



fraction genes in fg and expected value

plasma membrane GO:0005886 nucleolar preribosome GO:0030685 Rab-protein geranylgeranyltransferase co... GO:0005968 receptor complex GO:0043235 basolateral plasma membrane GO:0016323 basal plasma membrane GO:0009925 basal part of cell GO:0045178 p=1.3E-03 n=11 p=4.7E-03 n=1 p=7.1E-03 n=1 p=4.4E-02 n=2 bg=0.25 bg=0.00 fg=0.06 fg=0.06 fg=0.11 bg=0.00 bg=0.02 p=4.8E-02 p=5.2E-02 n=2fg=0.11 bg=0.02 bg=0.02 bg=0.02 bg=0.00 fg=0.11 n=2p=5.6E-02 p=6.0E-02 fg=0.11 fg=0.06 n=2sautolysosome GO:0044754
secondary lysosome GO:0005767
autophagosome membrane GO:0000421
trans-Golgi network membrane GO:0032588
membrane raft GO:0045121
membrane microdomain GO:0098857 n=1 fg=0.06 fg=0.06 p=6.0E-02 p=6.2E-02 bg=0.00 bg=0.00 n=1 n=1 p=7.7E-02 p=1.1E-01 bg=0.00 fg=0.06 bg=0.03 bg=0.03 n=2fa=0.11p=1.1E-01 fg=0.11 fg=0.06 | bg=0.01 autophagosome GO:0005776 late endosome GO:0005770 p=1.7E-01 n=1p=2.9E-01vacuolar membrane GO:0005774 trans–Golgi network GO:0005802 fg=0.06 p=3.0E-01n=1bg=0.02 p=3.3E-01 p=3.7E-01 fg=0.06 bg=0.02 n=1membrane GO:0016020 microtubule GO:0005874 n = 14p=4.0E fg=0.06 bg=0.03 n=1microtubule GC:0005874
Golgi apparatus subcompartment GO:0098791
plasma membrane region GO:0098590
polymeric cytoskeletal fiber GO:0099513
perinuclear region of cytoplasm GO:0048471
glutamatergic synapse GO:0098978
lysosome GO:0005764
lytic vacuole GO:0000323 p=4.0E-01n=1fg=0.06 bg=0.03 p=4.4E-01 fg=0.11 n=2bg=0.08 n=1 fg=0.06 fg=0.06 p=4.7E-01bg=0.04 p=4.9E bg=0.04 -01 n=1p=5.3E-01 p=5.4E-01 n=1fg=0.06 bg=0.04 bg=0.04 fg=0.06 n=1p=5.4E-01 p=5.7E-01 p=5.7E-01 p=5.9E-01 n=1fg=0.06 bg=0.04 bg=0.05  $f_{q=0.06}$ supramolecular fiber GO:0099512 n=1supramolecular polymer GO:0099081 n=1 fg=0.06 bg=0.05 fg=0.06 bq=0.05 vacuole GO:0005773 n=1p=6.3E-01 mitochondrial inner membrane GO:0005743 fg=0.06 bg=0.05 0 2 3 5 0.0 1 0.2 0.4 0.6 0.8 1.0 fraction -log(p) n=18/45 input genes with annotations

GO:CC

gc015