity acetyltransferase complex kinase regulator activity phagocytic cup regulation of cellular component movement import into cell maintenance of protein location regulation of cell migration protein phosphatase 2A binding COPI-coated vesicle S-adenosylmethionine-dependent methyltransferase activity condensed chromosome kinase inhibitor activity cis-trans isomerase activity GABA-ergic synapse ubiquitin-protein transferase regulator activity cell adhesion - regulation of cellular senescence -U2-type spliceosomal complex proline-rich region binding exocytic vesicle · response to growth factor -positive regulation of microtubule polymerization oxidoreductase activity, oxidizing metal ions positive regulation of microtubule polymerization negative regulation of protein localization to membrane cellular response to vitamin establishment of protein localization to membrane plasma membrane bounded cell projection morphogenesis positive regulation of chromatin organization regulation of mitotic nuclear division vesicle targeting regulation of ubiquitin-protein transferase activity regulation of mitotic nuclear division selenocysteine metabolic process response to hypobaric hypoxia response to carbon monoxide regulation of nuclear receptor transcription coactivator activity regulation of mitotic cell cycle DNA replication fegulation of establishment of T cell polarity regulation of collagen catabolic process spindle pole -H4 histone acetyltransferase activity · plasma membrane region metalloendopeptidase activity transcription factor TFTC complex translation initiation factor binding RNA polymerase II core promoter sequence-specific DNA binding dendrite terminus DNA polymerase activity replisome disordered domain specific binding INO80-type complex calcium ion binding nuclear periphery carbon-carbon lyase activity synaptic vesicle solute:proton antiporter activity synaptic membrane · protein tyrosine kinase activator activity oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP a... rough endoplasmic reticulum membrane lysophospholipase activity sarcoplasm adrenergic receptor binding phagocytic vesicle regulation of establishment of I cell polarity regulation of collagen catabolic process positive regulation of retinoic acid receptor signaling pathway positive regulation of clathrin-dependent endocytosis peptidyl-glycine modification neurotransmitter receptor metabolic process negative regulation of hepatocyte proliferation JUN phosphorylation Golgi to plasma membrane CFTR protein transport glomerular visceral epithelial cell migration calcium-independent cell-matrix adhesion sodium channel regulator activity node of Ranvier phosphatase activity integral component of presynaptic active zone membrane · P-P-bond-hydrolysis-driven transmembrane transporter activity ATPase activity, coupled to transmembrane movement of ions, phosphorylative. COPI vesicle coat phosphatidylinositol bisphosphate binding compact myelin -RNA polymerase II basal transcription factor binding Golgi cisterna protein phosphatase 1 binding endoplasmic reticulum subcompartment calcium-independent cell-matrix adhesion chromatin remodeling organelle inner membrane nuclear import signal receptor activity regulation of epithelial cell migration positive regulation of autophagy of mitochondrion asymmetric cell division regulation of lamellipodium morphogenesis U2-type catalytic step 2 spliceosome alcohol dehydrogenase (NADP+) activity primary active transmembrane transporter activity endoribonuclease complex phosphatidylinositol binding ciliary tip ubiquitin-like protein conjugating enzyme binding cytoplasmic stress granule ion channel inhibitor activity positive regulation of synaptic vesicle transport Notch receptor processing Sin3-type complex Nótch receptor processing membrane raft assembly biological adhesion regulation of potassium ion transmembrane transport negative regulation of response to DNA damage stimulus positive regulation of supramolecular fiber organization cell projection morphogenesis positive regulation of epidermal growth factor receptor signaling pathway positive regulation of protein complex assembly mitotic DNA damage checkpoint negative regulation of autophagy protein autophosphorylation cellular response to epidermal growth factor stimulus cellular component disassembly wound healing eukaryotic translation initiation factor 3 complex sterol binding core promoter binding endocytic patch nuclear receptor binding Ada2/Gcn5/Ada3 transcription activator complex L-ascorbic acid binding actin cortical patch · cyclosporin A binding endonuclease complex ribonucleoprotein complex binding histone acetyltransferase complex -Ran GTPase binding distal axon peptidase activator activity channel inhibitor activity cytoplasmic vesicle membrane -Number of genes enriched protein binding, bridging condensed chromosome, centromeric region negative regulation of transcription from RNA polymerase II promoter in res... small GTPase mediated signal transduction cellular response to reactive oxygen species alpha—amino acid biosynthetic process regulation of systemic arterial blood pressure - CD4—positive or CD8—positive, alpha—beta T cell lineage commitment response to metal ion regulation of response to oxidative stress—positive regulation of GTPase activity—positive regulation of hydrolase activity—positive regulation of cartilage development—negative regulation of signal transduction by p53 class mediator—regulation of protein deacetylation—regulation of nitric—oxide synthase activity—membrane organization—protein targeting—vesicle coating—vesicle coating—vesic phosphatidylserine binding wound healing presynaptic membrane oxidoreductase activity, acting on CH-OH group of donors endoplasmic reticulum membrane scaffold protein binding nuclear outer membrane-endoplasmic reticulum membrane network basal transcription machinery binding basal RNA polymerase II transcription machinery binding mitochondrial matrix -60 sulfur compound binding presynapse telomerase RNA binding dendritic spine protein disulfide oxidoreductase activity -30 presynaptic active zone cytoplasmic component microfilament motor activity Ino80 complex · extracellular matrix structural constituent conferring compression resistance DNA helicase complex molecular adaptor activity integral component of endoplasmic reticulum membrane -ATPase activity, coupled disulfide oxidoreductase activity neuron spine · transforming growth factor beta binding Schaffer collateral - CA1 synapse · poly(U) RNA binding regulation of response to endoplasmic reticulum stress organelle localization by membrane tethering replicative senescence positive regulation of fibroblast migration neuron projection cytoplasm phosphatidylinositol bisphosphate phosphatase activity microvillus -GTP-dependent protein binding organelle envelope oxidoreductase activity, acting on a sulfur group of donors phosphatase regulator activity envelope negative regulation of necroptotic process L–serine metabolic process RNA polymerase II proximal promoter sequence-specific DNA binding dendrite cytoplasm phosphoric ester hydrolase activity neuron migration lung development nuclear chromosome, telomeric region receptor signaling complex scaffold activity lung development response to radiation regulation of protein localization to membrane regulation of sodium ion transport execution phase of apoptosis peptidyl—cysteine modification regulation of endoplasmic reticulum stress—induced intrinsic apoptotic sign... positive regulation of ERBB signaling pathway positive regulation of cytoskeleton organization positive regulation of mRNA splicing, via spliceosome positive regulation of mRNA splicing, via spliceosome negative regulation of protein localization to plasma membrane negative regulation of intrinsic apoptotic signaling pathway by p53 class m... mitophagy mitochondrion morphogenesis membrane raft organization ficolin-1-rich granule lumen -DNA replication origin binding myelin sheath -ATPase activity, coupled to transmembrane movement of substances cytosolic ribosome -ATPase activity, coupled to movement of substances motor activity sarcoplasmic reticulum · growth factor binding extracellular matrix ligase activity glycoprotein complex enzyme inhibitor activity dystrophin-associated glycoprotein complex structural constituent of muscle protein-lysine N-methyltransferase activity intrinsic component of endoplasmic reticulum membrane endoplasmic reticulum-Golgi intermediate compartment deoxyribonuclease activity chemorepellent activity basal part of cell endodeoxyribonuclease activity membrane raft organization kinetochore organization Golgi stack protein kinase inhibitor activity release of cytochrome c from mitochondria regulation of potassium ion transmembrane transporter activity
positive regulation of cellular protein localization DN repair telomerase holoenzyme complex lysine N-methyltransferase activity intraciliary transport particle B endoribonuclease activity exocyst: protein phosphatase regulator activity response to ionizing radiation -plasma membrane organization -regulation of actin filament polymerization endolysosome syntaxin-1 binding poly-pyrimidine tract binding COPI-coated vesicle membrane poly-purine tract binding -NAD+ ADP-ribosyltransferase activity regulation of nuclear division receptor metabolic process tertiary granule lumen · misfolded protein binding circulatory system process nuclear division ribosomal subunit -MAP kinase kinase kinase activity ER to Golgi vesicle-mediated transport - regulation of cellular localization sarcoplasmic reticulum membrane gamma-tubulin binding aspartic-type endopeptidase activity regulation of cellular localization nucleurs organization nucleurs organization cell junction assembly actin filament polymerization pteridine-containing compound metabolic process positive regulation of microtubule polymerization or depolymerization negative regulation of DNA replication developmental cell growth kinesin complex aldo-keto reductase (NADP) activity extrinsic component of membrane oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP a. early endosome Rac GTPase binding small nucleolar ribonucleoprotein complex nucleobase-containing compound kinase activity lamellipodium membrane histone–lysine N–methyltransferase activity developmental cell growth synaptic vesicle recycling via endosome stress granule disassembly response to hydrostatic pressure regulation of stress granule assembly regulation of skeletal muscle contraction by calcium ion signaling protein de-ADP-ribosylation positive regulation of protein localization to cilium positive regulation of protein localization to cilium positive regulation of protein localization to cell cortex positive regulation of high voltage—gated calcium channel activity positive regulation of attachment of spindle microtubules to kinetochore negative regulation of DNA damage checkpoint negative regulation of cell volume intrinsic apoptotic signaling pathway in response to hydrogen peroxide hematopoietic stem cell nomeostasis cap—independent translational initiation proximal promoter sequence-specific DNA binding gamma-tubulin complex purine nucleoside binding BLOC complex beta-catenin binding transferase complex catalytic activity, acting on RNA dendrite translation elongation factor activity cytosolic large ribosomal subunit phosphatidylinositol phosphate phosphatase activity aspartic-type peptidase activity protein tyrosine kinase activity endoplasmic reticulum tubular network microtubule motor activity anaphase-promoting complex alcohol binding nuclear chromosome protein phosphatase inhibitor activity large ribosomal subunit non-membrane spanning protein tyrosine kinase activity cap-independent translational initiation 10-formyltetrahydrofolate metabolic process late endosome p53 binding negative regulation of Skeletal muscles at ellipse call process water—soluble vitamin metabolic process water—soluble vitamin metabolic process negative regulation of chromosome organization eye development nuclear chromosome segregation telomere localization signal transduction involved in G2 DNA damage checkpoint regulation of skeletal muscle satellite cell proliferation mitochondrial intermembrane space · oxidoreductase activity, acting on single donors with incorporation of mole. modified amino acid binding extrinsic component of plasma membrane signal sequence binding cullin-RING ubiquitin ligase complex phosphoprotein phosphatase activity protein-cysteine S-palmitoyltransferase activity protein-cysteine S-acyltransferase activity phosphatidylinositol-3,5-bisphosphate binding laminin binding nuclear replication fork -H4 histone acetyltransferase complex regulation of skeletal muscle satellite cell proliferation regulation of histone H4 acetylation embryonic brain development respiratory tube development vascular associated smooth muscle cell migration regulation of mitochondrial fission negative regulation of G1/S transition of mitotic cell cycle cellular response to transforming growth factor beta stimulus dendrite morphogenesis -U12-type spliceosomal complex ribosome -DNA-directed DNA polymerase activity ficolin-1-rich granule bHLH transcription factor binding nuclear replisome actin monomer binding protein serine/threonine phosphatase complex catalytic activity, acting on a tRNA dendrite morphogenesis histone H3 acetylation phosphatase complex oxidoreductase activity, acting on NAD(P)H establishment of protein localization to plasma membrane -amide biosynthetic process nuclear ubiquitin ligase complex histone acetyltransferase activity cytosolic small ribosomal subunit coenzyme binding response to ketone response to ketone response to ketone response to ketone response to epidermal growth factor vesicle targeting, to, from or within Golgi regulation of G1/S transition of mitotic cell cyclescertion by tissue positive regulation of viral genome replication necroptotic process endonuclease activity intrinsic component of mitochondrial inner membrane nucleoside binding integral component of mitochondrial inner membrane activating transcription factor binding platelet alpha granule lumen oxidoreductase activity, acting on the CH-NH group of donors nuclear outer membrane histone demethylase activity mitotic spindle pole cyclin-dependent protein serine/threonine kinase activity bone cell development phosphatase inhibitor activity intrinsic component of synaptic membrane visual system development androgen receptor signaling pathway -muscle cell differentiation -endothelial cell migration -purine nucleoside metabolic process peptide-lysine-N-acetyltransferase activity clathrin-coated vesicle cation-transporting ATPase activity extrinsic component of organelle membrane yclin–dependent protein kinase activit cis-Golgi network purine nucleoside metabolic process - maintenance of protein location in cell - regulation of cell aging - cellular response to oxygen-containing compound - response to prostaglandin E - regulation of ubiquitin protein ligase activity - regulation of receptor recycling - negative regulation of synapse organization - negative regulation to cell periphery - membrane docking ATPase coupled ion transmembrane transporter activity nuclear chromosome part active ion transmembrane transporter activity lumenal side of endoplasmic reticulum membrane carbohydrate binding guanyl ribonucleotide binding intraciliary transport particle guanyl nucleotide binding integral component of lumenal side of endoplasmic reticulum membrane -GTP binding oxidoreductase activity plasma membrane raft pasitive regulation of protein localization to cell periphery membrane docking apoptotic mitochondrial changes positive regulation of peptidyl-serine phosphorylation negative regulation of cell cycle G1/S phase transition MRNA 3'-end processing collagen metabolic process regulation of response to DNA damage stimulation of processing positive regulation of intracellular transports. myosin binding -PcG protein complex -E-box binding cell-cell adhesion mediator activity endocytic vesicle WW domain binding Golgi cisterna membrane solute:cation antiporter activity photoreceptor inner segment · phosphatidylinositol 3-kinase binding organelle envelope lumen negative regulation of intrinsic apoptotic signaling pathway in response to the mitochondrial fission cell morphogenesis involved in neuron differentiation outflow tract morphogenesis nucleocytoplasmic carrier activity microtubule associated complex cyclin binding purine ribonucleoside binding cytoplasmic microtubule mRNA 3'-UTR binding cell division site stress response to copper ion skeletal muscle satellite cell proliferation regulation of translation, ncRNA-mediated regulation of skeletal muscle cell proliferation ubiquitin conjugating enzyme binding endosome membrane S-acyltransferase activity mitochondrial membrane part protein heterodimerization activity regulation of skeletal muscle cell proliferation regulation of hepatocyte proliferation negative regulation of translation, ncRNA-mediated negative regulation of anion transmembrane transport miRNA mediated inhibition of translation detoxification of copper ion deoxyribonucleotide biosynthetic process cargo loading into COPII-coated vesicle positive regulation of developmental process chromosome separation response to transforming growth factor heta. peroxisome single-stranded DNA binding microbody · Rho GTPase binding peroxisomal matrix nucleotidyltransferase activity ribonucleoside binding microbody lumen · scavenger receptor activity apical part of cell peptide hormone binding integral component of synaptic membrane monosaccharide binding nuclear transcriptional repressor complex chromosome separation response to transforming growth factor beta positive regulation of neuron projection development cellular response to steroid hormone stimulus respiratory system development sensory system development positive regulation of neuron differentiation regulation of anatomical structure size -N-acetyltransferase activity integrin complex · peptide transmembrane transporter activity apical plasma membrane -N-acyltransferase activity terminal bouton calcium-dependent phospholipid binding cell-cell contact zone phosphatidylinositol-4,5-bisphosphate binding somatodendritic compartment · SMAD binding regulation of cell motility microtubule polymerization endosomal part carboxy-lyase activity positive regulation of protein localization to cell periphery negative regulation of nuclear division molecular carrier activity vacuolar membrane hydrolase activity, acting on ester bonds lysosomal lumen mitotic nuclear division somatic stem cell division ubiquitin protein ligase binding somatic stem cell division regulation of necrotic cell death positive regulation of focal adhesion assembly negative regulation of locomotion Schwann cell differentiation regulation of perine phosphorylation establishment of cell polarity negative regulation of leukocyte mediated immunity heart morphogenesis regulation of endothelial cell migration regulation of gene expression, epigenetic viral genome replication transcription-dependent tethering of RNA polymerase II gene DNA at nuclear ... telomere tethering at nuclear periphery selenium compound metabolic process response to UV-A autophagosome steroid hormone receptor activity. phagophore assembly site hydro-lyase activity MLL1/2 complex · peptide N-acetyltransferase activity MLL1 complex nuclease activity heterotrimeric G-protein complex carboxylic acid binding protein self-association GTPase complex SH2 domain binding small ribosomal subunit -RNA polymerase II complex binding phagocytic vesicle membrane -Rab guanyl-nucleotide exchange factor activity methyltransferase complex cysteine-type peptidase activity palmitoyltransferase activity lytic vacuole demethylase activity response to UV-A
regulation of metalloendopeptidase activity
regulation of mesenchymal stem cell differentiation
regulation of isotype switching to IgE isotypes lysosome transition metal ion transmembrane transporter activity cleavage furrow snRNA binding trans-Golgi network transport vesicle phosphatidylinositol-3-phosphate binding protein répair positive regulation of thymocyte apoptotic process neural crest cell migration involved in autonomic nervous system development negative regulation of vascular associated smooth muscle cell migration negative regulation of type B pancreatic cell apoptotic process negative regulation of cysteine—type endopeptidase activity involved in apo... negative regulation of cell cycle checkpoint isotype switching to IgE isotypes formate metabolic process asymmetric neuroblast division regulation of chromosome separation protein complex involved in cell adhesion actinin binding Cul4-RING E3 ubiquitin ligase complex magnesium ion binding ciliary base lyase activity ubiquitin-like protein ligase binding lytic vacuole membrane organic acid binding lysosomal membrane thiolester hydrolase activity protein-DNA complex chemoattractant activity axon cytoplasm transmembrane receptor protein tyrosine kinase activity regulation of chromosome separation histone H4 acetylation anatomical structure formation involved in morphogenesis regulation of DNA replication positive regulation of protein localization neuron projection morphogenesis positive regulation of protein localization to membrane telomere maintenance via telomere trimming tocicle formation skeletal muscle cell proliferation regulation of podosome assembly pteridine—containing compound biosynthetic process pre—miRNA processing positive regulation of ruffle assembly positive regulation of ruffle assembly positive regulation of necrotic cell death negative regulation of necrotic cell death intra—S DNA damage checkpoint formation of extrachromosomal circular DNA muscle cell development cellular response to endogenous stimulus response to endogenous stimulus response to growth hormone negative regulation of protein complex assembly cellular component assembly involved in morphogenesis regulation of oxidative stress—induced intrinsic apoptotic signaling pathway regulation of actin nucleation positive regulation of protein autophosphorylation maintenance of location in cell regulation of actin filament organization translation cell junction organization of cell junction organization cell junction organization or cell junction organization cell junction organization organization cell junction organization organization cell junction organization cell junction organization cell junction organization organization cell junction organization cell regulation of chromosome separation histone H4 acetylation site of DNA damage cargo receptor activity condensed nuclear chromosome protein N-terminus binding smooth endoplasmic reticulum -RNA methyltransferase activity nuclear chromatin peptide binding vacuole · transcription cofactor binding nuclear heterochromatin estrogen receptor binding transferase activity, transferring glycosyl groups iron ion binding caveola organellar large ribosomal subunit methylation-dependent protein binding mitochondrial large ribosomal subunit methylated histone binding lateral plasma membrane metallopeptidase activity intrinsic component of presynaptic membrane acetyltransferase activity site of double-strand break tau protein binding RNA polymerase core enzyme binding neuron projection membrane clathrin-coated endocytic vesicle coreceptor activity DNA-dependent ATPase activity inclusion body dioxygenase activity spindle microtubule calcium ion transmembrane transporter activity vacuolar part tumor necrosis factor receptor superfamily binding pigment granule · steroid binding cyclin-dependent protein serine/threonine kinase regulator activity melanosome amide binding protein-lipid complex cysteine-type endopeptidase activity phosphoric diester hydrolase activity cell division site part franslation - Golgi vesicle budding - cell junction organization - positive regulation of histone modification - activation of GTPase activity - ruffle organization - negative regulation of blood coagulation - vesicle targeting, rough ER to cis-Golgi - COPII vesicle coating - negative regulation of mitotic metaphase/anaphase transition - cellular response to radiation - neuron apoptotic process - muscle cell migration - regulation of protein localization to plasma membrane - T cell lineage commitment rough endoplasmic reticulum · channel regulator activity SCF ubiquitin ligase complex · ion channel regulator activity · dendrite membrane acetylgalactosaminyltransferase activity synaptic vesicle membrane calcium channel regulator activity ATP-dependent microtubule motor activity exocytic vesicle membrane aminopeptidase activity myosin complex amide transmembrane transporter activity plasma membrane bounded cell projection cytoplasm AP-type membrane coat adaptor complex voltage-gated calcium channel activity organellar ribosome transferase activity, transferring sulfur-containing groups carbon-oxygen lyase activity mitochondrial ribosome -T cell lineage commitment regulation of oxidative stress-induced neuron death adherens junction organization isomerase activity platelet alpha granule ciliary membrane protein phosphorylated amino acid binding T-helper cell lineage commitment stress response to metal ion regulation of retinoic acid receptor signaling pathway regulation of DNA damage checkpoint positive regulation of T cell chemotaxis secretory vesicle potassium channel regulator activity spliceosomal snRNP complex -NADP binding SH3/SH2 adaptor activity extrinsic component of cytoplasmic side of plasma membrane positive regulation of T cell chemotaxis positive regulation of sodium ion transmembrane transporter activity positive regulation of keratinocyte differentiation negative regulation of natural killer cell mediated cytotoxicity detoxification of inorganic compound negative regulation of hemostasis peptide biosynthetic process negative regulation of cell proliferation osteoblast differentiation negative regulation of cell morphogenesis involved in differentiation regulation of Ras protein signal transduction rhythmic process programmed necrotic cell death protein kinase C binding tertiary granule · protein serine/threonine phosphatase activity cell-cell adherens junction -RNA polymerase II activating transcription factor binding tethering complex antigen binding endoplasmic reticulum-Golgi intermediate compartment membrane phospholipase activity integral component of presynaptic membrane exonuclease activity ubiquitin–like protein–specific protease activity sulfotransferase activity polysome · SNARE complex signaling adaptor activity multivesicular body programmed necrotic cell death negative regulation of metaphase/anaphase transition of cell cycle negative regulation of lymphocyte mediated immunity maintenance of protein localization in organelle positive regulation of neurogenesis endopeptidase activity vacuolar lumen transmembrane receptor protein kinase activity early endosome membrane oxidoreductase activity, acting on peroxide as acceptor sperm part hormone binding proton transmembrane transporter activity small nuclear ribonucleoprotein complex negative regulation of cytoskeleton organization regulation of mitotic metaphase/anaphase transition regulation of histone acetylation positive regulation of receptor-mediated endocytosis cell migration involved in sprouting angiogenesis regulation of actin polymerization or depolymerization antiporter activity cell body · oxidoreductase activity, acting on paired donors, with incorporation or red... carboxylic ester hydrolase activity stereocilium intercalated disc ubiquitin-like protein ligase activity transferase activity, transferring acyl groups other than amino-acyl groups -SNARE binding secretory granule lumen urinary bladder smooth muscle contraction urinary bladder smooth muscle contraction tail—anchored membrane protein insertion into ER membrane spindle assembly involved in meiosis ribonucleoprotein granule transferase activity, transferring alkyl or aryl (other than methyl) groups integral component of postsynaptic specialization membrane · rRNA binding nuclear membrane relaxation of vascular smooth muscle regulation of metaphase plate congression regulation of DNA-dependent DNA replication initiation pre-replicative complex assembly involved in nuclear cell cycle DNA replication pre-replicative complex assembly involved in cell cycle DNA replication pre-replicative complex assembly involved in cell cycle DNA replication pre-replicative complex assembly positive regulation of protein localization to synapse positive regulation of pricrotubule motor activity. ribonuclease activity heterochromatin exopeptidase activity cytoplasmic side of plasma membrane -DNA-binding transcription factor activity proton-transporting two-sector ATPase complex amino acid binding acetylglucosaminyltransferase activity DNA-binding transcription factor activity, RNA polymerase II-specific cytoplasmic side of membrane lipid droplet positive regulation of protein localization to synapse positive regulation of microtubule motor activity positive regulation of histone H4 acetylation platelet–derived growth factor receptor–alpha signaling pathway peptidyl–diphthamide metabolic process peptidyl–diphthamide biosynthetic process from peptidyl–histidine paranodal junction assembly nucleotide transmembrane transport brush border membrane oxidoreductase activity, acting on the CH-CH group of donors intrinsic component of postsynaptic specialization membrane transferase activity, transferring acyl groups stereocilium bundle manganese ion binding anchored component of plasma membrane transferase activity, transferring hexosyl groups protein tyrosine kinase binding acrosomal vesicle negative regulation of synapse assembly negative regulation of nuclease activity negative regulation of cellular response to hypoxia histone H3–K9 dimethylation tRNA binding · endocytic vesicle membrane metal cluster binding negative regulătion of čellular response to hypoxiá histone H3–K9 dimethylation adenylate cyclase—activating adrenergic receptor signaling pathway involved... neuron death in response to oxidative stress cellular response to copper ion cell proliferation in forebrain transmembrane receptor protein serine/threonine kinase signaling pathway regulation of actin filament length positive regulation of protein modification process ruffle assembly negative regulation of mitotic sister chromatid separation translational initiation establishment of organelle localization regulation of cartilage development regulation of hydrolase activity protein catabolic process positive regulation of cell differentiation positive regulation of cell differentiation positive regulation of cell cycle extrinsic apoptotic signaling pathway via death domain receptors regulation of extrinsic apoptotic signaling pathway via death domain receptors regulation of extrinsic apoptotic signaling pathway via death domain receptors regulation of extrinsic apoptotic signaling pathway via death domain receptors regulation of extrinsic apoptotic signaling pathway via death domain receptors regulation of protein ubiquitination cellular response to vascular endothelial growth factor stimulus glycosyl compound metabolic process positive regulation of protein ubiquitination regulation of T cell chemotaxis regulation of nuclear cell cycle DNA replication regulation of mitophagy regulation of defense response to bacterium blood microparticle iron-sulfur cluster binding cytoplasmic ribonucleoprotein granule · heat shock protein binding peptidase regulator activity damaged DNA binding cytoplasmic vesicle lumen · late endosome membrane serine-type endopeptidase inhibitor activity unfolded protein binding Sm-like protein family complex vesicle lumen thiol-dependent ubiquitinyl hydrolase activity ubiquitin protein ligase activity postsynaptic membrane clathrin-coated vesicle membrane histone binding neuron projection terminus ubiquitinyl hydrolase activity receptor tyrosine kinase binding specific granule lumen peptidase activity, acting on L-amino acid peptides nuclear inner membrane chemokine receptor binding ficolin-1-rich granule membrane peptidase activity histone methyltransferase complex lipase activity azurophil granule lumen ion channel binding external side of plasma membrane monocarboxylic acid binding nuclear envelope cytokine receptor activity DNA-binding transcription activator activity, RNA polymerase II-specific apical junction complex · UDP-glycosyltransferase activity regulation of nuclear cell cycle DNA replication regulation of mitophagy regulation of defense response to bacterium regulation of cysteine—type endopeptidase activity involved in apoptotic si... preganglionic parasympathetic fiber development positive regulation of cellular response to oxidative stress negative regulation of natural killer cell mediated immunity CD4—positive, alpha—beta T cell lineage commitment peptidyl—lysine modification internal peptidyl—lysine acetylation protein complex oligomerization substrate—dependent cell migration regulation of ruffle assembly regulation of ruffle assembly regulation of cytoplasmic translation negative regulation of reactive oxygen species biosynthetic process regulation of membrane permeability stem cell proliferation microtubule polymerization or depolymerization on morphogenesis signal transduction in response to DNA damage stem cell division regulation of lamellipodium organization side of membrane chaperone binding trans-Golgi network membrane chloride channel activity secretory granule virus receptor activity integral component of postsynaptic membrane hijacked molecular function active transmembrane transporter activity sperm flagellum · thiol-dependent ubiquitin-specific protease activity RNA polymerase II, holoenzyme -ATPase binding bicellular tight junction phosphoprotein binding -Golgi lumen · G protein-coupled receptor binding motile cilium · voltage-gated cation channel activity intrinsic component of postsynaptic membrane anion channel activity cofactor binding · peroxisomal part endopeptidase inhibitor activity microbody part voltage-gated potassium channel activity 9+2 motile cilium · hydrolase activity, acting on glycosyl bonds calcium channel activity tight junction stem cell division regulation of lamellipodium organization specific granule peptidase inhibitor activity endopeptidase regulator activity negative regulation of chromosome separation clathrin-dependent endocytosis protein kinase complex hydrolase activity, hydrolyzing O-glycosyl compounds regulation of metaphase/anaphase transition of cell cycleplatelet-derived growth factor receptor signaling pathway negative regulation of reactive oxygen species metabolic process negative regulation of coagulation host cell DNA-binding transcription repressor activity, RNA polymerase II-specific host chloride transmembrane transporter activity ubiquitin-like protein transferase activity secretory granule membrane négative regulation of coagulation animal organ morphogenesis regulation of cell development regulation of locomotion actin filament—based movement cellular response to alcohol cellular amino acid biosynthetic process regulation of mitochondrial membrane potential myeloid cell development positive regulation of nervous system development negative regulation of establishment of protein localization cytoskeleton—dependent intracellular transport regulation of protein ubiquitination neuron projection development neuronal cell body ubiquitin-protein transferase activity anchored component of membrane · monooxygenase activity solute:cation symporter activity voltage-gated ion channel activity recycling endosome membrane · voltage-gated channel activity other organism part serine-type peptidase activity · other organism cell serine hydrolase activity other organism · potassium channel activity postsynaptic specialization membrane · serine-type endopeptidase activity potassium ion transmembrane transporter activity intermediate filament cytoskeleton · neuron projection development
negative regulation of transcription by RNA polymerase II
regulation of potassium ion transport
regulation of sterol biosynthetic process
regulation of cholesterol biosynthetic process lipid transporter activity serine/threonine protein kinase complex growth factor receptor binding axoneme · secondary active transmembrane transporter activity receptor complex metal ion transmembrane transporter activity intrinsic apoptotic signaling pathway in response to oxidative stress establishment or maintenance of epithelial cell apical/basal polarity cell surface · organic anion transmembrane transporter activity myelination of I-kappaB kinase/NF-kappaB signaling positive regulation of pourse. ciliary plasm axon terminus positive regulation of neuron apoptotic process metaphase/anaphase transition of mitotic cell cycle symporter activity nuclear DNA-directed RNA polymerase complex endosome to lysosome transport cellular response to glucocorticoid stimulus cellular response to fatty acid DNA-directed RNA polymerase complex tetrapyrrole binding primary lysosome sodium ion transmembrane transporter activity regulation of transmembrane transporter activity I–kappaB kinase/NF-kappaB signaling azurophil granule growth factor activity cytokine receptor binding specific granule membrane regulation of intrinsic apoptotic signaling pathway in response to DNA dama...

positive regulation of cardiac muscle cell differentiation osteoclast development anion transmembrane transporter activity oxidoreductase complex monovalent inorganic cation transmembrane transporter activity transferase complex, transferring phosphorus-containing groups inorganic cation transmembrane transporter activity negative regulation of release of cytochrome c from mitochondria negative regulation of cellular senescence immune response to tumor cell RNA polymerase complex ion gated channel activity plasma membrane receptor complex gated channel activity retinoic acid receptor signaling pathway regulation of intrinsic apoptotic signaling pathway by p53 class mediator positive regulation of release of cytochrome c from mitochondria positive regulation of filopodium assembly negative regulation of insulin receptor signaling pathway cellular response to dexamethasone stimulus cellular response to graanic cyclic compound. intermediate filament cation channel activity cation transmembrane transporter activity mitochondrial protein complex ion channel activity inner mitochondrial membrane protein complex transporter activity membrane protein complex substrate-specific channel activity cellular response to dexametriasone stimulus cellular response to organic cyclic compound eye morphogenesis positive regulation of cell adhesion skeletal system development signal transduction involved in DNA integrity checkpoint regulation of protein acetylation nucleosome · transmembrane transporter activity DNA packaging complex channel activity plasma membrane protein complex passive transmembrane transporter activity perikaryon ion transmembrane transporter activity · receptor ligand activity transporter complex inorganic molecular entity transmembrane transporter activity transmembrane transporter complex positive regulation of organelle assembly COPII-coated vesicle budding receptor regulator activity cation channel complex G protein–coupled receptor activity optic cup morphogenesis involved in camera—type eye development -citrulline metabolic process ion channel complex · transmembrane signaling receptor activity 6 6 $log_{10}(P_{b-hoch})$

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