GO:BP
Ncol_Nvec_v1g19278

fraction genes in fg and expected value

detection of external stimulus GO:0009581	p=2.6E−03	n=6	fg=0.09 bg=0.02
detection of abiotic stimulus GO:0009582	p=3.3E−03	n=6	fg=0.09 bg=0.02
retina vasculature morphogenesis in came... GO:0061299	p=3.6E−03	n=2	fg=0.03 bg=0.00
sensory perception GO:0007600	p=3.7E−03	n=10	fg=0.16 bg=0.06
regulated exocytosis GO:0045055	p=4.8E−03	n=10	fg=0.16 bg=0.06
regulation of heart rate GO:0002027	p=5.4E−03	n=4	fg=0.06 bg=0.01
toxin transport GO:1901998	p=5.6E−03	n=3	fg=0.05 bg=0.01
cellular response to calcium ion GO:0071277	p=5.6E−03	n=3	fg=0.05 bg=0.01
positive regulation of axon extension in... GO:0048842	p=7.0E−03	n=2	fg=0.03 bg=0.00
response to hepatocyte growth factor GO:0035728	p=7.0E−03	n=2	fg=0.03 bg=0.00
dendrite arborization GO:0140059	p=7.0E−03	n=2	fg=0.03 bg=0.00
photoreceptor cell fate commitment GO:0046552	p=7.3E−03	n=3	fg=0.05 bg=0.01
inorganic ion transmembrane transport GO:0098660	p=9.3E−03	n=10	fg=0.16 bg=0.07
cation transmembrane transport GO:0098655	p=1.0E−02	n=10	fg=0.16 bg=0.07
regulation of membrane potential GO:0042391	p=1.1E−02	n=7	fg=0.11 bg=0.04
regulation of synapse structural plastic... GO:0051823	p=1.1E−02	n=2	fg=0.03 bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214	p=1.1E−02	n=2	fg=0.03 bg=0.00
response to hypoxia GO:0001666	p=1.2E−02	n=7	fg=0.11 bg=0.04
calcium−mediated signaling GO:0019722	p=1.2E−02	n=5	fg=0.08 bg=0.02
detection of light stimulus GO:0009583	p=1.3E−02	n=4	fg=0.06 bg=0.01
response to decreased oxygen levels GO:0036293	p=1.3E−02	n=7	fg=0.11 bg=0.04
detection of stimulus involved in sensor... GO:0050906	p=1.5E−02	n=4	fg=0.06 bg=0.02
cranial nerve structural organization GO:0021604	p=1.7E−02	n=2	fg=0.03 bg=0.00
negative regulation of calcium−mediated ... GO:0050849	p=1.7E−02	n=2	fg=0.03 bg=0.00
vascular endothelial growth factor signa... GO:0038084	p=1.7E−02	n=2	fg=0.03 bg=0.00
branched−chain amino acid metabolic proc... GO:0009081	p=1.7E−02	n=2	fg=0.03 bg=0.00
branched−chain amino acid catabolic proc... GO:0009083	p=1.7E−02	n=2	fg=0.03 bg=0.00
actin cytoskeleton reorganization GO:0031532	p=1.7E−02	n=3	fg=0.05 bg=0.01
regulation of calcium ion transport into... GO:0010522	p=1.7E−02	n=3	fg=0.05 bg=0.01
detection of mechanical stimulus GO:0050982	p=1.7E−02	n=3	fg=0.05 bg=0.01

−log(p)
n=64/286 input genes with annotations

fraction

GO:MF
Ncol_Nvec_v1g19278

fraction genes in fg and expected valu

ion gated channel activity GO:0022839	p=7.3E−04	n=7	fg=0.12 bg=0.03
high voltage−gated calcium channel activ... GO:0008331	p=1.4E−03	n=2	fg=0.03 bg=0.00
peroxidase activity GO:0004601	p=4.1E−03	n=2	fg=0.03 bg=0.00
phosphatidylinositol binding GO:0035091	p=6.4E−03	n=6	fg=0.10 bg=0.03
acyltransferase activity, transferring g... GO:0016747	p=6.7E−03	n=4	fg=0.07 bg=0.01
calcium−dependent phospholipid binding GO:0005544	p=8.0E−03	n=2	fg=0.03 bg=0.00
phosphatidylethanolamine binding GO:0008429	p=8.0E−03	n=2	fg=0.03 bg=0.00
ammonium ion binding GO:0070405	p=8.8E−03	n=3	fg=0.05 bg=0.01
acetyltransferase activity GO:0016407	p=1.1E−02	n=3	fg=0.05 bg=0.01
transmitter−gated ion channel activity GO:0022824	p=1.3E−02	n=2	fg=0.03 bg=0.00
transmitter−gated channel activity GO:0022835	p=1.3E−02	n=2	fg=0.03 bg=0.00
anion channel activity GO:0005253	p=1.7E−02	n=3	fg=0.05 bg=0.01
chloride channel activity GO:0005254	p=1.7E−02	n=3	fg=0.05 bg=0.01
ion channel activity GO:0005216	p=1.7E−02	n=8	fg=0.13 bg=0.04
voltage−gated anion channel activity GO:0008308	p=1.9E−02	n=2	fg=0.03 bg=0.00
voltage−gated chloride channel activity GO:0005247	p=1.9E−02	n=2	fg=0.03 bg=0.00
phospholipase activity GO:0004620	p=2.0E−02	n=3	fg=0.05 bg=0.01
quaternary ammonium group binding GO:0050997	p=2.6E−02	n=2	fg=0.03 bg=0.00
phosphatidylcholine binding GO:0031210	p=2.6E−02	n=2	fg=0.03 bg=0.00
phosphatidylinositol phosphate binding GO:1901981	p=2.7E−02	n=4	fg=0.07 bg=0.02
chloride transmembrane transporter activ... GO:0015108	p=2.8E−02	n=3	fg=0.05 bg=0.01
phosphoprotein binding GO:0051219	p=3.2E−02	n=3	fg=0.05 bg=0.01
lipase activity GO:0016298	p=3.2E−02	n=3	fg=0.05 bg=0.01
identical protein binding GO:0042802	p=3.4E−02	n=16	fg=0.27 bg=0.17
phosphatidylinositol bisphosphate bindin... GO:1902936	p=3.7E−02	n=3	fg=0.05 bg=0.01
glycogen binding GO:2001069	p=3.8E−02	n=1	fg=0.02 bg=0.00
semaphorin receptor activity GO:0017154	p=3.8E−02	n=1	fg=0.02 bg=0.00
[phosphorylase] phosphatase activity GO:0050196	p=3.8E−02	n=1	fg=0.02 bg=0.00
C−acetyltransferase activity GO:0016453	p=3.8E−02	n=1	fg=0.02 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985	p=3.8E−02	n=1	fg=0.02 bg=0.00

−log(p)
n=60/286 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=7.8E−04	n=3	fg=0.05 bg=0.00
presynapse GO:0098793	p=2.3E−03	n=12	fg=0.19 bg=0.05
apical plasma membrane GO:0016324	p=3.1E−03	n=8	fg=0.12 bg=0.04
integral component of synaptic vesicle m... GO:0030285	p=5.7E−03	n=3	fg=0.05 bg=0.01
side of membrane GO:0098552	p=7.4E−03	n=7	fg=0.11 bg=0.04
ion channel complex GO:0034702	p=7.6E−03	n=4	fg=0.06 bg=0.01
cell surface GO:0009986	p=8.1E−03	n=7	fg=0.11 bg=0.04
voltage−gated calcium channel complex GO:0005891	p=1.1E−02	n=2	fg=0.03 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234	p=1.4E−02	n=3	fg=0.05 bg=0.01
cytoplasmic side of plasma membrane GO:0009898	p=1.5E−02	n=5	fg=0.08 bg=0.02
organelle membrane contact site GO:0044232	p=1.7E−02	n=2	fg=0.03 bg=0.00
cytoplasmic side of membrane GO:0098562	p=2.3E−02	n=5	fg=0.08 bg=0.03
calcium channel complex GO:0034704	p=2.3E−02	n=2	fg=0.03 bg=0.00
cell projection membrane GO:0031253	p=2.8E−02	n=6	fg=0.09 bg=0.04
L−type voltage−gated calcium channel com... GO:1990454	p=3.5E−02	n=1	fg=0.02 bg=0.00
UBC13−UEV1A complex GO:0035370	p=3.5E−02	n=1	fg=0.02 bg=0.00
semaphorin receptor complex GO:0002116	p=3.5E−02	n=1	fg=0.02 bg=0.00
extrinsic component of plasma membrane GO:0019897	p=3.6E−02	n=3	fg=0.05 bg=0.01
cation channel complex GO:0034703	p=3.6E−02	n=3	fg=0.05 bg=0.01
lysosome GO:0005764	p=4.9E−02	n=7	fg=0.11 bg=0.05
brush border GO:0005903	p=5.0E−02	n=3	fg=0.05 bg=0.01
leading edge membrane GO:0031256	p=5.6E−02	n=3	fg=0.05 bg=0.01
lytic vacuole GO:0000323	p=5.9E−02	n=7	fg=0.11 bg=0.06
plasma membrane protein complex GO:0098797	p=6.5E−02	n=5	fg=0.08 bg=0.03
vacuolar membrane GO:0005774	p=6.5E−02	n=5	fg=0.08 bg=0.03
cell periphery GO:0071944	p=6.8E−02	n=28	fg=0.44 bg=0.29
cell body fiber GO:0070852	p=7.0E−02	n=1	fg=0.02 bg=0.00
acetylcholine−gated channel complex GO:0005892	p=7.0E−02	n=1	fg=0.02 bg=0.00
outer kinetochore GO:0000940	p=7.0E−02	n=1	fg=0.02 bg=0.00
transcription factor AP−1 complex GO:0035976	p=7.0E−02	n=1	fg=0.02 bg=0.00

−log(p)
n=64/286 input genes with annotations

fraction