

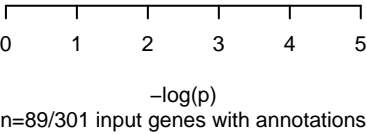
GO:BP
Elav_Nvec_vc1.1_XM_032382466.2

fraction genes in fg and expected value

positive regulation of insulin secretion	GO:0032024
actin cortical patch localization	GO:0051666
regulation of cellular response to manga...	GO:1905802
positive regulation of transcription fac...	GO:1901485
negative regulation of vascular associat...	GO:1904753
lysine transport	GO:0015819
endodermal cell fate specification	GO:0001714
cellular response to parathyroid hormone...	GO:0071374
cellular response to glucagon stimulus	GO:0071377
cellular response to glucocorticoid stim...	GO:0071385
nucleobase-containing small molecule bio...	GO:0034404
regulation of defense response to bacter...	GO:1900424
positive regulation of glucose import	GO:0046326
regulation of transcription by glucose	GO:0046015
lactate biosynthetic process	GO:0019249
glycerol catabolic process	GO:0019563
glycerol biosynthetic process from pyruv...	GO:0046327
lactate oxidation	GO:0019516
propionate catabolic process	GO:0019543
positive regulation of transcription fro...	GO:0061402
negative regulation of synaptic vesicle ...	GO:2000301
glucose catabolic process to lactate via...	GO:0019661
nitrogenous compound fermentation	GO:0019666
malate transport	GO:0015743
negative regulation of blood vessel endo...	GO:0043537
cellular response to potassium ion starv...	GO:0051365
cellular response to fructose stimulus	GO:0071332
response to methionine	GO:1904640
kidney interstitial fibroblast different...	GO:0072071
mesendoderm development	GO:0048382

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p=1.1E-03	n=4
p=1.3E-03	n=6
p=1.7E-03	n=3
p=2.5E-03	n=3
p=3.2E-03	n=2
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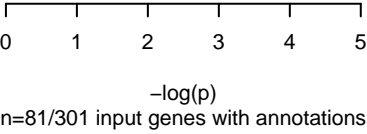
GO:MF
Elav_Nvec_vc1.1_XM_032382466.2

fraction genes in fg and expected value

oxidoreductase activity, acting on the C...	GO:0016899
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
inosine kinase activity	GO:0008906
manganese ion binding	GO:0030145
DNA binding domain binding	GO:0050692
lactate dehydrogenase activity	GO:0004457
nucleobase-containing compound kinase ac...	GO:0019205
carbohydrate derivative binding	GO:0097367
epinephrine binding	GO:0051379
poly(A) binding	GO:0008143
nucleoside diphosphate kinase activity	GO:0004550
catecholamine binding	GO:1901338
anion binding	GO:0043168
GTP binding	GO:0005525
cytoskeletal anchor activity	GO:0008093
poly-purine tract binding	GO:0070717
ribonucleotide binding	GO:0032553
purine ribonucleotide binding	GO:0032555
p53 binding	GO:0002039
purine ribonucleoside binding	GO:0032550
ribonucleoside binding	GO:0032549
purine ribonucleoside triphosphate bindi...	GO:0035639
purine nucleotide binding	GO:0017076
protein kinase binding	GO:0019901
purine nucleoside binding	GO:0001883
nucleoside binding	GO:0001882
guanyl ribonucleotide binding	GO:0032561
guanyl nucleotide binding	GO:0019001
cytoskeletal protein binding	GO:0008092
protein serine/threonine kinase inhibito...	GO:0030291

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p=4.9E-03	n=4
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p=6.6E-03	n=2
p=6.8E-03	n=3
p=8.7E-03	n=13
p=1.1E-02	n=2
p=1.1E-02	n=2
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p=1.1E-02	n=18
p=1.6E-02	n=5
p=1.6E-02	n=2
p=1.6E-02	n=2
p=1.6E-02	n=11
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p=1.8E-02	n=3
p=1.9E-02	n=5
p=1.9E-02	n=5
p=1.9E-02	n=10
p=2.1E-02	n=11
p=2.2E-02	n=11
p=2.2E-02	n=5
p=2.2E-02	n=5
p=2.4E-02	n=5
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p=2.5E-02	n=12
p=2.8E-02	n=2

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GO:CC
Elav_Nvec_vc1.1_XM_032382466.2

fraction genes in fg and expected value

dendrite cytoplasm	GO:0032839
lytic vacuole	GO:0000323
cell division site	GO:0032153
integral component of endoplasmic reticu...	GO:0030176
fungal-type vacuole	GO:0000324
fungal-type vacuole membrane	GO:0000329
intrinsic component of Golgi membrane	GO:0031228
cell tip	GO:0051286
lysosome	GO:0005764
storage vacuole	GO:0000322
germinal vesicle	GO:0042585
cell pole	GO:0060187
excitatory synapse	GO:0060076
female germ cell nucleus	GO:0001674
ciliary plasm	GO:0097014
microvesicle	GO:1990742
AMPA glutamate receptor complex	GO:0032281
intrinsic component of autophagosome mem...	GO:0097636
integral component of autophagosome memb...	GO:0097637
intrinsic component of endosome membrane	GO:0031302
centralspindlin complex	GO:0097149
dense core granule membrane	GO:0032127
interleukin-5 receptor complex	GO:0005895
neuronal ribonucleoprotein granule	GO:0071598
stereocilia ankle link	GO:0002141
stereocilia ankle link complex	GO:0002142
stereocilia coupling link	GO:0002139
USH2 complex	GO:1990696
FACT complex	GO:0035101
plasma membrane bounded cell projection ...	GO:0032838

p=3.4E-04	n=3
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p=3.1E-03	n=4
p=8.3E-03	n=6
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p=1.0E-02	n=2
p=1.2E-02	n=3
p=1.5E-02	n=2
p=1.6E-02	n=9
p=2.1E-02	n=2
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p=2.1E-02	n=2
p=2.7E-02	n=2
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