

p=9.7E-03 | n=4 p=1.1E-02 | n=2 ∥fg=0.02 ion channel inhibitor activity GO:0008200 bg=0.01 fg=0.01 bg=0.00 tRNA-specific ribonuclease activity GO:0004549 p=1.1E-02 n=2 p=1.1E-02 n=2 fg=0.01 telomerase RNA binding GO:0070034 bg=0.00 N4–(beta–N–acetylglucosaminyl)–L–asparag... GO:0003948 potassium channel inhibitor activity GO:0019870 potassium ion transmembrane transporter ... GO:0015079 spectrin binding GO:0030507 fg=0.01 bg=0.00 fg=0.02 n=3 p=1.8E-02 bg=0.00 p=2.6E-02fg=0.03 bg=0.01 n=5potassium ion transmembrane transporter ... GO:0015079
spectrin binding GO:0030507
transferase activity, transferring nitro... GO:0016769
miRNA binding GO:0035198
WW domain binding GO:0050699
acylglycerol O-acyltransferase activity GO:0016411
1-acylglycerol-3-phosphate O-acyltransfe... GO:0003841
triglyceride lipase activity GO:0004806
phosphoric diester hydrolase activity GO:0008081
nucleic acid binding GO:0003676
phosphotyrosine residue binding GO:0001784
Notch binding GO:0005112
GTPase regulator activity GO:0030695
GTPase activator activity GO:0030695
GTPase activator activity GO:0005267
kinesin binding GO:0019894
nucleoside-triphosphatase regulator acti... GO:006589
hydrolase activity, acting on ester bond... GO:0016788
cyclin-dependent protein kinase activity GO:0097472
cyclin-dependent protein serine/threonin... GO:00061980
O-acyltransferase activity GO:0003371
sphosphatidic acid binding GO:00703007 p=2.9E-02 p=2.9E-02 fg=0.02 fg=0.02 n=3 bg=0.00 ba=0.00n=3p=3.1E-02 p=3.1E-02 n=2 n=2 fg=0.01 fg=0.01 bg=0.00 bq=0.00 bg=0.00 p=3.1E-02 fg=0.01 p=3.1E-02bg=0.00 bg=0.00 n=2fa=0.01fg=0.01 p=3.3E-02n=5fg=0.03 ba = 0.01bğ=0.19 p=3.9E-02 g=0.02 bg=0.01 p=4.3E-02n=3p=4.3E=02 p=4.3E=02 p=4.4E=02 p=5.1E=02 p=5.1E=02 bg=0.01 n = 13fg = 0.08bg=0.05 n=8 fg=0.05 bg=0.02 n=4**∥** fg=0.02 bg=0.01 n=4fg=0.02 bg=0.01 fg=0.08 p=5.4E-02 p=5.6E-02 n=14 bg=0.05 bg=0.07 fg=0.10 n=17p=5.0E-02 p=5.7E-02 p=5.7E-02 p=5.7E-02 p=5.7E-02 p=5.7E-02 fg=0.01 bg=0.00 n=2n=2fg=0.01 bg=0.00 fg=0.01 n=2bg=0.00 bg=0.00 bg=0.00 fg=0.01 n=2n=2 n=2 fg=0.01 fg=0.01 translation repressor activity GO:0030371 phosphatidic acid binding GO:0070300 bq = 0.00p=5.7E-02 fg=0.01 bg=0.00 0 2 0.0 1 3 5 0.2 0.4 0.6 0.8 1.0 fraction –log(p) n=167/599 input genes with annotations

GO:CC Elav_Nvec_vc1.1_XM_032378403.2

fraction genes in fg and expected valu

