

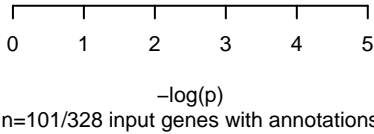
GO:BP
Ncol_Nvec_vc1.1_XM_032387164.2

fraction genes in fg and expected value

negative regulation of activated T cell ... GO:0046007
negative regulation of B cell proliferat... GO:0030889
positive regulation of inclusion body as... GO:0090261
adherens junction organization GO:0034332
protein polyubiquitination GO:0000209
cellular macromolecule catabolic process GO:0044265
regulation of protein exit from endoplas... GO:0070861
protein N-linked glycosylation via aspar... GO:0018279
B cell homeostasis GO:0001782
DNA catabolic process, endonucleolytic GO:0000737
retrograde transport, endosome to Golgi GO:0042147
cellular response to interferon-beta GO:0035458
cellular response to low-density lipopro... GO:0071404
dephosphorylation GO:0016311
regulation of alpha-beta T cell differen... GO:0046637
T cell homeostasis GO:0043029
positive regulation of catabolic process GO:0009896
regulation of catabolic process GO:0009894
intracellular protein transport GO:0006886
protein catabolic process GO:0030163
cellular protein catabolic process GO:0044257
glomerulus morphogenesis GO:0072102
negative regulation of endoplasmic retic... GO:1902236
regulation of cellular catabolic process GO:0031329
proteolysis involved in cellular protein... GO:0051603
intrinsic apoptotic signaling pathway in... GO:0070059
amide transport GO:0042886
vesicle-mediated transport to the plasma... GO:0098876
in utero embryonic development GO:0001701
regulation of adherens junction organiza... GO:1903391

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p=1.5E-02	n=18
p=1.5E-02	n=20
p=1.6E-02	n=16
p=1.7E-02	n=14
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p=1.7E-02	n=16
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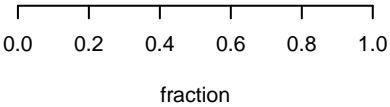
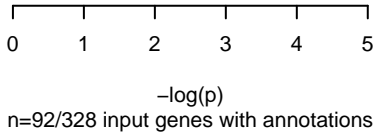
GO:MF
Ncol_Nvec_vc1.1_XM_032387164.2

fraction genes in fg and expected value

catalytic activity, acting on a protein GO:0140096
phosphatidylinositol-4,5-bisphosphate ph... GO:0106019
ubiquitin-protein transferase activity GO:0004842
ubiquitin-like protein transferase activ... GO:0019787
sterol transporter activity GO:0015248
ubiquitin conjugating enzyme activity GO:0061631
SNAP receptor activity GO:0005484
ubiquitin-like protein conjugating enzym... GO:0061650
acyltransferase activity, transferring g... GO:0016747
ubiquitin protein ligase binding GO:0031625
acetyltransferase activity GO:0016407
myosin binding GO:0017022
acyltransferase activity GO:0016746
ubiquitin-like protein ligase binding GO:0044389
phosphatase activity GO:0016791
signaling receptor complex adaptor activ... GO:0030159
cis-trans isomerase activity GO:0016859
peptidyl-prolyl cis-trans isomerase acti... GO:0003755
5S rDNA binding GO:0080084
CoA carboxylase activity GO:0016421
neuropilin binding GO:0038191
low-density lipoprotein particle binding GO:0030169
Toll-like receptor binding GO:0035325
protein phosphatase 5 binding GO:1990634
myosin VI binding GO:0070853
myosin VI heavy chain binding GO:0070854
growth hormone-releasing hormone recepto... GO:0016520
RNA polymerase III core binding GO:0000994
BH4 domain binding GO:0051435
Roundabout binding GO:0048495

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p=2.8E-02	n=3
p=2.9E-02	n=4
p=3.0E-02	n=8
p=3.5E-02	n=3
p=3.5E-02	n=3
p=4.0E-02	n=4
p=4.5E-02	n=8
p=4.9E-02	n=7
p=5.7E-02	n=2
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GO:CC
Ncol_Nvec_vc1.1_XM_032387164.2

fraction genes in fg and expected value

nuclear stress granule GO:0097165
organelle subcompartment GO:0031984
TIM23 mitochondrial import inner membran... GO:0005744
transport vesicle GO:0030133
perinuclear region of cytoplasm GO:0048471
Golgi apparatus subcompartment GO:0098791
Golgi stack GO:0005795
smooth endoplasmic reticulum GO:0005790
transport vesicle membrane GO:0030658
SNARE complex GO:0031201
Golgi membrane GO:0000139
acrosomal vesicle GO:0001669
microtubule cytoskeleton GO:0015630
Golgi apparatus GO:0005794
ER to Golgi transport vesicle membrane GO:0012507
apical dendrite GO:0097440
death-inducing signaling complex GO:0031264
insulin-responsive compartment GO:0032593
telomerase holoenzyme complex GO:0005697
protein farnesyltransferase complex GO:0005965
palmitoyltransferase complex GO:0002178
immunoglobulin complex GO:0019814
B cell receptor complex GO:0019815
radial spoke GO:0001534
dendritic microtubule GO:1901588
cuticular plate GO:0032437
fusome GO:0045169
site of double-strand break GO:0035861
site of DNA damage GO:0090734
cytoplasmic microtubule GO:0005881

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p=8.1E-03	n=24
p=9.3E-03	n=2
p=1.4E-02	n=10
p=1.5E-02	n=14
p=1.6E-02	n=15
p=2.6E-02	n=6
p=2.7E-02	n=3
p=2.8E-02	n=5
p=4.1E-02	n=3
p=4.1E-02	n=11
p=4.1E-02	n=2
p=4.3E-02	n=16
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