



GO:CC

Elav\_Nvec\_vc1.1\_XM\_001633819.3

plasma membrane	GO:0005886	p=4.8E-03	n=35	fg=0.43	bg=0.27
exon-exon junction complex	GO:0035145	p=5.9E-03	n=2	fg=0.02	bg=0.00
voltage-gated potassium channel complex	GO:0008076	p=6.2E-03	n=3	fg=0.04	bg=0.01
type I terminal bouton	GO:0061174	p=8.6E-03	n=3	fg=0.04	bg=0.01
lipid droplet	GO:0005811	p=9.0E-03	n=4	fg=0.05	bg=0.01
cell junction	GO:0030054	p=1.0E-02	n=21	fg=0.26	bg=0.13
dendrite	GO:0030425	p=1.2E-02	n=12	fg=0.15	bg=0.07
dendritic tree	GO:0097447	p=1.2E-02	n=12	fg=0.15	bg=0.07
synapse	GO:0045202	p=1.3E-02	n=17	fg=0.21	bg=0.10
plasma membrane raft	GO:0044853	p=1.3E-02	n=4	fg=0.05	bg=0.01
actomyosin	GO:0042641	p=1.8E-02	n=3	fg=0.04	bg=0.01
synaptic vesicle	GO:0008021	p=1.9E-02	n=6	fg=0.07	bg=0.03
integral component of membrane	GO:0016021	p=2.0E-02	n=23	fg=0.28	bg=0.16
endoplasmic reticulum subcompartment	GO:0098827	p=2.6E-02	n=12	fg=0.15	bg=0.08
focal adhesion	GO:0005925	p=2.8E-02	n=3	fg=0.04	bg=0.01
somatodendritic compartment	GO:0036477	p=2.8E-02	n=14	fg=0.17	bg=0.10
nuclear chromosome	GO:0000228	p=2.9E-02	n=7	fg=0.09	bg=0.04
membrane raft	GO:0045121	p=3.0E-02	n=6	fg=0.07	bg=0.03
membrane microdomain	GO:0098857	p=3.0E-02	n=6	fg=0.07	bg=0.03
intrinsic component of membrane	GO:0031224	p=3.3E-02	n=23	fg=0.28	bg=0.17
caveola	GO:0005901	p=3.3E-02	n=3	fg=0.04	bg=0.01
histone methyltransferase complex	GO:0035097	p=3.3E-02	n=3	fg=0.04	bg=0.01
intrinsic component of endoplasmic retic...	GO:0031227	p=3.5E-02	n=5	fg=0.06	bg=0.02
integral component of endoplasmic reticu...	GO:0030176	p=3.5E-02	n=5	fg=0.06	bg=0.02
exocytic vesicle	GO:0070382	p=3.5E-02	n=6	fg=0.07	bg=0.03
cell-substrate junction	GO:0030055	p=4.5E-02	n=3	fg=0.04	bg=0.01
endoplasmic reticulum membrane	GO:0005789	p=4.5E-02	n=11	fg=0.13	bg=0.08
transverse filament	GO:0000802	p=4.5E-02	n=1	fg=0.01	bg=0.00
RNA polymerase II transcription represso...	GO:0090571	p=4.5E-02	n=1	fg=0.01	bg=0.00
integrin alpha9-beta1 complex	GO:0034679	p=4.5E-02	n=1	fg=0.01	bg=0.00

012345

-log(p)

n=82/314 input genes with annotations

fraction genes in fg and expected value

0.00.20.40.60.81.0

fg=0.43bg=0.27

fg=0.02bg=0.00

fg=0.04bg=0.01

fg=0.04bg=0.01

fg=0.05bg=0.01

fg=0.26bg=0.13

fg=0.15bg=0.07

fg=0.15bg=0.07

fg=0.21bg=0.10

fg=0.05bg=0.01

fg=0.04bg=0.01

fg=0.07bg=0.03

fg=0.28bg=0.16

fg=0.15bg=0.08

fg=0.04bg=0.01

fg=0.17bg=0.10

fg=0.09bg=0.04

fg=0.07bg=0.03

fg=0.07bg=0.03

fg=0.28bg=0.17

fg=0.04bg=0.01

fg=0.04bg=0.01

fg=0.06bg=0.02

fg=0.06bg=0.02

fg=0.07bg=0.03

fg=0.04bg=0.01

fg=0.13bg=0.08

fg=0.01bg=0.00

fg=0.01bg=0.00

fg=0.01bg=0.00

0.00.20.40.60.81.0

fraction