

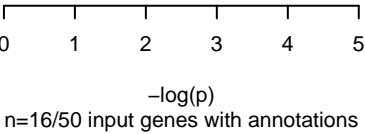
GO:BP
gc010

fraction genes in fg and expected value

G protein-coupled receptor signaling pat...	GO:0007186
regulation of multicellular organismal p...	GO:0051239
peptidyl-glutamic acid carboxylation	GO:0017187
modulation of chemical synaptic transmis...	GO:0050804
vitamin K biosynthetic process	GO:0042371
retinal bipolar neuron differentiation	GO:0060040
antifungal innate immune response	GO:0061760
negative regulation of IRE1-mediated unf...	GO:1903895
behavior	GO:0007610
system process	GO:0003008
Fc-gamma receptor signaling pathway	GO:0038094
visual perception	GO:0007601
cell surface receptor signaling pathway	GO:0007166
peptidyl-proline hydroxylation to 4-hydr...	GO:0018401
negative regulation of telomeric DNA bin...	GO:1904743
peptidyl-proline hydroxylation	GO:0019511
inner ear morphogenesis	GO:0042472
ear morphogenesis	GO:0042471
regulation of smooth muscle contraction	GO:0006940
positive regulation of amine transport	GO:0051954
negative regulation of maintenance of mi...	GO:0034183
positive regulation of protein localizat...	GO:2000010
regulation of maintenance of mitotic sis...	GO:1904907
negative regulation of maintenance of mi...	GO:1904908
negative regulation of maintenance of si...	GO:0034092
regulation of telomeric DNA binding	GO:1904742
maintenance of mitotic sister chromatid ...	GO:0099403
mitotic sister chromatid cohesion, telom...	GO:0099404
animal organ development	GO:0048513
positive regulation of multicellular org...	GO:0051240

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p=1.2E-03	n=8
p=2.1E-03	n=1
p=3.6E-03	n=4
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p=4.2E-03	n=1
p=6.3E-03	n=1
p=6.3E-03	n=1
p=7.9E-03	n=4
p=8.3E-03	n=7
p=8.4E-03	n=1
p=9.5E-03	n=2
p=1.0E-02	n=7
p=1.1E-02	n=1
p=1.1E-02	n=1
p=1.1E-02	n=1
p=1.1E-02	n=2
p=1.2E-02	n=2
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.3E-02	n=1
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p=1.3E-02	n=8
p=1.3E-02	n=5

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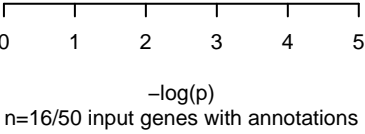
GO:MF
gc010

fraction genes in fg and expected value

G protein-coupled receptor activity	GO:0004930
vitamin-K-epoxide reductase (warfarin-se...	GO:0047057
vitamin-K-epoxide reductase (warfarin-in...	GO:0047058
procollagen-proline 4-dioxygenase activi...	GO:0004656
thioredoxin-disulfide reductase activity	GO:0004791
acetylcholine receptor regulator activit...	GO:0030548
pattern recognition receptor activity	GO:0038187
L-ascorbic acid binding	GO:0031418
calcium ion binding	GO:0005509
protein disulfide isomerase activity	GO:0003756
quinone binding	GO:0048038
intramolecular oxidoreductase activity, ...	GO:0016864
glycolipid binding	GO:0051861
group II metabotropic glutamate receptor...	GO:0001641
protein-disulfide reductase activity	GO:0015035
G protein-coupled peptide receptor activ...	GO:0008528
peptide receptor activity	GO:0001653
NAD+ ADP-ribosyltransferase activity	GO:0003950
protein ADP-ribosylase activity	GO:1990404
adenylate cyclase inhibiting G protein-c...	GO:0001640
G protein-coupled glutamate receptor act...	GO:0098988
11-cis retinal binding	GO:0005502
glutamate receptor activity	GO:0008066
disulfide oxidoreductase activity	GO:0015036
thyroid-stimulating hormone receptor act...	GO:0004996
metalloaminopeptidase activity	GO:0070006
substance K receptor activity	GO:0016497
G protein-coupled photoreceptor activity	GO:0008020
G protein-coupled adenosine receptor act...	GO:0001609
retinal binding	GO:0016918

p=2.7E-04	n=6
p=2.1E-03	n=1
p=2.1E-03	n=1
p=4.2E-03	n=1
p=6.3E-03	n=1
p=6.3E-03	n=1
p=8.5E-03	n=1
p=8.5E-03	n=1
p=1.1E-02	n=3
p=1.7E-02	n=1
p=1.7E-02	n=1
p=1.7E-02	n=1
p=2.3E-02	n=1
p=2.7E-02	n=1
p=3.7E-02	n=2
p=4.2E-02	n=2
p=4.7E-02	n=2
p=4.8E-02	n=1
p=4.8E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.6E-02	n=1
p=5.6E-02	n=2
p=5.8E-02	n=1
p=6.0E-02	n=1
p=6.2E-02	n=1
p=6.2E-02	n=1
p=6.4E-02	n=1
p=6.6E-02	n=1

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fg=0.06	bg=0.00



GO:CC
gc010

fraction genes in fg and expected value

membrane	GO:0016020
sperm head	GO:0061827
plasma membrane	GO:0005886
phagocytic vesicle membrane	GO:0030670
insulin-responsive compartment	GO:0032593
endoplasmic reticulum chaperone complex	GO:0034663
cell surface	GO:0009986
endocytic vesicle membrane	GO:0030666
astrocyte projection	GO:0097449
smooth endoplasmic reticulum	GO:0005790
sperm head plasma membrane	GO:1990913
glial cell projection	GO:0097386
mitotic spindle pole	GO:0097431
endoplasmic reticulum	GO:0005783
sperm plasma membrane	GO:0097524
endoplasmic reticulum-Golgi intermediate...	GO:0005793
phagocytic vesicle	GO:0045335
nuclear pore	GO:0005643
sperm midpiece	GO:0097225
endomembrane system	GO:0012505
plasma membrane region	GO:0098590
endoplasmic reticulum lumen	GO:0005788
presynaptic active zone	GO:0048786
glutamatergic synapse	GO:0098978
cytoplasmic vesicle membrane	GO:0030659
spindle pole	GO:0000922
endoplasmic reticulum protein-containing...	GO:0140534
vesicle membrane	GO:0012506
chromosome, telomeric region	GO:0000781
endocytic vesicle	GO:0030139

p=4.4E-03	n=15
p=6.4E-03	n=2
p=7.7E-03	n=9
p=1.9E-02	n=1
p=1.9E-02	n=1
p=2.1E-02	n=1
p=2.9E-02	n=3
p=3.3E-02	n=1
p=3.5E-02	n=1
p=4.1E-02	n=1
p=4.3E-02	n=1
p=4.9E-02	n=1
p=4.9E-02	n=1
p=5.3E-02	n=5
p=5.3E-02	n=1
p=8.3E-02	n=1
p=8.6E-02	n=1
p=1.1E-01	n=1
p=1.1E-01	n=1
p=1.3E-01	n=7
p=1.4E-01	n=3
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p=1.4E-01	n=1
p=1.4E-01	n=1
p=1.4E-01	n=2
p=1.6E-01	n=2
p=1.6E-01	n=1
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p=1.7E-01	n=2
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p=1.8E-01	n=1

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