GO:BP
Ncol_Nvec_vc1.1_XM_048730283.1

fraction genes in fg and expected valu

GO term	p-value	n	fg	bg
response to water deprivation GO:0009414	p=3.6E−04	n=3	fg=0.04	bg=0.00
regulation of lipid localization GO:1905952	p=8.4E−04	n=6	fg=0.07	bg=0.01
protein localization to Golgi apparatus GO:0034067	p=8.6E−04	n=3	fg=0.04	bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890	p=9.5E−04	n=5	fg=0.06	bg=0.01
peptide transport GO:0015833	p=1.2E−03	n=28	fg=0.34	bg=0.16
regulation of deacetylase activity GO:0150065	p=2.1E−03	n=2	fg=0.02	bg=0.00
regulation of macrophage derived foam ce... GO:0010743	p=2.1E−03	n=2	fg=0.02	bg=0.00
positive regulation of ER to Golgi vesic... GO:1902953	p=2.1E−03	n=2	fg=0.02	bg=0.00
positive regulation of prostaglandin bio... GO:0031394	p=2.1E−03	n=2	fg=0.02	bg=0.00
regulation of protein exit from endoplas... GO:0070861	p=2.8E−03	n=3	fg=0.04	bg=0.00
dsRNA transport GO:0033227	p=2.8E−03	n=3	fg=0.04	bg=0.00
lipid droplet organization GO:0034389	p=2.8E−03	n=3	fg=0.04	bg=0.00
regulation of lipid storage GO:0010883	p=2.9E−03	n=4	fg=0.05	bg=0.01
vesicle coating GO:0006901	p=3.8E−03	n=4	fg=0.05	bg=0.01
positive regulation of intracellular pro... GO:0090316	p=3.8E−03	n=5	fg=0.06	bg=0.01
B cell homeostasis GO:0001782	p=4.4E−03	n=3	fg=0.04	bg=0.00
vesicle targeting, to, from or within Go... GO:0048199	p=4.9E−03	n=4	fg=0.05	bg=0.01
regulation of determination of dorsal id... GO:2000015	p=6.0E−03	n=2	fg=0.02	bg=0.00
SRP−dependent cotranslational protein ta... GO:0006616	p=6.0E−03	n=2	fg=0.02	bg=0.00
regulation of histone deacetylation GO:0031063	p=6.0E−03	n=2	fg=0.02	bg=0.00
negative regulation of JUN kinase activi... GO:0043508	p=6.0E−03	n=2	fg=0.02	bg=0.00
COPII−coated vesicle cargo loading GO:0090110	p=6.0E−03	n=2	fg=0.02	bg=0.00
Golgi vesicle budding GO:0048194	p=6.2E−03	n=4	fg=0.05	bg=0.01
transmembrane transport GO:0055085	p=6.5E−03	n=19	fg=0.23	bg=0.11
membrane organization GO:0061024	p=7.0E−03	n=17	fg=0.20	bg=0.09
regulation of biological quality GO:0065008	p=7.3E−03	n=39	fg=0.47	bg=0.32
positive regulation of secretion by cell GO:1903532	p=7.5E−03	n=8	fg=0.10	bg=0.04
regulation of peptide transport GO:0090087	p=9.0E−03	n=12	fg=0.14	bg=0.07
imaginal disc morphogenesis GO:0007560	p=9.9E−03	n=9	fg=0.11	bg=0.04
signal release GO:0023061	p=1.0E−02	n=11	fg=0.13	bg=0.06

−log(p)
n=83/258 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_048730283.1

fraction genes in fg and expected valu

GO term	p-value	n	fg	bg
cysteine−type endopeptidase activator ac... GO:0008656	p=6.5E−03	n=2	fg=0.03	bg=0.00
triglyceride lipase activity GO:0004806	p=6.5E−03	n=2	fg=0.03	bg=0.00
voltage−gated potassium channel activity GO:0005249	p=9.8E−03	n=3	fg=0.04	bg=0.01
acyltransferase activity, transferring g... GO:0016747	p=1.5E−02	n=4	fg=0.05	bg=0.01
small GTPase binding GO:0031267	p=1.8E−02	n=9	fg=0.12	bg=0.05
dynactin binding GO:0034452	p=2.1E−02	n=2	fg=0.03	bg=0.00
acyltransferase activity GO:0016746	p=2.1E−02	n=4	fg=0.05	bg=0.01
GTPase activity GO:0003924	p=2.6E−02	n=5	fg=0.07	bg=0.02
DNA−binding transcription factor activit... GO:0000981	p=2.7E−02	n=10	fg=0.13	bg=0.05
enzyme binding GO:0019899	p=3.0E−02	n=26	fg=0.34	bg=0.24
DNA−binding transcription factor activit... GO:0003700	p=4.0E−02	n=11	fg=0.14	bg=0.08
GTP binding GO:0005525	p=4.6E−02	n=4	fg=0.05	bg=0.02
purine ribonucleoside binding GO:0032550	p=4.6E−02	n=4	fg=0.05	bg=0.02
ribonucleoside binding GO:0032549	p=4.6E−02	n=4	fg=0.05	bg=0.02
3'−phosphoadenosine 5'−phosphosulfate tr... GO:0046964	p=4.8E−02	n=1	fg=0.01	bg=0.00
open rectifier potassium channel activit... GO:0005252	p=4.8E−02	n=1	fg=0.01	bg=0.00
low−density lipoprotein particle binding GO:0030169	p=4.8E−02	n=1	fg=0.01	bg=0.00
taste receptor binding GO:0031883	p=4.8E−02	n=1	fg=0.01	bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045	p=4.8E−02	n=1	fg=0.01	bg=0.00
glutamate−ammonia ligase activity GO:0004356	p=4.8E−02	n=1	fg=0.01	bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837	p=4.8E−02	n=1	fg=0.01	bg=0.00
intracellular sodium activated potassium... GO:0005228	p=4.8E−02	n=1	fg=0.01	bg=0.00
mono−olein transacylation activity GO:0051264	p=4.8E−02	n=1	fg=0.01	bg=0.00
diolein transacylation activity GO:0051265	p=4.8E−02	n=1	fg=0.01	bg=0.00
ABC−type sterol transporter activity GO:0034041	p=4.8E−02	n=1	fg=0.01	bg=0.00
protein−membrane adaptor activity GO:0043495	p=4.8E−02	n=1	fg=0.01	bg=0.00
C−acyltransferase activity GO:0016408	p=4.8E−02	n=1	fg=0.01	bg=0.00
tricarboxylate secondary active transmem... GO:0005371	p=4.8E−02	n=1	fg=0.01	bg=0.00
phospholipase D activator activity GO:1990583	p=4.8E−02	n=1	fg=0.01	bg=0.00
steroid dehydrogenase activity GO:0016229	p=4.8E−02	n=1	fg=0.01	bg=0.00

−log(p)
n=76/258 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_048730283.1

fraction genes in fg and expected valu

GO term	p-value	n	fg	bg
Golgi membrane GO:0000139	p=4.2E−04	n=14	fg=0.16	bg=0.06
Golgi apparatus subcompartment GO:0098791	p=3.0E−03	n=15	fg=0.17	bg=0.08
endoplasmic reticulum−Golgi intermediate... GO:0033116	p=7.1E−03	n=3	fg=0.03	bg=0.01
cytoplasmic vesicle membrane GO:0030659	p=7.3E−03	n=14	fg=0.16	bg=0.08
endoplasmic reticulum GO:0005783	p=8.5E−03	n=21	fg=0.24	bg=0.14
endoplasmic reticulum membrane GO:0005789	p=1.2E−02	n=13	fg=0.15	bg=0.08
basal dendrite GO:0097441	p=1.3E−02	n=2	fg=0.02	bg=0.00
transport vesicle GO:0030133	p=1.3E−02	n=9	fg=0.10	bg=0.04
nuclear outer membrane−endoplasmic retic... GO:0042175	p=1.3E−02	n=13	fg=0.15	bg=0.08
transport vesicle membrane GO:0030658	p=1.4E−02	n=5	fg=0.06	bg=0.02
endosome GO:0005768	p=1.5E−02	n=14	fg=0.16	bg=0.09
endoplasmic reticulum subcompartment GO:0098827	p=1.6E−02	n=13	fg=0.15	bg=0.08
anchored component of membrane GO:0031225	p=2.0E−02	n=2	fg=0.02	bg=0.00
endosome membrane GO:0010008	p=2.7E−02	n=7	fg=0.08	bg=0.03
cell division site GO:0032153	p=3.1E−02	n=3	fg=0.03	bg=0.01
intrinsic component of plasma membrane GO:0031226	p=3.9E−02	n=12	fg=0.14	bg=0.08
vesicle coat GO:0030120	p=4.2E−02	n=2	fg=0.02	bg=0.00
Golgi stack GO:0005795	p=4.2E−02	n=5	fg=0.06	bg=0.02
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540	p=4.8E−02	n=1	fg=0.01	bg=0.00
signal recognition particle GO:0048500	p=4.8E−02	n=1	fg=0.01	bg=0.00
apical cytoplasm GO:0090651	p=4.8E−02	n=1	fg=0.01	bg=0.00
intrinsic component of autophagosome mem... GO:0097636	p=4.8E−02	n=1	fg=0.01	bg=0.00
integral component of autophagosome memb... GO:0097637	p=4.8E−02	n=1	fg=0.01	bg=0.00
actin cortical patch GO:0030479	p=4.8E−02	n=1	fg=0.01	bg=0.00
signal recognition particle, endoplasmic... GO:0005786	p=4.8E−02	n=1	fg=0.01	bg=0.00
endocytic patch GO:0061645	p=4.8E−02	n=1	fg=0.01	bg=0.00
periciliary membrane compartment GO:1990075	p=4.8E−02	n=1	fg=0.01	bg=0.00
apoptosome GO:0043293	p=4.8E−02	n=1	fg=0.01	bg=0.00
Golgi lumen GO:0005796	p=5.2E−02	n=2	fg=0.02	bg=0.00
proton−transporting V−type ATPase comple... GO:0033176	p=5.2E−02	n=2	fg=0.02	bg=0.00

−log(p)
n=86/258 input genes with annotations

fraction