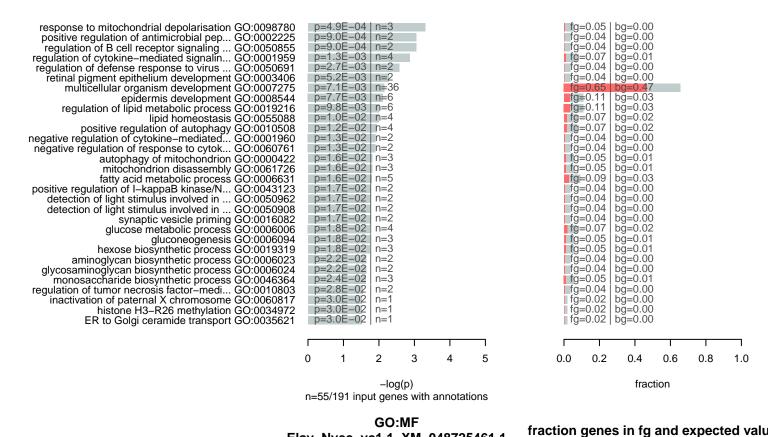
fraction



amino acid binding GO:0016597
DNA-binding transcription repressor acti... GO:0001227
phospholipase A2 activity GO:0004623
Wnt-protein binding GO:0017147
arrestin family protein binding GO:099763
carboxylic acid binding GO:0997001
L-tyrosine:2-oxoglutarate aminotransfera... GO:0004838
D5 dopamine receptor binding GO:0031752
leucine binding GO:0031752
leucine binding GO:0070728
galactosylxylosylprotein 3-beta-galactos... GO:0047220
lipoprotein lipase activity GO:0004465
sphingolipid transporter activity GO:0044654
G-protein beta-subunit binding GO:0031681
L-tyrosine aminotransferase activity GO:0004884
lysophosphatidic acid binding GO:0035727
mono-olein transacylation activity GO:0051264
diolein transacylation activity GO:0051265
cyclic GMP-AMP synthase activity GO:0120016
ceramide transfer activity GO:0120017
calcium channel inhibitor activity GO:0019855
sulfiredoxin activity GO:0032542
2',3'-cyclic GMP-AMP synthase activity GO:0061501 p=3.0E-03 | n=3 p=3.5E-03 | n=4 bg=0.01 bg=0.01 fg=0.06 fg=0.08 p=5.5E-03 n=2 p=9.1E-03 n=2 p=9.1E-03 n=2 p=1.5E-02 n=3 fg=0.04 bg=0.00 fg=0.04 bg=0.00 fğ=0.04 bg=0.00 bg=0.01 fg=0.06 p=3.1E-02 p=3.1E-02 fg=0.02 fg=0.02 n=1bg=0.00 bg=0.00 n=1p=3.1E-02 p=3.1E-02 n=1fg=0.02 bg=0.00 fg=0.02 bg=0.00 n=1bg=0.00 fg=0.02 p=3.1E-02 p=3.1E-02fa = 0.02bg=0.00 bg=0.00 n=1p=3.1E-02 p=3.1E-02 p=3.1E-02 fg=0.02 fg=0.02 n=1bg = 0.00bg=0.00 p=3.1E-02 fg=0.02 fg=0.02 bg=0.00 p=3.1E-02n=1p=3.1E bg=0.00 n=1p=3.1E-02 p=3.1E-02 fg=0.02 n=1bg=0.00 fg=0.02 bg=0.00 n=1fg=0.02 p=3.1E-02 p=3.1E-02 n=1bg=0.00 fg=0.02 bg=0.00 n=1fg=0.02 p=3.1E-02 p=3.1E-02 n=1 bg=0.00 fg=0.02 bg=0.00 n=1sulfiredoxin activity GO:0019835
sulfiredoxin activity GO:0019835
2',3'-cyclic GMP-AMP synthase activity GO:0061501
serine binding GO:0070905
platelet-activating factor acetyltransfe... GO:0047179
GDP-dissociation inhibitor activity GO:0005092 p=3.1E-02 p=3.1E-02 n=1fg=0.02 bg=0.00 fg=0.02 bg=0.00 n=1fg=0.02 p=6.2E-02 p=6.2E-02 n=1bg=0.00 bg=0.00 bg=0.00 fg=0.02 n=1p=6.2E-02 p=6.2E-02 fg=0.02 fg=0.02 n=1 sphingolipid binding GO:0046625 long-chain fatty acyl-CoA binding GO:0036042 n=1bq = 0.00fg=0.02 p=6.2E-02 bg=0.00 0 2 0.0 0.2 1 3 5 0.4 0.6 8.0 1.0

Elav\_Nvec\_vc1.1\_XM\_048725461.1

GO:CC
Elav\_Nvec\_vc1.1\_XM\_048725461.1 fraction genes in fg and expected value

-log(p)
n=50/191 input genes with annotations

