

ammonium ion binding GO:0070405

[3-methyl-2-oxobutanoate dehydrogenase (... GO:0047323
histone pre-mRNA stem-loop binding GO:0071207
phosphatidylcholine transporter activity GO:0008525
beta1-adrenergic receptor activity GO:0004940
beta2-adrenergic receptor activity GO:0004941
bradykinin receptor binding GO:0031711
aminomethyltransferase activity GO:0004047
B2 bradykinin receptor binding GO:0031713
methylenetetrahydrofolate dehydrogenase ... GO:0004486
methylenetetrahydrofolate dehydrogenase ... GO:0004487
methylenetetrahydrofolate dehydrogenase ... GO:0004487
methylenetetrahydrofolate dehydrogenase ... GO:0004487
methylenetetrahydrofolate dehydrogenase ... GO:0004487
methylenetetrahydrofolate cyclohydrolase ... GO:000477
formate-tetrahydrofolate cyclohydrolase ... GO:0004329
dopamine binding GO:0035240
T cell receptor binding GO:0042608 fg=0.03 p=1.4E-02 | n=1 bg=0.00 p=1.4E-02 n=1 fg=0.03 bg=0.00 fg=0.03 p=1.4E-02 n=1 p=1.4E-02 n=1 bg=0.00 bg=0.00 fg=0.03 p=1.4E-02 n=1 p=1.4E-02 n=1 fg=0.03 bg=0.00 fg=0.03 bg=0.00 dopartific binding GO:003240

T cell receptor binding GO:0042608

D-xylose 1-dehydrogenase (NADP+) activit... GO:0047837

estradiol 17-beta-dehydrogenase activity GO:0004303
testosterone 17-beta-dehydrogenase (NADP... GO:0047045

protein domain specific binding GO:0019904 p=1.4E-02 n=1 p=1.4E-02 n=1 fg=0.03 bg=0.00 fg=0.03 bg=0.00 fğ=0.03 p=1.4E-02 n=1 p=1.4E-02 n=1 bg=0.00 fg=0.03 fg=0.21 fg=0.06 bg=0.00 bg=0.08 p=1.6E-02 n=7 p=2.0E-02 n=2 ATPase–coupled ion transmembrane transpo... GO:0042625 adenyl ribonucleotide binding GO:0032559 bq = 0.01p=2.1E-02 fg=0.15 bg=0.05 2 0.0 0.2 1 3 5 0.4 0.6 0.8 1.0 fraction –log(p) n=33/137 input genes with annotations

GO:CC Elav_Nvec_vc1.1_XM_001647488.3

fraction genes in fg and expected valu

