

Elav\_Nvec\_vc1.1\_XM\_032377792.2

p=1.9E-03 n=2 p=5.0E-03 n=6 p=5.7E-03 n=2 p=5.7E-03 n=2 fg=0.02 fg=0.06 bg=0.00 bg=0.02 histone threonine kinase activity GO:0035184 transcription corepressor activity GO:003714
adenyl–nucleotide exchange factor activit... GO:0000774
SUMO transferase activity GO:0019789
DNA–binding transcription factor activit... GO:0000981
regulatory RNA binding GO:0061980
DNA topoisomerase binding GO:0044547
DNA–binding transcription activator acti fg=0.02 bg=0.00 bg=0.00 fg=0.02 p=7.2E-03 n=13 p=1.1E-02 n=2 fg = 0.12bg=0.06 bg=0.00 fg=0.02 p=1.1E-02 n=2 p=1.5E-02 n=8 fg=0.02 fg=0.08 bg=0.00 DNA-binding transcription activator acti... GO:0001228
DNA-binding transcription activator acti... GO:0001216
cis-regulatory region sequence-specific ... GO:0000987
RNA polymerase II cis-regulatory region ... GO:0000978
12-hydroxyheptadecatrienoic acid synthas... GO:0036134
thromboxane-A synthase activity GO:0004796 bq=0.03 p=1.5E-02 p=1.6E-02 fg=0.08 fg=0.08 n=8 bg=0.03 n=8 ba = 0.03fg=0.08 bg=0.03 p=1.6E-02 p=1.8F-02fg=0.02 bg=0.00 bg=0.00 n=2thromboxane—A synthase activity GO:0004796
ribosome binding GO:0043022
hydrolase activity, acting on carbon—nit... GO:0016810
CoA carboxylase activity GO:0016421
histone kinase activity (H3—T3 specific) GO:0072354
siRNA binding GO:0035197
glutathione—disulfide reductase (NADPH) ... GO:0004362
proteinase activated receptor binding GO:0031871
very long—chain fatty acid—CoA ligase ac... GO:0031957
sterol response element binding GO:0032810
5'-3' DNA helicase activity GO:0043139
farnesyltranstransferase activity GO:0004311
histone pre—mRNA stem—loop binding GO:0071207
large conductance calcium—activated pota... GO:0060072
polyamine oxidase activity GO:00046592
adenosylhomocysteinase activity GO:00046692
protein farnesyltransferase activity GO:00046680 fg=0.02 p=1.8E-02 fa=0.03 p=2.2E-02n=3bg=0.01 bğ=0.01 p=4.1E-02 fg=0.04 p=4.4E-02fg=0.01 fg=0.01 n=1bg=0.00 p=4.4E-02 p=4.4E-02 p=4.4E-02 p=4.4E-02 bg=0.00 n=1fg = 0.01n=1bg=0.00 fg=0.01 bg=0.00 n=1fg=0.01 n=1bg=0.00 p=4.4E-02 fg=0.01 bg=0.00 n=1p=4.4E-02 p=4.4E-02 n=1fg=0.01 bg=0.00 fg=0.01 bg=0.00 n=1p=4.4E-02 p=4.4E-02 fg=0.01 bg=0.00 n=1fg=0.01 bg=0.00 n=1n=1 fg=0.01 p=4.4E-02 bg=0.00 p=4.4E-02 p=4.4E-02 p=4.4E-02 fg=0.01 bg=0.00 bg=0.00 n=1fg=0.01 fg=0.01 n=1 protein farnesyltransferase activity GO:0004660 beta-1,4-mannosylglycoprotein 4-beta-N-a... GO:0003830 n=1bq = 0.00p=4.4E-02 fg=0.01 bg=0.00 0 1 2 3 0.0 0.2 5 0.4 0.6 8.0 1.0 fraction –log(p)

GO:CC Elav\_Nvec\_vc1.1\_XM\_032377792.2

n=105/365 input genes with annotations

fraction genes in fg and expected valu

