

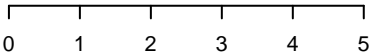
GO:BP
gc028

fraction genes in fg and expected value

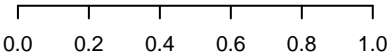
positive regulation of transcription fro...	GO:0061400
positive regulation of arachidonic acid ...	GO:0090238
GDP catabolic process	GO:0046712
UDP catabolic process	GO:0006256
positive regulation of phospholipase A2 ...	GO:0032430
regulation of systemic arterial blood pr...	GO:0001992
negative regulation of regulatory T cell...	GO:0045590
plasmacytoid dendritic cell activation	GO:0002270
positive regulation of viral entry into ...	GO:0046598
CTP metabolic process	GO:0046036
positive regulation of natural killer ce...	GO:0045954
regulation of Golgi organization	GO:1903358
regulation of DNA-binding transcription ...	GO:0051090
negative regulation of interleukin-2 pro...	GO:0032703
regulation of natural killer cell mediat...	GO:0042269
positive regulation of natural killer ce...	GO:0002717
protein autoprocessing	GO:0016540
viral entry into host cell	GO:0046718
regulation of natural killer cell mediat...	GO:0002715
nucleobase-containing small molecule cat...	GO:0034656
activation of phospholipase C activity	GO:0007202
entry into host	GO:0044409
positive regulation of inositol phosphat...	GO:0060732
regulation of inositol phosphate biosynt...	GO:0010919
positive regulation of phospholipase C a...	GO:0010863
natural killer cell mediated cytotoxicit...	GO:0042267
positive regulation of leukocyte mediate...	GO:0001912
regulation of phospholipase C activity	GO:1900274
regulation of interleukin-2 production	GO:0032663
interleukin-2 production	GO:0032623

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p=1.6E-03	n=1
p=1.8E-03	n=1
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p=4.8E-03	n=1
p=5.2E-03	n=1
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p=1.0E-02	n=1
p=1.1E-02	n=1
p=1.1E-02	n=2
p=1.1E-02	n=1
p=1.3E-02	n=1
p=1.4E-02	n=1
p=1.4E-02	n=1
p=1.6E-02	n=2
p=1.7E-02	n=1
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-log(p)
n=7/33 input genes with annotations



fraction

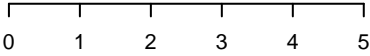
GO:MF
gc028

fraction genes in fg and expected value

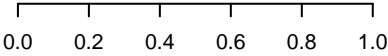
CTPase activity	GO:0043273
cytidine-diphosphatase activity	GO:0036384
DNA-binding transcription activator acti...	GO:0001228
vasopressin receptor activity	GO:0005000
uridine-diphosphatase activity	GO:0045134
guanosine-diphosphatase activity	GO:0004382
MHC class II protein binding	GO:0042289
scavenger receptor activity	GO:0005044
RNA polymerase II cis-regulatory region ...	GO:0000978
cis-regulatory region sequence-specific ...	GO:0000987
RNA polymerase II transcription regulato...	GO:0000977
transcription cis-regulatory region bind...	GO:0000976
transcription regulatory region nucleic ...	GO:0001067
sequence-specific double-stranded DNA bi...	GO:1990837
double-stranded DNA binding	GO:0003690
sequence-specific DNA binding	GO:0043565
serine-type endopeptidase activity	GO:0004252
serine-type peptidase activity	GO:0008236
serine hydrolase activity	GO:0017171
endopeptidase activity	GO:0004175
DNA binding	GO:0003677
peptide binding	GO:0042277
amide binding	GO:0033218
peptidase activity	GO:0008233
nucleic acid binding	GO:0003676
transmembrane signaling receptor activit...	GO:0004888
signaling receptor activity	GO:0038023
molecular transducer activity	GO:0060089
hydrolase activity	GO:0016787
catalytic activity, acting on a protein	GO:0140096

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p=3.0E-03	n=2
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p=3.7E-03	n=1
p=4.8E-03	n=1
p=9.3E-03	n=1
p=1.2E-02	n=2
p=1.3E-02	n=2
p=1.7E-02	n=2
p=2.5E-02	n=2
p=2.5E-02	n=2
p=2.9E-02	n=2
p=3.7E-02	n=2
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-log(p)
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fraction

GO:CC
gc028

fraction genes in fg and expected value

granular component	GO:0001652
Golgi membrane	GO:0000139
autophagosome membrane	GO:0000421
autophagosome	GO:0005776
extracellular region	GO:0005576
external side of plasma membrane	GO:0009897
vacuolar membrane	GO:0005774
side of membrane	GO:0098552
plasma membrane	GO:0005886
cell surface	GO:0009986
vacuole	GO:0005773
cell periphery	GO:0071944
Golgi apparatus	GO:0005794
membrane	GO:0016020
endomembrane system	GO:0012505
nuclear lumen	GO:0031981
intracellular membrane-bounded organelle	GO:0043231
membrane-bounded organelle	GO:0043227
intracellular organelle lumen	GO:0070013
organelle lumen	GO:0043233
membrane-enclosed lumen	GO:0031974
nucleoplasm	GO:0005654
intracellular organelle	GO:0043229
cellular anatomical entity	GO:0110165
cytosol	GO:0005829
organelle	GO:0043226
nucleus	GO:0005634
intracellular anatomical structure	GO:0005622
cytoplasm	GO:0005737
non-membrane-bounded organelle	GO:0043228

p=2.4E-06	n=2
p=8.9E-03	n=2
p=2.4E-02	n=1
p=6.5E-02	n=1
p=7.2E-02	n=2
p=7.8E-02	n=1
p=1.2E-01	n=1
p=1.6E-01	n=1
p=2.4E-01	n=3
p=2.5E-01	n=1
p=2.8E-01	n=1
p=2.8E-01	n=3
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p=8.5E-01	n=1
p=8.6E-01	n=6
p=8.7E-01	n=7
p=8.8E-01	n=1
p=8.9E-01	n=6
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-log(p)
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fraction