GO term	−log(p)	n	fg	bg
response to water deprivation GO:0009414	p=5.3E−04	n=3	fg=0.14	bg=0.01
positive regulation of cellular carbohyd... GO:0010676	p=2.8E−03	n=2	fg=0.09	bg=0.01
negative regulation of JUN kinase activi... GO:0043508	p=2.8E−03	n=2	fg=0.09	bg=0.01
engulfment of apoptotic cell GO:0043652	p=2.8E−03	n=2	fg=0.09	bg=0.01
positive regulation of prostaglandin bio... GO:0031394	p=2.8E−03	n=2	fg=0.09	bg=0.01
regulation of determination of dorsal id... GO:2000015	p=2.8E−03	n=2	fg=0.09	bg=0.01
positive regulation of organic acid tran... GO:0032892	p=2.8E−03	n=2	fg=0.09	bg=0.01
amelogenesis GO:0097186	p=2.8E−03	n=2	fg=0.09	bg=0.01
regulation of macrophage derived foam ce... GO:0010743	p=2.8E−03	n=2	fg=0.09	bg=0.01
cellular response to interleukin−1 GO:0071347	p=2.8E−03	n=2	fg=0.09	bg=0.01
positive regulation of intracellular pro... GO:0090316	p=4.2E−03	n=3	fg=0.14	bg=0.02
positive regulation of neuron apoptotic ... GO:0043525	p=6.4E−03	n=3	fg=0.14	bg=0.02
B cell homeostasis GO:0001782	p=8.1E−03	n=2	fg=0.09	bg=0.01
positive regulation of anion transport GO:1903793	p=8.1E−03	n=2	fg=0.09	bg=0.01
protein transmembrane transport GO:0071806	p=8.1E−03	n=2	fg=0.09	bg=0.01
apoptotic mitochondrial changes GO:0008637	p=9.3E−03	n=3	fg=0.14	bg=0.02
wing disc morphogenesis GO:0007472	p=9.5E−03	n=4	fg=0.18	bg=0.04
positive regulation of cellular cataboli... GO:0031331	p=9.5E−03	n=4	fg=0.18	bg=0.04
response to starvation GO:0042594	p=9.5E−03	n=4	fg=0.18	bg=0.04
determination of adult lifespan GO:0008340	p=1.3E−02	n=3	fg=0.14	bg=0.02
regulation of biological quality GO:0065008	p=1.3E−02	n=15	fg=0.68	bg=0.39
positive regulation of secretion by cell GO:1903532	p=1.4E−02	n=4	fg=0.18	bg=0.05
activation of cysteine−type endopeptidas... GO:0006919	p=1.6E−02	n=2	fg=0.09	bg=0.01
positive regulation of lipid localizatio... GO:1905954	p=1.6E−02	n=2	fg=0.09	bg=0.01
regulation of lipid transport GO:0032368	p=1.6E−02	n=2	fg=0.09	bg=0.01
positive regulation of lipid transport GO:0032370	p=1.6E−02	n=2	fg=0.09	bg=0.01
response to peptide GO:1901652	p=1.7E−02	n=5	fg=0.23	bg=0.07
positive regulation of cytoskeleton orga... GO:0051495	p=1.7E−02	n=3	fg=0.14	bg=0.03
multicellular organism aging GO:0010259	p=1.7E−02	n=3	fg=0.14	bg=0.03
biomineral tissue development GO:0031214	p=1.7E−02	n=3	fg=0.14	bg=0.03

0   1   2   3   4   5

−log(p)
n=22/83 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction

GO term	−log(p)	n	fg	bg
ATP binding GO:0005524	p=6.8E−03	n=4	fg=0.18	bg=0.04
voltage−gated potassium channel activity GO:0005249	p=1.3E−02	n=3	fg=0.14	bg=0.02
transmembrane transporter activity GO:0022857	p=2.5E−02	n=7	fg=0.32	bg=0.14
potassium channel activity GO:0005267	p=3.0E−02	n=3	fg=0.14	bg=0.03
potassium ion transmembrane transporter ... GO:0015079	p=3.0E−02	n=3	fg=0.14	bg=0.03
transporter activity GO:0005215	p=4.4E−02	n=7	fg=0.32	bg=0.16
voltage−gated cation channel activity GO:0022843	p=4.5E−02	n=3	fg=0.14	bg=0.04
channel activity GO:0015267	p=5.4E−02	n=5	fg=0.23	bg=0.10
passive transmembrane transporter activi... GO:0022803	p=5.4E−02	n=5	fg=0.23	bg=0.10
voltage−gated ion channel activity GO:0005244	p=5.4E−02	n=3	fg=0.14	bg=0.04
voltage−gated channel activity GO:0022832	p=5.4E−02	n=3	fg=0.14	bg=0.04
inorganic molecular entity transmembrane... GO:0015318	p=5.4E−02	n=6	fg=0.27	bg=0.13
tricarboxylate secondary active transmem... GO:0005371	p=6.0E−02	n=1	fg=0.05	bg=0.00
BH3 domain binding GO:0051434	p=6.0E−02	n=1	fg=0.05	bg=0.00
nucleotidyltransferase activity GO:0016779	p=6.0E−02	n=1	fg=0.05	bg=0.00
V1A vasopressin receptor binding GO:0031894	p=6.0E−02	n=1	fg=0.05	bg=0.00
cysteine−type endopeptidase activator ac... GO:0008656	p=6.0E−02	n=1	fg=0.05	bg=0.00
open rectifier potassium channel activit... GO:0005252	p=6.0E−02	n=1	fg=0.05	bg=0.00
choline−phosphate cytidylyltransferase a... GO:0004105	p=6.0E−02	n=1	fg=0.05	bg=0.00
cytidylyltransferase activity GO:0070567	p=6.0E−02	n=1	fg=0.05	bg=0.00
macromolecule transmembrane transporter ... GO:0022884	p=6.0E−02	n=1	fg=0.05	bg=0.00
fructose−6−phosphate binding GO:0070095	p=6.0E−02	n=1	fg=0.05	bg=0.00
protein phosphatase activator activity GO:0072542	p=6.0E−02	n=1	fg=0.05	bg=0.00
histone deacetylase regulator activity GO:0035033	p=6.0E−02	n=1	fg=0.05	bg=0.00
JUN kinase activity GO:0004705	p=6.0E−02	n=1	fg=0.05	bg=0.00
MAP kinase activity GO:0004707	p=6.0E−02	n=1	fg=0.05	bg=0.00
glucuronosyltransferase activity GO:0015020	p=6.0E−02	n=1	fg=0.05	bg=0.00
intracellular sodium activated potassium... GO:0005228	p=6.0E−02	n=1	fg=0.05	bg=0.00
carbohydrate kinase activity GO:0019200	p=6.0E−02	n=1	fg=0.05	bg=0.00
carbohydrate phosphatase activity GO:0019203	p=6.0E−02	n=1	fg=0.05	bg=0.00

0   1   2   3   4   5

−log(p)
n=22/83 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction

GO term	−log(p)	n	fg	bg
Golgi lumen GO:0005796	p=3.7E−03	n=2	fg=0.08	bg=0.00
anchored component of membrane GO:0031225	p=3.7E−03	n=2	fg=0.08	bg=0.00
organelle envelope GO:0031967	p=2.3E−02	n=5	fg=0.20	bg=0.07
envelope GO:0031975	p=2.3E−02	n=5	fg=0.20	bg=0.07
intrinsic component of plasma membrane GO:0031226	p=3.0E−02	n=8	fg=0.32	bg=0.16
mitochondrion GO:0005739	p=3.4E−02	n=5	fg=0.20	bg=0.08
organelle outer membrane GO:0031968	p=4.8E−02	n=2	fg=0.08	bg=0.01
outer membrane GO:0019867	p=4.8E−02	n=2	fg=0.08	bg=0.01
mitochondrial outer membrane GO:0005741	p=4.8E−02	n=2	fg=0.08	bg=0.01
mitochondrial membrane GO:0031966	p=4.9E−02	n=3	fg=0.12	bg=0.03
anchored component of plasma membrane GO:0046658	p=6.2E−02	n=1	fg=0.04	bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540	p=6.2E−02	n=1	fg=0.04	bg=0.00
glycogen granule GO:0042587	p=6.2E−02	n=1	fg=0.04	bg=0.00
Bcl−2 family protein complex GO:0097136	p=6.2E−02	n=1	fg=0.04	bg=0.00
dendrite cytoplasm GO:0032839	p=6.2E−02	n=1	fg=0.04	bg=0.00
podosome GO:0002102	p=6.2E−02	n=1	fg=0.04	bg=0.00
neuron projection cytoplasm GO:0120111	p=6.2E−02	n=1	fg=0.04	bg=0.00
muscle cell projection GO:0036194	p=6.2E−02	n=1	fg=0.04	bg=0.00
muscle cell projection membrane GO:0036195	p=6.2E−02	n=1	fg=0.04	bg=0.00
sarcoplasmic reticulum membrane GO:0033017	p=6.2E−02	n=1	fg=0.04	bg=0.00
mitochondrial envelope GO:0005740	p=7.0E−02	n=3	fg=0.12	bg=0.04
voltage−gated potassium channel complex GO:0008076	p=8.3E−02	n=2	fg=0.08	bg=0.02
potassium channel complex GO:0034705	p=8.3E−02	n=2	fg=0.08	bg=0.02
sarcoplasm GO:0016528	p=1.2E−01	n=1	fg=0.04	bg=0.00
sarcoplasmic reticulum GO:0016529	p=1.2E−01	n=1	fg=0.04	bg=0.00
cortical endoplasmic reticulum GO:0032541	p=1.2E−01	n=1	fg=0.04	bg=0.00
site of double−strand break GO:0035861	p=1.2E−01	n=1	fg=0.04	bg=0.00
site of DNA damage GO:0090734	p=1.2E−01	n=1	fg=0.04	bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235	p=1.2E−01	n=1	fg=0.04	bg=0.00
endoplasmic reticulum tubular network GO:0071782	p=1.2E−01	n=1	fg=0.04	bg=0.00

0   1   2   3   4   5

−log(p)
n=25/83 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction