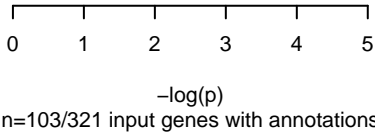


GO:BP
Elav_Nvec_vc1.1_XM_032384172.2

fraction genes in fg and expected value

positive regulation of Notch signaling p...	GO:0045747	p=4.2E-04	n=5
epithelial cell differentiation	GO:0030855	p=1.9E-03	n=16
glial cell proliferation	GO:0014009	p=2.0E-03	n=4
pro-B cell differentiation	GO:0002328	p=4.2E-03	n=2
S-adenosylmethionine biosynthetic proces...	GO:0006556	p=4.2E-03	n=2
primitive hemopoiesis	GO:0060215	p=8.2E-03	n=2
establishment of blood-brain barrier	GO:0060856	p=8.2E-03	n=2
sperm DNA decondensation	GO:0035041	p=8.2E-03	n=2
protein targeting to lysosome	GO:0006622	p=9.2E-03	n=3
epidermis development	GO:0008544	p=1.1E-02	n=8
cleavage furrow ingression	GO:0036090	p=1.3E-02	n=2
NAD biosynthesis via nicotinamide ribosi...	GO:0034356	p=1.3E-02	n=2
adherens junction maintenance	GO:0034334	p=1.3E-02	n=2
positive regulation of cAMP-mediated sig...	GO:0043950	p=1.3E-02	n=2
antigen processing and presentation of p...	GO:0002504	p=1.4E-02	n=4
antigen processing and presentation of p...	GO:0002495	p=1.4E-02	n=4
response to organic cyclic compound	GO:0014070	p=1.7E-02	n=15
response to cocaine	GO:0042220	p=1.8E-02	n=3
neuroepithelial cell differentiation	GO:0060563	p=1.8E-02	n=4
response to anesthetic	GO:0072347	p=1.8E-02	n=4
response to cycloheximide	GO:0046898	p=2.0E-02	n=2
MyD88-dependent toll-like receptor signa...	GO:0002755	p=2.0E-02	n=2
cell-cell junction maintenance	GO:0045217	p=2.0E-02	n=2
positive regulation of membrane protein ...	GO:0051044	p=2.0E-02	n=2
C4-dicarboxylate transport	GO:0015740	p=2.0E-02	n=2
negative regulation of extrinsic apoptot...	GO:1902042	p=2.0E-02	n=2
signaling	GO:0023052	p=2.0E-02	n=52
epithelial cell development	GO:0002064	p=2.1E-02	n=10
antigen processing and presentation of p...	GO:0048002	p=2.3E-02	n=4
endoplasmic reticulum to Golgi vesicle-m...	GO:0006888	p=2.4E-02	n=5

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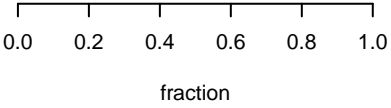
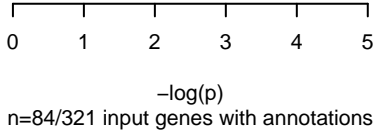


GO:MF
Elav_Nvec_vc1.1_XM_032384172.2

fraction genes in fg and expected value

LIM domain binding	GO:0030274	p=3.6E-03	n=2
regulatory RNA binding	GO:0061980	p=7.1E-03	n=2
transcription coregulator activity	GO:0003712	p=8.2E-03	n=10
sequence-specific double-stranded DNA bi...	GO:1990837	p=9.2E-03	n=10
arrestin family protein binding	GO:1990763	p=1.2E-02	n=2
molecular function inhibitor activity	GO:0140678	p=1.4E-02	n=3
transcription cis-regulatory region bind...	GO:0000976	p=1.6E-02	n=9
spectrin binding	GO:0030507	p=2.3E-02	n=2
G-protein alpha-subunit binding	GO:0001965	p=3.0E-02	n=2
alkanesulfonate transmembrane transporte...	GO:0042959	p=3.5E-02	n=1
siRNA binding	GO:0035197	p=3.5E-02	n=1
amino acid:sodium symporter activity	GO:0005283	p=3.5E-02	n=1
beta-1,4-N-acetylgalactosaminyltransfera...	GO:0033207	p=3.5E-02	n=1
pre-miRNA binding	GO:0070883	p=3.5E-02	n=1
taurine transmembrane transporter activi...	GO:0005368	p=3.5E-02	n=1
taurine:sodium symporter activity	GO:0005369	p=3.5E-02	n=1
3-hydroxyisobutryl-CoA hydrolase activi...	GO:0003860	p=3.5E-02	n=1
pyridine N-methyltransferase activity	GO:0030760	p=3.5E-02	n=1
RNA-3'-phosphate cyclase activity	GO:0003963	p=3.5E-02	n=1
G-protein beta-subunit binding	GO:0031681	p=3.5E-02	n=1
high-affinity glutamate transmembrane tr...	GO:0005314	p=3.5E-02	n=1
leucine-tRNA ligase activity	GO:0004823	p=3.5E-02	n=1
glutamate:sodium symporter activity	GO:0015501	p=3.5E-02	n=1
organic acid:sodium symporter activity	GO:0005343	p=3.5E-02	n=1
glutamine-tRNA ligase activity	GO:0004819	p=3.5E-02	n=1
mitochondrial promoter sequence-specific...	GO:0001018	p=3.5E-02	n=1
thioether S-methyltransferase activity	GO:0004790	p=3.5E-02	n=1
ATP-dependent peptidase activity	GO:0004176	p=3.5E-02	n=1
valine-tRNA ligase activity	GO:0004832	p=3.5E-02	n=1
alditol:NADP+ 1-oxidoreductase activity	GO:0004032	p=3.5E-02	n=1

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GO:CC
Elav_Nvec_vc1.1_XM_032384172.2

fraction genes in fg and expected value

methionine adenosyltransferase complex	GO:0048269	p=4.2E-03	n=2
NuRD complex	GO:0016581	p=8.2E-03	n=2
nuclear body	GO:0016604	p=8.4E-03	n=13
bicellular tight junction	GO:0005923	p=9.2E-03	n=3
extrinsic component of organelle membran...	GO:0031312	p=1.2E-02	n=3
autolysosome	GO:0044754	p=1.3E-02	n=2
germ cell nucleus	GO:0043073	p=1.8E-02	n=3
cell cortex	GO:0005938	p=2.5E-02	n=8
secondary lysosome	GO:0005767	p=2.7E-02	n=2
dynactin complex	GO:0005869	p=2.7E-02	n=2
kinetochore	GO:0000776	p=3.2E-02	n=4
female germ cell nucleus	GO:0001674	p=3.5E-02	n=2
Ndc80 complex	GO:0031262	p=3.8E-02	n=1
ATF4-CREB1 transcription factor complex	GO:1990589	p=3.8E-02	n=1
NMS complex	GO:0031617	p=3.8E-02	n=1
ciliary cap	GO:0061822	p=3.8E-02	n=1
shelterin complex	GO:0070187	p=3.8E-02	n=1
nuclear RNA export factor complex	GO:0042272	p=3.8E-02	n=1
RNA nuclear export complex	GO:0042565	p=3.8E-02	n=1
polysomal ribosome	GO:0042788	p=5.3E-02	n=2
polymeric cytoskeletal fiber	GO:0099513	p=5.4E-02	n=6
condensed chromosome, centromeric region	GO:0000779	p=5.5E-02	n=4
pronucleus	GO:0045120	p=6.3E-02	n=2
Cajal body	GO:0015030	p=6.3E-02	n=2
apical junction complex	GO:0043296	p=7.1E-02	n=5
cytoplasmic region	GO:0099568	p=7.2E-02	n=9
ruffle membrane	GO:0032587	p=7.4E-02	n=2
actomyosin contractile ring	GO:0005826	p=7.5E-02	n=1
extrinsic component of Golgi membrane	GO:0090498	p=7.5E-02	n=1
extrinsic component of mitochondrial inn...	GO:0031314	p=7.5E-02	n=1

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