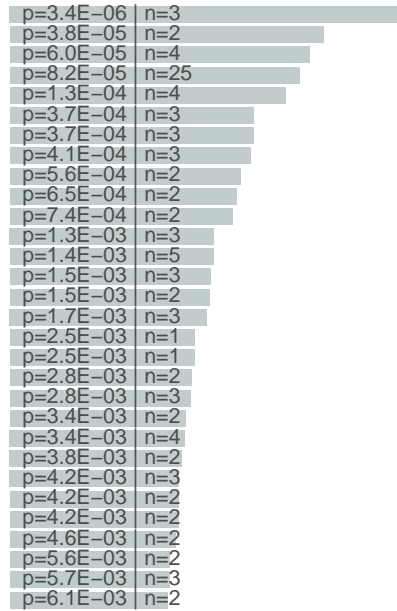


GO:BP
gc017

fraction genes in fg and expected value

positive regulation of cytochrome–c oxid...	GO:1904960
response to symbiotic bacterium	GO:0009609
negative regulation of BMP signaling pat...	GO:0030514
G protein–coupled receptor signaling pat...	GO:0007186
blastocyst hatching	GO:0001835
positive regulation of osteoclast prolifer...	GO:0090290
bombesin receptor signaling pathway	GO:0031989
positive regulation of respiratory gaseo...	GO:1903942
negative regulation of telomeric DNA bin...	GO:1904743
negative regulation of maintenance of mi...	GO:1904908
negative regulation of inflammatory resp...	GO:0002862
antiviral innate immune response	GO:0140374
positive regulation of amine transport	GO:0051954
neuropeptide signaling pathway	GO:0007218
cellular response to estradiol stimulus	GO:0071392
positive regulation of interferon–alpha ...	GO:0032727
tolerance induction to nonself antigen	GO:0002462
positive regulation of glomerular mesang...	GO:0072126
neuropeptide catabolic process	GO:0010813
regulation of sensory perception of pain	GO:0051930
regulation of angiotensin levels in bloo...	GO:0002002
regulation of synaptic transmission, glu...	GO:0051966
receptor guanylyl cyclase signaling path...	GO:0007168
positive regulation of cytosolic calcium...	GO:0051482
adenylate cyclase–inhibiting G protein–c...	GO:0007196
natural killer cell differentiation	GO:0001779
cGMP biosynthetic process	GO:0006182
positive regulation of telomere capping	GO:1904355
SMAD protein signal transduction	GO:0060395
detection of light stimulus involved in ...	GO:0050908



–log(p)
n=78/232 input genes with annotations

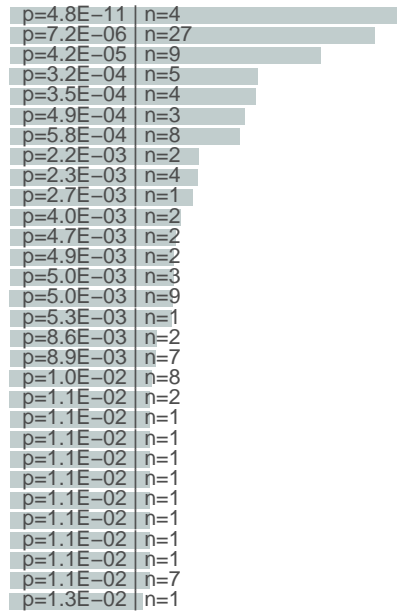
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fraction
n=78/232 input genes with annotations

GO:MF
gc017

fraction genes in fg and expected value

pyroglutamyl–peptidase activity	GO:0016920
G protein–coupled receptor activity	GO:0004930
neuropeptide receptor activity	GO:0008188
olfactory receptor activity	GO:0004984
SMAD binding	GO:0046332
bombesin receptor activity	GO:0004946
DNA–binding transcription factor activit...	GO:0000981
natriuretic peptide receptor activity	GO:0016941
metalloexopeptidase activity	GO:0008235
complement component C3a receptor activi...	GO:0004876
glutathione peroxidase activity	GO:0004602
group III metabotropic glutamate recepto...	GO:0001642
lysophosphatidic acid receptor activity	GO:0070915
carboxypeptidase activity	GO:0004180
zinc ion binding	GO:0008270
arsenite methyltransferase activity	GO:0030791
guanylate cyclase activity	GO:0004383
peptide binding	GO:0042277
transcription cis–regulatory region bind...	GO:0000976
metallocarboxypeptidase activity	GO:0004181
calcium–dependent protein kinase regulat...	GO:0010858
heparan sulfate 2–O–sulfotransferase act...	GO:0004394
tRNA (guanine(37)–N(1))–methyltransferas...	GO:0052906
potassium ion leak channel activity	GO:0022841
orotidine–5′–phosphate decarboxylase act...	GO:0004590
outward rectifier potassium channel acti...	GO:0015271
calcium–dependent protein kinase inhibit...	GO:0008427
orotate phosphoribosyltransferase activi...	GO:0004588
RNA polymerase II transcription regulato...	GO:0000977
complement component C3a binding	GO:0001850



–log(p)
n=82/232 input genes with annotations

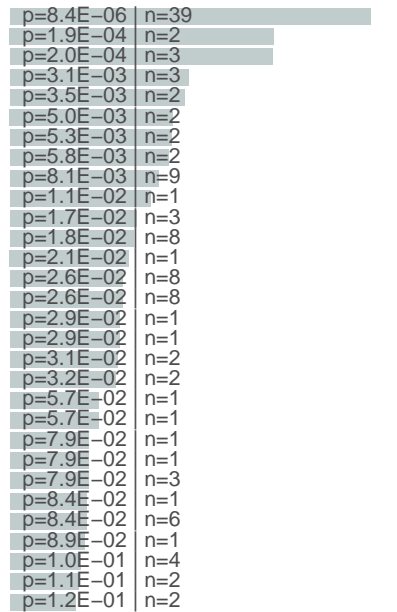
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fraction
n=82/232 input genes with annotations

GO:CC
gc017

fraction genes in fg and expected value

plasma membrane	GO:0005886
core TFIIF complex portion of holo TFIIF...	GO:0000438
mitochondrial respiratory chain complex ...	GO:0005751
mitochondrial respiratory chain complex ...	GO:0005747
new growing cell tip	GO:0035841
transcription preinitiation complex	GO:0097550
insulin–responsive compartment	GO:0032593
inhibitory synapse	GO:0060077
neuronal cell body	GO:0043025
junctional membrane complex	GO:0030314
acrosomal vesicle	GO:0001669
transcription regulator complex	GO:0005667
rough endoplasmic reticulum lumen	GO:0048237
dendrite	GO:0030425
dendritic tree	GO:0097447
peptidase inhibitor complex	GO:1904090
protein complex involved in cell–matrix ...	GO:0098637
mitotic spindle pole	GO:0097431
transcription factor TFIID complex	GO:0005669
Golgi lumen	GO:0005796
filopodium tip	GO:0032433
secretory granule lumen	GO:0034774
cytoplasmic vesicle lumen	GO:0060205
non–motile cilium	GO:0097730
protein complex involved in cell adhesio...	GO:0098636
secretory granule	GO:0030141
vesicle lumen	GO:0031983
postsynaptic membrane	GO:0045211
rough endoplasmic reticulum	GO:0005791
nuclear pore	GO:0005643



–log(p)
n=82/232 input genes with annotations

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fraction
n=82/232 input genes with annotations