GO:BP
Ncol_Nvec_v1g19278

fraction genes in fg and expected valu...

DNA dealkylation involved in DNA repair GO:0006307	p=6.3E−04	n=3	fg=0.02	bg=0.00
negative regulation of purine nucleotide... GO:1900543	p=9.0E−04	n=4	fg=0.03	bg=0.00
negative regulation of histone H3−K4 met... GO:0051572	p=3.0E−03	n=2	fg=0.01	bg=0.00
negative regulation of oxidative phospho... GO:0090324	p=3.0E−03	n=2	fg=0.01	bg=0.00
axonemal dynein complex assembly GO:0070286	p=3.1E−03	n=4	fg=0.03	bg=0.00
interleukin−12−mediated signaling pathwa... GO:0035722	p=4.3E−03	n=4	fg=0.03	bg=0.00
cyclic nucleotide metabolic process GO:0009187	p=4.3E−03	n=4	fg=0.03	bg=0.00
actin cytoskeleton reorganization GO:0031532	p=4.7E−03	n=5	fg=0.03	bg=0.01
positive chemotaxis GO:0050918	p=4.9E−03	n=3	fg=0.02	bg=0.00
cellular response to nitrogen compound GO:1901699	p=5.1E−03	n=18	fg=0.12	bg=0.06
regulation of heart contraction GO:0008016	p=6.7E−03	n=8	fg=0.05	bg=0.02
negative regulation of calcium−mediated ... GO:0050849	p=7.5E−03	n=3	fg=0.02	bg=0.00
glutamate secretion, neurotransmission GO:0061535	p=8.8E−03	n=2	fg=0.01	bg=0.00
hepatocyte growth factor receptor signal... GO:0048012	p=8.8E−03	n=2	fg=0.01	bg=0.00
retina vasculature morphogenesis in came... GO:0061299	p=8.8E−03	n=2	fg=0.01	bg=0.00
cellular response to calcium ion GO:0071277	p=9.6E−03	n=4	fg=0.03	bg=0.01
cellular response to organonitrogen comp... GO:0071417	p=1.0E−02	n=16	fg=0.11	bg=0.06
regulation of intrinsic apoptotic signal... GO:1902229	p=1.1E−02	n=3	fg=0.02	bg=0.00
detection of external stimulus GO:0009581	p=1.2E−02	n=8	fg=0.05	bg=0.02
cellular oxidant detoxification GO:0098869	p=1.2E−02	n=4	fg=0.03	bg=0.01
positive regulation of neuron differenti... GO:0045666	p=1.2E−02	n=12	fg=0.08	bg=0.04
response to abiotic stimulus GO:0009628	p=1.2E−02	n=30	fg=0.20	bg=0.13
regulation of cellular localization GO:0060341	p=1.3E−02	n=21	fg=0.14	bg=0.09
exocytosis GO:0006887	p=1.4E−02	n=17	fg=0.11	bg=0.06
response to oxygen levels GO:0070482	p=1.4E−02	n=12	fg=0.08	bg=0.04
regulation of heart rate GO:0002027	p=1.4E−02	n=5	fg=0.03	bg=0.01
positive regulation of neuron projection... GO:0010976	p=1.5E−02	n=10	fg=0.07	bg=0.03
cellular detoxification GO:1990748	p=1.5E−02	n=4	fg=0.03	bg=0.01
detection of abiotic stimulus GO:0009582	p=1.6E−02	n=8	fg=0.05	bg=0.02
positive regulation of vasculature devel... GO:1904018	p=1.7E−02	n=5	fg=0.03	bg=0.01

−log(p)
n=149/570 input genes with annotations

fraction

GO:MF
Ncol_Nvec_v1g19278

fraction genes in fg and expected valu...

dynein heavy chain binding GO:0045504	p=1.2E−04	n=4	fg=0.03	bg=0.00
phosphatidylethanolamine binding GO:0008429	p=6.1E−04	n=3	fg=0.02	bg=0.00
calcium−dependent phospholipid binding GO:0005544	p=1.5E−03	n=3	fg=0.02	bg=0.00
high voltage−gated calcium channel activ... GO:0008331	p=2.9E−03	n=2	fg=0.02	bg=0.00
antioxidant activity GO:0016209	p=4.1E−03	n=4	fg=0.03	bg=0.01
ammonium ion binding GO:0070405	p=4.1E−03	n=4	fg=0.03	bg=0.01
MAP kinase kinase kinase activity GO:0004709	p=4.7E−03	n=3	fg=0.02	bg=0.00
phosphatidylcholine binding GO:0031210	p=4.7E−03	n=3	fg=0.02	bg=0.00
ion gated channel activity GO:0022839	p=9.7E−03	n=8	fg=0.06	bg=0.02
receptor ligand activity GO:0048018	p=1.4E−02	n=3	fg=0.02	bg=0.00
syntaxin−1 binding GO:0017075	p=1.6E−02	n=2	fg=0.02	bg=0.00
signaling receptor activator activity GO:0030546	p=1.9E−02	n=3	fg=0.02	bg=0.00
flavin adenine dinucleotide binding GO:0050660	p=2.4E−02	n=3	fg=0.02	bg=0.01
signaling receptor regulator activity GO:0030545	p=2.4E−02	n=3	fg=0.02	bg=0.01
mannosyltransferase activity GO:0000030	p=2.6E−02	n=2	fg=0.02	bg=0.00
chemoattractant activity GO:0042056	p=2.6E−02	n=2	fg=0.02	bg=0.00
dynein light chain binding GO:0045503	p=2.6E−02	n=2	fg=0.02	bg=0.00
calcium ion binding GO:0005509	p=2.7E−02	n=7	fg=0.05	bg=0.02
cytoskeletal motor activity GO:0003774	p=2.9E−02	n=4	fg=0.03	bg=0.01
oxidoreductase activity GO:0016491	p=3.2E−02	n=13	fg=0.10	bg=0.06
peroxidase activity GO:0004601	p=3.8E−02	n=2	fg=0.02	bg=0.00
cyclic−nucleotide phosphodiesterase acti... GO:0004112	p=3.8E−02	n=2	fg=0.02	bg=0.00
3',5'−cyclic−nucleotide phosphodiesteras... GO:0004114	p=3.8E−02	n=2	fg=0.02	bg=0.00
DNA−(apurinic or apyrimidinic site) endo... GO:0003906	p=3.8E−02	n=2	fg=0.02	bg=0.00
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555	p=3.8E−02	n=2	fg=0.02	bg=0.00
O−methyltransferase activity GO:0008171	p=3.8E−02	n=2	fg=0.02	bg=0.00
acyltransferase activity, transferring g... GO:0016747	p=4.3E−02	n=5	fg=0.04	bg=0.02
2−oxoglutarate−dependent dioxygenase act... GO:0016706	p=4.4E−02	n=3	fg=0.02	bg=0.01
transmitter−gated channel activity GO:0022835	p=5.2E−02	n=2	fg=0.02	bg=0.00
voltage−gated anion channel activity GO:0008308	p=5.2E−02	n=2	fg=0.02	bg=0.00

−log(p)
n=129/570 input genes with annotations

fraction

GO:CC
Ncol_Nvec_v1g19278

fraction genes in fg and expected valu...

ficolin−1−rich granule membrane GO:0101003	p=5.1E−04	n=4	fg=0.03	bg=0.00
organelle membrane contact site GO:0044232	p=2.9E−03	n=3	fg=0.02	bg=0.00
hippocampal mossy fiber GO:0097457	p=3.0E−03	n=2	fg=0.01	bg=0.00
integral component of synaptic vesicle m... GO:0030285	p=4.2E−03	n=4	fg=0.03	bg=0.00
presynapse GO:0098793	p=4.7E−03	n=17	fg=0.11	bg=0.05
outer dynein arm GO:0036157	p=8.6E−03	n=2	fg=0.01	bg=0.00
side of membrane GO:0098552	p=9.8E−03	n=11	fg=0.07	bg=0.03
extrinsic component of plasma membrane GO:0019897	p=2.5E−02	n=5	fg=0.03	bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234	p=2.5E−02	n=4	fg=0.03	bg=0.01
cytoplasmic side of plasma membrane GO:0009898	p=2.6E−02	n=7	fg=0.05	bg=0.02
Prp19 complex GO:0000974	p=2.7E−02	n=2	fg=0.01	bg=0.00
neuronal cell body GO:0043025	p=2.8E−02	n=15	fg=0.10	bg=0.06
apical plasma membrane GO:0016324	p=3.1E−02	n=10	fg=0.07	bg=0.03
presynaptic membrane GO:0042734	p=3.2E−02	n=5	fg=0.03	bg=0.01
presynaptic active zone GO:0048786	p=3.4E−02	n=4	fg=0.03	bg=0.01
cell surface GO:0009986	p=3.5E−02	n=10	fg=0.07	bg=0.04
synaptic membrane GO:0097060	p=3.7E−02	n=7	fg=0.05	bg=0.02
axon cytoplasm GO:1904115	p=3.9E−02	n=2	fg=0.01	bg=0.00
voltage−gated calcium channel complex GO:0005891	p=3.9E−02	n=2	fg=0.01	bg=0.00
perikaryon GO:0043204	p=3.9E−02	n=4	fg=0.03	bg=0.01
brush border GO:0005903	p=4.0E−02	n=5	fg=0.03	bg=0.01
somatodendritic compartment GO:0036477	p=4.4E−02	n=19	fg=0.13	bg=0.09
distal axon GO:0150034	p=4.7E−02	n=10	fg=0.07	bg=0.04
nuclear membrane GO:0031965	p=5.0E−02	n=7	fg=0.05	bg=0.02
cytoplasmic side of membrane GO:0098562	p=5.0E−02	n=7	fg=0.05	bg=0.02
phagocytic vesicle GO:0045335	p=5.1E−02	n=4	fg=0.03	bg=0.01
axon GO:0030424	p=5.2E−02	n=17	fg=0.11	bg=0.07
UBC13−UEV1A complex GO:0035370	p=5.5E−02	n=1	fg=0.01	bg=0.00
L−type voltage−gated calcium channel com... GO:1990454	p=5.5E−02	n=1	fg=0.01	bg=0.00
Shu complex GO:0097196	p=5.5E−02	n=1	fg=0.01	bg=0.00

−log(p)
n=148/570 input genes with annotations

fraction