GO:BP
gc010

fraction genes in fg and expected val...

Term	p-value	n	fg	bg
peptidyl−glutamic acid carboxylation GO:0017187	p=6.0E−09	n=3	fg=0.20	bg=0.00
poly−N−acetyllactosamine biosynthetic pr... GO:0030311	p=1.2E−07	n=4	fg=0.27	bg=0.00
protein glycosylation GO:0006486	p=1.7E−04	n=4	fg=0.27	bg=0.02
regulation of blood coagulation GO:0030193	p=6.0E−04	n=2	fg=0.13	bg=0.00
negative regulation of secretion by cell GO:1903531	p=1.9E−03	n=3	fg=0.20	bg=0.02
positive regulation of I−kappaB kinase/N... GO:0043123	p=1.9E−03	n=2	fg=0.13	bg=0.00
retinal bipolar neuron differentiation GO:0060040	p=1.9E−03	n=1	fg=0.07	bg=0.00
vitamin K biosynthetic process GO:0042371	p=3.9E−03	n=1	fg=0.07	bg=0.00
detection of yeast GO:0001879	p=3.9E−03	n=1	fg=0.07	bg=0.00
lysine transport GO:0015819	p=3.9E−03	n=1	fg=0.07	bg=0.00
L−histidine import across plasma membran... GO:1903810	p=3.9E−03	n=1	fg=0.07	bg=0.00
peptide hormone secretion GO:0030072	p=5.8E−03	n=3	fg=0.20	bg=0.03
L−arginine import across plasma membrane GO:0097638	p=5.9E−03	n=1	fg=0.07	bg=0.00
stimulatory C−type lectin receptor signa... GO:0002223	p=5.9E−03	n=1	fg=0.07	bg=0.00
regulation of hormone secretion GO:0046883	p=6.4E−03	n=3	fg=0.20	bg=0.03
positive regulation of neutrophil mediat... GO:0070963	p=7.8E−03	n=1	fg=0.07	bg=0.00
positive regulation of T−helper 17 type ... GO:2000318	p=7.8E−03	n=1	fg=0.07	bg=0.00
negative regulation of toll−like recepto... GO:0034140	p=7.8E−03	n=1	fg=0.07	bg=0.00
positive regulation of renin secretion i... GO:1900135	p=7.8E−03	n=1	fg=0.07	bg=0.00
antifungal innate immune response GO:0061760	p=7.8E−03	n=1	fg=0.07	bg=0.00
potassium channel activating, G protein−... GO:0099109	p=7.8E−03	n=1	fg=0.07	bg=0.00
L−ornithine transmembrane transport GO:1903352	p=7.8E−03	n=1	fg=0.07	bg=0.00
positive regulation of eosinophil degran... GO:0043311	p=7.8E−03	n=1	fg=0.07	bg=0.00
regulation of chemokine (C−X−C motif) li... GO:2000341	p=9.7E−03	n=1	fg=0.07	bg=0.00
positive regulation of toll−like recepto... GO:0034141	p=9.7E−03	n=1	fg=0.07	bg=0.00
positive regulation of toll−like recepto... GO:0034145	p=9.7E−03	n=1	fg=0.07	bg=0.00
positive regulation of glomerular filtra... GO:0003104	p=9.7E−03	n=1	fg=0.07	bg=0.00
positive regulation of amine transport GO:0051954	p=1.1E−02	n=2	fg=0.13	bg=0.01
negative regulation of hormone secretion GO:0046888	p=1.2E−02	n=2	fg=0.13	bg=0.01
pseudopodium organization GO:0031268	p=1.2E−02	n=1	fg=0.07	bg=0.00

−log(p) axis: 0 1 2 3 4 5

−log(p)
n=15/58 input genes with annotations

fraction axis: 0.0 0.2 0.4 0.6 0.8 1.0

fraction

GO:MF
gc010

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
beta−galactosyl−N−acetylglucosaminylgala... GO:0008457	p=1.2E−07	n=4	fg=0.27	bg=0.00
N−acetyllactosaminide beta−1,3−N−acetylg... GO:0008532	p=1.2E−07	n=4	fg=0.27	bg=0.00
gamma−glutamyl carboxylase activity GO:0008488	p=3.6E−06	n=2	fg=0.13	bg=0.00
vitamin−K−epoxide reductase (warfarin−se... GO:0047057	p=2.0E−03	n=1	fg=0.07	bg=0.00
vitamin−K−epoxide reductase (warfarin−in... GO:0047058	p=2.0E−03	n=1	fg=0.07	bg=0.00
L−histidine transmembrane transporter ac... GO:0005290	p=3.9E−03	n=1	fg=0.07	bg=0.00
L−ornithine transmembrane transporter ac... GO:0099064	p=5.9E−03	n=1	fg=0.07	bg=0.00
proteinase activated receptor activity GO:0001648	p=7.8E−03	n=1	fg=0.07	bg=0.00
L−arginine transmembrane transporter act... GO:0061459	p=7.8E−03	n=1	fg=0.07	bg=0.00
potassium channel activator activity inv... GO:0099108	p=7.8E−03	n=1	fg=0.07	bg=0.00
thrombin−activated receptor activity GO:0015057	p=7.8E−03	n=1	fg=0.07	bg=0.00
L−lysine transmembrane transporter activ... GO:0015189	p=7.8E−03	n=1	fg=0.07	bg=0.00
adenylate cyclase inhibitor activity GO:0010855	p=9.8E−03	n=1	fg=0.07	bg=0.00
G−protein beta−subunit binding GO:0031681	p=9.8E−03	n=1	fg=0.07	bg=0.00
heterotrimeric G−protein binding GO:0032795	p=9.8E−03	n=1	fg=0.07	bg=0.00
pattern recognition receptor activity GO:0038187	p=9.8E−03	n=1	fg=0.07	bg=0.00
acetylcholine receptor regulator activit... GO:0030548	p=9.8E−03	n=1	fg=0.07	bg=0.00
quinone binding GO:0048038	p=1.6E−02	n=1	fg=0.07	bg=0.00
calcium channel inhibitor activity GO:0019855	p=1.8E−02	n=1	fg=0.07	bg=0.00
vitamin binding GO:0019842	p=2.1E−02	n=2	fg=0.13	bg=0.02
exogenous protein binding GO:0140272	p=2.5E−02	n=1	fg=0.07	bg=0.00
virus receptor activity GO:0001618	p=2.5E−02	n=1	fg=0.07	bg=0.00
mannose binding GO:0005537	p=2.7E−02	n=1	fg=0.07	bg=0.00
channel inhibitor activity GO:0016248	p=2.9E−02	n=1	fg=0.07	bg=0.00
ion channel inhibitor activity GO:0008200	p=2.9E−02	n=1	fg=0.07	bg=0.00
G protein−coupled peptide receptor activ... GO:0008528	p=3.2E−02	n=3	fg=0.20	bg=0.02
peptide receptor activity GO:0001653	p=3.6E−02	n=3	fg=0.20	bg=0.02
extracellular matrix protein binding GO:1990430	p=4.2E−02	n=1	fg=0.07	bg=0.00
G protein−coupled receptor activity invo... GO:0099530	p=4.2E−02	n=1	fg=0.07	bg=0.00
G protein−coupled neurotransmitter recep... GO:0150047	p=4.2E−02	n=1	fg=0.07	bg=0.00

−log(p) axis: 0 1 2 3 4 5

−log(p)
n=15/58 input genes with annotations

fraction axis: 0.0 0.2 0.4 0.6 0.8 1.0

fraction

GO:CC
gc010

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
Golgi membrane GO:0000139	p=2.1E−04	n=4	fg=0.27	bg=0.02
membrane GO:0016020	p=3.3E−03	n=14	fg=0.93	bg=0.48
pseudopodium GO:0031143	p=1.4E−02	n=1	fg=0.07	bg=0.00
basolateral plasma membrane GO:0016323	p=3.1E−02	n=2	fg=0.13	bg=0.02
basal plasma membrane GO:0009925	p=3.3E−02	n=2	fg=0.13	bg=0.02
receptor complex GO:0043235	p=3.5E−02	n=2	fg=0.13	bg=0.02
basal part of cell GO:0045178	p=3.6E−02	n=2	fg=0.13	bg=0.02
endoplasmic reticulum GO:0005783	p=3.7E−02	n=5	fg=0.33	bg=0.13
endomembrane system GO:0012505	p=4.2E−02	n=10	fg=0.67	bg=0.28
GABA receptor complex GO:1902710	p=4.4E−02	n=1	fg=0.07	bg=0.00
G protein−coupled GABA receptor complex GO:1902712	p=4.4E−02	n=1	fg=0.07	bg=0.00
G protein−coupled receptor complex GO:0097648	p=4.9E−02	n=1	fg=0.07	bg=0.00
G protein−coupled receptor dimeric compl... GO:0038037	p=4.9E−02	n=1	fg=0.07	bg=0.00
G protein−coupled receptor heterodimeric... GO:0038039	p=4.9E−02	n=1	fg=0.07	bg=0.00
axolemma GO:0030673	p=6.2E−02	n=1	fg=0.07	bg=0.00
neuron projection membrane GO:0032589	p=7.0E−02	n=1	fg=0.07	bg=0.00
membrane raft GO:0045121	p=7.2E−02	n=2	fg=0.13	bg=0.03
membrane microdomain GO:0098857	p=7.2E−02	n=2	fg=0.13	bg=0.03
main axon GO:0044304	p=8.8E−02	n=1	fg=0.07	bg=0.01
plasma membrane signaling receptor compl... GO:0098802	p=9.6E−02	n=1	fg=0.07	bg=0.01
sperm head GO:0061827	p=1.1E−01	n=1	fg=0.07	bg=0.01
sperm midpiece GO:0097225	p=1.1E−01	n=1	fg=0.07	bg=0.01
plasma membrane region GO:0098590	p=1.1E−01	n=3	fg=0.20	bg=0.08
dendritic shaft GO:0043198	p=1.1E−01	n=1	fg=0.07	bg=0.01
leading edge membrane GO:0031256	p=1.1E−01	n=1	fg=0.07	bg=0.01
intrinsic component of plasma membrane GO:0031226	p=1.3E−01	n=1	fg=0.07	bg=0.01
integral component of plasma membrane GO:0005887	p=1.3E−01	n=1	fg=0.07	bg=0.01
plasma membrane GO:0005886	p=1.5E−01	n=6	fg=0.40	bg=0.25
GABA−ergic synapse GO:0098982	p=1.6E−01	n=1	fg=0.07	bg=0.01
external side of plasma membrane GO:0009897	p=1.6E−01	n=1	fg=0.07	bg=0.01

−log(p) axis: 0 1 2 3 4 5

−log(p)
n=15/58 input genes with annotations

fraction axis: 0.0 0.2 0.4 0.6 0.8 1.0

fraction