fraction genes in fg and expected valu

regulation of neutrophil mediated cytoto... GO:0070948	p=2.1E−05	n=2
regulation of acute inflammatory respons... GO:0002673	p=3.2E−05	n=2
neutrophil activation involved in immune... GO:0002283	p=1.2E−04	n=2
DNA catabolic process, endonucleolytic GO:0000737	p=1.8E−03	n=2
visual behavior GO:0007632	p=1.9E−03	n=2
eating behavior GO:0042755	p=2.0E−03	n=2
G protein−coupled receptor signaling pat... GO:0007186	p=2.6E−03	n=6
G protein−coupled purinergic nucleotide ... GO:0035589	p=4.6E−03	n=1
sensory perception GO:0007600	p=4.6E−03	n=3
regulation of circadian rhythm GO:0042752	p=5.1E−03	n=2
phospholipase C−activating G protein−cou... GO:0007200	p=5.7E−03	n=2
positive regulation of inositol trisphos... GO:0032962	p=6.1E−03	n=1
blood circulation GO:0008015	p=7.0E−03	n=3
positive regulation of penile erection GO:0060406	p=9.1E−03	n=1
conditioned taste aversion GO:0001661	p=9.1E−03	n=1
cellular response to purine−containing c... GO:0071415	p=9.1E−03	n=1
sensitization GO:0046960	p=9.1E−03	n=1
adenylate cyclase−activating adrenergic ... GO:0071880	p=1.1E−02	n=1
phospholipase C−activating dopamine rece... GO:0060158	p=1.1E−02	n=1
catecholamine transport GO:0051937	p=1.1E−02	n=2
cerebral cortex GABAergic interneuron mi... GO:0021853	p=1.2E−02	n=1
adenylate cyclase−activating dopamine re... GO:0007191	p=1.2E−02	n=1
regulation of angiotensin levels in bloo... GO:0002002	p=1.2E−02	n=1
regulation of presynaptic cytosolic calc... GO:0099509	p=1.2E−02	n=1
regulation of tube size GO:0035150	p=1.4E−02	n=2
regulation of tube diameter GO:0035296	p=1.4E−02	n=2
blood vessel diameter maintenance GO:0097746	p=1.4E−02	n=2
interneuron migration GO:1904936	p=1.4E−02	n=1
cerebral cortex GABAergic interneuron di... GO:0021892	p=1.4E−02	n=1
cerebral cortex GABAergic interneuron de... GO:0021894	p=1.4E−02	n=1

fg=0.17 | bg=0.00
fg=0.17 | bg=0.00
fg=0.17 | bg=0.00
fg=0.17 | bg=0.01
fg=0.17 | bg=0.01
fg=0.17 | bg=0.01
fg=0.50 | bg=0.07
fg=0.08 | bg=0.00
fg=0.25 | bg=0.03
fg=0.17 | bg=0.01
fg=0.17 | bg=0.01
fg=0.08 | bg=0.00
fg=0.25 | bg=0.03
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.17 | bg=0.01
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.17 | bg=0.01
fg=0.17 | bg=0.01
fg=0.17 | bg=0.01
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00

−log(p)
n=12/43 input genes with annotations
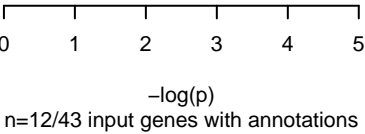
fraction

fraction genes in fg and expected valu

deoxyribonuclease I activity GO:0004530	p=2.5E−06	n=2
G protein−coupled receptor activity GO:0004930	p=4.2E−04	n=6
olfactory receptor activity GO:0004984	p=3.5E−03	n=2
G protein−coupled ADP receptor activity GO:0001621	p=5.0E−03	n=1
A1 adenosine receptor binding GO:0031686	p=5.0E−03	n=1
G protein−coupled ATP receptor activity GO:0045031	p=5.0E−03	n=1
D3 dopamine receptor binding GO:0031750	p=9.9E−03	n=1
dopamine neurotransmitter receptor activ... GO:0001588	p=9.9E−03	n=1
angiotensin receptor binding GO:0031701	p=1.6E−02	n=1
dopamine binding GO:0035240	p=2.0E−02	n=1
catecholamine binding GO:1901338	p=2.0E−02	n=1
bombesin receptor activity GO:0004946	p=2.3E−02	n=1
metallocarboxypeptidase activity GO:0004181	p=2.6E−02	n=1
actin binding GO:0003779	p=2.7E−02	n=2
11−cis retinal binding GO:0005502	p=3.4E−02	n=1
G protein−coupled photoreceptor activity GO:0008020	p=3.8E−02	n=1
photoreceptor activity GO:0009881	p=4.4E−02	n=1
retinal binding GO:0016918	p=4.7E−02	n=1
G−protein alpha−subunit binding GO:0001965	p=4.7E−02	n=1
carboxypeptidase activity GO:0004180	p=5.3E−02	n=1
retinoid binding GO:0005501	p=5.5E−02	n=1
isoprenoid binding GO:0019840	p=5.7E−02	n=1
scaffold protein binding GO:0097110	p=5.8E−02	n=1
metalloexopeptidase activity GO:0008235	p=8.4E−02	n=1
ADP binding GO:0043531	p=9.1E−02	n=1
ATPase binding GO:0051117	p=1.0E−01	n=1
neuropeptide receptor activity GO:0008188	p=1.2E−01	n=1
exopeptidase activity GO:0008238	p=1.3E−01	n=1
metallopeptidase activity GO:0008237	p=1.4E−01	n=1
protein phosphatase binding GO:0019903	p=1.4E−01	n=1

fg=0.15 | bg=0.00
fg=0.46 | bg=0.06
fg=0.15 | bg=0.01
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.15 | bg=0.02
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01

−log(p)
n=13/43 input genes with annotations
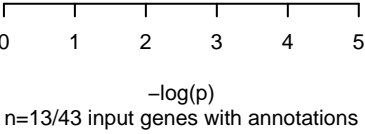
fraction

fraction genes in fg and expected valu

dendritic spine neck GO:0044326	p=1.1E−02	n=1
dendritic spine head GO:0044327	p=1.5E−02	n=1
sperm head plasma membrane GO:1990913	p=2.1E−02	n=1
plasma membrane GO:0005886	p=2.5E−02	n=7
sperm plasma membrane GO:0097524	p=3.1E−02	n=1
postsynaptic membrane GO:0045211	p=3.1E−02	n=2
presynaptic membrane GO:0042734	p=3.3E−02	n=2
cell periphery GO:0071944	p=3.4E−02	n=7
cilium GO:0005929	p=3.9E−02	n=3
presynaptic active zone membrane GO:0048787	p=4.0E−02	n=1
ciliary membrane GO:0060170	p=4.0E−02	n=1
extracellular region GO:0005576	p=4.9E−02	n=3
caveola GO:0005901	p=7.0E−02	n=1
synaptic membrane GO:0097060	p=7.3E−02	n=2
dendritic shaft GO:0043198	p=7.6E−02	n=1
sperm head GO:0061827	p=8.4E−02	n=1
plasma membrane raft GO:0044853	p=8.4E−02	n=1
plasma membrane region GO:0098590	p=8.6E−02	n=3
glutamatergic synapse GO:0098978	p=9.0E−02	n=2
dendritic tree GO:0097447	p=1.0E−01	n=2
dendrite GO:0030425	p=1.0E−01	n=2
presynaptic active zone GO:0048786	p=1.0E−01	n=1
axon terminus GO:0043679	p=1.1E−01	n=1
GABA−ergic synapse GO:0098982	p=1.1E−01	n=1
cell body GO:0044297	p=1.3E−01	n=2
neuron projection terminus GO:0044306	p=1.3E−01	n=1
postsynapse GO:0098794	p=1.4E−01	n=2
non−motile cilium GO:0097730	p=1.4E−01	n=1
dendritic spine GO:0043197	p=1.5E−01	n=1
cell projection GO:0042995	p=1.5E−01	n=4

fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.54 | bg=0.25
fg=0.08 | bg=0.00
fg=0.15 | bg=0.02
fg=0.15 | bg=0.02
fg=0.54 | bg=0.27
fg=0.23 | bg=0.06
fg=0.08 | bg=0.00
fg=0.08 | bg=0.00
fg=0.23 | bg=0.07
fg=0.08 | bg=0.01
fg=0.15 | bg=0.03
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.23 | bg=0.08
fg=0.15 | bg=0.04
fg=0.15 | bg=0.04
fg=0.15 | bg=0.04
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.15 | bg=0.05
fg=0.08 | bg=0.01
fg=0.15 | bg=0.05
fg=0.08 | bg=0.01
fg=0.08 | bg=0.01
fg=0.31 | bg=0.16

−log(p)
n=13/43 input genes with annotations

fraction