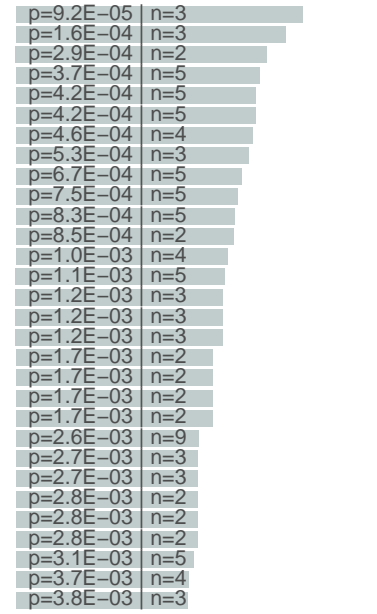


GO:BP
gc001a

fraction genes in fg and expected value

negative regulation of regulatory T cell...	GO:0045590
plasmacytoid dendritic cell activation	GO:0002270
chemorepulsion of axon	GO:0061643
positive regulation of acetylcholine sec...	GO:0014057
negative regulation of luteinizing hormo...	GO:0033685
prolactin secretion	GO:0070459
positive regulation of glucose import	GO:0046326
positive regulation of insulin receptor ...	GO:0046628
positive regulation of flagellated sperm...	GO:1902093
positive regulation of uterine smooth mu...	GO:0070474
positive regulation of vascular permeabi...	GO:0043117
positive regulation of estradiol secreti...	GO:2000866
negative regulation of Notch signaling p...	GO:0045746
operant conditioning	GO:0035106
negative regulation of interleukin-2 pro...	GO:0032703
negative regulation of cardiac muscle ce...	GO:0010667
positive regulation of natural killer ce...	GO:0045954
negative regulation of sarcomere organiz...	GO:0060299
positive regulation of hydrogen peroxide...	GO:0010729
positive regulation of progesterone secr...	GO:2000872
positive regulation of thyroid hormone g...	GO:2000611
epithelial tube morphogenesis	GO:0060562
regulation of glial cell proliferation	GO:0060251
cell-cell adhesion mediated by cadherin	GO:0044331
negative regulation of axon extension in...	GO:0048843
parkin-mediated stimulation of mitophagy...	GO:0061734
positive regulation of ovarian follicle ...	GO:2000386
intestine smooth muscle contraction	GO:0014827
regulation of cellular respiration	GO:0043457
negative regulation of gliogenesis	GO:0014014



0 1 2 3 4 5
-log(p)
n=130/342 input genes with annotations

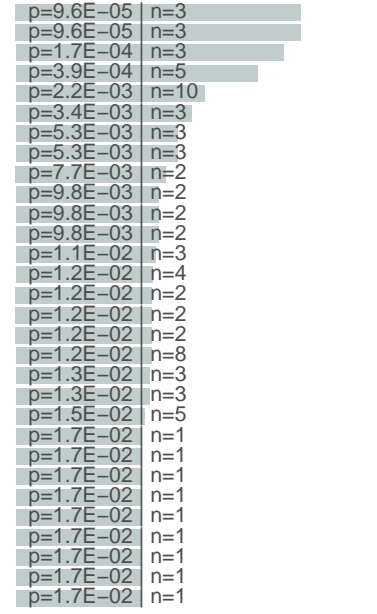
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0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
gc001a

fraction genes in fg and expected value

proteoglycan binding	GO:0043394
MHC class II protein binding	GO:0042289
mechanosensitive ion channel activity	GO:0008381
substance K receptor activity	GO:0016497
calcium ion binding	GO:0005509
thyroid hormone transmembrane transporte...	GO:0015349
NAD+ ADP-ribosyltransferase activity	GO:0003950
protein ADP-ribosylase activity	GO:1990404
ADP-D-ribose binding	GO:0072570
GDP-dissociation inhibitor activity	GO:0005092
dopamine beta-monooxygenase activity	GO:0004500
double-stranded methylated DNA binding	GO:0010385
laminin binding	GO:0043236
cytoskeletal motor activity	GO:0003774
ADP-D-ribose modification-dependent prot...	GO:0160002
ligand-gated sodium channel activity	GO:0015280
serine-type carboxypeptidase activity	GO:0004185
monooxygenase activity	GO:0004497
sodium-independent organic anion transme...	GO:0015347
extracellular matrix binding	GO:0050840
flavin adenine dinucleotide binding	GO:0050660
oxysterol 7-alpha-hydroxylase activity	GO:0008396
insulin-like growth factor I binding	GO:0031994
steroid 7-alpha-hydroxylase activity	GO:0008387
calcium-dependent phospholipase A2 activ...	GO:0047498
glucagon receptor activity	GO:0004967
24-hydroxycholesterol 7alpha-hydroxylase...	GO:0033782
hedgehog family protein binding	GO:0097108
L-threonine 3-dehydrogenase activity	GO:0008743
delta-catenin binding	GO:0070097



0 1 2 3 4 5
-log(p)
n=131/342 input genes with annotations

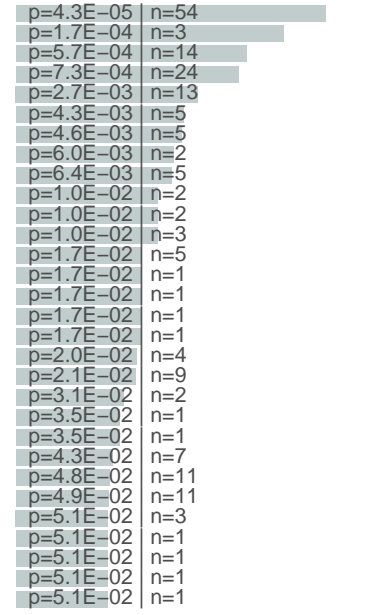
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fg=0.01	bg=0.00

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
gc001a

fraction genes in fg and expected value

plasma membrane	GO:0005886
stereocilium tip	GO:0032426
extracellular space	GO:0005615
extracellular region	GO:0005576
cell surface	GO:0009986
sperm midpiece	GO:0097225
sperm head	GO:0061827
cuticular plate	GO:0032437
endoplasmic reticulum lumen	GO:0005788
Barr body	GO:0001740
kinocilium	GO:0060091
apoptosome	GO:0043293
external side of plasma membrane	GO:0009897
type III intermediate filament	GO:0045098
glycocalyx	GO:0030112
subapical part of cell	GO:0120219
stereocilium coat	GO:0120234
sarcolemma	GO:0042383
actin cytoskeleton	GO:0015629
photoreceptor inner segment	GO:0001917
muscle tendon junction	GO:0005927
BRCA1-BARD1 complex	GO:0031436
side of membrane	GO:0098552
supramolecular fiber	GO:0099512
supramolecular polymer	GO:0099081
basement membrane	GO:0005604
cone photoreceptor outer segment	GO:0120199
protein complex involved in cell-matrix ...	GO:0098637
kinociliary basal body	GO:1902636
varicosity	GO:0043196



0 1 2 3 4 5
-log(p)
n=134/342 input genes with annotations

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0.0 0.2 0.4 0.6 0.8 1.0
fraction