0.0213961289892364 lyase activity ATPase–coupled transmembrane transporter activity serine–type endopeptidase activity nuclear estrogen receptor binding 0.043614464687815 0.0484710037177856 0.0313338706325175 0.0487975251925066 disulfide oxidoreductase activity proteoglycan binding P-type ion transporter activity oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor 0.0131999331464268 0.00831059118673907 0.00676125148555323 0.0404416383291701 ATPase-coupled monoatomic cation transmembrane transporter activity 0.0404416383291701 ATPase-coupled ion transmembrane transporter activity 0.0404416383291701 active monoatomic ion transmembrane transporter activity protein-disulfide reductase (NAD(P)) activity 0.00334868585221767 0.0239051095993992 histone threonine kinase activity 0.00621196300785242 histone H2AT120 kinase activity 0.0263879850494558 heparan sulfate proteoglycan binding 0.00511547855108191 steroid hormone binding 0.0192775326900274 sodium ion binding 0.0349639539623603 retinoid binding 0.0349639539623603 retinoic acid binding 0.0339834470388699 protein-glutamine gamma-glutamyltransferase activity 0.0146077848002757 pótassium ion binding phosphatidyl–N–methylethanolamine N–methyltransferase activity 0.010187095084592 phosphatidyl-N-dimethylethanolamine N-methyltransferase activity
P-type sodium:potassium-exchanging transporter activity involved in regulation of cardiac muscle cell membrane potential 0.010187095084592 0.00511547855108191 0.0334996214411417 P-type sodium:potassium-exchanging transporter activity 0.00512992134634551 P-type sodium transporter activity
P-type potassium transmembrane transporter activity
nucleosomal DNA binding 0.0334996214411417 0.0451579688405942 0.0349639539623603 isoprenoid binding 0.00512992134634551 canalicular bile acid transmembrane transporter activity 0.0294318142721398 bubble DNA binding arylesterase activity alkali metal ion binding 0.00521679190633421 0.0342054530160391 0.0341164616410537 ribosome 0.0474881770752229 ribosomal subunit 0.00295039550819325 cytosolic ribosome small ribosomal subunit cytosolic small ribosomal subunit 0.00536016679143596 0.00261775960689683 0.0427372980682783 tight junction
cation–transporting ATPase complex
ATPase dependent transmembrane transport complex
sodium:potassium–exchanging ATPase complex
SMAD protein complex 0.0396025124444228 0.00185141937542532 0.00794740307737601 0.0187586678220476 0.0436361615230777 0.0285989578616407 lateral part of cell intercellular canaliculus gut granule membrane gut granule dendritic spine neck 0.0316612782047095 0.0201584170748269 0.0201584170748269 0.0283834683097093 0.0149307166490357 cornified envelope cell body fiber
basolateral part of cell
cytoplasmic translation
steroid metabolic process 0.0301537139760874 0.0151187704738394 0.00649743440721415 0.01181509318998 0.0316582607326541 response to carbohydrate 0.0205949601946672 cellular response to oxygen levels cellular response to light stimulus response to monosaccharide 0.0154620388697445 0.0343593032971241 0.0117235757506834 cellular response to hypoxia 0.0225671353621078 cellular response to decreased oxygen levels response to glucose cellular response to UV sterol metabolic process 0.044614989524485 0.0374382345565196 0.0179130484236726 0.034875418310097 response to type II interferon 0.0271924509109925 iron ion homeostasis 0.0301088569244055 intracellular glucose homeostasis 0.0207932999818711 0.0424797467183851 cellular response to type II interferon modulation by host of symbiont process 0.0102088975278969 cellular response to retinoic acid 0.0445835731929671 cellular response to monosaccharide stimulus 0.0445835731929671 cellular response to hexose stimulus cellular response to glucose 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0.0287597253252263 negative regulation of blood circulation 0.0490084415012761 molting cycle, collagen and cuticulin-based cuticle 0.0206738127139464 modulation by host of viral transcription modulation by host of symbiont transcription 0.0206738127139464 0.00370111783170307 keratinization 0.0213543542184582 estrogen metabolic process deoxyribonucleoside triphosphate metabolic process 0.00462703924343249 0.00195659289670612 cornification collagen metabolic process 0.00190577686515445 cellular response to ethanol ADP metabolic process 0.00336553620402049 0.038859223057326 0.0334280781550842 acute inflammatory response V(D)J recombination UV-damage excision repair type II interferon-mediated signaling pathway 0.0498504925416026 0.029215458935528 0.014647931527368 0.00257435571293307 tetrapyrrole cătabolic process 0.0497841493919641 septate junction assembly respiratory chain complex III assembly 0.00750115893230685 relaxation of muscle 0.00412880680420328 relaxation of cardiac muscle 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hormone biosynthetic process 0.0253621885322588 negative regulation of heart contraction 0.00756740707674772 negative regulation of glucocorticoid metabolic process negative regulation of glucocorticoid biosynthetic process mRNA 3'-splice site recognition mitochondrial respiratory chain complex III assembly 0.00756740707674772 0.0443909843413803 0.0203886003384286 0.0456818052197723 hydrogen peroxide catabolic process 0.00257435571293307 heme catabolic process 0.0127896196925424 enteric nervous system development endocardial cushion morphogenesis chondrocyte development 0.0186796884547307 0.0424611305859304 0.0153750127079245 benzene-containing compound metabolic process 0.00995943724857844 AMP metabolic process 0.0400273232393604 acute–phase response xenobiotic glucuronidation wound healing involved in inflammatory response 0.0191128701589056 0.00853817457876929 0.0187586678220476 sodium ion export across plasma membrane 0.0349639539623603 retinoic acid metabolic process 0.00511547855108191 response to glycoside regulation of transforming growth factor beta2 production regulation of respiratory system process 0.032650614414536 0.0297620567571268 0.015763229574808 regulation of respiratory gaseous exchange by nervous system process 0.00511547855108191 regulation of glutamate uptake involved in transmission of nerve impulse regulation of glucuronosyltransferase activity regulation of cytokine activity regulation of cellular glucuronidation regulation of calcium:sodium antiporter activity 0.0191128701589056 0.0151389997736609 0.0340346719394298 0.0187586678220476 regulation of amino acid uptake involved in synaptic transmission purine deoxyribonucleoside triphosphate biosynthetic process potassium ion import across plasma membrane positive regulation of keratinocyte proliferation 0.00511547855108191 0.00551668070286775 0.0343999010505464 0.00522226131014057 0.0356414506874158 positive regulation of glomerulus development 0.0191128701589056 phenylpropanoid 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metabolic process 0.0217570131542441 0.0191109864387245 0.0191128701589056 coumarin metabolic process 0.0191128701589056 coumarin catabolic process 0.0345022671910838 collagen catabolic process cellular response to UV–C cellular glucuronidation 0.00627785314159582 0.0472120195658257 0.00522226131014057 cell envelope organization 0.0377952867484893 cell communication by electrical coupling involved in cardiac conduction 0.0350070850079867 biphenyl metabolic process biphenyl catabolic process bilirubin conjugation 0.0191128701589056 0.0191128701589056 0.0468931306666031 basement membrane disassembly 0.0223505693214311 'de novo' IMP biosynthetic process

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