GO:BP
Ncol_Nvec_vc1.1_XM_001630131.3

fraction genes in fg and expected val...

Term	p-value	n	fg	bg
spermidine biosynthetic process GO:0008295	p=1.7E−04	n=2	fg=0.08	bg=0.00
spermine metabolic process GO:0008215	p=1.7E−04	n=2	fg=0.08	bg=0.00
negative regulation of extrinsic apoptot... GO:2001240	p=1.7E−04	n=2	fg=0.08	bg=0.00
inorganic ion transmembrane transport GO:0098660	p=7.3E−04	n=7	fg=0.29	bg=0.07
regulation of olfactory learning GO:0090328	p=9.9E−04	n=2	fg=0.08	bg=0.00
neurotransmitter transport GO:0006836	p=1.6E−03	n=5	fg=0.21	bg=0.04
gamma−aminobutyric acid signaling pathwa... GO:0007214	p=1.6E−03	n=2	fg=0.08	bg=0.00
inter−male aggressive behavior GO:0002121	p=2.4E−03	n=2	fg=0.08	bg=0.00
regulation of backward locomotion GO:0043058	p=3.4E−03	n=2	fg=0.08	bg=0.00
cochlea morphogenesis GO:0090103	p=3.4E−03	n=2	fg=0.08	bg=0.00
membrane depolarization during action po... GO:0086010	p=3.4E−03	n=2	fg=0.08	bg=0.00
ammonium ion metabolic process GO:0097164	p=5.9E−03	n=3	fg=0.12	bg=0.02
positive regulation of DNA repair GO:0045739	p=8.6E−03	n=2	fg=0.08	bg=0.01
neuron fate specification GO:0048665	p=1.0E−02	n=2	fg=0.08	bg=0.01
inorganic cation transmembrane transport GO:0098662	p=1.3E−02	n=5	fg=0.21	bg=0.06
spermidine catabolic process GO:0046203	p=1.3E−02	n=1	fg=0.04	bg=0.00
spermine catabolic process GO:0046208	p=1.3E−02	n=1	fg=0.04	bg=0.00
spermine biosynthetic process GO:0006597	p=1.3E−02	n=1	fg=0.04	bg=0.00
polyamine catabolic process GO:0006598	p=1.3E−02	n=1	fg=0.04	bg=0.00
positive regulation of oxidative stress−... GO:1902177	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of sequestering of zinc ion GO:0061088	p=1.3E−02	n=1	fg=0.04	bg=0.00
sex determination, establishment of X:A ... GO:0007540	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of membrane potential in phot... GO:0016057	p=1.3E−02	n=1	fg=0.04	bg=0.00
pigment cell development GO:0070285	p=1.3E−02	n=1	fg=0.04	bg=0.00
negative regulation of B cell apoptotic ... GO:0002903	p=1.3E−02	n=1	fg=0.04	bg=0.00
sequestering of zinc ion GO:0032119	p=1.3E−02	n=1	fg=0.04	bg=0.00
sequestering of metal ion GO:0051238	p=1.3E−02	n=1	fg=0.04	bg=0.00
histone dephosphorylation GO:0016576	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of guanylate cyclase activity GO:0031282	p=1.3E−02	n=1	fg=0.04	bg=0.00
positive regulation of guanylate cyclase... GO:0031284	p=1.3E−02	n=1	fg=0.04	bg=0.00

−log(p)
n=24/97 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_001630131.3

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
ion gated channel activity GO:0022839	p=1.5E−04	n=5	fg=0.24	bg=0.03
GABA−gated chloride ion channel activity GO:0022851	p=4.9E−04	n=2	fg=0.10	bg=0.00
GABA−A receptor activity GO:0004890	p=4.9E−04	n=2	fg=0.10	bg=0.00
benzodiazepine receptor activity GO:0008503	p=4.9E−04	n=2	fg=0.10	bg=0.00
phospholipase A2 activity GO:0004623	p=9.8E−04	n=2	fg=0.10	bg=0.00
voltage−gated calcium channel activity GO:0005245	p=4.4E−03	n=2	fg=0.10	bg=0.01
polyamine binding GO:0019808	p=1.3E−02	n=1	fg=0.05	bg=0.00
polyamine oxidase activity GO:0046592	p=1.3E−02	n=1	fg=0.05	bg=0.00
calcium−independent phospholipase A2 act... GO:0047499	p=1.3E−02	n=1	fg=0.05	bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946	p=1.3E−02	n=1	fg=0.05	bg=0.00
oxidoreductase activity, acting on the C... GO:0016647	p=1.3E−02	n=1	fg=0.05	bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014	p=1.3E−02	n=1	fg=0.05	bg=0.00
cyclase activator activity GO:0010853	p=1.3E−02	n=1	fg=0.05	bg=0.00
guanylate cyclase regulator activity GO:0030249	p=1.3E−02	n=1	fg=0.05	bg=0.00
phospholipase A1 activity GO:0008970	p=1.3E−02	n=1	fg=0.05	bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901	p=1.3E−02	n=1	fg=0.05	bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904	p=1.3E−02	n=1	fg=0.05	bg=0.00
putrescine binding GO:0019810	p=1.3E−02	n=1	fg=0.05	bg=0.00
calcium sensitive guanylate cyclase acti... GO:0008048	p=1.3E−02	n=1	fg=0.05	bg=0.00
guanylate cyclase activator activity GO:0030250	p=1.3E−02	n=1	fg=0.05	bg=0.00
sodium ion transmembrane transporter act... GO:0015081	p=1.6E−02	n=2	fg=0.10	bg=0.01
transmembrane transporter activity GO:0022857	p=1.9E−02	n=9	fg=0.43	bg=0.09
metal ion transmembrane transporter acti... GO:0046873	p=2.0E−02	n=5	fg=0.24	bg=0.04
dephospho−CoA kinase activity GO:0004140	p=2.6E−02	n=1	fg=0.05	bg=0.00
neurotransmitter:sodium symporter activi... GO:0005328	p=2.6E−02	n=1	fg=0.05	bg=0.00
platelet−activating factor acetyltransfe... GO:0047179	p=2.6E−02	n=1	fg=0.05	bg=0.00
high voltage−gated calcium channel activ... GO:0008331	p=2.6E−02	n=1	fg=0.05	bg=0.00
low voltage−gated calcium channel activi... GO:0008332	p=2.6E−02	n=1	fg=0.05	bg=0.00
calcium−dependent protein kinase regulat... GO:0010858	p=2.6E−02	n=1	fg=0.05	bg=0.00
BH3 domain binding GO:0051434	p=2.6E−02	n=1	fg=0.05	bg=0.00

−log(p)
n=21/97 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_001630131.3

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
postsynaptic membrane GO:0045211	p=5.8E−03	n=3	fg=0.13	bg=0.02
neuromuscular junction GO:0031594	p=7.6E−03	n=3	fg=0.13	bg=0.02
integral component of synaptic vesicle m... GO:0030285	p=7.9E−03	n=2	fg=0.09	bg=0.01
neuronal cell body membrane GO:0032809	p=1.3E−02	n=2	fg=0.09	bg=0.01
neuron projection membrane GO:0032589	p=1.5E−02	n=2	fg=0.09	bg=0.01
cell body membrane GO:0044298	p=1.5E−02	n=2	fg=0.09	bg=0.01
Seh1−associated complex GO:0035859	p=2.5E−02	n=1	fg=0.04	bg=0.00
growth cone filopodium GO:1990812	p=2.5E−02	n=1	fg=0.04	bg=0.00
GATOR2 complex GO:0061700	p=2.5E−02	n=1	fg=0.04	bg=0.00
growth cone lamellipodium GO:1990761	p=3.8E−02	n=1	fg=0.04	bg=0.00
Bcl−2 family protein complex GO:0097136	p=3.8E−02	n=1	fg=0.04	bg=0.00
leading edge membrane GO:0031256	p=3.9E−02	n=2	fg=0.09	bg=0.01
cell leading edge GO:0031252	p=4.7E−02	n=3	fg=0.13	bg=0.04
peroxisomal matrix GO:0005782	p=5.0E−02	n=1	fg=0.04	bg=0.00
microbody lumen GO:0031907	p=5.0E−02	n=1	fg=0.04	bg=0.00
voltage−gated calcium channel comlpex GO:0005891	p=6.2E−02	n=1	fg=0.04	bg=0.00
neuronal cell body GO:0043025	p=7.2E−02	n=4	fg=0.17	bg=0.07
dynactin complex GO:0005869	p=7.4E−02	n=1	fg=0.04	bg=0.00
dendritic tree GO:0097447	p=7.8E−02	n=4	fg=0.17	bg=0.07
dendrite GO:0030425	p=7.8E−02	n=4	fg=0.17	bg=0.07
presynapse GO:0098793	p=8.0E−02	n=5	fg=0.22	bg=0.05
transmembrane transporter complex GO:1902495	p=8.2E−02	n=2	fg=0.09	bg=0.02
calcium channel complex GO:0034704	p=8.6E−02	n=1	fg=0.04	bg=0.00
transporter complex GO:1990351	p=9.0E−02	n=2	fg=0.09	bg=0.02
cell body GO:0044297	p=9.0E−02	n=4	fg=0.17	bg=0.08
axon GO:0030424	p=9.8E−02	n=4	fg=0.17	bg=0.08
membrane GO:0016020	p=1.3E−01	n=15	fg=0.65	bg=0.46
respiratory chain complex I GO:0045271	p=1.4E−01	n=1	fg=0.04	bg=0.01
mitochondrial respiratory chain complex ... GO:0005747	p=1.4E−01	n=1	fg=0.04	bg=0.01
NADH dehydrogenase complex GO:0030964	p=1.4E−01	n=1	fg=0.04	bg=0.01

−log(p)
n=23/97 input genes with annotations

fraction