

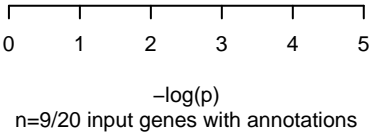
GO:BP
gc003a

fraction genes in fg and expected value

positive regulation of DNA helicase acti...	GO:1905776
intestine smooth muscle contraction	GO:0014827
positive regulation of mitochondrial DNA...	GO:0090297
positive regulation of smooth muscle con...	GO:0045987
regulation of systemic arterial blood pr...	GO:0003050
regulation of stem cell division	GO:2000035
negative regulation of hormone secretion	GO:0046888
intestinal epithelial cell differentiati...	GO:0060575
positive regulation of cell communicatio...	GO:0010647
positive regulation of signaling	GO:0023056
regulation of peptide hormone secretion	GO:0090276
regulation of amine transport	GO:0051952
amine transport	GO:0015837
learning or memory	GO:0007611
cognition	GO:0050890
signal transduction	GO:0007165
G protein-coupled receptor signaling pat...	GO:0007186
DNA unwinding involved in DNA replicatio...	GO:0006268
negative regulation of macrophage apopto...	GO:2000110
hindgut contraction	GO:0043133
regulation of hindgut contraction	GO:0043134
ghrelin secretion	GO:0036321
intestinal motility	GO:0120054
small intestinal transit	GO:0120055
regulation of small intestinal transit	GO:0120057
positive regulation of small intestinal ...	GO:0120058
regulation of small intestine smooth mus...	GO:1904347
positive regulation of small intestine s...	GO:1904349
regulation of gastro-intestinal system s...	GO:1904304
positive regulation of gastro-intestinal...	GO:1904306

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p=2.0E-03	n=2
p=2.3E-03	n=1
p=3.0E-03	n=2
p=3.5E-03	n=1
p=4.7E-03	n=1
p=5.2E-03	n=2
p=5.9E-03	n=1
p=8.5E-03	n=4
p=8.6E-03	n=4
p=9.7E-03	n=2
p=1.2E-02	n=2
p=1.3E-02	n=2
p=1.4E-02	n=2
p=1.7E-02	n=2
p=1.8E-02	n=6
p=2.3E-02	n=3
p=2.4E-02	n=1
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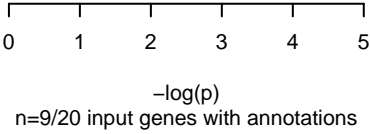
GO:MF
gc003a

fraction genes in fg and expected value

G protein activity	GO:0003925
G protein-coupled receptor activity	GO:0004930
GTP-dependent protein binding	GO:0030742
transmembrane signaling receptor activit...	GO:0004888
GTP binding	GO:0005525
peptide binding	GO:0042277
growth hormone-releasing hormone recepto...	GO:0016520
growth hormone secretagogue receptor act...	GO:0001616
guanyl nucleotide binding	GO:0019001
guanyl ribonucleotide binding	GO:0032561
molecular transducer activity	GO:0060089
signaling receptor activity	GO:0038023
amide binding	GO:0033218
chromatin binding	GO:0003682
GDP binding	GO:0019003
substance K receptor activity	GO:0016497
tachykinin receptor activity	GO:0004995
promoter-specific chromatin binding	GO:1990841
peptide hormone binding	GO:0017046
transcription corepressor activity	GO:0003714
hormone binding	GO:0042562
neuropeptide receptor activity	GO:0008188
single-stranded DNA binding	GO:0003697
methyltransferase activity	GO:0008168
transferase activity, transferring one-c...	GO:0016741
G protein-coupled peptide receptor activ...	GO:0008528
peptide receptor activity	GO:0001653
RNA polymerase II cis-regulatory region ...	GO:0000978
DNA binding	GO:0003677
cis-regulatory region sequence-specific ...	GO:0000987

p=2.6E-04	n=2
p=1.4E-02	n=3
p=1.4E-02	n=1
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p=2.5E-02	n=1
p=2.5E-02	n=2
p=2.7E-02	n=3
p=2.7E-02	n=3
p=3.7E-02	n=2
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p=4.3E-02	n=1
p=4.7E-02	n=1
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p=7.3E-02	n=1
p=8.0E-02	n=1
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p=8.5E-02	n=1
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p=2.2E-01	n=1

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GO:CC
gc003a

fraction genes in fg and expected value

plasma membrane	GO:0005886
cell periphery	GO:0071944
nucleoid	GO:0009295
mitochondrial nucleoid	GO:0042645
sperm midpiece	GO:0097225
sperm head	GO:0061827
cilium	GO:0005929
plasma membrane bounded cell projection	GO:0120025
Schaffer collateral - CA1 synapse	GO:0098685
sperm flagellum	GO:0036126
9+2 motile cilium	GO:0097729
cell projection	GO:0042995
motile cilium	GO:0031514
membrane microdomain	GO:0098857
membrane raft	GO:0045121
mitochondrial matrix	GO:0005759
synaptic membrane	GO:0097060
glutamatergic synapse	GO:0098978
cell surface	GO:0009986
membrane	GO:0016020
nuclear body	GO:0016604
plasma membrane region	GO:0098590
neuron projection	GO:0043005
synapse	GO:0045202
cell junction	GO:0030054
cellular anatomical entity	GO:0110165
mitochondrion	GO:0005739
intracellular organelle lumen	GO:0070013
organelle lumen	GO:0043233
membrane-enclosed lumen	GO:0031974

p=2.6E-02	n=5
p=3.3E-02	n=5
p=4.1E-02	n=1
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p=6.3E-02	n=1
p=6.4E-02	n=1
p=8.6E-02	n=2
p=1.1E-01	n=3
p=1.1E-01	n=1
p=1.2E-01	n=1
p=1.3E-01	n=1
p=1.4E-01	n=3
p=1.7E-01	n=1
p=2.2E-01	n=1
p=2.2E-01	n=1
p=2.3E-01	n=1
p=2.4E-01	n=1
p=2.8E-01	n=1
p=2.8E-01	n=1
p=3.1E-01	n=5
p=3.4E-01	n=1
p=4.8E-01	n=1
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p=6.6E-01	n=1
p=7.0E-01	n=8
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