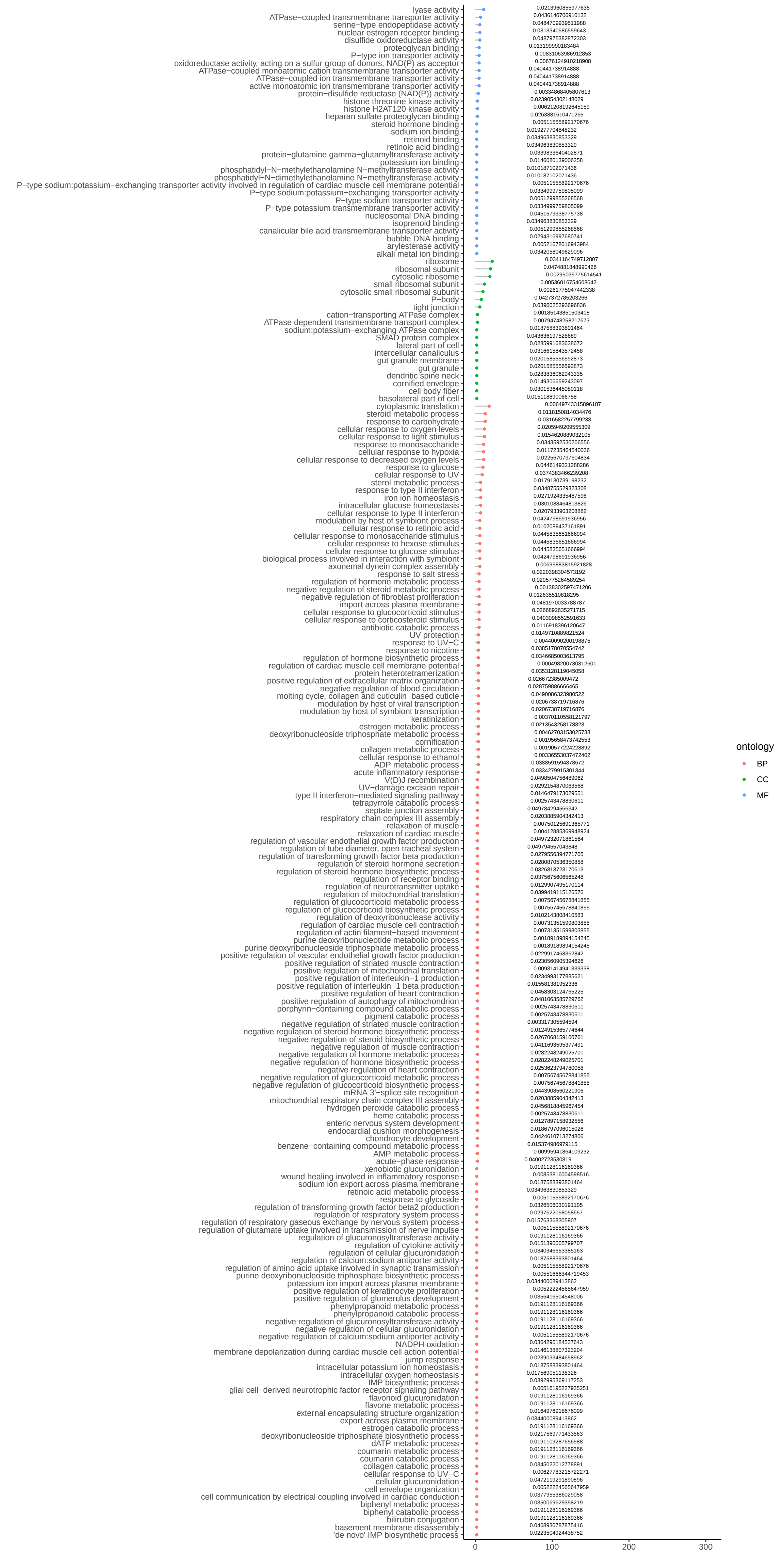
lyase activity 0.0213960855977635
ATPase−coupled transmembrane transporter activity 0.0436146706910132
serine−type endopeptidase activity 0.0484709939511988
nuclear estrogen receptor binding 0.0313340586559643
disulfide oxidoreductase activity 0.0487975382872303
proteoglycan binding 0.013199990183484
P−type ion transporter activity 0.00831063986912853
oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor 0.00676124910218908
ATPase−coupled monoatomic cation transmembrane transporter activity 0.040441738914888
ATPase−coupled ion transmembrane transporter activity 0.040441738914888
active monoatomic ion transmembrane transporter activity 0.040441738914888
protein−disulfide reductase (NAD(P)) activity 0.00334868405807613
histone threonine kinase activity 0.0239054302148029
histone H2AT120 kinase activity 0.00621208192645159
heparan sulfate proteoglycan binding 0.0263881610471265
steroid hormone binding 0.00511555892170676
sodium ion binding 0.019277704848232
retinoid binding 0.034963830853329
retinoic acid binding 0.034963830853329
protein−glutamine gamma−glutamyltransferase activity 0.0339833640402871
potassium ion binding 0.0146080139006258
phosphatidyl−N−methylethanolamine N−methyltransferase activity 0.010187102071436
phosphatidyl−N−dimethylethanolamine N−methyltransferase activity 0.010187102071436
P−type sodium:potassium−exchanging transporter activity involved in regulation of cardiac muscle cell membrane potential 0.00511555892170676
P−type sodium:potassium−exchanging transporter activity 0.0334999759805099
P−type sodium transporter activity 0.0051299855268568
P−type potassium transmembrane transporter activity 0.0334999759805099
nucleosomal DNA binding 0.0451579338775738
isoprenoid binding 0.034963830853329
canalicular bile acid transmembrane transporter activity 0.0051299855268568
bubble DNA binding 0.0294316997680741
arylesterase activity 0.00521678016943984
alkali metal ion binding 0.0342058049629096
ribosome 0.0341164749712807
ribosomal subunit 0.0474881848990426
cytosolic ribosome 0.00295039775614541
small ribosomal subunit 0.00536016754608642
cytosolic small ribosomal subunit 0.00261775947442338
P−body 0.0427372785203266
tight junction 0.0396025293696836
cation−transporting ATPase complex 0.00185143851503418
ATPase dependent transmembrane transport complex 0.00794748258217673
sodium:potassium−exchanging ATPase complex 0.0187588393801464
SMAD protein complex 0.043636197528689
lateral part of cell 0.0285991683638672
intercellular canaliculus 0.0316615843572458
gut granule membrane 0.0201585556592873
gut granule 0.0201585556592873
dendritic spine neck 0.0283836062043335
cornified envelope 0.0149306659243097
cell body fiber 0.0301536445080118
basolateral part of cell 0.015118890066758
cytoplasmic translation 0.00649743315896187
steroid metabolic process 0.0118150814034476
response to carbohydrate 0.0316582257799238
cellular response to oxygen levels 0.0205949209555309
cellular response to light stimulus 0.0154620889032105
response to monosaccharide 0.0343592530206556
cellular response to hypoxia 0.0117235464540036
cellular response to decreased oxygen levels 0.0225670797604834
response to glucose 0.0446149321288286
cellular response to UV 0.0374383466239208
sterol metabolic process 0.0179130739198232
response to type II interferon 0.0348755529323308
iron ion homeostasis 0.0271924335487596
intracellular glucose homeostasis 0.0301088464813826
cellular response to type II interferon 0.0207933903208882
modulation by host of symbiont process 0.0424798691936956
cellular response to retinoic acid 0.0102089437161891
cellular response to monosaccharide stimulus 0.0445835651666994
cellular response to hexose stimulus 0.0445835651666994
cellular response to glucose stimulus 0.0445835651666994
biological process involved in interaction with symbiont 0.0424798691936956
axonemal dynein complex assembly 0.00699883815921828
response to salt stress 0.0220398304573192
regulation of hormone metabolic process 0.0205775264589254
negative regulation of steroid metabolic process 0.00138302597471206
negative regulation of fibroblast proliferation 0.012635510818295
import across plasma membrane 0.0481970033788787
cellular response to glucocorticoid stimulus 0.0266892635271715
cellular response to corticosteroid stimulus 0.0403098552591633
antibiotic catabolic process 0.0116918396120647
UV protection 0.0149710889821524
response to UV−C 0.00440090200198875
response to nicotine 0.0385178070554742
regulation of hormone biosynthetic process 0.0346685003613795
regulation of cardiac muscle cell membrane potential 0.000498200730312601
protein heterotetramerization 0.0353128119045058
positive regulation of extracellular matrix organization 0.026672385009472
negative regulation of blood circulation 0.028759886666465
molting cycle, collagen and cuticulin−based cuticle 0.0490086323980522
modulation by host of viral transcription 0.0206738719716876
modulation by host of symbiont transcription 0.0206738719716876
keratinization 0.00370110558121797
estrogen metabolic process 0.0213543258178823
deoxyribonucleoside triphosphate metabolic process 0.00462703153025733
cornification 0.00195658473742553
collagen metabolic process 0.00190577224228892
cellular response to ethanol 0.00336553037472402
ADP metabolic process 0.0388591594878672
acute inflammatory response 0.0334279915301344
V(D)J recombination 0.0498504756489062
UV−damage excision repair 0.0292154870063568
type II interferon−mediated signaling pathway 0.0146479173029551
tetrapyrrole catabolic process 0.0025743478830611
septate junction assembly 0.049784294566342
respiratory chain complex III assembly 0.0203885904342413
relaxation of muscle 0.00750125691365771
relaxation of cardiac muscle 0.00412885369948924
regulation of vascular endothelial growth factor production 0.0497232071861564
regulation of tube diameter, open tracheal system 0.049794557043848
regulation of transforming growth factor beta production 0.0279556394771705
regulation of steroid hormone secretion 0.0280870536350858
regulation of steroid hormone biosynthetic process 0.0326813723170613
regulation of receptor binding 0.0375675606565248
regulation of neurotransmitter uptake 0.0129907495170114
regulation of mitochondrial translation 0.0399419115126576
regulation of glucocorticoid metabolic process 0.00756745678841855
regulation of glucocorticoid biosynthetic process 0.00756745678841855
regulation of deoxyribonuclease activity 0.0102143808410583
regulation of cardiac muscle cell contraction 0.00731351599803855
regulation of actin filament−based movement 0.00731351599803855
purine deoxyribonucleotide metabolic process 0.00189189894154245
purine deoxyribonucleoside triphosphate metabolic process 0.00189189894154245
positive regulation of vascular endothelial growth factor production 0.0229917468362842
positive regulation of striated muscle contraction 0.0230560905394626
positive regulation of mitochondrial translation 0.00931414941339338
positive regulation of interleukin−1 production 0.0234993177885621
positive regulation of interleukin−1 beta production 0.015581381952336
positive regulation of heart contraction 0.0458303124765225
positive regulation of autophagy of mitochondrion 0.0481063585729762
porphyrin−containing compound catabolic process 0.0025743478830611
pigment catabolic process 0.0025743478830611
negative regulation of striated muscle contraction 0.003317305594594
negative regulation of steroid hormone biosynthetic process 0.0124915365774644
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negative regulation of hormone biosynthetic process 0.0282248249025701
negative regulation of heart contraction 0.0253623794780058
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negative regulation of glucocorticoid biosynthetic process 0.00756745678841855
mRNA 3'−splice site recognition 0.0443908560221906
mitochondrial respiratory chain complex III assembly 0.0203885904342413
hydrogen peroxide catabolic process 0.0456818845967454
heme catabolic process 0.0025743478830611
enteric nervous system development 0.0127897158932556
endocardial cushion morphogenesis 0.0186797096015026
chondrocyte development 0.0424610713274806
benzene−containing compound metabolic process 0.015374986979115
AMP metabolic process 0.00995941864109232
acute−phase response 0.04002723530819
xenobiotic glucuronidation 0.0191128116169366
wound healing involved in inflammatory response 0.00853816004598516
sodium ion export across plasma membrane 0.0187588393801464
retinoic acid metabolic process 0.034963830853329
response to glycoside 0.00511555892170676
regulation of transforming growth factor beta2 production 0.0326506030191105
regulation of respiratory system process 0.0297622058058657
regulation of respiratory gaseous exchange by nervous system process 0.015763368305907
regulation of glutamate uptake involved in transmission of nerve impulse 0.00511555892170676
regulation of glucuronosyltransferase activity 0.0191128116169366
regulation of cytokine activity 0.0151390005799707
regulation of cellular glucuronidation 0.0340346653385163
regulation of calcium:sodium antiporter activity 0.0187588393801464
regulation of amino acid uptake involved in synaptic transmission 0.00511555892170676
purine deoxyribonucleoside triphosphate biosynthetic process 0.00551666344719453
potassium ion import across plasma membrane 0.034400089413862
positive regulation of keratinocyte proliferation 0.00522224565647959
positive regulation of glomerulus development 0.0356416504548006
phenylpropanoid metabolic process 0.0191128116169366
phenylpropanoid catabolic process 0.0191128116169366
negative regulation of glucuronosyltransferase activity 0.0191128116169366
negative regulation of cellular glucuronidation 0.0191128116169366
negative regulation of calcium:sodium antiporter activity 0.00511555892170676
NADPH oxidation 0.0364296184537643
membrane depolarization during cardiac muscle cell action potential 0.0146138807323204
jump response 0.0239033484658962
intracellular potassium ion homeostasis 0.0187588393801464
intracellular oxygen homeostasis 0.017569051138326
IMP biosynthetic process 0.0392995369117253
glial cell−derived neurotrophic factor receptor signaling pathway 0.00516195227935251
flavonoid glucuronidation 0.0191128116169366
flavone metabolic process 0.0191128116169366
external encapsulating structure organization 0.0164976918676099
export across plasma membrane 0.034400089413862
estrogen catabolic process 0.0191128116169366
deoxyribonucleoside triphosphate biosynthetic process 0.0217569771433563
dATP metabolic process 0.0191109287656588
coumarin metabolic process 0.0191128116169366
coumarin catabolic process 0.0191128116169366
collagen catabolic process 0.0345022012778891
cellular response to UV−C 0.00627783215722271
cellular glucuronidation 0.0472119291890896
cell envelope organization 0.00522224565647959
cell communication by electrical coupling involved in cardiac conduction 0.0377955386029058
biphenyl metabolic process 0.0350069629358219
biphenyl catabolic process 0.0191128116169366
bilirubin conjugation 0.0191128116169366
basement membrane disassembly 0.0468930787875416
'de novo' IMP biosynthetic process 0.0223504924438752
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ontology
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MF