Top 10 significantly over–represented GO terms for OB series for dPSI cutoff of 0.15 and any sig qvalue 0.01 encompassing 983 genes MF BP regulation of organelle organization -cytoskeleton organization -positive regulation of organelle organization -actin filament-based process cell adhesion molecule binding cell-substrate junction cytoskeletal protein binding focal adhesion protein domain specific binding cell-substrate adherens junction cadherin binding positive regulation of cellular component organization regulation of RNA splicing RNA splicing RNA splicing adherens junction actin binding anchoring junction + SH3 domain binding microtubule binding microtubule cytoskeleton supramolecular fiber organization regulation of mRNA splicing, via spliceosome protein-containing complex localization cell cycle process -14-3-3 protein binding cell junction peroxisome proliferator activated receptor binding nucleoplasm part chromatin binding actin cytoskeleton cell cycle process regulation of cell—substrate adhesion—RNA splicing, via transesterification reactions with bulged adenosine as nu...mRNA splicing, via spliceosome—organelle disassembly—intrinsic apoptotic signaling pathway—regulation of mRNA processing—microtubule—based process—apoptotic signaling pathway—apoptotic signaling pathwa protein-containing complex binding lamellipodium protease binding cell leading edge integrin binding nuclear body protein-lysine 6-oxidase activity Golgi subcompartment transcription coregulator activity Golgi apparatus part + microtubule—based process apoptotic signaling pathway - RNA splicing, via transesterification reactions - RNA processing - Alternative mRNA splicing, via spliceosome - cellular response to DNA damage stimulus - mRNA processing - regulation of cellular component biogenesis - mitotic cell cycle - regulation of intrinsic apoptotic signaling pathway - circulatory system development - positive regulation of apoptotic signaling pathway - mitotic cell cycle process - mitotic cell cycle - mitotic c 1 retinoic acid receptor binding cell cortex transcription factor binding platelet-derived growth factor binding 5-formyltetrahydrofolate cyclo-ligase activity nucleolus - I supramolecular fiber supramolecular polymer transferase activity, transferring phosphorus–containing groups -structural molecule activity supramolecular complex -Golgi membrane tRNA-specific adenosine deaminase activity cell cortex part histone deacetylase binding positive regulation of apoptotic signaling pathway - mitotic cell cycle process - positive regulation of chromosome organization - negative regulation of peptidyl-cysteine S-nitrosylation - regulation of integrin-mediated signaling pathway - regulation of cell cycle - cell cycle G2/M phase transition - regulation of alternative mRNA splicing, via spliceosome - chromosome organization - mitochondrion organization - mito nuclear speck protein serine/threonine kinase activity -hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds -phosphatase binding interstitial matrix midbody glutamatergic synapse structural constituent of cytoskeleton microtubule plasma membrane bounded cell projection part oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as ac. mitochondrion organization cell projection part regulation of mitochondrion organization regulation of mitochondrion organization positive regulation of chromosome segregation regulation of cell - matrix adhesion main axon pre-mRNA binding SAP kinase activity synapse phosphothreonine residue binding CCAAT-binding factor complex + regulation of cell-matrix adnesion organelle assembly regulation of mitotic cell cycle actin filament organization positive regulation of mitochondrion organization plasma membrane bounded cell projection assembly
positive regulation of apoptotic process integrin-mediated signaling pathway positive regulation of programmed cell death cardiovascular system development
microtubule cytoskeleton organization -JUN kinase activity histone deacetylase complex cyclo-ligase activity perinuclear region of cytoplasm alkylglycerophosphoethanolamine phosphodiesterase activity cytoplasmic region deacetylase activity uridylyltransferase activity fibrillar center -D1 dopamine receptor binding spindle nucleosome binding nucleolar part retinoid X receptor binding trans-Golgi network microtubule cytoskeleton organization tetrahydrofolate interconversion microtubule organizing center transcription corepressor activity - Ras GTPase binding - nuclear hormone receptor binding - I histone deacetylation - vasçulature development axon initial segment regulation of chromosome organization - chromatin organization cortical actin cytoskeleton ciliary basal body repressing transcription factor binding chromatin organization regulation of peptidyl-cysteine S-nitrosylation positive regulation of integrin-mediated signaling pathway mitotic cell cycle phase transition positive regulation of cell projection organization negative regulation of mitotic cell cycle
regulation of apoptotic signaling pathway extracellular matrix organization blood vessel development mitochondrion disassembly autophagy of mitochondrion cortical cytoskeleton double-stranded RNA binding chromosomal region calcium–transporting ATPase activity BH domain binding 1 synapse part adenosine deaminase activity ruffle polyubiquitin modification-dependent protein binding invadopodium membrane actin filament nucleosomal DNA binding collagen type I trimer + RNA strand annealing activity - methylenetetrahydrofolate dehydrogenase (NADP+) activity - protein C-terminus binding -MKS complex -SWI/SNF superfamily-type complex bone development -mRNA metabolic process modification-dependent protein binding microtubule end + regulation of cellular response to stress negative regulation of organelle organization chromatin remodeling cell—substrate junction assembly microtubule plus-end phosphotransferase activity, alcohol group as acceptor cytosolic part profilin binding small GTPase binding axon part cell-substrate junction assembly - organelle localization - G2/M transition of mitotic cell cycle - cellular component morphogenesis - protein localization to cell periphery - regulation of androgen receptor signaling pathway - regulation of cell cycle phase transition - regulation of cytoskeleton organization - regulation of nuclear cell cycle DNA replication - nucleobase-containing compound transport - RNA export from nucleus - G2 DNA damage checkpoint - regulation of cell cycle process polymeric cytoskeletal fiber oxidoreductase activity, acting on the CH–NH2 group of donors extracellular matrix structural constituent filopodium vinculin binding contractile fiber structural molecule activity conferring elasticity node of Ranvier sequence-specific mRNA binding neuron projection hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in c... single-stranded RNA binding contractile fiber part Cajal body collagen binding ubiquitin-like protein binding spectrin -1 regulation of cell cycle process -cell division androgen receptor binding postsynapse scaffold protein binding myofibril + isopeptidase activity protein deacylation positive regulation of cell death ribonucleoprotein complex export from nucleus regulation of organelle assembly positive regulation of intrinsic apoptotic signaling pathway cell aging ribonucleoprotein complex localization protein deacetylation cell matrix adhesion positive regulation of cellular component biogenesis collagen type VI trimer inositol hexakisphosphate kinase activity collagen beaded filament + inositol hexakisphosphate 5-kinase activity H3 histone acetyltransferase activity glial cell projection double-stranded RNA adenosine deaminase activity ciliary transition zone chondroitin sulfotransferase activity neuron projection cytoplasm microtubule minus-end binding BORC complex chloride ion binding positive regulation of cellular component biogenesis negative regulation of cellular component organization regulation of autophagy of mitochondrion axon protein phosphatase binding spliceosomal complex + ÷ protein tyrosine/serine/threonine phosphatase activity regulation of autophagy of illium assembly regulation of substrate adhesion–dependent cell spreading ciliary basal body–plasma membrane docking regulation of cell cycle G2/M phase transition establishment of RNA localization filopodium tip phosphatidylinositol phosphate binding postsynaptic specialization -PDZ domain binding neuron to neuron synapse cysteine-type endopeptidase activity involved in apoptotic process centrosome kinase binding actin-based cell projection + angiogenesis macromolecule deacylation regulation of autophagy positive regulation of cell-substrate adhesion histone modification negative regulation of cell cycle regulation of cell morphogenesis intracellular protein transport peptidyl-lysine oxidation covalent chromatin modification mRNA export from nucleus ribonucleoprotein complex export from pucleus angiogenesis regulatory RNA binding extracellular matrix component proteoglycan binding GTPase activator activity lateral loop protein kinase activity FANCM-MHF complex -Ral GTPase binding elastic fiber nitric-oxide synthase binding dendritic filopodium ubiquitin binding actin cap centriolar satellite 🕂 steroid hormone receptor binding beta-catenin-TCF complex ng ribonucleoprotein complex export from nucleus protein localization to organelle cell cycle checkpoint cell morphogenesis peripheral nervous system axon ensheathment myelination in peripheral nervous system peptidyl-serine modification regulation of cell projection organization positive regulation of histone deacetylation negative regulation of sodium ion transport DNA-dependent DNA replication establishment or maintenance of cell polarity skeletal system development regulation of GTPase activity regulation of cellular protein localization nucleic acid transport regulation of protein binding lamellipodium organization cilium organization care posterness activity regulation of protein binding lamellipodium organization contents. microtubule plus-end binding mRNA-containing ribonucleoprotein complex export from nucleus -glucocorticoid receptor binding postsynaptic density enzyme activator activity sarcolemma phosphotransferase activity, phosphate group as acceptor actomyosin phosphatidylinositol-3,4,5-trisphosphate binding basement membrane vascular endothelial growth factor-activated receptor activity type 1 angiotensin receptor binding -thioredoxin–disulfide reductase activity -sodium channel inhibitor activity autophagosome asymmetric synapse cell-cell junction clathrin light chain binding npBAF complex calcium-dependent protein serine/threonine phosphatase activity fibrillar collagen trimer glycosaminoglycan binding -protein homodimerization activity banded collagen fibril ATPase complex hormone receptor binding spectrin binding centriole phosphatidylinositol-3,5-bisphosphate binding membrane raft lămellipodium organization cilium organization one-carbon metabolic process peptidyl-amino acid modification regulation of actin cytoskeleton organization regulation of plasma membrane bounded cell projection organization cellular component disassembly tetrahydrofolate metabolic process nucleosome disassembly negative regulation of DNA-dependent DNA replication cytoskeleton-dependent intracellular transport nuclear export proteasome binding catalytic step 2 spliceosome extracellular matrix structural constituent conferring tensile strength I band carbohydrate derivative transmembrane transporter activity BLOC complex phospholipid binding -RNA polymerase II transcription factor binding -GTPase regulator activity nuclear transcription factor complex integral component of organelle membrane transcription coactivator activity membrane microdomain protein kinase binding dendrite cytoplasm histone deacetylase activity NAD binding nuclear export peptidyl-serine phosphorylation regulation of protein localization to cell periphery intrinsic apoptotic signaling pathway in response to DNA damage regulation of potassium ion transmembrane transporter activity chromosome, telomeric region + RNA polymerase I regulatory region sequence–specific DNA binding RNA polymerase I regulatory region DNA binding RNA polymerase I CORE element sequence–specific DNA binding collagen-containing extracellular matrix transcription export complex paranode region of axon primary miRNA binding regulation of potassium for transferribrate transporter activity tube morphogenesis regulation of potassium ion transmembrane transporter activity hepatocyte apoptotic process 1 eukaryotic translation initiation factor 4F complex transcriptional repressor complex non-membrane spanning protein tyrosine phosphatase activity nitric-oxide synthase regulator activity N6-methyladenosine-containing RNA binding negative regulation of sodium ion transmembrane transporter activity hepatocyte apoptotic process cellular response to oxidative stress positive regulation of oxidative stress—induced intrinsic apoptotic signali... regulation of small GTPase mediated signal transduction muscle structure development blood vessel morphogenesis cellular response to ketone negative regulation of autophagy cell junction assembly symbiont process regulation of cellular amino acid biosynthetic process negative regulation of protein localization to chromosome, telomeric region negative regulation of mitotic cell cycle DNA replication glycoside transport extracellular structure organization regulation of plasma membrane bounded cell projection assembly positive regulation of autophagy of mitochondrion maintenance of protein location tube development to protein localization to membrane transport along microtubule microtubule—based transport regulation of mitotic cell cycle phase transition regulation of mitotic cell cycle phase transition regulation of histone deacetylation regulation of bNA replication regulation of DNA-dependent DNA replication positive regulation of chromatin organization myelination cellular response to growth factor stimulus— Z disc synaptic membrane DEAD/H-box RNA helicase binding endoplasmic reticulum lumen + cAMP response element binding protein binding ribonucleoprotein complex angiotensin receptor binding dendritic spine ubiquitin—specific protease binding nucleotide diphosphatase activity extracellular matrix binding catalytic complex growth cone protein deacetylase activity integral component of mitochondrial membrane intrinsic component of organelle membrane enzyme regulator activity neuron spine adrenergic receptor binding endoribonuclease activity, producing 5'-phosphomonoesters protein serine/threonine/tyrosine kinase activity nucleobase-containing compound transmembrane transporter activity RNA polymerase II transcription factor complex septin ring septin complex endonuclease activity, active with either ribo- or deoxyribonucleic acids a. core promoter sequence-specific DNA binding intrinsic component of mitochondrial membrane rDNA binding GABA-ergic synapse pre-mRNA intronic binding actin filament bundle potassium channel inhibitor activity chromosome, centromeric region + phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity interleukin-1 binding membrane region guanylate kinase activity 9+0 non-motile cilium cysteine-type endopeptidase activity involved in apoptotic signaling pathway ribosome binding myelin sheath abaxonal region + microtubule bundle nucleotide transmembrane transporter activity regulation of critornatin organization myelination cellular response to growth factor stimulus negative regulation of organelle assembly regulation of cell projection assembly regulation of anatomical structure morphogenesis neural precursor cell proliferation chromosome segregation regulation of chromatin organization protein nitrosylation protein nitrosylation peptidyl—cysteine S—nitrosylation peptidyl—cysteine S—nitrosylation negative regulation of sodium ion transmembrane transport regulation of focal adhesion assembly regulation of cell—substrate junction assembly regulation of histone modification regulation of histone modification heart development extrinsic component of presynaptic membrane protein methyltransferase activity zinc ion binding dendritic spine neck RNA polymerase binding A band cell adhesion mediator activity neuromuscular junction chromatin DNA binding non-motile cilium + protein dimerization activity site of polarized growth calcium ion binding septin cytoskeleton -K63-linked polyubiquitin modification-dependent protein binding nBAF complex G-rich strand telomeric DNA binding extracellular matrix constituent conferring elasticity endocytic adaptor activity kinetochore endoplasmic reticulum exit site ruffle membrane dystroglycan binding basolateral plasma membrane regulation of protein localization to synapse protein-DNA complex disassembly chromatin disassembly cyclic nucleotide-dependent protein kinase activity sarcomere clathrin adaptor activity translation initiation factor binding microtubule organizing center part FAD binding actin polymerization or depolymerization cellular response to vitamin filamentous actin disordered domain specific binding - hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds, in l... - ligase activity, forming carbon–nitrogen bonds integral component of Golgi membrane ensheathment of neurons invadopodium + regulation of protein localization to membrane mRNA transport regulation of sodium ion transmembrane transport negative regulation of cell-substrate adhesion positive regulation of cell-matrix adhesion viral process -endocytic patch phosphatidylinositol bisphosphate binding actin cortical patch Ras guanyl-nucleotide exchange factor activity guanyl-nucleotide exchange factor activity nucleoside-triphosphatase regulator activity enhancer sequence-specific DNA binding leading edge membrane ciliary part Bcl-2 family protein complex positive regulation of plasma membrane bounded cell projection assembly pantothenate metabolic process - L-serine biosynthetic process - L-serine biosynthetic process - Golgi to plasma membrane protein transport positive regulation of epidermal growth factor receptor signaling pathway protein export from nucleus cell morphogenesis involved in differentiation process utilizing autophagic mechanism autophagy helicase activity INO80-type complex phospholipid scramblase activity Flemming body cardiolipin binding aldehyde–lyase activity phosphatidylinositol binding RNA polymerase II repressing transcription factor binding stress fiber contractile actin filament bundle Ino80 complex DNA helicase complex process utilizing autophagic mechanism autophagy autophagy maintenance of protein location in cell positive regulation of protein deacetylation neuron projection arborization negative regulation of neural precursor cell proliferation membrane raft organization collagen fibril organization positive regulation of GTPase activity cell migration response to growth factor poly(U) RNA binding cytoplasmic ubiquitin ligase complex catalytic activity, acting on a glycoprotein PML body N-methyltransferase activity collagen trimer telomeric DNA binding protein kinase activator activity mitochondrial envelope cytokine binding Golgi-associated vesicle membrane methylation-dependent protein binding podosome methylated histone binding nuclear periphery sequence—specific DNA binding -single—stranded telomeric DNA binding -phosphatidylinositol phosphate 5—phosphatase activity response to growth factor mitotic cell cycle checkpoint coated vesicle protein oxidation mitochondrial part cell adhesion · oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acce. plasma membrane region + aging substrate adhesion–dependent cell spreading cell cycle DNA replication regulation of myelination organelle fission postsynaptic density, intracellular component protein heterodimerization activity s, in phosphorus—containing RNA N6-methyladenosine methyltransferase complex hydrolase activity, acting on acid anhy mRNA editing complex hydrolase activity, acting on acid anhydrides regulation of transmembrane transporter activity regulatory region nucleic acid binding intrinsic component of Golgi membrane protein localization to plasma membrane cytoplasmic microtubule organization phosphorič ester hydrolase activity presynaptic active zone membrane cytoplasmic microtubule organization activation of protein kinase B activity protein targeting positive regulation of endocytosis biological adhesion biological adhesion cellular response to prostaglandin stimulus cell part morphogenesis sequence-specific double-stranded DNA binding cell cortex region receptor activator activity protein binding involved in heterotypic cell-cell adhesion phosphatidylinositol-4,5-bisphosphate phosphatase activity Golgi stack spindle pole photoreceptor cell cilium myosin II binding fucosyltransferase activity mitochondrial outer membrane adenylate cyclase binding phosphatidylinositol–3–phosphate binding response to copper ion regulation of cilium assembly positive regulation of receptor-mediated endocytosis-regulation of cell morphogenesis involved in differentiation positive regulation of ERBB signaling pathway membrane assembly regulation of cell adhesion mitochondrial membrane sex chromosome poly–pyrimidine tract binding
poly–purine tract binding
nuclear localization sequence binding endosome intrinsic component of presynaptic active zone membrane glycoprotein complex + transferase activity, transferring pentosyl groups regulation of cell adhesion positive regulation of catalytic activity ribonucleoprotein complex disassembly positive regulation of mitochondrial fission neuronal stem cell division -dystrophin-associated glycoprotein complex core promoter binding phosphatidylserine binding histone methyltransferase activity apicolateral plasma membrane chromatin - Hrd1p ubiquitin ligase complex pyrophosphatase activity neuronal stem cell division neuroblast division regulation of chromosome segregation post—Golgi vesicle—mediated transport protein polymerization nuclear transport protein polymerization nuclear transport production of miRNAs involved in gene silencing by miRNA regulation of actin filament—based process ameboidal—type cell migration regulation of platelet—derived growth factor receptor—beta signaling pathway positive regulation of synaptic vesicle endocytosis plus—end—directed vesicle transport along microfubule adenosine to inosine editing regulation of response to DNA damage stimulus epithelial cell migration—DNA damage checkpoint—neuron migration— RNA polymerase II distal enhancer sequence-specific DNA binding autolysosome metalloendopeptidase activity ciliary tip phosphatidylinositol phosphate phosphatase activity hyaluronic acid binding retromer complex fibronectin binding intraciliary transport particle B sequence–specific single stranded DNA binding MAP kinase activity condensed chromosome kinetochore ubiquitin ligase complex histone demethylase activity (H3-K9 specific DNA-(apurinic or apyrimidinic site) endonuclease activity organelle outer membrane arylsulfatase activity extrinsic component of membrane acetylcholine receptor binding transition metal ion binding nuclear matrix presynaptic membrane transcription regulatory region sequence-specific DNA binding regulation of ion transmembrane transporter activity cell cycle G1/S phase transition regulation of adherens junction organization positive regulation of cellular protein localization of cellular protein localization positive regulation of cellular protein localization of cellular protein locali extracellular matrix kinase activator activity SWI/SNF complex growth factor binding enhancer binding catalytic activity, acting on DNA DNA helicase activity postsynaptic specialization, intracellular component complex of collagen trimers cell projection membrane phosphatase activity outer membrane epithelium migration response to water transcription regulatory region DNA binding phosphatidylinositol-3,4-bisphosphate binding X chromosome lamellipodium morphogenesis vesicle–mediated transport to the plasma membrane maintenance of location in cell bone cell development unconventional myosin complex + organophosphate ester transmembrane transporter activity juxtaparanode region of axon calmodulin-dependent protein kinase activity signal transduction by trans—phosphorylation—retrograde trans—synaptic signaling by trans—synaptic protein complex—response to flavonoid—regulation of transcription from RNA polymerase II promoter in response to ...—regulation of the provision ER ubiquitin ligase complex RNA helicase activity cytoplasmic stress granule structural constituent of muscle COP9 signalosome double-stranded DNA binding mitotic spindle endoplasmic reticulum part phosphatidylinositol-4,5-bisphosphate binding regulation of leionneit loop disasseribly regulation of peroxisome organization positive regulation of platelet–derived growth factor receptor–beta signali... neuroblast division in subventricular zone NADPH regeneration actin filament binding extrinsic component of plasma membrane S100 protein binding U2-type precatalytic spliceosome purine ribonucleotide transmembrane transporter activity NADPH regeneration melanocyte proliferation development involved in symbiotic interaction Golgi vesicle transport regulation of sister chromatid segregation focal adhesion assembly cell–substrate adherens junction assembly regulation of transporter activity positive regulation of histone modification activation of GTPase activity response to oxidative stress regulation of mitotic sister chromatid segregation regulation of supramolecular fiber organization negative regulation of cell cycle process response to inorganic substance endoplasmic reticulum-Golgi intermediate compartment platelet-derived growth factor receptor binding autophagosome membrane phosphatidylglycerol binding dendrite oligosaccharide binding NAD-dependent histone deacetylase activity mitogen-activated protein kinase kinase binding mitochondrial inner membrane precatalytic spliceosome intronic transcription regulatory region sequence-specific DNA binding myelin sheath intronic transcription regulatory region DNA binding dendritic tree adenine nucleotide transmembrane transporter activity dendritic shaft thyroid hormone receptor binding phosphatidylinositol-4-phosphate binding histone demethylase activity Golgi cisterna regulation of supramolecular fiber organization negative regulation of cell cycle process response to inorganic substance negative regulation of extrinsic apoptotic signaling pathway via death doma... cellular response to cadmium ion negative regulation of intrinsic apoptotic signaling pathway positive regulation of neurogenesis regulation of release of cytochrome c from mitochondria interspecies interaction between organisms postsynaptic signal transduction postsynaptic signal transduction postsynaptic signal transduction postsynapse to nucleus signaling pathway positive regulation of synaptic vesicle exocytosis plus—end—directed organelle transport along microtubule actin filament reorganization regulation of G2/M transition of mitotic cell cycle animal organ morphogenesis myeloid cell development positive regulation of neuron projection development nuclear DNA replication serine family amino acid biosynthetic process protein localization to postsynaptic specialization membrane positive regulation of mitotic sister chromatid segregation neurotransmitter receptor localization to postsynaptic specialization membrane kinetochore assembly cellular response to prostaglandin E stimulus positive regulation of protein localization to membrane nucleocytoplasmic transport peptide metabolic process production of small RNA involved in gene silencing by RNA changle metabolic process production of cellular component size regulation of cellular component size regulation of sodium ion transport regulation of membrane permeability regulation of morphiane permeability regulation of sodium ion transport regulation of membrane permeability regulation of sodium in transport regulation of sodium in transport regu cis-Golgi network ligase activity, forming carbon-oxygen bonds T-tubule + region of cytosol aminoacyl-tRNA ligase activity phagocytic vesicle molecular adaptor activity
mRNA 3'-UTR binding
nucleobase-containing compound kinase activity sarcoplasmic reticulum membrane condensed chromosome protein-containing complex scaffold activity Golgi-associated vesicle purine nucleotide transmembrane transporter activity Schmidt-Lanterman incisure -NAD-dependent protein deacetylase activity plasma membrane bounded cell projection cytoplasm -GABA receptor binding peptidyl-prolyl cis-trans isomerase activity protein-lysine N-methyltransferase activity transcription factor complex nucleoside-triphosphatase activity U12-type spliceosomal complex ribonucleoprotein complex binding M band protein serine/threonine kinase activator activity presynapse condensed chromosome, centromeric region electron transfer activity organelle envelope lysine N-methyltransferase activity envelope calcium-dependent protein binding nuclear inclusion body + transcription factor activity, direct ligand regulated sequence-specific DN. meiotic spindle single-stranded DNA-dependent ATPase activity single-stranded DNA-dependent ATP-dependent DNA helicase activity phosphatidylinositol-5-phosphate binding Fanconi anaemia nuclear complex + SAGA-type complex presynaptic active zone -NAD+ kinase activity endodeoxyribonuclease activity, producing 5'-phosphomonoesters flavin adenine dinucleotide binding brush border regulation of cellular component size regulation of sodium ion transport regulation of membrane permeability positive regulation of hydrolase activity regulation of oxidative stress—induced neuron death plasma membrane bounded cell projection morphogenesis cellular protein—containing complex assembly cellular response to transforming growth factor beta stimulus Golgi to plasma membrane transport androgen receptor signaling pathway negative regulation of cell migration regulation of cellular localization establishment of organelle localization negative regulation of cellular protein localization localization in localization within membrane recycling endosome protein serine/threonine kinase inhibitor activity
Rac GTPase binding replication fork cell-cell contact zone ATPase activity phagocytic cup protein binding, bridging Rho guanyl–nucleotide exchange factor activity COPI-coated vesicle photoreceptor outer segment + protein phosphatase 2A binding ubiquitin-protein transferase regulator activity purine NTP-dependent helicase activity proline-rich region binding H4 histone acetyltransferase activity photoreceptor connecting cilium + integral component of endoplasmic reticulum membrane transcription factor TFTC complex + secondary lysosome ATP-dependent helicase activity presynaptic cytosol -ATP-dependent DNA helicase activity localization within membrane negative regulation of cell-matrix adhesion protein kinase A binding extrinsic component of synaptic membrane + regative regulation of cell-matrix addression membrane biogenesis negative regulation of cell motility regulation of gene expression, epigenetic membrane organization plasma membrane organization regulation of protein complex assembly cell projection morphogenesis promoter-specific chromatin binding dendrite terminus heparin binding chromocenter phosphoprotein phosphatase activity RNA polymerase II regulatory region DNA binding organelle inner membrane + intraciliary transport particle cis-trans isomerase activity protein acetyltransferase complex -RNA polymerase II core promoter sequence-specific DNA binding regulation of mitochondrial membrane permeability G1/S transition of mitotic cell cycle DNA polymerase activity kinase inhibitor activity acetyltransferase complex coated vesicle membrane regulation of blood pressure connective tissue development positive regulation of synaptic vesicle recycling positive regulation of sister chromatid cohesion sulfuric ester hydrolase activity mitochondrial matrix solute:proton antiporter activity U2-type spliceosomal complex + protein tyrosine kinase activator activitý positive regulation of sister chromatid cohesion folic acid-containing compound biosynthetic process asymmetric stem cell division negative regulation of cellular component movement neuron death in response to oxidative stress folic acid-containing compound metabolic process cell proliferation in forebrain positive regulation of intracellular transport positive regulation of supramolecular fiber organization cytoplasmic translation DNA integrity checkpoint purine nucleoside metabolic process regulation of intrinsic apoptotic signaling pathway in response to DNA damage fibroblast migration RNA 3'-end processing positive regulation of protein localization to cell periphery integral component of presynaptic active zone membrane oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP a. COPII vesicle coat lysophospholipase activity protein tyrosine phosphatase activity potassium channel regulator activity COPI vesicle coat Number of genes enriched compact myelin cell-cell adhesion mediator activity rough endoplasmic reticulum membrane carbon-carbon lyase activity membrane coat structural constituent of ribosome 90 coated membrane nuclear receptor transcription coactivator activity sodium channel regulator activity distal axon modified amino acid binding -ER to Golgi transport vesicle membrane 60 RNA polymerase II regulatory region sequence–specific DNA binding protein serine/threonine phosphatase complex hydrolase activity, acting on ester bonds phosphatase complex -30 positive regulation of protein localization to cell periphery regulation of potassium ion transport negative regulation of protein binding regulation of protein polymerization mitotic G2 DNA damage checkpoint folic acid metabolic process regulation of cell days formers. S-adenosylmethionine-dependent methyltransferase activity U2-type catalytic step 2 spliceosome RNA polymerase II basal transcription factor binding endoribonuclease complex protein phosphatase 1 binding poly(A) binding Sin3-type complex nuclear import signal receptor activity Ada2/Gcn5/Ada3 transcription activator complex + regulation of cell development positive regulation of nervous system development response to transforming growth factor beta nucleobase-containing small molecule interconversion organelle localization by membrane tethering maintenance of protein localization in organelle selenocysteine metabolic process response to vitamin K intrinsic component of mitochondrial inner membrane alcohol dehydrogenase (NADP+) activity
ATPase activity, coupled to transmembrane movement of ions, phosphorylative... integral component of mitochondrial inner membrane sarcoplasm + enzyme inhibitor activity -Rho GTPase binding intrinsic component of endoplasmic reticulum membrane proximal promoter sequence-specific DNA binding exocytic vesicle selenocysteine metabolic process response to vitamin K-response to hypobaric hypoxia-response to carbon monoxide-regulation of mitotic cell cycle DNA replication regulation of establishment of T 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 prostatic bud formation negative regulation of hepatocyte proliferation—JUN phosphorylation—Golgi to plasma membrane CFTR protein transport-glomerular visceral epithelial cell migration calcium—independent cell—matrix adhesion regulation of sodium ion transmembrane transporter activity—lung development ubiquitin–like protein conjugating enzyme binding SH2 domain binding COPII-coated ER to Golgi transport vesicle nuclear transcriptional repressor complex ion channel inhibitor activity endonuclease complex nuclear receptor binding extrinsic component of organelle membrane L-ascorbic acid binding synaptic vesicle cyclosporin A binding RNA polymerase II proximal promoter sequence—specific DNA binding Ran GTPase binding mitochondrial intermembrane space presynaptic active zone cytoplasmic component peptidase activator activity NuRD complex channel inhibitor activity CHD-type complex beta-tubulin binding BLOC-1 complex + catalytic activity, acting on a tRNA phagophore assembly site telomerase KNA binding microfilament motor activity PcG protein complex extracellular matrix structural constituent conferring compression resistance histone acetyltransferase complex dynein complex binding methyltransferase activity lung development establishment of protein localization to membrane cellular amide metabolic process peroxisome establishment of protein localization to membrane - cellular amide metabolic process protein—containing complex disassembly regulation of hydrolase activity regulation of cell junction assembly regulation of cell junction assembly regulation of cell junction assembly response to muscle inactivity involved in regulation of muscle adaptation response to denervation involved in regulation of muscle adaptation regulation of protein homooligomerization regulation of neuron projection arborization regulation of lamellipodium morphogenesis positive regulation of synaptic vesicle transport pancreatic juice secretion Notch receptor processing membrane raft assembly regulation of cellular senescence wound healing regulation of neurogenesis positive regulation of microtubule polymerization positive regulation of filopodium assembly negative regulation of protein localization to membrane positive regulation of protein polymerization actin filament—based movement regulation of nervous system development mitotic nuclear division negative regulation of oxidative stress—induced neuron death asymmetric cell division nuclear div microbody translation initiation factor activity catalytic activity, acting on RNA methyltransferase complex cytoplasmic side of plasma membrane demethylase activity protein kinase regulator activity
basal transcription machinery binding
basal RNA polymerase II transcription machinery binding growth cone part -Schaffer collateral - CA1 synapse microvillus transforming growth factor beta binding phosphatidylinositol bisphosphate phosphatase activity peroxisomal matrix microbody lumen + nucleoside monophosphate kinase activity GTP-dependent protein binding snRNA binding exon-exon junction complex somatodendritic compartment actinin binding sarcoplasmic reticulum SMAD binding vesicle membrane oxidoreductase activity, acting on CH-OH group of donors receptor signaling complex scaffold activity

DNA replication origin binding nuclear chromosome, telomeric region ficolin-1-rich granule lumen + phosphoric diester hydrolase activity phosphatase regulator activity telomerase holoenzyme complex integral component of mitochondrial outer membrane translation repressor activity chemorepellent activity endolysosome transferase activity, transferring one-carbon groups COPI-coated vesicle membrane translation factor activity, RNA binding transcription cofactor binding nucleotidyltransferase activity endoplasmic reticulum subcompartment + transferase complex nuclear division dendrite morphogenesis exonuclease activity cullin-RING ubiquitin ligase complex + syntaxin-1 binding adherens junction assembly regulation of cellular response to growth factor stimulus positive regulation of cell development transport vesicle NAD+ ADP-ribosyltransferase activity cytoplasmic side of membrane misfolded protein binding regulation of nuclear division MAP kinase kinase kinase activity cytosolic ribosome transmembrane receptor protein serine/threonine kinase signaling pathway apoptotic mitochondrial changes positive regulation of cytoskeleton organization positive regulation of developmental process regulation of ubiquitin—protein transferase activity regulation of monoxygenase activity negative regulation of mitotic nuclear division respiratory tube development positive regulation of cell differentiation negative regulation of transmembrane transport ER to Golgi vesicle—mediated transport muscle organ development cell ular senescence cell morphogenesis involved in neuron differentiation muscle cell cellular homeostasis cellular response to vitamin D CD4—positive or CD8—positive, alpha—beta T cell lineage commitment regulation of DNA replication development acell growth passal valents. réceptor metabolic process gamma-tubulin binding aspartic-type endopeptidase activity aldo-keto reductase (NADP) activity Golgi cisterna membrane vesicle coat basal part of cell ubiquitin protein ligase binding apical part of cell kinase regulator activity organelle envelope lumen -ATPase activity, coupled protein kinase inhibitor activity endoribonuclease activity postsynaptic membrane sperm midpiece + motor activity pericentriolar material ion channel regulator activity intrinsic component of mitochondrial outer membrane -RNA polymerase core enzyme binding histone–lysine N–methyltransferase activity plasma membrane raft + glutamate receptor binding translation elongation factor activity ionotropic glutamate receptor binding tertiary granule lumen polysome · endocytic vesicle + aspartic-type peptidase activity endoplasmic reticulum membrane protein phosphatase regulator activity oxidoreductase activity, acting on single donors with incorporation of mole... protein phosphatase inhibitor activity non-membrane spanning protein tyrosine kinase activity kinesin complex developmental cell growth establishment or maintenance of epithelial cell apical/basal polarity cellular response to epidermal growth factor stimulus axon cytoplasm small nucleolar ribonucleoprotein complex lamellipodium membrane negative regulation of response to DNA damage stimulus muscle cell migration gamma-tubulin complex + carbohydrate binding nuclear outer membrane-endoplasmic reticulum membrane network circulatory system process regulation of cellular component movement regulation of postsynaptic membrane neurotransmitter receptor levels response to the component of the beta-catenin binding late endosome protein-cysteine S-palmitoyltransferase activity protein-lipid complex protein-cysteine S-acyltransferase activity extrinsic component of cytoplasmic side of plasma membrane response to muscle inactivity replicative senescence replicative senescence positive regulation of fibroblast migration negative regulation of necroptotic process L-serine metabolic process cellular response to nitrogen starvation cellular response to nitrogen levels viral genome replication onent assembly involved in morphogenesis -DNA-directed DNA polymerase activity phagocytic vesicle membrane bHLH transcription factor binding actin monomer binding oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP a. ribosome + signal sequence binding microtubule motor activity intrinsic component of synaptic membrane lateral plasma membrane cellular component assembly involved in morphogenesis response to prostaglandin positive regulation of cartilage development negative regulation of signal transduction by p53 class mediator anatomical structure formation involved in morphogenesis endothelial cell migration platelet derived growth factor recentor signaling pathway p53 binding channel regulator activity sperm principal piece lipid binding pore complex oxidoreductase activity, acting on the CH-NH group of donors endoplasmic reticulum tubular network histone acetyltransferase binding adenylyltransferase activity endoplasmic reticulum quality control compartment platelet–derived growth factor receptor signaling pathway -negative regulation of cell proliferation anaphase-promoting complex histone acetyltransferase activity lysosomal lumen ion channel binding regulation of mitotic nuclear division alpha–amino acid biosynthetic process ribosomal subunit cholesterol binding site of double-strand break protein tyrosine kinase activity nuclear chromosome segregation regulation of protein deacetylation cargo receptor activity neuron projection membrane P-P-bond-hydrolysis-driven transmembrane transporter activity regulation of nitric-oxide synthase activity regulation of protein localization to plasma membrane regulation of cation transmembrane transport cytosolic large ribosomal subunit oxidoreductase activity, acting on NAD(P)F dendrite membrane phosphatase inhibitor activity regulation of cation transmerhorane transport
peptidyl—lysine modification
regulation of ventricular cardiac muscle cell membrane repolarization
positive regulation of mRNA splicing, via spliceosome
positive regulation of gene silencing by miRNA
negative regulation of protein localization to plasma membrane
negative regulation of intrinsic apoptotic signaling pathway by p53 class m...
mitophagy 3',5'-cyclic-nucleotide phosphodiesterase activity site of DNA damage activating transcription factor binding apical plasma membrane peptide–lysine–N–acetyltransferase activity
DNA–dependent ATPass activity vacuole · cell-cell adherens junction + cation-transporting ATPase activity cluster of actin-based cell projections primary active transmembrane transporter activity mitochondrion morphogenesis kinetochore organization neuron projection development regulation of response to oxidative stress cellular response to endogenous stimulus synaptic vesicle recycling via endosome stress granule disassembly response to hydrostatic pressure regulation of stress granule assembly regulation of stress granule assembly regulation of skeletal muscle contraction by calcium ion signaling regulation of basement membrane organization regulation of basement membrane organization 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 basement membrane assembly involved in embryonic bod... positive regulation of statchment of spindle microtubules to kinetochore negative regulation of DNA damage checkpoint negative regulation of DNA damage checkpoint negative regulation of DNA damage checkpoint negative regulation of cell volume intrinsic apoptotic signaling pathway in response to hydrogen peroxide interkinetic nuclear migration hematopoietic stem cell homeostasis cap-independent translational initiation basement membrane assembly involved in embryonic body morphogenesis integral component of synaptic membrane mitochondrion morphogenesis ubiquitin-like protein ligase binding WW domain binding H4 histone acetyltransferase complex large ribosomal subunit solute:cation antiporter activity phosphatidylinositol 3–kinase binding cytoplasmic vesicle membrane nuclear chromosome part nucleocytoplasmic carrier activity side of membrane cyclic-nucleotide phosphodiesterase activity vacuolar membrane alpha-actinin binding ATPase coupled ion transmembrane transporter activity nuclear ubiquitin ligase complex + active ion transmembrane transporter activity cytosolic small ribosomal subunit -GTPase activity SCF ubiquitin ligase complex -E-box binding nuclear outer membrane + myosin binding mitotic spindle pole sulfur compound binding high-density lipoprotein particle ubiquitin conjugating enzyme binding S-acyltransferase activity mitochondrial membrane part + coenzyme binding cysteine–type peptidase activity nuclear chromatin platelet alpha granule lumen peptide transmembrane transporter activity replisome ribonuclease activity mRNA cleavage factor complex dioxygenase activity lumenal side of endoplasmic reticulum membrane scavenger receptor activity peptide hormone binding nematopoletic stem cell nomeostasis cap-independent translational initiation basement membrane assembly involved in embryonic body morphogenesis 10-formyltetrahydrofolate metabolic process centromere complex assembly regulation of systemic arterial blood pressure negative regulation of protein complex assembly regulation of epithelial cell migration regulation of epithelial cell migration integral component of lumenal side of endoplasmic reticulum membrane monosaccharide binding lytic vacuole calcium-dependent phospholipid binding lysosome + carboxy-lyase activity ficolin-1-rich granule acetyltransferase activity
N-acetyltransferase activity
transferase activity, transferring sulfur-containing groups
sulfotransferase activity rough endoplasmic reticulum regulation of epithelial cell migration respiratory system development peptidyl-cysteine modification regulation of response to endoplasmic reticulum stress cellular response to reactive oxygen species small GTPase mediated signal transduction telomere localization signal transduction involved in G2 DNA damage checkpoint
regulation of skeletal muscle satellite cell proliferation regulation of histone phosphorylation regulation of histone H4 acetylation embryonic brain development neuron projection morphogenesis clathrin-coated pit cell body photoreceptor inner segment molecular carrier activity endoplasmic reticulum-Golgi intermediate compartment membrane exonuclease activity, active with either ribo- or deoxyribonucleic acids an. cytoplasmic microtubule + magnesium ion binding 3'-5'-exoribonuclease activity ciliary membrane clathrin-coated vesicle -N-acyltransferase activity hydro-lyase activity regulation of histone H4 acetylation embryonic brain development neuron projection morphogenesis regulation of binding regulation of mitochondrial membrane potential release of cytochrome c from mitochondria regulation of cell migration glial cell development execution phase of apoptosis ventricular cardiac muscle cell action potential regulation of membrane repolarization pteridine-containing compound metabolic process positive regulation of microtubule polymerization or depolymerization negative regulation of DNA replication attachment of spindle microtubules to kinetochore vascular associated smooth muscle cell migration regulation of mitochondrial fission positive regulation of potassium ion transport cellular response to inorganic substance regulation of macroautophagy gene silencing by miRNA regulation of circadian rhythm microtubule-based movement cellular response to alcohol integrin complex -ATPase activity, coupled to transmembrane movement of substances ATPase activity, coupled to movement of substances histone methyltransferase complex early endosome protein self-association intercalated disc cysteine–type endopeptidase inhibitor activity peptide N–acetyltransferase activity microtubule associated complex calcium ion transmembrane transporter activity terminal bouton cytokine receptor activity ionotropic glutamate receptor complex oxidoreductase activity, acting on paired donors, with incorporation or red... polysomal ribosome peptidase regulator activity metallopeptidase activity MLL1/2 complex exoribonuclease activity, producing 5'-phosphomonoesters protein serine/threonine phosphatase activity MLL1 complex heterotrimeric G-protein complex oxidoreductase activity, acting on a sulfur group of donors GTPase complex -RNA polymerase II complex binding postsynaptic specialization membrane Rab guanyl-nucleotide exchange factor activity nuclear membrane carboxylic acid binding palmitoyltransferase activity trans-Golgi network membrane transport vesicle membrane exoribonuclease activity oxidoreductase activity small ribosomal subunit mičrotubule-based movement cellular response to alcohol negative regulation of ion transmembrane transport heart morphogenesis response to epidermal growth factor regulation of filopodium assembly interleukin-12-mediated signaling pathway establishment or maintenance of bipolar cell polarity establishment or maintenance of apical/basal cell polarity positive regulation of viral genome replication necroptotic process regulation of neuron differentiation histone H3 acetylation establishment of protein localization to plasma membrane regulation of neuron projection development transferase activity, transferring glycosyl groups lytic vacuole membrane ubiquitin conjugating enzyme activity -transition metal ion transmembrane transporter activity -disulfide oxidoreductase activity lysosomal membrane neurotransmitter receptor complex spindle midzone translation regulator activity protein complex involved in cell adhesion + deoxyribonuclease activity Cul4-RING E3 ubiquitin ligase complex phospholipase activity DNA-binding transcription factor activity ciliary base thiolester hydrolase activity cleavage furrow alcohol binding vacuolar part endonuclease activity neuron projection terminus + ubiquitin-like protein ligase activity regulation of neuron projection development response to prostaglandin E regulation of ubiquitin protein ligase activity regulation of receptor recycling regulation of platelet–derived growth factor receptor signaling pathway positive regulation of meiotic cell cycle smooth endoplasmic reticulum transmembrane receptor protein tyrosine kinase activity ubiquitin-like protein-specific protease activity tRNA binding Golgi lumen ribonucleoprotein granule antioxidant activity endocytic vesicle membrane ubiquitin-like protein conjugating enzyme activity integral component of postsynaptic specialization membrane estrogen receptor binding nuclear migration negative regulation of synapse organization negative regulation of protein localization to cell periphery negative regulation of potassium ion transmembrane transport cellular response to radiation nuclear heterochromatin 4 iron, 4 sulfur cluster binding lyase activity protein N-terminus binding endodeoxyribonuclease activity peroxisomal part microbody part stress response to radiation stress response to radiation stress response to copper ion skeletal muscle satellite cell proliferation regulation of translation, ncRNA-mediated regulation of skeletal muscle cell proliferation regulation of hepatocyte proliferation positive regulation of meiotic nuclear division growth factor receptor-beta signaling pathway condensed nuclear chromosome organic acid binding organellar large ribosomal subunit mitochondrial large ribosomal subunit proton transmembrane transporter activity plasma lipoprotein particle tau protein binding lipoprotein particle coreceptor activity platelet-derived growth factor receptor-beta signaling pathway negative regulation of translation, ncRNA-mediated negative regulation of anion transmembrane transport miRNA mediated inhibition of translation GMP metabolic process endopeptidase inhibitor activity immunological synapse ubiquitin protein ligase activity caveola peptide binding intrinsic component of presynaptic membrane acetylgalactosaminyltransferase activity detoxification of copper ion -deoxyribonucleotide biosynthetic process spindle microtubule calcium channel regulator activity ATP-dependent microtubule motor activity apical junction complex negative regulation of intrinsic apoptotic signaling pathway in response to...
mitochondrial transport
regulation of actin filament polymerization aminopeptidase activity bicellular tight junction + amide transmembrane transporter activity intrinsic component of postsynaptic specialization membrane regulation of cellular response to oxidative stress regulation of receptor—mediated endocytosis negative regulation of cell cycle G2/M phase transition regulations of cell cycle G2/M phase transition regulation r cysteine-type endopeptidase activity inclusion body peptidase inhibitor activity endosomal part endopeptidase regulator activity cytoplasmic ribonucleoprotein granule voltage-gated calcium channel activity regulation of cell aging cortical cytoskeleton organization syntaxin binding -unfolded protein binding nuclear envelope protein stabilization negative regulation of locomotion mitochondrial outer membrane permeabilization involved in programmed cell d... external side of plasma membrane thiol-dependent ubiquitinyl hydrolase activity vacuolar lumen virus receptor activity postsynaptic density membrane hijacked molecular function negative regulation of chromosome organization glycosyl compound metabolic process cellular response to oxygen-containing compound regulation of actin filament organization transcription-dependent tethering of RNA polymerase II gene DNA at nuclear ... telomere tethering at nuclear periphery selenium compound metabolic process -selenium compound metabolic process -telomere tethering at nuclear periphery selenium compound metabolic process -telomere tethering at nuclear periphery cell division site part carbon-oxygen lyase activity -protein phosphorylated amino acid binding tight junction -AP-type membrane coat adaptor complex -NADP binding ubiquitinyl hydrolase activity myosin complex transferase activity, transferring acyl groups other than amino-acyl groups nuclear replication fork amyloid-beta binding endosome membrane response to UV-A regulation of prostatic bud formation phospholipid transporter activity purine nucleoside binding -SH3/SH2 adaptor activity organellar ribosome regulation of pancreatic juice secretion regulation of metalloendopeptidase activity regulation of mesenchymal stem cell differentiation regulation of isotype switching to IgE isotypes mitochondrial ribosome platelet alpha granule protein kinase C binding spliceosomal snRNP complex amide binding 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 p38MAPK cascade negative regulation of cysteine-type endopeptidase activity involved in apo... negative regulation of cell cycle checkpoint isotype switching to IgE isotypes formate metabolic process late endosome membrane ubiquitin-protein transferase activity - RNA polymerase II activating transcription factor binding tethering complex cell division site antigen binding isomerase activity -endopeptidase activity sperm flagellum tertiary granule ubiquitin–like protein transferase activity – nucleoside binding – protein-DNA complex integral component of presynaptic membrane transferase activity, transferring hexosyl groups - signaling adaptor activity asymmetric neuroblast division actin filament polymerization roof of mouth development SNARE complex multivesicular body steroid hormone receptor activity oxidoreductase activity, acting on peroxide as acceptor - 3'-5' exonuclease activity integral component of postsynaptic membrane head development small nuclear ribonucleoprotein complex cellular response to organic cyclic compound positive regulation of protein modification process transferase activity, transferring acyl groups host cell osteoblast differentiation somatic stem cell division regulation of receptor binding regulation of necrotic cell death transmembrane receptor protein kinase activity -guanyl ribonucleotide binding host neuronal cell body guanyl nucleotide binding -hormone binding -9+2 motile cilium positive regulation of receptor internalization positive regulation of focal adhesion assembly GTP binding excitatory synapse antiporter activity melanosome organization sperm part · DNA-binding transcription factor activity, RNA polymerase II-specific integral component of postsynaptic density membrane epithelial to mesenchymal transition thiol-dependent ubiquitin-specific protease activity negative regulation of mitotic cell cycle phase transition central nervous system development heterochromatin iron ion binding proton-transporting two-sector ATPase complex · purine ribonucleoside binding -rRNA binding cellular response to interleukin–12 transforming growth factor beta receptor signaling pathway limb development intrinsic component of postsynaptic membrane carboxylic ester hydrolase activity other organism part appendage development appendage development vesicle budding from membrane proteasome-mediated ubiquitin-dependent protein catabolic process positive regulation of dendrite development amino acid binding other organism cell acetylglucosaminyltransferase activity - ribonucleoside binding - exopeptidase activity other organism pigment granule outflow tract morphogenesis blood circulation melanosome oxidoreductase activity, acting on the CH-CH group of donors transcription elongation factor complex peptidase activity, acting on L-amino acid peptides negative regulation of protein metabolic process telomere maintenance via telomere trimming voltage-gated potassium channel activity lipid droplet manganese ion binding -single-stranded DNA binding t-circle formation skeletal muscle cell proliferation intrinsic component of postsynaptic density membrane response to inactivity
regulation of podosome assembly
pteridine–containing compound biosynthetic process
pre–miRNA processing
positive regulation of ruffle assembly
positive regulation of receptor recycling
positive regulation of processing
positive regulation of processing azurophil granule membrane vitamin binding anchored component of plasma membrane peptidase activity RNA methyltransferase activity secretory granule lumen motile cilium iron-sulfur cluster binding clathrin-coated endocytic vesicle protein tyrosine kinase binding synaptic vesicle membrane negative regulation of oxidative stress—induced cell death negative regulation of necrotic cell death negative regulation of androgen receptor signaling pathway intra—S DNA damage checkpoint formation of extrachromosomal circular DNA damaged DNA binding exocytic vesicle membrane steroid binding blood microparticle serine-type endopeptidase inhibitor activity response to ketone regulation of cell cycle G1/S phase transition regulation of Ras protein localization regulation of Ras protein signal transduction positive regulation of peptidyl—serine phosphorylation mRNA 3'—end processing collagen metabolic processing regulation of evidative stress induced cell death Sm-like protein family complex heat shock protein binding voltage–gated cation channel activity hydrolase activity, acting on glycosyl bonds clathrin-coated vesicle membrane specific granule lumen receptor tyrosine kinase binding DNA-binding transcription activator activity, RNA polymerase II-specific nuclear inner membrane ficolin-1-rich granule membrane + hydrolase activity, hydrolyzing O-glycosyl compounds secretory vesicle regulation of oxidative stress-induced cell death positive regulation of mitochondrial membrane permeability negative regulation of nuclear division response to interleukin-12 negative regulation of leukocyte mediated immunity ATP-dependent chromatin remodeling monocarboxylic acid binding voltage-gated potassium channel complex calcium channel activity UDP-glycosyltransferase activity plasma membrane receptor complex chaperone binding cell surface chloride channel activity peptidase complex monooxygenase activity microtubule polymerization intrinsic apoptotic signaling pathway by p53 class mediato growth factor receptor binding -ATPase binding azurophil granule lumen cytoplasmic vesicle lumen macroautophagy regulation of anatomical structure size ventricular cardiac muscle cell membrane repolarization phosphoprotein binding vesicle lumen anion channel activity axoneme regulation of oxidative stress-induced intrinsic cell membrane repolarization regulation of cardiac muscle cell membrane repolarization prostate gland epithelium morphogenesis pigment granule organization DNA-binding transcription repressor activity, RNA polymerase II-specific ciliary plasm · voltage-gated ion channel activity axon terminus voltage-gated channel activity inner mitochondrial membrane protein complex -G protein–coupled receptor binding – potassium channel activity – protein polyubiquitination response to growth hormone early endosome membrane serine-type peptidase activity RNA polymerase II, holoenzyme autophagosome maturation regulation of chromosome separation active transmembrane transporter activity potassium channel complex histone H4 acetylation cofactor binding positive regulation of catabolic process regulation of mRNA metabolic process peripheral nervous system development nucleosome organization cardiac muscle cell action potential involved in contraction posttranscriptional gaps silencing by RNA posttranscriptional gaps silencing silencing gaps silencing mitochondrial protein complex lipid transporter activity primary lysosome chloride transmembrane transporter activity - serine hydrolase activity - serine-type endopeptidase activity azurophil granule protein kinase complex potassium ion transmembrane transporter activity specific granule posttranscriptional gene silencing by RNA eye development solute:cation symporter activity preribosome metal ion transmembrane transporter activity cellular response to nutrient levels
regulation of protein stability
posttranscriptional gene silencing
mitotic sister chromatid segregation recycling endosome membrane hormone activity acrosomal vesicle growth factor activity secondary active transme ane transporter activity ligand-gated ion channel activity - ligand-gated channel activity positive regulation of membrane permeability perikaryon regulation of memorane permeability amide biosynthetic process T-helper cell lineage commitment stress response to metal ion response to stimulus involved in regulation of muscle adaptation regulation of retinoic acid receptor signaling pathway regulation of DNA damage checkpoint potassium ion export across plasma memorane receptor complex organic anion transmembrane transporter activity secretory granule membrane inorganic anion transmembrane transporter activity serine/threonine protein kinase complex symporter activity regulation of retinoic acid receptor signaling pathway regulation of DNA damage checkpoint potassium ion export across plasma membrane potassium ion export positive regulation of T cell chemotaxis positive regulation of transmembrane transporter activity positive regulation of keratinocyte differentiation nucleoside salvage negative regulation of natural killer cell mediated cytotoxicity detoxification of inorganic compound DNA repair regulation of peptidyl—serine phosphorylation secretory granule monovalent inorganic cation transmembrane transporter activity nuclear DNA-directed RNA polymerase complex inorganic cation transmembrane transporter activity ion gated channel activity - gated channel activity specific granule membrane DNA-directed RNA polymerase complex sodium ion transmembrane transporter activity oxidoreductase complex cation channel activity -RNA polymerase complex cation transmembrane transporter activity mitochondrial respiratory chain cytokine activity anion transmembrane transporter activity transferase complex, transferring phosphorus-containing groups regulation of peptidyl-serine phosphorylation establishment of cell polarity ion channel activity membrane protein complex substrate-specific channel activity + protein localization to postsynaptic membrane negative regulation of mitotic metaphase/anaphase transition
T cell lineage commitment chondroitin sulfate biosynthetic process plasma membrane protein complex transporter activity intermediate filament channel activity transporter complex passive transmembrane transporter activity sister chromatid segregation ruffle organization negative regulation of blood coagulation protein—DNA complex subunit organization regulation of endothelial cell migration intermediate filament cytoskeleton transmembrane transporter activity respiratory chain ion transmembrane transporter activity cytokine receptor binding nucleosome inorganic molecular entity transmembrane transporter activity - receptor ligand activity ion channel complex regulation of endotheral ceri highauon urinary tract smooth muscle contraction - urinary bladder smooth muscle contraction - regulation of DNA-dependent DNA replication initiation - pre-replicative complex assembly involved in nuclear cell cycle DNA replica... DNA packaging complex receptor regulator activity cation channel complex transmembrane signaling receptor activity transmembrane transporter complex -G protein-coupled receptor activity ന 6 ന ന $log_{10}(P_{b-hoch})$

term

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