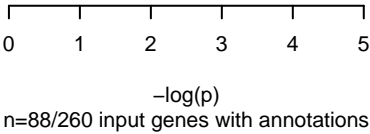


GO:BP
Ncol_Nvec_vc1.1_XM_048720726.1

fraction genes in fg and expected value

cellular response to peptide hormone sti...	GO:0071375	p=1.4E-03	n=10
antigen processing and presentation	GO:0019882	p=1.4E-03	n=6
positive regulation of apoptotic signal...	GO:2001235	p=1.7E-03	n=6
B cell activation	GO:0042113	p=1.9E-03	n=8
intracellular signal transduction	GO:0035556	p=2.2E-03	n=29
regulation of B cell differentiation	GO:0045577	p=2.3E-03	n=2
regulation of fibroblast apoptotic proce...	GO:2000269	p=2.3E-03	n=2
positive thymic T cell selection	GO:0045059	p=2.3E-03	n=2
positive regulation of heart rate	GO:0010460	p=3.4E-03	n=3
vesicle coating	GO:0006901	p=4.7E-03	n=4
homeostatic process	GO:0042592	p=5.0E-03	n=25
B cell homeostasis	GO:0001782	p=5.2E-03	n=3
integrin-mediated signaling pathway	GO:0007229	p=5.2E-03	n=3
DNA catabolic process, endonucleolytic	GO:0000737	p=5.2E-03	n=3
vesicle targeting, to, from or within Go...	GO:0048199	p=6.0E-03	n=4
regulation of receptor localization to s...	GO:1902683	p=6.8E-03	n=2
negative regulation of cyclin-dependent ...	GO:0045736	p=6.8E-03	n=2
interleukin-2-mediated signaling pathway	GO:0038110	p=6.8E-03	n=2
negative regulation of anoikis	GO:2000811	p=6.8E-03	n=2
regulation of female receptivity	GO:0045924	p=6.8E-03	n=2
regulation of growth hormone secretion	GO:0060123	p=6.8E-03	n=2
COPII-coated vesicle cargo loading	GO:0090110	p=6.8E-03	n=2
cellular response to stress	GO:0033554	p=7.3E-03	n=28
regulation of tumor necrosis factor-medi...	GO:0010803	p=7.5E-03	n=3
positive regulation of peptide secretion	GO:0002793	p=7.6E-03	n=6
Golgi vesicle budding	GO:0048194	p=7.6E-03	n=4
T cell receptor signaling pathway	GO:0050852	p=9.4E-03	n=4
anatomical structure morphogenesis	GO:0009653	p=1.0E-02	n=34
circadian regulation of gene expression	GO:0032922	p=1.0E-02	n=3
positive regulation of secretion by cell	GO:1903532	p=1.1E-02	n=8

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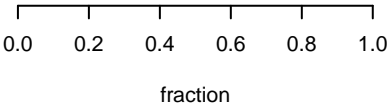
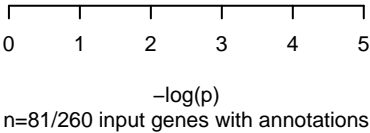


GO:MF
Ncol_Nvec_vc1.1_XM_048720726.1

fraction genes in fg and expected value

GTPase activity	GO:0003924	p=3.0E-04	n=8
cyclin-dependent protein serine/threonin...	GO:0004861	p=2.6E-03	n=2
phospholipase activator activity	GO:0016004	p=2.6E-03	n=2
ion binding	GO:0043167	p=4.3E-03	n=27
nucleotide binding	GO:0000166	p=6.9E-03	n=13
cysteine-type endopeptidase activator ac...	GO:0008656	p=7.4E-03	n=2
GDP binding	GO:0019003	p=1.2E-02	n=3
GTP binding	GO:0005525	p=1.4E-02	n=5
purine ribonucleoside binding	GO:0032550	p=1.4E-02	n=5
ribonucleoside binding	GO:0032549	p=1.4E-02	n=5
purine ribonucleoside triphosphate bindi...	GO:0035639	p=1.7E-02	n=10
ribonucleotide binding	GO:0032553	p=1.7E-02	n=11
purine ribonucleotide binding	GO:0032555	p=1.7E-02	n=11
nucleoside binding	GO:0001882	p=1.8E-02	n=5
purine nucleoside binding	GO:0001883	p=1.8E-02	n=5
integrin binding	GO:0005178	p=2.0E-02	n=3
purine nucleotide binding	GO:0017076	p=2.0E-02	n=11
guanyl ribonucleotide binding	GO:0032561	p=2.1E-02	n=5
guanyl nucleotide binding	GO:0019001	p=2.1E-02	n=5
proline-rich region binding	GO:0070064	p=2.3E-02	n=2
BH domain binding	GO:0051400	p=2.3E-02	n=2
carbohydrate derivative binding	GO:0097367	p=2.4E-02	n=12
signaling adaptor activity	GO:0035591	p=2.5E-02	n=3
beta-catenin binding	GO:0008013	p=3.4E-02	n=2
zinc ion binding	GO:0008270	p=3.5E-02	n=8
protein kinase binding	GO:0019901	p=3.6E-02	n=11
anion binding	GO:0043168	p=3.9E-02	n=16
protein heterodimerization activity	GO:0046982	p=4.0E-02	n=9
histone binding	GO:0042393	p=4.5E-02	n=4
signaling receptor complex adaptor activ...	GO:0030159	p=4.5E-02	n=2

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GO:CC
Ncol_Nvec_vc1.1_XM_048720726.1

fraction genes in fg and expected value

endoplasmic reticulum membrane	GO:0005789	p=1.9E-03	n=15
site of double-strand break	GO:0035861	p=5.0E-03	n=3
vacuolar proton-transporting V-type ATPa...	GO:0000221	p=6.6E-03	n=2
endoplasmic reticulum-Golgi intermediate...	GO:0033116	p=7.3E-03	n=3
cleavage furrow	GO:0032154	p=1.0E-02	n=3
cell periphery	GO:0071944	p=1.4E-02	n=35
transport vesicle membrane	GO:0030658	p=1.5E-02	n=5
plasma membrane	GO:0005886	p=1.7E-02	n=33
supramolecular fiber	GO:0099512	p=2.4E-02	n=9
supramolecular polymer	GO:0099081	p=2.4E-02	n=9
plasma membrane proton-transporting V-ty...	GO:0033181	p=3.0E-02	n=2
mitochondrial envelope	GO:0005740	p=3.1E-02	n=10
cell division site	GO:0032153	p=3.2E-02	n=3
extrinsic component of cytoplasmic side ...	GO:0031234	p=3.2E-02	n=3
membrane	GO:0016020	p=3.6E-02	n=54
transport vesicle	GO:0030133	p=3.7E-02	n=8
endoplasmic reticulum tubular network	GO:0071782	p=4.1E-02	n=2
ER to Golgi transport vesicle membrane	GO:0012507	p=4.1E-02	n=2
polymeric cytoskeletal fiber	GO:0099513	p=4.4E-02	n=5
death-inducing signaling complex	GO:0031264	p=4.8E-02	n=1
Sec61 translocon complex	GO:0005784	p=4.8E-02	n=1
signal recognition particle, endoplasmic...	GO:0005786	p=4.8E-02	n=1
insulin-responsive compartment	GO:0032593	p=4.8E-02	n=1
H zone	GO:0031673	p=4.8E-02	n=1
septin filament array	GO:0032160	p=4.8E-02	n=1
signal recognition particle	GO:0048500	p=4.8E-02	n=1
glycerol-3-phosphate dehydrogenase compl...	GO:0009331	p=4.8E-02	n=1
apoptosome	GO:0043293	p=4.8E-02	n=1
mitochondrial pyruvate dehydrogenase com...	GO:0005967	p=4.8E-02	n=1
translocon complex	GO:0071256	p=4.8E-02	n=1

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