

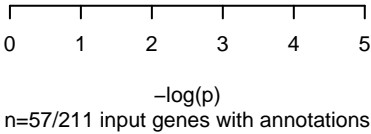
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032385496.2

fraction genes in fg and expected value

protein heterooligomerization	GO:0051291
renal water homeostasis	GO:0003091
heart valve morphogenesis	GO:0003179
ventral spinal cord development	GO:0021517
nephric duct formation	GO:0072179
negative regulation of cAMP-dependent pr...	GO:2000480
positive regulation of meiotic cell cycl...	GO:1904146
negative regulation of interleukin-2 pro...	GO:0032703
phosphatidylglycerol acyl-chain remodeli...	GO:0036148
positive regulation of superoxide anion ...	GO:0032930
renal tubule morphogenesis	GO:0061333
cell differentiation in spinal cord	GO:0021515
regulation of inflammatory response	GO:0050727
lymphoid progenitor cell differentiation	GO:0002320
regulation of nephron tubule epithelial ...	GO:0072182
negative regulation of blood vessel endo...	GO:0043537
cardiac ventricle formation	GO:0003211
activation of protein kinase A activity	GO:0034199
autonomic nervous system development	GO:0048483
cellular response to peptide hormone sti...	GO:0071375
uterus development	GO:0060065
metanephric renal vesicle morphogenesis	GO:0072283
retina layer formation	GO:0010842
positive regulation of mesonephros devel...	GO:0061213
regulation of phospholipid biosynthetic ...	GO:0071071
response to antipsychotic drug	GO:0097332
response to clozapine	GO:0097338
cardiac right ventricle morphogenesis	GO:0003215
positive regulation of urine volume	GO:0035810
definitive hemopoiesis	GO:0060216

p=9.2E-04	n=4
p=9.4E-04	n=3
p=9.4E-04	n=3
p=9.4E-04	n=3
p=9.7E-04	n=2
p=9.7E-04	n=2
p=9.7E-04	n=2
p=9.7E-04	n=2
p=9.7E-04	n=2
p=1.2E-03	n=5
p=1.5E-03	n=3
p=1.7E-03	n=5
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=4.1E-03	n=3
p=4.9E-03	n=7
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=2

fg=0.07	bg=0.01
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.09	bg=0.01
fg=0.05	bg=0.00
fg=0.09	bg=0.02
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.05	bg=0.01
fg=0.12	bg=0.04
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00



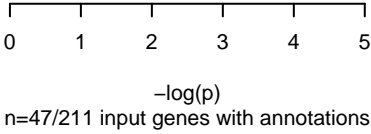
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032385496.2

fraction genes in fg and expected value

protein kinase A catalytic subunit bindi...	GO:0034236
cAMP-dependent protein kinase inhibitor ...	GO:0004862
beta-2 adrenergic receptor binding	GO:0031698
peptide hormone binding	GO:0017046
cAMP binding	GO:0030552
ephrin receptor binding	GO:0046875
cytokine receptor binding	GO:0005126
HMG box domain binding	GO:0071837
voltage-gated cation channel activity	GO:0022843
outward rectifier potassium channel acti...	GO:0015271
purine ribonucleoside triphosphate bindi...	GO:0035639
carbohydrate derivative binding	GO:0097367
metalloendopeptidase activity	GO:0004222
ribonucleotide binding	GO:0032553
purine ribonucleotide binding	GO:0032555
purine nucleotide binding	GO:0017076
protein domain specific binding	GO:0019904
type I transforming growth factor beta r...	GO:0034713
heparan sulfate binding	GO:1904399
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159
Roundabout binding	GO:0048495
tRNA (uracil) methyltransferase activity	GO:0016300
calcitonin family binding	GO:0097644
amylin binding	GO:0097645
BH4 domain binding	GO:0051435
neuropilin binding	GO:0038191
beta-endorphin binding	GO:0031626
acetylcholine receptor regulator activit...	GO:0030548
acetylcholine receptor activator activit...	GO:0030549
phorbol ester receptor activity	GO:0001565

p=8.5E-04	n=2
p=8.5E-04	n=2
p=8.5E-04	n=2
p=2.5E-03	n=2
p=4.9E-03	n=2
p=8.1E-03	n=2
p=1.0E-02	n=3
p=1.2E-02	n=2
p=1.4E-02	n=3
p=1.6E-02	n=2
p=1.7E-02	n=7
p=1.9E-02	n=10
p=2.1E-02	n=2
p=2.3E-02	n=9
p=2.3E-02	n=9
p=2.7E-02	n=9
p=2.9E-02	n=9
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1

fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.06	bg=0.01
fg=0.04	bg=0.00
fg=0.06	bg=0.01
fg=0.04	bg=0.00
fg=0.15	bg=0.06
fg=0.21	bg=0.08
fg=0.04	bg=0.01
fg=0.19	bg=0.07
fg=0.19	bg=0.07
fg=0.19	bg=0.07
fg=0.19	bg=0.09
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032385496.2

fraction genes in fg and expected value

germinal vesicle	GO:0042585
dendritic shaft	GO:0043198
nucleotide-activated protein kinase comp...	GO:0031588
cAMP-dependent protein kinase complex	GO:0005952
T-tubule	GO:0030315
actomyosin	GO:0042641
dendritic spine	GO:0043197
precatalytic spliceosome	GO:0071011
sarcomere	GO:0030017
membrane raft	GO:0045121
membrane microdomain	GO:0098857
azurophil granule membrane	GO:0035577
cation channel complex	GO:0034703
secretory granule membrane	GO:0030667
cell periphery	GO:0071944
stress fiber	GO:0001725
contractile actin filament bundle	GO:0097517
actin filament bundle	GO:0032432
voltage-gated potassium channel complex	GO:0008076
potassium channel complex	GO:0034705
lipoprotein particle	GO:1990777
interphase microtubule organizing center	GO:0031021
L-type voltage-gated calcium channel com...	GO:1990454
amyloid-beta complex	GO:0106003
RNA polymerase II transcription represso...	GO:0090571
male pronucleus	GO:0001940
intermediate-density lipoprotein particl...	GO:0034363
endosome to plasma membrane transport ve...	GO:0070381
high-density lipoprotein particle	GO:0034364
DNA ligase III-XRCC1 complex	GO:0070421

p=1.1E-04	n=3
p=1.5E-04	n=5
p=2.8E-03	n=2
p=2.8E-03	n=2
p=2.9E-03	n=3
p=6.5E-03	n=3
p=6.8E-03	n=5
p=1.8E-02	n=2
p=2.1E-02	n=4
p=2.2E-02	n=5
p=2.2E-02	n=5
p=2.3E-02	n=2
p=2.5E-02	n=3
p=2.8E-02	n=4
p=2.8E-02	n=25
p=2.9E-02	n=2
p=2.9E-02	n=2
p=2.9E-02	n=2
p=2.9E-02	n=2
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1
p=3.1E-02	n=1

fg=0.05	bg=0.00
fg=0.09	bg=0.01
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.05	bg=0.01
fg=0.05	bg=0.01
fg=0.09	bg=0.02
fg=0.04	bg=0.00
fg=0.07	bg=0.02
fg=0.09	bg=0.03
fg=0.09	bg=0.03
fg=0.04	bg=0.00
fg=0.05	bg=0.01
fg=0.07	bg=0.02
fg=0.45	bg=0.29
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00

