

gc017 fraction genes in fg and expected valu

peptidase inhibitor complex GO:1904090
protein complex involved in cell-matrix ... GO:0098637
rough endoplasmic reticulum lumen GO:0048237
rough endoplasmic reticulum GO:0005791
cell periphery GO:0071944
Golgi lumen GO:0005788
endoplasmic reticulum lumen GO:0005788 p=1.2E-02 | n=1 p=1.2E-02 | n=1 fg=0.03 | bg=0.00 fg=0.03 | bg=0.00 p=1.2E-02 n=1 p=1.8E-02 n=2 fg=0.03 bg=0.00 fg=0.06 bg=0.01 p=2.1E-02 p=2.4E-02 n=14 bg=0.27 fg=0.03 bg=0.00 bg=0.01 n=1 p=3.0E-02 p=3.0E-02 fg=0.06 plasma membrane GO:0005788
plasma membrane GO:0005788
secretory granule GO:0030141
protein complex involved in cell adhesio... GO:0098636
secretory granule lumen GO:0034774
cytoplasmic vesicle lumen GO:0060205
insulin-responsive compartment GO:0032593 bg=0.02 bg=0.02 bg=0.00 bg=0.00 n = 13p=3.1E-02 p=3.2E-02 fg=0.10 fg=0.03 n=3 n=1p=3.9E-02 p=3.9E-02 fg=0.03 bg=0.00 bg=0.00 fg=0.03 n=1p=4.3E-02 p=4.3E-02 fg=0.03 fg=0.03 | bg=0.00 | bg=0.00 vesicle lumen GO:0031983 inhibitory synapse GO:0060077 n=1p=4.3E-02perinuclear region of cytoplasm GO:0048471 mitotic spindle pole GO:0097431 extracellular space GO:0005615 neuronal cell body GO:0043025 p=1.1E-01fg=0.10 fg=0.03 n=3bg=0.04 p=1.1E-01 n=1bg=0.00 fg=0.10 fg=0.10 p=1.3E-01n=3bg=0.04 p=1.5E-01 n=3bg=0.04 bg=0.04 bg=0.01 secretory vesicle GO:0099503 basement membrane GO:0005604 p=1.5E-01fg=0.10 fg=0.03 n=3p=1.7E-01 n=1membrane GO:0016020 trans-Golgi network membrane GO:0032588 p=1.7E-01n=18 p=1.8E -01 fg=0.03 bg=0.01 n=1p=1.8E-01 fğ=0.06 trans–Golgi network GO:0005802 acrosomal vesicle GO:0001669 cell body GO:0044297 n=2bg=0.02 p=1.8E-01 fg=0.03 bg=0.01 n=1p=2.0E-01 n=3fg=0.10 bg=0.05 transcription regulator complex GO:0005667 nuclear pore GO:0005643 p=2.0E-01 fg=0.06 bg=0.03 n=2p=2.0E-01 p=2.0E-01 fg=0.03 fg=0.03 n=1 bg=0.01 sperm head GO:0061827 sperm midpiece GO:0097225 bg=0.01 n=1p=2.0E-01 fg=0.03 bg=0.01 0 2 3 5 0.0 1 4 0.2 0.4 0.6 0.8 1.0 fraction -log(p) n=31/76 input genes with annotations