

purine ribonucleoside binding GO:0032550
ribonucleoside binding GO:0032549
3'-phosphoadenosine 5'-phosphosulfate tr... GO:0046964
open rectifier potassium channel activit... GO:0005252
low-density lipoprotein particle binding GO:0030169
taste receptor binding GO:0031883
testosterone 17-beta-dehydrogenase (NADP-.. GO:0047045
glutamate-ammonia ligase activity GO:0004356
D-xylose 1-dehydrogenase (NADP+) activit... GO:0047837
intracellular sodium activated potassium... GO:005228
mono-olein transacylation activity GO:0051264
diolein transacylation activity GO:0034041
protein-membrane adaptor activity GO:0043495
C-acyltransferase activity GO:0016408 bg=0.00 p=4.8E-02 p=4.8E-02 bg=0.00 n=1fg=0.01 n=1bg=0.00 p=4.8E-02 fg=0.01 bg=0.00 n=1n=1fg=0.01 bg=0.00 p=4.8E-02p=4.8E-02 fg=0.01 bg=0.00 n=1p=4.8E-02 fg=0.01 bg=0.00 n=1p=4.8E-02 fg=0.01 bg=0.00 n=1fg=0.01 n=1 p=4.8E-02 bg=0.00 bg=0.00 bg=0.00 C-acyltransferase activity GO:0016408 tricarboxylate secondary active transmem... GO:0005371 p=4.8E-02 fg=0.01 n=1p=4.8E-02 p=4.8E-02 fg=0.01 fg=0.01 n=1 phospholipase D activator activity GO:1990583 steroid dehydrogenase activity GO:0016229 n=1bq = 0.00fg=0.01 p=4.8E-02 bg=0.00 2 0.0 3 5 0.2 0.4 0.6 8.0 1.0 fraction –log(p) n=76/258 input genes with annotations

GO:CC Ncol\_Nvec\_vc1.1\_XM\_048730161.1

fraction genes in fg and expected valu

