

translation repressor activity GO:0030371
protein kinase binding GO:0019901
mRNA binding GO:0003729
ubiquitin–like protein ligase binding GO:0044389
adenyl ribonucleotide binding GO:0032559
signaling receptor binding GO:0005102
ATPase binding GO:0051117
purine ribonucleoside triphosphate bindi... GO:0035639
manganese ion binding GO:0030145
phosphoprotein phosphatase activity GO:0004721
mRNA regulatory element binding translat... GO:000900
Wnt-activated receptor activity GO:0042813
hydrolase activity GO:0042813
hydrolase activity GO:0042813
catalytic activity, acting on a protein GO:0140096
ubiquitin protein ligase binding GO:0031625
phosphoprotein binding GO:003678
actin binding GO:0003678
actin binding GO:0003779
ubiquitin–like protein ligase activity GO:0061630
ATP hydrolysis activity GO:0016887
cytoskeletal protein binding GO:0008092 p=2.9E-03 | n=4 p=3.4E-03 | n=41 p=4.3E-03 | n=20 p=5.6E-03 | n=26 fg=0.01 bg=0.00 bg=0.08 fg = 0.05bg=0.03 fg=0.07 bg=0.04 p=6.5E-03 n=29 p=7.1E-03 n=52 p=8.1E-03 n=10 p=8.5E-03 n=32 fg=0.08 bg=0.05 bg=0.10 fq = 0.14fg=0.03 bg=0.01 fg=0.09 bg=0.06 p=1.1E-02 n=8 p=1.2E-02 n=12 bg=0.01 fg=0.02 fg=0.03 bg=0.02 fg=0.01 bg=0.00 p=1.3E-02 bg=0.00 bg=0.20 p=1.3F-02 n=3fg=0.01 p=1.4E-02 fg=0.24 fg=0.06 p=1.6F-02ba = 0.04n=24 bg=0.20 p=1.6E-02 n=89 fg=0.06 bg=0.04 p=1.7E-02n = 23p=1.8E -02 bg=0.01 p=2.0E-02 p=2.5E-02 p=2.8E-02 p=2.8E-02 n=5fg=0.01 bg=0.01 n=6bg=0.01 n = 13■fg=0.03 bg=0.02 bğ=0.04 n=20 fg=0.05 fg=0.05 p=2.8E-02n=20 bg=0.04 fg=0.07 p=2.9E-02 bg=0.05 cytoskeletal protein binding GO:0018092
nucleoside–triphosphatase activity GO:0017111
identical protein binding GO:0042802
ATP–dependent activity GO:0140657
E–box binding GO:0070888 p=2.9E-02n = 39fg=0.10 fg=0.10 bg=0.08 p=3.0E-02 bg=0.07 n = 36p=3.2E-02 p=3.2E-02 fg=0.20 fg=0.07 n=75 bg=0.17 bg=0.05 bg=0.01 n=27 p=3.7E-02 p=3.9E-02 fg=0.01 n=5 n=12 transcription corepressor activity GO:0003714 snRNA binding GO:0017069 bq = 0.02fg=0.01 p=4.2E-02 bg=0.00

Elav_Nvec_vc1.1_XM_001628964.3

GO:CC Elav_Nvec_vc1.1_XM_001628964.3

-log(p)
n=372/1453 input genes with annotations

3

5

0.0

0.2

2

0

1

fraction genes in fg and expected valu

fraction

0.4

0.6

0.8

1.0

