

JUN kinase binding GO:0008432
outward rectifier potassium channel acti... GO:0015271
protein self-association GO:0043621
phosphatidyl-N-dimethylethanolamine N-me... GO:0080101
translation elongation factor binding GO:0061770
phosphatidyl-N-methylethanolamine N-meth... GO:0000773
oxidoreductase activity, acting on the C... GO:0016649
electron-transferring-flavoprotein dehyd... GO:0004174
cysteine-tRNA ligase activity GO:0004817
oxidoreductase activity, acting on NAD(P... GO:0050664
NAD(P)H oxidase H2O2-forming activity GO:0016174
intracellular sodium activated potassium... GO:0005228
co-SMAD binding GO:0070410
STAT family protein binding GO:00797677
sequence-specific single stranded DNA bi... GO:0098847
uridine kinase activity GO:0004849
nucleoside kinase activity GO:0015206
heparan-alpha-glucosaminide N-acetyltran... GO:0015019
gamma-butyrobetaine dioxygenase activity GO:0008336
DNA-binding transcription repressor acti... GO:0001227
DNA-binding transcription repressor acti... GO:0001227
DNA-binding transcription repressor acti... GO:00015269
RNA polymerase II intronic transcription... GO:00015269
RNA polymerase II intronic transcription... GO:0001162
fibroblast growth factor-activated recep... GO:00071949
receptor-receptor interaction GO:0090722
transcription regulator activity GO:00140110
phosphatidylinositol bisphosphate kinase... GO:00052813 p=2.5E-03 | n=2 p=5.1E-03 | n=2 fg=0.08 fg=0.08 bg=0.00 bg=0.00 p=1.3E-02 n=2 p=1.6E-02 n=1 fg=0.08 bg=0.01 fg=0.04 bg=0.00 p=1.6E-02 p=1.6E-02 fg=0.04 n=1bg=0.00 fg=0.04 bg=0.00 n=1bg=0.00 p=1.6E-02 fg=0.04 fg=0.04 p=1.6E-02ba = 0.00n=1p=1.6E-02 p=1.6E-02 fg=0.04 bg=0.00 fg=0.04 bq=0.00 n=1bg=0.00 p=1.6E-02 fg=0.04 p=1.6F-02fg=0.04 bg=0.00 bg=0.00 n=1p=3.2E-02 p=3.2E-02 fg=0.04 fa=0.04 n=1bg = 0.00bg=0.00 p=3.2E-02 fg=0.04 fg=0.04 p=3.2E-02n=1bg=0.00 fg=0.04 bg=0.00 n=1p=3.2F-0.2fg=0.04 n=1bg=0.00 p=3.2E-02 p=4.4E-02 bg=0.00 n=1n=2fg=0.08 bg=0.01 p=4.4E-02 n=2fg=0.08 bg=0.01 n=1fg=0.04 p=4.8E-02 bg=0.00 p=4.8E-02 fg=0.04 bg=0.00 n=1p=4.8E-02 n=1fg=0.04 bg=0.00 p=4.8E-02 fg=0.04 bg=0.00 n=1p=4.8E-02 n=1fg=0.04 bg=0.00 p=4.8E-02 p=4.8E-02 p=7.3E-02 bg=0.00 bg=0.00 fg=0.04 n=1fg=0.04 n=1 transcription regulator activity GO:0140110 phosphatidylinositol bisphosphate kinase... GO:0052813 =0.23n=6 bq = 0.12p=7.9E-02 fg=0.04 bg=0.00 2 0.0 1 3 5 0.2 0.4 0.6 0.8 1.0

GO:CC Fox\_Nvec\_vc1.1\_XM\_032365096.2

-log(p)
n=26/117 input genes with annotations

fraction genes in fg and expected valu

fraction

