

poly-pyrimidine tract binding GO:0008187
mRNA 3'-UTR AU-rich region binding GO:0035925
poly(U) RNA binding GO:0008266
myosin heavy chain binding GO:00032036
miRNA binding GO:00032198
DNA secondary structure binding GO:0000217
minor groove of adenine-thymine-rich DNA... GO:0003680
palmitoyl-(protein) hydrolase activity GO:0008474
palmitoyl hydrolase activity GO:0098599
double-stranded RNA binding GO:0003725
transforming growth factor beta receptor... GO:0005160
microfilament motor activity GO:00061980
small GTPase binding GO:0061980
small GTPase binding GO:0031267
translation regulator activity, nucleic ... GO:0090079
translation regulator activity GO:0045182
structural constituent of muscle GO:0008307
Wnt-protein binding GO:0017147
thiolester hydrolase activity GO:0016790
translation repressor activity GO:0030371
single-stranded RNA binding GO:0003727
mRNA regulatory element binding translat... GO:0009000
identical protein binding GO:0017022
HMG box domain binding GO:0017022
HMG box domain binding GO:00071837
mRNA 3'-UTR binding GO:0005126
GTPase regulator activity GO:0030695
cytoskeletal motor activity GO:0030377 p=2.7E-02 p=2.7E-02 fg=0.10 fg=0.10 bg=0.00 bg=0.00 n=1fg=0.10 p=2.7E-02 p=5.4E-02 n=1bg=0.00 bg=0.01 fg=0.10 n=1p=5.4E-02 p=5.4E-02 n=1fg=0.10 bg=0.01 fg=0.10 bg=0.01 n=1p=5.4E-02 p=5.4E-02 n=1 fg=0.10 bg=0.01 fg=0.10 bg=0.01 n=1fg=0.10 fg=0.10 p=5.4E-02 p=5.4E-02 n=1bg=0.01 bg=0.01 n=1p=5.4E-02 p=5.4E-02 fg=0.10 bg=0.01 n=1fa=0.10 bg=0.01 p=5.4E-02 p=7.4E-02 bg=0.01 $f_{q=0.20}$ n=2ba = 0.05bg=0.01 p=8.0E-02 fg=0.10 fg=0.10 fg=0.10 bg=0.01 p=8.0E-02n=1p=8.0E-02 p=8.0E-02 bg=0.01 n=1fg=0.10 fg=0.10 bg=0.01 n=1-02 -02 p=8.0E bg=0.01 n=1p=8.0E n=1fg=0.10 bg=0.01 fg=0.10 p=8.0E -02 bg=0.01 n=1n=1p=8.0E-02fg=0.10 bg=0.01 p=9.6E -02 bg=0.19 n=4fg=0.10 fg=0.10 p=1.1E-01 bg=0.01 n=1-01 bg=0.01 p=1.1E n=1p=1.1E-01 n=1fg=0.10 bg=0.01 bg=0.01 bg=0.06 p=1.1E-01 fg=0.10 n=1 p=1.1E-01 p=1.1E-01 n=2 n=2 fg=0.20 fg=0.20 GTPase regulator activity GO:0030695 cytoskeletal motor activity GO:0003774 bq=0.06 p=1.3E-01 fg=0.10 bg=0.01 0 2 0.0 0.2 1 3 5 0.4 0.6 0.8 1.0 fraction -log(p) n=10/53 input genes with annotations

GO:CC Elav_Nvec_vc1.1_XM_032385556.2

fraction genes in fg and expected valu

