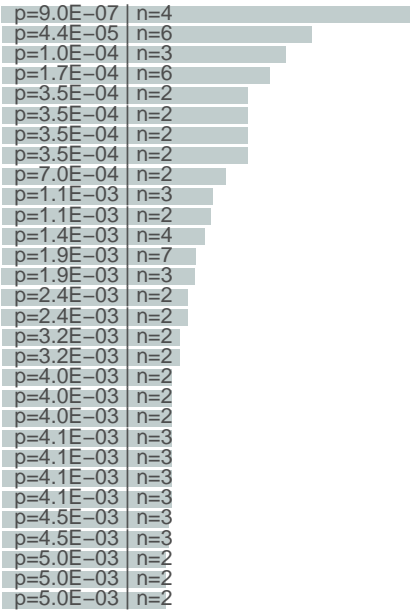


GO:BP
gc001a

fraction genes in fg and expected value

serotonin uptake	GO:0051610
ubiquitin-dependent ERAD pathway	GO:0030433
adenohypophysis development	GO:0021984
sodium ion transmembrane transport	GO:0035725
negative regulation of cerebellar granul...	GO:0021941
positive regulation of serotonin secreti...	GO:0014064
regulation of thalamus size	GO:0090067
cellular response to cGMP	GO:0071321
negative regulation of synaptic transmis...	GO:0032227
negative regulation of fat cell differen...	GO:0045599
negative chemotaxis	GO:0050919
negative regulation of small molecule me...	GO:0062014
negative regulation of response to exter...	GO:0032102
brain morphogenesis	GO:0048854
sperm ejaculation	GO:0042713
quaternary ammonium group transport	GO:0015697
cardiac atrium morphogenesis	GO:0003209
choline transport	GO:0015871
dopamine biosynthetic process	GO:0042416
dopamine uptake involved in synaptic tra...	GO:0051583
positive regulation of mitochondrial dep...	GO:0051901
cellular biogenic amine catabolic proces...	GO:0042402
positive regulation of acetylcholine sec...	GO:0014057
response to cocaine	GO:0042220
negative regulation of luteinizing hormo...	GO:0033685
regulation of cellular amine metabolic p...	GO:0033238
prolactin secretion	GO:0070459
atrioventricular valve morphogenesis	GO:0003181
aortic valve development	GO:0003176
cell surface receptor signaling pathway ...	GO:0061311



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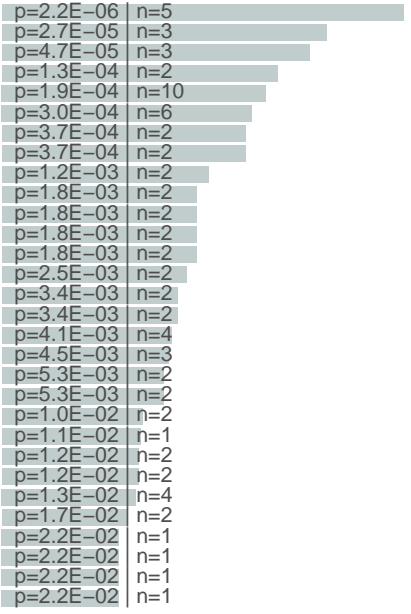
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-log(p)
n=83/230 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
gc001a

fraction genes in fg and expected value

neurotransmitter transmembrane transport...	GO:0005326
serotonin:sodium symporter activity	GO:0005335
mechanosensitive ion channel activity	GO:0008381
choline transmembrane transporter activi...	GO:0015220
calcium ion binding	GO:0005509
flavin adenine dinucleotide binding	GO:0050660
serotonin binding	GO:0051378
cocaine binding	GO:0019811
BMP receptor binding	GO:0070700
mercury ion binding	GO:0045340
lead ion binding	GO:0032791
quaternary ammonium group transmembrane ...	GO:0015651
hormone activity	GO:0005179
nitric-oxide synthase binding	GO:0050998
dopamine:sodium symporter activity	GO:0005330
norepinephrine:sodium symporter activity	GO:0005334
amine binding	GO:0043176
substance K receptor activity	GO:0016497
ligand-gated sodium channel activity	GO:0015280
WW domain binding	GO:0050699
phospholipid scramblase activity	GO:0017128
S-methyl-5-thioribose-1-phosphate isomer...	GO:0046523
catecholamine binding	GO:1901338
dopamine binding	GO:0035240
protein N-terminus binding	GO:0047485
dynein light intermediate chain binding	GO:0051959
thiamine pyrophosphate transmembrane tra...	GO:0090422
glucagon receptor activity	GO:0004967
toxin transmembrane transporter activity	GO:0019534
co-receptor binding	GO:0039706



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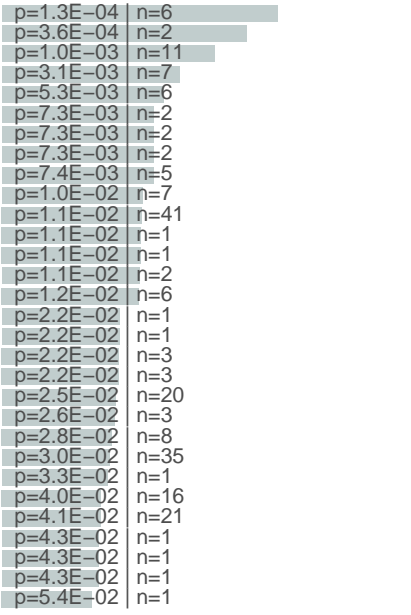
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-log(p)
n=85/230 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
gc001a

fraction genes in fg and expected value

endoplasmic reticulum lumen	GO:0005788
serotonergic synapse	GO:0099154
extracellular space	GO:0005615
presynaptic membrane	GO:0042734
apical plasma membrane	GO:0016324
dopaminergic synapse	GO:0098691
neuronal cell body membrane	GO:0032809
flotillin complex	GO:0016600
collagen-containing extracellular matrix	GO:0062023
external encapsulating structure	GO:0030312
cell periphery	GO:0071944
stereocilium coat	GO:0120234
glycocalyx	GO:0030112
pericentriolar material	GO:0000242
postsynaptic membrane	GO:0045211
BMP receptor complex	GO:0070724
ciliary inversin compartment	GO:0097543
basement membrane	GO:0005604
sperm midpiece	GO:0097225
plasma membrane bounded cell projection	GO:0120025
sperm head	GO:0061827
cell surface	GO:0009986
plasma membrane	GO:0005886
cholinergic synapse	GO:0098981
extracellular region	GO:0005576
cell projection	GO:0042995
apical plasma membrane urothelial plaque	GO:0120001
stereocilium tip	GO:0032426
CRD-mediated mRNA stability complex	GO:0070937
cytoplasmic side of late endosome membra...	GO:0098560



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0 1 2 3 4 5
-log(p)
n=84/230 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction