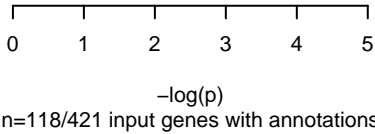


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032373640.2

fraction genes in fg and expected value

embryonic placenta development	GO:0001892	p=1.9E-03	n=5
lung epithelium development	GO:0060428	p=2.4E-03	n=3
cellular response to oxygen levels	GO:0071453	p=3.9E-03	n=8
regulation of odontoblast differentiatio...	GO:1901329	p=4.2E-03	n=2
swim bladder development	GO:0048794	p=4.2E-03	n=2
positive regulation of transcription fro...	GO:0061408	p=4.2E-03	n=2
magnesium ion transmembrane transport	GO:1903830	p=4.2E-03	n=2
positive regulation of transcription fro...	GO:0006990	p=4.2E-03	n=2
liver morphogenesis	GO:0072576	p=4.2E-03	n=2
positive regulation of DNA recombination	GO:0045911	p=4.6E-03	n=3
protein maturation	GO:0051604	p=5.3E-03	n=8
cellular response to lipid	GO:0071396	p=7.7E-03	n=11
somatic muscle development	GO:0007525	p=7.7E-03	n=4
antigen processing and presentation of p...	GO:0002474	p=7.7E-03	n=3
double-strand break repair via homologou...	GO:0000724	p=9.4E-03	n=5
regulation of osteoclast differentiation	GO:0045670	p=1.0E-02	n=4
apoptotic process	GO:0006915	p=1.1E-02	n=26
regulation of apoptotic process	GO:0042981	p=1.1E-02	n=23
determination of left/right symmetry	GO:0007368	p=1.1E-02	n=7
determination of heart left/right asymme...	GO:0061371	p=1.1E-02	n=5
adenylate cyclase-activating adrenergic ...	GO:0086023	p=1.2E-02	n=2
negative regulation of adenylate cyclase...	GO:0071878	p=1.2E-02	n=2
positive regulation of tyrosine phosphor...	GO:0042531	p=1.2E-02	n=2
cellular response to insulin-like growth...	GO:1990314	p=1.2E-02	n=2
regulation of adenylate cyclase-activati...	GO:0140192	p=1.2E-02	n=2
negative regulation of adenylate cyclase...	GO:0140199	p=1.2E-02	n=2
response to herbicide	GO:0009635	p=1.2E-02	n=2
G protein-coupled receptor signaling pat...	GO:0086103	p=1.2E-02	n=2
regulation of neurotrophin TRK receptor ...	GO:0051386	p=1.2E-02	n=2
positive regulation of neurotrophin TRK ...	GO:0051388	p=1.2E-02	n=2

fg=0.04	bg=0.01
fg=0.03	bg=0.00
fg=0.07	bg=0.02
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=0.03	bg=0.00
fg=0.07	bg=0.02
fg=0.09	bg=0.04
fg=0.03	bg=0.01
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.22	bg=0.14
fg=0.19	bg=0.12
fg=0.06	bg=0.02
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

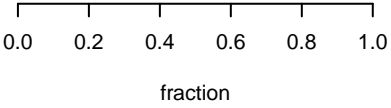
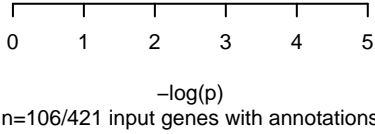


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032373640.2

fraction genes in fg and expected value

protein self-association	GO:0043621	p=4.3E-03	n=4
magnesium ion transmembrane transporter ...	GO:0015095	p=4.4E-03	n=2
N4-(beta-N-acetylglucosaminy)-L-asparag...	GO:0003948	p=4.4E-03	n=2
3'-5' DNA helicase activity	GO:0043138	p=1.3E-02	n=2
pre-mRNA intronic binding	GO:0097157	p=1.3E-02	n=2
G-quadruplex DNA binding	GO:0051880	p=1.3E-02	n=2
ATP hydrolysis activity	GO:0016887	p=2.4E-02	n=10
cis-regulatory region sequence-specific ...	GO:0000987	p=3.2E-02	n=8
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.2E-02	n=8
DNA helicase activity	GO:0003678	p=3.2E-02	n=3
intronic transcription regulatory region...	GO:0001161	p=3.8E-02	n=2
misfolded protein binding	GO:0051787	p=3.8E-02	n=2
nucleoside-triphosphatase activity	GO:0017111	p=3.9E-02	n=13
ATP-dependent activity	GO:0140657	p=4.4E-02	n=10
DNA-binding transcription repressor acti...	GO:0001227	p=4.6E-02	n=4
DNA-binding transcription repressor acti...	GO:0001217	p=4.6E-02	n=4
hydrolase activity, acting on acid anhyd...	GO:0016817	p=4.7E-02	n=13
hydrolase activity, acting on acid anhyd...	GO:0016818	p=4.7E-02	n=13
pyrophosphatase activity	GO:0016462	p=4.7E-02	n=13
chromatin DNA binding	GO:0031490	p=5.0E-02	n=3
DNA-binding transcription factor binding	GO:0140297	p=5.0E-02	n=6
aryl hydrocarbon receptor binding	GO:0017162	p=5.5E-02	n=2
transcription regulatory region nucleic ...	GO:0001067	p=5.6E-02	n=11
DNA binding	GO:0003677	p=5.7E-02	n=18
hydrolase activity	GO:0016787	p=6.5E-02	n=29
transcription cis-regulatory region bind...	GO:0000976	p=6.6E-02	n=10
insulin-like growth factor II binding	GO:0031995	p=6.7E-02	n=1
four-way junction DNA binding	GO:0000400	p=6.7E-02	n=1
poly(A)-specific ribonuclease activity	GO:0004535	p=6.7E-02	n=1
lipopolysaccharide binding	GO:0001530	p=6.7E-02	n=1

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=0.09	bg=0.05
fg=0.08	bg=0.04
fg=0.08	bg=0.04
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.12	bg=0.07
fg=0.09	bg=0.05
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.12	bg=0.07
fg=0.12	bg=0.07
fg=0.12	bg=0.07
fg=0.03	bg=0.01
fg=0.06	bg=0.03
fg=0.02	bg=0.00
fg=0.10	bg=0.06
fg=0.17	bg=0.12
fg=0.27	bg=0.20
fg=0.09	bg=0.06
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032373640.2

fraction genes in fg and expected value

euchromatin	GO:0000791	p=9.8E-04	n=4
M band	GO:0031430	p=2.7E-03	n=4
COPII vesicle coat	GO:0030127	p=4.2E-03	n=2
I band	GO:0031674	p=5.3E-03	n=6
endoplasmic reticulum membrane	GO:0005789	p=6.9E-03	n=17
Golgi-associated vesicle	GO:0005798	p=7.2E-03	n=7
extracellular space	GO:0005615	p=7.8E-03	n=9
Golgi-associated vesicle membrane	GO:0030660	p=1.0E-02	n=4
Prp19 complex	GO:0000974	p=1.2E-02	n=2
Fanconi anaemia nuclear complex	GO:0043240	p=1.2E-02	n=2
condensed chromosome	GO:0000793	p=1.3E-02	n=6
membrane-enclosed lumen	GO:0031974	p=1.4E-02	n=58
intracellular organelle lumen	GO:0070013	p=1.4E-02	n=58
organelle lumen	GO:0043233	p=1.4E-02	n=58
nucleoplasm	GO:0005654	p=1.5E-02	n=43
Z disc	GO:0030018	p=2.0E-02	n=5
intracellular organelle	GO:0043229	p=2.0E-02	n=109
secretory granule lumen	GO:0034774	p=2.6E-02	n=6
transport vesicle	GO:0030133	p=2.7E-02	n=12
nuclear lumen	GO:0031981	p=3.0E-02	n=47
secretory vesicle	GO:0099503	p=3.0E-02	n=15
centrosome	GO:0005813	p=3.3E-02	n=11
vesicle lumen	GO:0031983	p=3.4E-02	n=6
cytoplasmic vesicle lumen	GO:0060205	p=3.4E-02	n=6
protein phosphatase type 2A complex	GO:0000159	p=3.7E-02	n=2
mitotic spindle pole	GO:0097431	p=3.7E-02	n=2
smooth endoplasmic reticulum	GO:0005790	p=3.9E-02	n=3
condensed chromosome, centromeric region	GO:0000779	p=4.3E-02	n=4
lysosome	GO:0005764	p=4.4E-02	n=11
integral component of endoplasmic reticu...	GO:0030176	p=4.7E-02	n=6

fg=0.03	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.14	bg=0.08
fg=0.06	bg=0.02
fg=0.08	bg=0.03
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.49	bg=0.39
fg=0.49	bg=0.39
fg=0.49	bg=0.39
fg=0.36	bg=0.27
fg=0.04	bg=0.01
fg=0.92	bg=0.84
fg=0.05	bg=0.02
fg=0.10	bg=0.04
fg=0.40	bg=0.32
fg=0.13	bg=0.08
fg=0.09	bg=0.05
fg=0.05	bg=0.02
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.09	bg=0.05
fg=0.05	bg=0.02

