0.00990817451740252 0.00730455957372166 0.0477599277975415 RNA polymerase II cis–regulatory region sequence–specific DNA bindin
RNA polymerase II cis–regulatory region sequence–specific DNA bindin
iron ion bindin
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen 0.0289727093694421 0.0395976357180765 0.0332056879807899 0.0412715476473527 extracellular ligand-gated ion channel acetylcholine-gated cation-selective channel Wnt-protein 0.0164343004176902 0.00077458563095867 ubiquitin-protein transferase activator sulfide:quinone oxidoredu sugar transmembrane transp tow-density.lipoprotein pa hydrolase activity, hydrolyzing N-glycosy hydro-0.000129906505071814 0.00189678192624449 0.00900643580644367 0.00900643580644367 0.00634155867610618 0.00864431066535704 0.0385118836935883 0.00189678192624449 0.00542638565884791 fructose transmembrane t dehydroascorbic acid transmembrane t carbonate de 0.0182699192351686 0.0107617298324582 1–acylglycerol–3–phosphate O–acyltranstic trehalose transmembrane transper translation elongation TORC2 con 0.0452638671180801 0.0452638671180801 0.01213824730515 0.0346944819977501 0.0223261280232829 0.0241112827727401 0.0480722352977028 RNA polymerase II intronic transcription regulatory region sequence—spec 0.0241297469911859 0.0487701861333068 0.0325083983975035 peptide-methionine (R)-S-oxius oxidoreductase activity, acting on a sulfur group of donors, disulf methionine tRN methionine adenosyltra maleylacetoacetate 0.0479708277267661 0.0348591709280729 0.0499604316039794 0.0381900266846582 0.0332251321594218 0.0491664732917847 leukotriene–A4 hy isovaleryl–CoA dehydro intracellular cAMP–activated cation (insulin–like growth f insulin–like growth f 0.0349666652980894 0.012138258484023 J.012136256464023 0.0241297469911858 0.0359762333326238 0.0417818619656159 0.0350193293586195 0.0295908076541564 0.0241297469911859 inositol phosphate phosphatase a hydroxymethylglutaryl–CoA reductase (NADPH) a hexokinase a hydroxymethylglutaryl–CoA reductase (NADPH) a hexokinase a hydroxymethylglutarylguanylate cyclase activator a glutamate-5-semialdenyde denydrogenase a glutamate 5-kinase a 0.012138258484023 0.0241297466144361 gamma-glutamylcyclotransferase 0.0261106724809928 0.0155299883739537 0.0112363420446187 0.034527649442026 0.0111975299621082 0.0241297469911859 | glucosinolate \$-oxygenase activity | glucosinolate \$-oxygenase activity | de-dependent protein kinase binding | ha-steroid 4-dehydrogenase activity | integral component of membrane | plasma membrane | endoplasmic reticulum membrane | mitochondrial inner membrane 0.0436727641231035 0.0327134577510015 0.043185235967736 0.0413177504458941 0.041317750443 0.0196046737057152 7.74198850592343e-05 0.00129069100570861 anchored component of external side of plasma membrane anaphase—promoting complex acetylcholine—gated channel complex 0.0235719294829792 0.013888346559591 0.0159721074735391 0.0241297469911859 0.0241233277692679 0.0460312362703803 0.0416082735346487 0.0115252161709509 0.0298149899789816 0.0359762333326238 0.0121091299788679 methionine adenosyltransferase, comple medial corte insulin receptor comple HCN channel comple extrinsic component of neuronal dense core vesicle membran complement component C1 comple cellular response cell differentiation response to chemical response to abiotic stimulus inmune response small GTPase mediated signal transduction anatomical structure formation involved in morphogenesis telencephalon developmen I cell activation response to hea 0.00415559076387416 0.01354962058684 0.00443974974309006 0.0479936732462712 0.00803646683432793 0.038860439289548 0.0318678059015884 0.0318678059015884 0.000134469009868934 0.00368502619545193 0.00592653759084053 0.0322346857014407 0.00819438095543672 0.046029313137931 0.00887085752311918 0.0441701198077138 0.0125966744765192 0.0127414099770958 response to heaf positive regulation of transcription of nucleolar large rRNA by RNA polymerase I negative regulation of Whit signaling pathway negative regulation of Notch signaling bathway negative regulation of interleukin-1 beta productive 0.0125966744765192 0.0127418099770958 0.00198547727359717 0.00150278253475348 0.000644783829046549 0.00363422653401334 0.0391830446444601 0.000823093280072849 0.0007824277095869201 amyloid-beta clearand amino acid transpo zymogen activatio thyroid hormone metabolic proces synaptic transmission involved in micturitio sulfide oxidation, using sulfide:quinone oxidoreductas sexual reproductio 0.0223278026406943 0.0223278026406943 0.00984921588222467 0.0456057611380774 0.0168368512844144 0.0391901731510403 0.0212695115604595 0.00510968166510577 0.020739225857413 regulation of neurotransmitter leve 0.00194966846805742 0.024853121838675 positive regulation of protein—containing positive regulation of macrophage derived foar positive regulation of cysteine—type endopeptidase activity involved in 0.0024853121838675 0.000807616384867207 0.0209787232798976 0.00129589087904373 0.00130643438714983 0.0177959697132609 0.016571394960217 0.0236591638546465 0.0169732043267892 .0160922043267882 ontology negative regulation of synaptic assembly at neuromuscular ji negative regulation of insulin receptor signaling p multicellular organismal reproductive male r 0.0370617042714634 0.0370617042/14634 0.0071548551691393 0.0216263124070886 0.00720754891442395 0.00213067317775485 0.003691036228579 BP CC 0.0422798295127685 MF 0.00189678192624449 0.00189678192624449 0.00537869865886291 0.0204883086965827 0.0226571677281584 0.00542636565884791 0.0314464115813021 0.000129906505071814 cytolysis
cellular sulfide ion homeostasis
cellular response to cGMP
cellular detoxification of cadmium ion
aromatic amino acid family metabolic process
anaphase–promoting complex–dependent catabolic brocess
vitamin B6 metabolic process
type I pneumocyte differentiation 0.00143266431481449 0.00091051056071883 0.0046909121928866 0.0046909121928866 0.00744620813998211 0.00651051406793682 0.0348039306375569 0.0452638671180801 trehalose transport transpiration transmembrane receptor protein tyrosine phosphatase signaling pathway transformation of most cell by virus 0.0241297469911859 transformation or nost cell by virus subpallium development stem vascular tissue pattern formation spinal cord dorsal/ventral patterning specification of proximal tupule identity skin epidermis development skeletal muscle satellite cell migration rostrocaudal neural tube patterning retrograde neuronal dense core vesicle transport response to vanadate(3-) response to resveratro response to melanocyte-stimulating hormone response to cisplatin 0.017412978628415 0.0174129/8628415 0.0359738767369185 0.033805303029382 0.00642574295250061 0.0356652208769486 0.0329445153862531 0.0447763412375798 0.0241297469911859 0.0241297469911859 0.0439712493941624 response to melanocyte—stimulating hormone—response to cisplatin—regulation of the force of skeletal muscle contraction—regulation of slow—twitch skeletal muscle contraction—regulation of slow—twitch skeletal muscle fiber contraction—regulation of mejotic nuclear division—regulation of mejotic nuclear division—regulation of mejotic nuclear division—regulation of place of the metabolic process—regulation of leukocyte chemotaxis—regulation of leukocyte chemotaxis—regulation of female gonad development—regulation of place—regulation of place—regulation of place—regulation—regulation of DNA—endoreduplication—regulation of DNA—endoreduplication—regulation of adenylate cyclase—activating G protein—coupled receptor signaling pathway—regulation of acetylcholine secretion, neurotransmission—proximal/distal pattern formation involved in pronephric nephron development—protein repair—protein localization to mitotic spindle pole bady— 0.0116466054124757 0.0241297469911859 0.012138258484023 0.012138258484023 0.0455712895321962 0.012138258484023 0.0227050895240287 0.0359447257618312 0.040182875188102 0.0447972123794993 0.0121091299788679 protein transport along microtubul protein repair protein localization to mitotic spindle pole body protein adenylylation protein adenylylation protein adenylylation protein adenylylation protein adenylylation protein adenylylation protein catabolic process positive regulation of transcription from RNA polymerase II promoter in response to stress positive regulation of 1 ORC2 signaling positive regulation of 1 ORC2 signaling positive regulation of tau-protein kinase activity positive regulation of synapse maturation positive regulation of synapse maturation positive regulation of skeletal muscle tissue growth positive regulation of RNA biosynthetic process positive regulation of protein—containing complex disassembly positive regulation of protein—containing complex disassembly positive regulation of protein containing complex disassembly positive regulation of protein or protein localization to nucleolus $0.0487701861333068 \\ 0.0359744275442433$ 0.0350456453106365 0.0269197130754109 0.0359762333326238 0.0354963987523075 0.0189833918285996 0.0469700674721281 positive regulation of RNA biosynthetic process positive regulation of respiratory burst:

positive regulation of protein—containing complex disassembly positive regulation of protein—containing complex disassembly positive regulation of protein localization to nucleolus positive regulation of protein insertion into mitochondria outer membrane positive regulation of informative in the positive regulation of glycoper biosynthetic process positive regulation of glycoper biosynthetic process positive regulation of regulation of registrative process positive regulation of process pro 0.0446163739251871 0.0120354377573889 0.0276757613159293 .023200393712959 0.0329445153862531 0.0447763412375798 0.0241297469911859 0.045415061857558 0.0236440389699619 0.0359762333326238 0.01213824730515 0.0252049692623653 0.0252049692623653 0.035410618797926 0.0233890474537476 0.0205561579324701 0.012138258484023 0.0189099011284589 0.0348497591556249 0.0359762333326238 0.0120330028019449 0.0359762333326238 0.00642574295250061 0.012138258484023 0.012136256464023 0.0241273615494165 0.0461975470619448 0.0118321080685378 0.0241297469911859 0.0224243/91466000 0.00603818639889422 0.046841575966099 0.0170586610735208 0.0181318186509943 0.0243423268626165 0.0478027452162353 negative regulation of actin f muscle filament slidin?
molting cycle, collagen and cuticulin-based cuticulin-based cuticulin-based cuticulin-based cuticulin-based cuticulin-based cuticulin-based cuticulin methionine catabolic process membrane depolarization during cardiac muscle cell action potential 0.0381900266846582 0.0213449709714004 0.0476764460010193 0.0413738052707434 0.0355032216797281 0.0339391405150408 0.0241273615494165 0.012138258484023 0.0448385143624015 depolarization during cardiac muscle cell action potential membrane depolarization leukocyte migration involved in inflammatory, response leukocyte chemotaxis intercellular transport induced systemic resistance hematopoletic stem cell migration hematopoletics to recognification between loss for stellar busynthetic process. hematopoietic stem cell migration hemangioblast cell differentiation green leaf volatile piosynthetic process glucosinolate biosynthetic process glucose 6-phosphate metabolic process 0.0245985996429616 0.0121382579911195 glomus developmen GABAergic neuron differentiation in basal danglia . . forebrain neuron differentiation embryonic liver development cytokinin transport cytokinin transport cytokinin transport cytokinin transport cytogamy craniofacial suture morphogenesis converged vascular tissue pattern formation complement activation, classical pathway citruline piocsynthetic process chemotaxis to notate cerebral cortex GABAergic interneuron tate commitment cerebellar Purkinje cell layer structural organization cerebellar molecular layer formation cerebellar molecular layer formation cerebellar cortex development cellular response to sodium arsenite cellular response to gonadotropin—releasing hormone cellular response to chemical stress cardiolipin acyl—chain remodeling carbohydrate transmembrane transport blastoderm segmentation antigen transcytosis by M cells in mucosal—associated lymphoid tissue activation of transmembrane receptor protein tyrosine kinase activity activation of phospholipase D activity activation of phospholipase D activity activation of phospholipase D activity abscisic acid—activated signaling pathway abscisic acid fansport activated signaling pathway abscisic acid transport activated signaling pathway abscisic acid transport abscisic acid fansport activated signaling pathway act 0.0338788886125202 0.0359738767369185 0.00649223644728214 0.0310915459143382 0.0476771360121092 0.0356517076769704 0.0354588380983746 0.0231484707709921 0.0217677226708978 0.00603818639889422 0.0440412231221807 0.0241297469911859 0.0469833005429179 0.0353199817452191 0.012138258484023 0.012138258484023 0.01213824730515 0.030094706525895 0.0239542846012118 0.0442543106198402 0.0283048389092653 0.0256638723726583 0.0241297469911859 0.0241297469911859 0.0430988139913493 0.0241297469911859 0.0219926359148569 0.0225329658130557 0.00649223644728214 0.0181318186509943 0.0241273615494165 0.0241273615494165