

GO:BP  
gc005

fraction genes in fg and expected value

negative regulation of insulin receptor ...	GO:0046627
phosphatidylinositol dephosphorylation	GO:0046856
thyroid-stimulating hormone signaling pa...	GO:0038194
cellular response to thyrotropin-releasi...	GO:1905229
cellular response to glycoprotein	GO:1904588
positive regulation of cold-induced ther...	GO:0120162
dopaminergic neuron differentiation	GO:0071542
B cell differentiation	GO:0030183
positive regulation of testosterone secr...	GO:2000845
negative regulation of insulin-like grow...	GO:0043569
negative regulation of glucagon secretio...	GO:0070093
cochlea morphogenesis	GO:0090103
activation of adenylate cyclase activity	GO:0007190
inner ear receptor cell stereocilium org...	GO:0060122
negative regulation of platelet-derived ...	GO:0010642
adult locomotory behavior	GO:0008344
adenylate cyclase-activating G protein-c...	GO:0007189
positive regulation of multicellular org...	GO:0040018
negative regulation of mitochondrial fis...	GO:0090258
positive regulation of fatty acid oxidat...	GO:0046321
regulation of synaptic vesicle cycle	GO:0098693
endochondral ossification	GO:0001958
insulin metabolic process	GO:1901142
inositol trisphosphate metabolic process	GO:0032957
positive regulation of mitochondrial mem...	GO:0010918
ruffle assembly	GO:0097178
negative regulation of cAMP-mediated sig...	GO:0043951
hormone-mediated signaling pathway	GO:0009755
negative regulation of protein serine/th...	GO:0071901
negative regulation of fat cell differen...	GO:0045599



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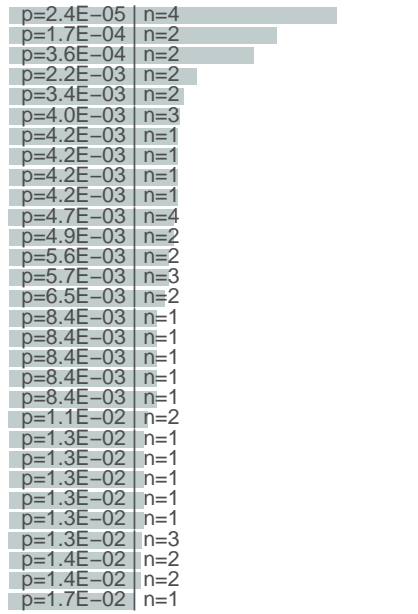
-log(p)  
n=32/122 input genes with annotations

fraction

GO:MF  
gc005

fraction genes in fg and expected value

thyroid-stimulating hormone receptor act...	GO:0004996
tumor necrosis factor receptor binding	GO:0005164
inositol-polyphosphate 5-phosphatase act...	GO:0004445
phosphatidylinositol phosphate phosphata...	GO:0052866
SH2 domain binding	GO:0042169
inositol trisphosphate phosphatase activ...	GO:0046030
RNA trimethylguanosine synthase activity	GO:0071164
neuroigin family protein binding	GO:0097109
inositol-4,5-bisphosphate 5-phosphatase ...	GO:0030487
type 1 fibroblast growth factor receptor...	GO:0005105
G protein-coupled peptide receptor activ...	GO:0008528
phosphatidylinositol-3,4,5-trisphosphate...	GO:0005547
protein serine/threonine kinase inhibito...	GO:0030291
guanyl-nucleotide exchange factor activi...	GO:0005085
G-protein alpha-subunit binding	GO:0001965
[protein]-3-O-(N-acetyl-D-glucosaminy)-...	GO:0102571
extracellular matrix structural constitu...	GO:0030021
[protein]-3-O-(N-acetyl-D-glucosaminy)-...	GO:0102166
[protein]-3-O-(N-acetyl-D-glucosaminy)-...	GO:0102167
asialoglycoprotein receptor activity	GO:0004873
organophosphate ester transmembrane tran...	GO:0015605
inositol-1,4,5-trisphosphate 5-phosphata...	GO:0052658
inositol-1,3,4,5-tetrakisphosphate 5-pho...	GO:0052659
histone methyltransferase activity (H3-K...	GO:0046974
cAMP binding	GO:0030552
acetylcholine receptor binding	GO:0033130
organic anion transmembrane transporter ...	GO:0008514
carbohydrate derivative transmembrane tr...	GO:1901505
promoter-specific chromatin binding	GO:1990841
potassium channel inhibitor activity	GO:0019870



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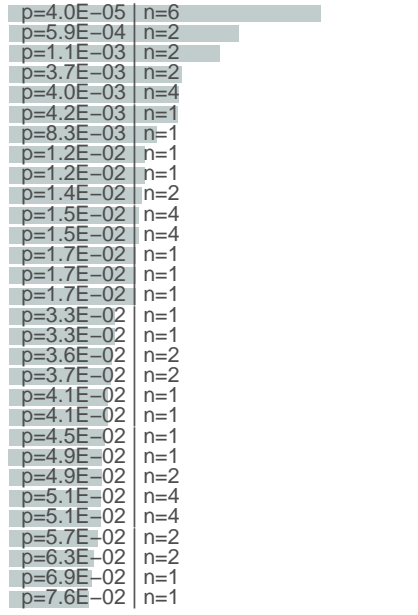
-log(p)  
n=33/122 input genes with annotations

fraction

GO:CC  
gc005

fraction genes in fg and expected value

basolateral plasma membrane	GO:0016323
nuclear outer membrane	GO:0005640
Golgi medial cisterna	GO:0005797
excitatory synapse	GO:0060076
receptor complex	GO:0043235
protein complex involved in cell-cell ad...	GO:0098635
cone cell pedicle	GO:0044316
cytoplasmic side of late endosome membra...	GO:0098560
cytoplasmic side of early endosome membr...	GO:0098559
endoplasmic reticulum-Golgi intermediate...	GO:0005793
membrane microdomain	GO:0098857
membrane raft	GO:0045121
filtration diaphragm	GO:0036056
slit diaphragm	GO:0036057
cytoplasmic side of endosome membrane	GO:0010009
Barr body	GO:0001740
outer mitochondrial membrane protein com...	GO:0098799
lamellipodium	GO:0030027
GABA-ergic synapse	GO:0098982
insulin-responsive compartment	GO:0032593
X chromosome	GO:0000805
cytoplasmic side of lysosomal membrane	GO:0098574
inhibitory synapse	GO:0060077
growth cone	GO:0030426
outer membrane	GO:0019867
organelle outer membrane	GO:0031968
mitochondrial outer membrane	GO:0005741
site of polarized growth	GO:0030427
photoreceptor inner segment	GO:0001917
hippocampal mossy fiber to CA3 synapse	GO:0098686



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