

poly(U) RNA binding GO:0008266
manganese ion binding GO:0030145
fibroblast growth factor-activated recep... GO:0005007
oxidoreductase activity, acting on the a... GO:0016620
polynucleotide adenylyltransferase activ... GO:0016769
oxidoreductase activity, transferring nitro... GO:0016769
oxidoreductase activity, acting on paire... GO:0016705
protein demethylase activity GO:0140457
fibroblast growth factor binding GO:0017134
histone demethylase activity GO:0032452
glyceraldehyde-3-phosphate dehydrogenase... GO:0043891
all-trans retinal binding GO:0005503
histone H3-methyl-arginine-2 demethylase... GO:0033746
histone H3-methyl-arginine-3 demethylase... GO:0033748
histone H3-methyl-arginine-3 demethylase... GO:0033749
L12 snRNA binding GO:0030626
oxidoreductase activity, acting on paire... GO:0016709
T cell receptor binding GO:0042608
peptidyl-lysine 5-dioxygenase activity GO:0070815
glutamate 5-kinase activity GO:0004349
all-trans-retinol binding GO:1904768
25-hydroxycholecalciferol-24-hydroxylase... GO:0061896
all-trans retinol 3,4-desaturase activit... GO:0061897
all-trans retinoic acid 3,4-desaturase activit... GO:0061898
11-cis-retinal 3,4-desaturase activit... GO:0061898
5-adenosyl-L-methionine transmembrane tr... GO:000095
poly(ADP-ribose) glycohydrolase activity GO:0004567
amidinotransferase activity GO:00015067 p=1.9E-03 | n=3 p=3.0E-03 | n=4 fg=0.04 fg=0.06 bg=0.00 bg=0.01 ■fg=0.03 bg=0.00 fg=0.03 bg=0.00 fg=0.03 bg=0.00 bg=0.00 fg=0.03 fğ=0.04 p=1.8E-02 p=2.2E-02 n=3 bg=0.01 fg=0.03 n=2bq = 0.00p=2.2E-02 p=2.2E-02 n=2 n=2 fg=0.03 fg=0.03 bg=0.00 bq=0.00 p=3.0E-02 p=3.0E-02 bg=0.00 fg=0.01 fa=0.01 bg=0.00 bg=0.00 n=1p=3.0E-02 p=3.0E-02 fg=0.01 fa=0.01ba = 0.00n=1bg=0.00 fg=0.01 fg=0.01 p=3.0E-02n=1bg=0.00 p=3.0E bg=0.00 n=1p=3.0E-02fg = 0.01bg=0.00 n=1p=3.0E bg=0.00 n=1p=3.0E-02 p=3.0E-02 fg=0.01 n=1bg=0.00 fg=0.01 bg=0.00 n=1p=3.0E-02 p=3.0E-02 n=1fg=0.01 bg=0.00 fg=0.01 bg=0.00 n=1p=3.0E-02 fg=0.01 bg=0.00 n=1p=3.0E-02 fg=0.01 bg=0.00 n=1fg=0.01 p=3.0E-02n=1bg=0.00 bg=0.00 bg=0.00 fg=0.01 p=3.0E-02 n=1p=3.0E-02 p=3.0E-02 fg=0.01 fg=0.01 n=1 amidinotransferase activity GO:0015067 glycine amidinotransferase activity GO:0015068 n=1bq = 0.00fg=0.01 p=3.0E-02 bg=0.00 2 3 0.0 1 5 0.2 0.4 0.6 8.0 1.0 fraction –log(p) n=71/233 input genes with annotations

GO:CC Elav_Nvec_vc1.1_XM_001625109.3

fraction genes in fg and expected valu

