

p=3.3E-03 n=2 p=1.0E-02 n=1 p=1.0E-02 n=1 p=1.0E-02 n=1 E-box binding GO:0070888 long-chain fatty acid transporter activi... GO:0005324 phosphatidylcholine transporter activity GO:0008525 fg=0.12 fg=0.06 bg=0.01 bg=0.00 fg=0.06 bg=0.00 estradiol 17-beta-dehydrogenase activity GO:0004303 interleukin-2 receptor binding GO:0005134 testosterone 17-beta-dehydrogenase (NADP... GO:0047045 steroid dehydrogenase activity GO:0016229 fg=0.06 bg=0.00 p=1.0E-02 | n=1 p=1.0E-02 | n=1 p=1.0E-02 | n=1 p=1.0E-02 | n=1 fg=0.06 bg=0.00 bg=0.00 fg=0.06 fg=0.06 bg=0.00 fğ=0.06 steroid dehydrogenase activity, acting o... GO:0033764
protein dimerization activity GO:0046983
protein homodimerization activity GO:0042803
metal ion transmembrane transporter acti... GO:0046873
DNA-binding transcription factor activit... GO:000981
ATPase-coupled transmembrane transporter... GO:0042626 ba=0.00p=1.1E-02 n=6 p=1.6E-02 n=5 p=1.8E-02 n=3 fg=0.38 fg=0.31 bg=0.13 bg=0.10 fg=0.19 bg=0.04 bg=0.07 bg=0.01 p=1.9F-02n=4fa = 0.25FPase-coupled transmembrane transporter... GO:0042626 lipid transporter activity GO:0005319 ferrous iron transmembrane transporter a... GO:0015093 phosphatidylinositol transfer activity GO:0008526 phosphatidic acid transfer activity GO:1990050 DNA-binding transcription activator acti... GO:0001228 DNA-binding transcription activator acti... GO:0001216 calcium ion transmembrane transporter ac... GO:0015085 D2 dopamine receptor binding GO:0031749 RNA polymerase II intronic transcription... GO:0001162 TFIID-class transcription factor complex... GO:0001094 fg=0.12 p=1.9F-02n=2bg=0.01 bg=0.00 p=2.0E-02 fg=0.06 fg=0.06 fg=0.06 p=2.0E-02 p=2.0E-02 n=1bg=0.00 bg=0.00 n=1p=2.1E-02 p=2.1E-02 fg=0.19 fg=0.19 n=3bg=0.04 bğ=0.04 n=3fg=0.12 fg=0.06 p=2.9E-02n=2bg=0.02 p=3.0E-02 bg=0.00 n=1p=3.0E-02 p=3.0E-02 n=1fg=0.06 bg=0.00 n=1fg=0.06 bg=0.00 P-type calcium transporter activity GO:00120014

P-type calcium transporter activity GO:0120014

DNA-binding transcription factor activit... GO:0003700

identical protein binding GO:0042802 fg=0.06 p=3.0E-02 p=3.0E-02 n=1bg=0.00 fg=0.06 bg=0.00 n=1fg=0.06 p=3.0E-02 n=1bg=0.00 fg=0.25 p=3.6E-02bg=0.08 n=4p=3.9E-02 p=4.0E-02 fg=0.38 fg=0.06 bg=0.17 n=6protein phosphatase inhibitor activity GO:0004864 C2H2 zinc finger domain binding GO:0070742 bg=0.00 n=1 p=4.0E-02 fg=0.06 bg=0.00 0 2 0.0 0.2 1 3 5 0.4 0.6 8.0 1.0 fraction -log(p)

GO:CC Elav_Nvec_vc1.1_XM_032385715.2

n=16/85 input genes with annotations

fraction genes in fg and expected valu

