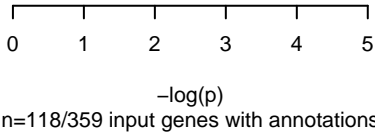


GO:BP
Elav_Nvec_vc1.1_XM_032382185.2

fraction genes in fg and expected value

positive regulation of T cell differenti...	GO:0033089	p=1.9E-03	n=2
negative regulation of cytokine producti...	GO:1900016	p=1.9E-03	n=2
mitochondrial cytochrome c oxidase assem...	GO:0033617	p=2.5E-03	n=3
germ-line cyst formation	GO:0048134	p=3.9E-03	n=3
positive regulation of RNA polymerase II...	GO:0045899	p=3.9E-03	n=3
carbohydrate derivative transport	GO:1901264	p=5.3E-03	n=4
activation of GTPase activity	GO:0090630	p=5.5E-03	n=5
positive regulation of non-canonical Wnt...	GO:2000052	p=5.5E-03	n=2
neural plate morphogenesis	GO:0001839	p=5.5E-03	n=2
protein N-linked glycosylation via aspar...	GO:0018279	p=7.8E-03	n=3
negative regulation of inflammatory resp...	GO:0050728	p=8.1E-03	n=4
negative regulation of systemic arterial...	GO:0003085	p=1.0E-02	n=3
convergent extension	GO:0060026	p=1.0E-02	n=3
regulation of endoplasmic reticulum stre...	GO:1902235	p=1.0E-02	n=3
alanine metabolic process	GO:0006522	p=1.1E-02	n=2
convergent extension involved in axis el...	GO:0060028	p=1.1E-02	n=2
negative regulation of cardiac muscle co...	GO:0055118	p=1.1E-02	n=2
positive regulation of fat cell differen...	GO:0045600	p=1.1E-02	n=2
pyruvate family amino acid metabolic pro...	GO:0009078	p=1.1E-02	n=2
histone H3-K36 demethylation	GO:0070544	p=1.1E-02	n=2
negative regulation of long-term synapti...	GO:1900272	p=1.1E-02	n=2
negative regulation of blood pressure	GO:0045776	p=1.3E-02	n=3
secretory granule organization	GO:0033363	p=1.3E-02	n=3
response to activity	GO:0014823	p=1.4E-02	n=4
regulation of organ growth	GO:0046620	p=1.5E-02	n=5
leuk development	GO:0007507	p=1.6E-02	n=12
regulation of myeloid leukocyte differen...	GO:0002761	p=1.6E-02	n=4
regulation of lymphocyte proliferation	GO:0050670	p=1.6E-02	n=4
regulation of leukocyte proliferation	GO:0070663	p=1.6E-02	n=4
regulation of mononuclear cell prolifera...	GO:0032944	p=1.6E-02	n=4

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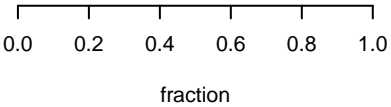
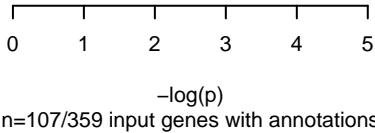


GO:MF
Elav_Nvec_vc1.1_XM_032382185.2

fraction genes in fg and expected value

protein tyrosine kinase binding	GO:1990782	p=4.7E-03	n=4
chaperone binding	GO:0051087	p=6.3E-03	n=6
cytochrome-c oxidase activity	GO:0004129	p=1.1E-02	n=2
oxidoreductase activity, acting on a hem...	GO:0016675	p=1.1E-02	n=2
histone H3-methyl-lysine-36 demethylase ...	GO:0051864	p=1.1E-02	n=2
primary active transmembrane transporter...	GO:0015399	p=1.3E-02	n=6
protein-disulfide reductase activity	GO:0015035	p=1.5E-02	n=3
receptor tyrosine kinase binding	GO:0030971	p=1.8E-02	n=3
ephrin receptor binding	GO:0046875	p=1.8E-02	n=2
G-protein beta/gamma-subunit complex bin...	GO:0031683	p=1.8E-02	n=2
transcription coactivator binding	GO:0001223	p=1.8E-02	n=2
histone H3-methyl-lysine-4 demethylase a...	GO:0032453	p=1.8E-02	n=2
disulfide oxidoreductase activity	GO:0015036	p=2.3E-02	n=3
unfolded protein binding	GO:0051082	p=2.9E-02	n=5
G protein-coupled receptor binding	GO:0001664	p=3.5E-02	n=5
dopamine receptor binding	GO:0050780	p=3.7E-02	n=2
phosphatidylcholine binding	GO:0031210	p=3.7E-02	n=2
oxidoreduction-driven active transmembra...	GO:0015453	p=3.8E-02	n=3
oxidoreductase activity	GO:0016491	p=4.2E-02	n=11
double-stranded methylated DNA binding	GO:0010385	p=4.5E-02	n=1
ACP phosphopantetheine attachment site b...	GO:0044620	p=4.5E-02	n=1
phosphatidylcholine transporter activity	GO:0008525	p=4.5E-02	n=1
acyl binding	GO:0000035	p=4.5E-02	n=1
acyl carrier activity	GO:0000036	p=4.5E-02	n=1
prosthetic group binding	GO:0051192	p=4.5E-02	n=1
panetheine hydrolase activity	GO:0017159	p=4.5E-02	n=1
unmethylated CpG binding	GO:0045322	p=4.5E-02	n=1
D5 dopamine receptor binding	GO:0031752	p=4.5E-02	n=1
chitinase activity	GO:0004568	p=4.5E-02	n=1
chitin binding	GO:0008061	p=4.5E-02	n=1

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GO:CC
Elav_Nvec_vc1.1_XM_032382185.2

fraction genes in fg and expected value

dendritic spine neck	GO:0044326	p=2.0E-03	n=2
protein serine/threonine phosphatase com...	GO:0008287	p=4.5E-03	n=4
endoplasmic reticulum quality control co...	GO:0044322	p=1.1E-02	n=2
smooth endoplasmic reticulum	GO:0005790	p=1.8E-02	n=3
PcG protein complex	GO:0031519	p=1.8E-02	n=3
presynaptic periaxial zone	GO:0036062	p=1.8E-02	n=2
protein phosphatase type 1 complex	GO:0000164	p=1.8E-02	n=2
intracellular organelle	GO:0043229	p=2.5E-02	n=108
organelle envelope lumen	GO:0031970	p=3.3E-02	n=4
chaperone complex	GO:0101031	p=3.5E-02	n=2
mitochondrion	GO:0005739	p=3.9E-02	n=24
cytoplasmic side of dendritic spine plas...	GO:1990780	p=4.4E-02	n=1
cytoplasmic periphery of the nuclear por...	GO:1990723	p=4.4E-02	n=1
cortical microtubule cytoskeleton	GO:0030981	p=4.4E-02	n=1
cortical microtubule plus-end	GO:1903754	p=4.4E-02	n=1
nuclear pore cytoplasmic filaments	GO:0044614	p=4.4E-02	n=1
ATF4-CREB1 transcription factor complex	GO:1990589	p=4.4E-02	n=1
FANCM-MHF complex	GO:0071821	p=4.4E-02	n=1
protein kinase CK2 complex	GO:0005956	p=4.4E-02	n=1
TSC1-TSC2 complex	GO:0033596	p=4.4E-02	n=1
centrosomal corona	GO:0031592	p=4.4E-02	n=1
UTP-C complex	GO:0034456	p=4.4E-02	n=1
cytoplasmic microtubule plus-end	GO:1904511	p=4.4E-02	n=1
tRNA methyltransferase complex	GO:0043527	p=4.4E-02	n=1
cortical microtubule	GO:0055028	p=4.4E-02	n=1
ATP-binding cassette (ABC) transporter c...	GO:0043190	p=4.4E-02	n=1
CUR1 complex	GO:0032545	p=4.4E-02	n=1
dendritic spine head	GO:0044327	p=4.4E-02	n=1
PR-DUB complex	GO:0035517	p=4.4E-02	n=1
proteasome core complex, beta-subunit co...	GO:0019774	p=4.4E-02	n=1

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