0.0164145839891849 0.00491715407549724 transmembrane transporter activity

RNA polymerase II cis–regulatory region sequence–specific DNA bindin
gated channel activity

FAD bindin ubiquitin-protein transferase activator Hsp90 protein 0.000219917335771021 0.00907364330420847 0.000271971834994988 extracellular ligand-gated ion channel ac 0.0462619875701501 0.00251554036021615 0.00667232523676928 0.0048581924906405 acetylcholine-gated cation-selective ch sulfide:quinone oxidoredu sugar transmembrane transporter activity oxidoreductase activity, acting on the CH–CH group of donors MAP kinase kinase activity 0.00129514562963975 0.0459427654037871 0.0439427654037871 0.0132643105243842 0.0063605005990236 0.00437836181742922 0.0275852290779128 0.00129514562963975 low-density lipoprotein pa hydrolase activity, hydrolyzing N-glycosy fructose transmembrane transporter act dehydroascorbic acid transmembrane transporter act carbonate dehydratase acid transmembrane transporter act carbonate dehydratase acid transmembrane transporter act carbonate dehydratase acid transmembrane transporter actor placetylcholine receptor acid transmembrane transporter acid trehalose transmembrane transporter acid translation elongation factor bir Torc2 complex bir RNA-3'-phosphate cyclase acid RNA polymerase II intronic transcription regulatory region sequence-specific DNA bir regulatory RNA bir acid transmit transmit transcription regulatory region sequence-specific DNA bir regulatory RNA bir regulato 0.00372824288158826 0.0126983456547531 0.00741485330523134 0.00410506064420614 0.0374033184934031 0.00989190501203163 0.0285371838318533 0.0196744467718901 0.0399672284542694 0.0456131888614059 0.0496131866014039 0.0196864286750625 0.0406189591929271 0.0268704835106488 0.0402924726759065 0.0296330264165162 peptide—methionine (R)—S—oxide reductase a oxidoreductase activity, acting on a sulfur group of donors, disulfide as acc methionine—tRNA ligase a methionine adenosyltransferase a 0.0317197039877475 0.0274384954171599 0.0406768436660201 0.0098919122498644 0.0160713676094626 0.0477888395664612 0.00989191224986444 0.0196864286750615 0.0293845037638754 0.0484951014245641 0.0287622397131757 0.0248168699824325 hydroxymethylglutaryl–CoA reductase (NADPH)
hexokinase guanylate cyclase activator glutamate-5-semialdehyde dehydrogenase 0.0196864286750587 0.00989191224986444 0.0196864284305752 gamma-glutamylcyclotransferase ethanolaminephosphotransferase activity
epoxide hydrolase activity
epoxide hydrolase activity
diamine N-acetyltransferase activity
D5 dopamine receptor binding
D-glucose transmembrane transporter activity
C-4 methylsterol oxidase activity
butyryl-CoA dehydrogenase activity
anaphase-promoting complex binding
adenylate cyclase activator activity
acetyltransferase activator activity
activity acetyltransferase activator activity
sthylthiopropyl glucosinolate S-oxygenase activity 0.0415907345131472 0.0178568879868916 0.00954512041495542 0.0284327406773449 0.00927985046564355 0.0248086594715024 0.0483884688513913 adenylate cyclase activator activity acetyltransferase activator activity acetyltransferase activator activity 4.

8-methylthiopropyl glucosinolate S-oxygenase activity 4.

4-methylthiopropyl glucosinolate S-oxygenase activity 3-phosphoripositide-dependent protein kinase binding 3-oxo-5-alpha-steroid 4-dehydrogenase activity endopalasmic reticulum membrane cell cortex SCF ubiquitin ligase complex low-density lipoprotein particle inwedensity lipoprotein particle integral component of postsynaptic specialization membrane dopaminergic synapse cholinergic synapse anaphase-promoting complex acetylcholine-gated channel complex syllapse acetylcholine-gated channel complex site of polarized growth radial spoke head pole plasm origin recognition complex nuclear outer membrane NuA3b histone acetyltransferase complex NuA3a histone acetyltransferase complex myosin filament muscle myosin tilament muscle myosin complex methionine adenosyltransferase complex methionine adenosyltransferase complex methionine adenosyltransferase complex extrinsic component of postsynaptic specialization membrane extrinsic component of neuronal dense core vesicle membrane extrinsic component of neuronal dense core vesicle membrane extrinsic component of neuronal dense core vesicle membrane extrinsic place in the property of 0.0478877942773201 0.00821748016785105 0.0426362493480774 0.00821748016785105 0.0196864286750615 0.0128189022062403 0.0298868068260177 0.00156759027270036 0.0482650646303643 0.0462690469303643 5.57709498992086e-05 0.0373957473451336 0.000875420769426579 0.0164055230544259 0.0111331165716247 0.0229195224087198 0.0196864286750615 0.019682263068846 0.0155566969080404 0.0162521564314761 0.0195672117642279 0.0480134391750351 0.0344676615566944 0.0247558250625274 0.0479055913608131 0.0364477375514469 0.0434684683385392 0.0293845037638766 0.0151936091561298 0.025839047181367 0.0309958034554238 0.0389494294724397 0.0353349064887013 positive regulation of macromolecule metabolic proces response to higher anatomical structure formation involved in morphogenesis response to heat regulation of protein metabolic process anatomical structure formation involved in morphogenesis response to heat response to heat response to heat regulation of protein metabolic process positive regulation of transcription of nucleolar large rRNA by RNA polymerase I negative regulation of Notch signaling pathway metal ion transport insulin receptor signaling pathway insulin receptor signaling pathway inorganic cation transmembrane transport glutathione biosynthetic process embryonic heart tube morphogenesis determination of heart left/right asymmetry detection of stimulus cholesterol transport behavioral response to nicotine amyloid—beta clearance zymogen activation telencephalon development synaptic transmission involved in micturition sulfide oxidation, using sulfide: quinone oxidoreductase service metabolic process sexual reproduction sensory perception of taste 0.0195641352101686 0.0466107307226148 7.392979309117246-0 0.00357081242269958 0.0383607686196744 0.00485679549594268 0.0282764268727103 0.00518600792738092 0.0137073682901894 0.0186071730508629 0.00754650614715909 0.00113754584737993 0451922822980799 0.000553698857509084 0.000531341627407495 0.0416811415750973 0.0322882093066899 0.0157695777856112 0.0320222743092636 0.0146778707779525 sexual reproduction
sensory perception of taste
response to food
regulation of dendrite morphogenesis
regulation of circadian rhythm
proximal/distal pattern formation
protein tetramerization
protein homotrimerization
protein heterooligomerization
positive regulation of macrophage derived foam cell differentiation
positive regulation of besterol storage
positive regulation of collecterol storage
positive particle clearance 0.0465741223578663 0.0143263625924656 0.000915768467976502 0.0165286290628434 0.0275219667789747 0.00843509089114696 0.0259445335684638 0.00497894196979645 0.0370768820910269 0.0149056723496495 ontology 0.0129923802754417 BP CC 0.0228357126234159 cerebellum development cellular sulfide ion homedstasis cellular protein—containing complex assembly cellular detoxification of cadmium ion anaphase–promoting complex–dependent catabolic process vitamin B6 metabolic process MF 8.82293230978269e-05 8.822932309782696-05 0.0127561829159979 0.000633146890229707 0.00517713859883704 0.00562655591166482 0.0474955373848549 0.0286110080959726 0.0374033184934031 transmembrane receptor protein tyrosine phosphatase signaling pathway transition between fast and slow fiber transformation of host cell by virus 0.0293671938710875 0.0444861710349183 0.044462106858233 tracnea lorrilation
telomeric D-loop disassembly
t-circle formation
subpallium development
stem vascular tissue pattern formation
spermine acetylation 0.0146251283908062 spermine acetylation
spermidine acetylation
specification of proximal tubule identity
skin epidermis development
skeletal muscle satellite cell migration
S-adenosylmethionine biosynthetic process
rostrocaudal neural tube patterning
retrograde neuronal dense core vesicle transport
response to vanadate(3-)
response to melanocyte-stimulating hormone 0.0272802349451954 0.0458363602753394 0.0458363602753394 0.0369883141067958 0.0196864286750625 0.0196864286750615 0.0362689775185403 0.00957361648791765 response to melanocyte—stimulating hormoneregulation of vascular endothelial growth factor signaling pathwayregulation of the force of skeletal muscle contractionregulation of slow—twitch skeletal muscle fiber contractionregulation of myosin—light—chain—phosphatase activityregulation of melotic huclear division—
regulation of melotic huclear division—
regulation of peroxide metabolic process—
regulation of Golgi inheritance—
regulation of fibroblast migration—
regulation of female gonad development—
regulation of bonad development—
regulation of adenylate cyclase—activating G protein—coupled receptor signaling bathway—
regulation of acetylcholine secretion, neurotransmission—
radial spoke assembly— 0.0468158277406676 0.00989191224986444 0.00989191224986444 0.0139962147597791 0.0379745189156147 0.037597257307427 0.037530939316006 0.0293640112677945 0.00989191224986046 0.00949745035750799 regulation of adenylate cyclase—activating G protein—bulled receptor sample pathway regulation of acetylation in PNA endoreduplication regulation of acetylation in Acetylation protein protei 0.0338259233893522 0.00804417815839422 0.0153479755182938 0.033455216293126 0.0380933467766953 0.00987305292266575 0.0406189591929271 0.0293833292743179 0.0223879615360345 0.0293845037638688 U.U.293845037638688 0.0290724454007274 0.0389224592512753 0.0389224592512763 0.0385243615806831 0.00988215129343921 0.0196864286750625 0.0196864286750615 0.0277866796471224 0.0927129937626578 0.0186889627553225 0.0368219551915269 0.00982534157710186 0.0228584397144987 0.0190803934718408 0.0369883141067958 0.0369663141067936 0.0196864286750615 0.0374238998115613 0.0193712669701054 0.0293845037638671 0.00989190501203163 0.00523223278344969 0.0211670087524286 0.0290166645522291 0.0495222503338872 0.0440852985699628 0.0160281561786426 0.0286519910407783 0.0293845037638757 0.00804417815839422 0.0478428375078687 0.00982376510922541 0.0293845037638754 0.00555591379929181 0.00989191224986046 0.0196848806964317 0.0379966207807066 0.00969370417261411 0.0484675741478377 0.0479549212597359 0.00957361648791765 0.0479537149320135 0.0196864286750615 0.0196864215084961 0.0185761747600404 0.00523223278344969 0.0476392538424452 0.0384392794462642 0.0142887953088749 0.0195672117642279 0.0463484060610621 0.0195672117642279 0.0290768822780172 0.0196848806964317 0.0370288050251584 0.0206465248893091 0.00989191193072672 green jear voigure glucosinolate biosynthetic b glucose 6-phosphate metabolic b glomus develo 0.0124913479342755 0.0393366859310994 0.0335595596696143 0.00864539437111826 GABAergic neuron differentiation forebrain neuron fatty acid derivative biosy epithelial cell proliferation involved in lung morphogenesis endothelial tip cell fate specification involved in lung morphogenesis endothelial tip cell fate specification embryonic liver development cell fate specification embryonic liver development endothelial tip cell fate specification embryonic liver development cell fate specification embryonic liver development cell fate specification embryonic liver development cell fate specification cytokinn transport cytokinn transport cytokinn transport cetter formation complement activation, classical pathway citrulline biosynthetic process chondrocyte intercalation involved in growth plate cartilage morphogenesis chondrocyte intercalation involved in growth plate cartilage morphogenesis cerebellar cortex GABAergic interneuron fate commitment cerebellar molecular layer formation cerebellar molecular layer formation cerebellar cortex development cellular response to sodium arsenite cellular response to sodium arsenite cellular response to gonadotropin—releasing hormone cellular response to cital cellular response to cital carbohydrate transmembrane transport batoderm segmentation asexual reproduction anterograde neuronal dense core vesicle transport activation of transmembrane receptor protein tyrosine kinase activity abscisic acid—activated signaling pathway abscisic acid transport 4—hydroxyproline catabolic process 0.0196756331306769 0.0196864286750624 0.02794021088814 0.02794021088814 0.0313418903091349 0.0293829710279301 0.0162961395722762 0.0389855650516757 0.0300371445723502 0.0290480203044908 0.0290480203044908 0.0190454888289534 0.0180469364763027 0.00523223278344969 0.036325825320005 0.0196864286750624 0.0385331844550362 0.0385331844550362 0.0289577271411745 0.00989191224986046 0.00989190501203163 0.0484951014245568 0.03652432419351552 0.0238571793955853 0.0217017606463134 0.0217917606163134 0.0196864286750584 0.0196864286750625 0.0182694174142019 0.0196848806964317 0.0293833367892727