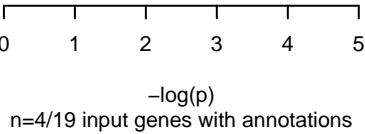


GO:BP
Fox_Nvec_vc1.1_XM_001624941.3

lipid metabolic process	GO:0006629
synaptic vesicle priming	GO:0016082
negative regulation of cAMP-dependent pr...	GO:2000480
positive regulation of meiotic cell cycl...	GO:1904146
monocarboxylic acid metabolic process	GO:0032787
asparagine catabolic process	GO:0006530
activation of protein kinase A activity	GO:0034199
aspartate family amino acid metabolic pr...	GO:0009066
aspartate family amino acid catabolic pr...	GO:0009068
asparagine metabolic process	GO:0006528
response to antipsychotic drug	GO:0097332
response to clozapine	GO:0097338
organelle localization	GO:0051640
cellular lipid metabolic process	GO:0044255
cellular response to glucagon stimulus	GO:0071377
monocarboxylic acid catabolic process	GO:0072329
glutamine family amino acid catabolic pr...	GO:0009065
carboxylic acid metabolic process	GO:0019752
oxoacid metabolic process	GO:0043436
organic acid metabolic process	GO:0006082
response to auditory stimulus	GO:0010996
ciliary basal body-plasma membrane docki...	GO:0097711
alpha-amino acid catabolic process	GO:1901606
protein heterooligomerization	GO:0051291
response to glucagon	GO:0033762
regulation of oocyte maturation	GO:1900193
positive regulation of oocyte maturation	GO:1900195
regulation of cell cycle G2/M phase tran...	GO:1902749
multicellular organismal water homeostas...	GO:0050891
renal water homeostasis	GO:0003091

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p=2.7E-02	n=2
p=2.9E-02	n=1
p=2.9E-02	n=1
p=2.9E-02	n=1
p=3.0E-02	n=2
p=3.2E-02	n=2
p=3.4E-02	n=2
p=3.9E-02	n=1
p=3.9E-02	n=1
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fraction genes in fg and expected value

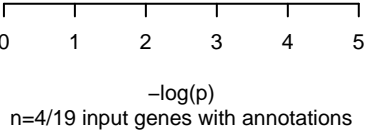
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GO:MF
Fox_Nvec_vc1.1_XM_001624941.3

carboxylic ester hydrolase activity	GO:0052689
phospholipase activity	GO:0004620
phospholipase A2 activity	GO:0004623
platelet-activating factor acetyltransfe...	GO:0047179
protein kinase A catalytic subunit bindi...	GO:0034236
cAMP-dependent protein kinase regulator ...	GO:0008603
protein serine/threonine kinase inhibito...	GO:0030291
beta-2 adrenergic receptor binding	GO:0031698
1-alkyl-2-acetylglycerophosphocholine es...	GO:0003847
cAMP-dependent protein kinase inhibitor ...	GO:0004862
asparaginase activity	GO:0004067
cAMP binding	GO:0030552
kinase inhibitor activity	GO:0019210
protein kinase A binding	GO:0051018
protein kinase inhibitor activity	GO:0004860
lysophospholipase activity	GO:0004622
cyclic nucleotide binding	GO:0030551
AP-2 adaptor complex binding	GO:0035612
protein kinase regulator activity	GO:0019887
kinase regulator activity	GO:0019207
acetyltransferase activity	GO:0016407
hydrolase activity, acting on carbon-nit...	GO:0016811
adrenergic receptor binding	GO:0031690
hydrolase activity, acting on carbon-nit...	GO:0016810
protein homodimerization activity	GO:0042803
acyltransferase activity	GO:0016746
acyltransferase activity, transferring g...	GO:0016747
enzyme inhibitor activity	GO:0004857
G protein-coupled receptor binding	GO:0001664
ubiquitin-like protein ligase binding	GO:0044389

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p=2.2E-02	n=1
p=3.3E-02	n=1
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p=4.3E-02	n=1
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p=7.5E-02	n=1
p=7.5E-02	n=1
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fraction genes in fg and expected value

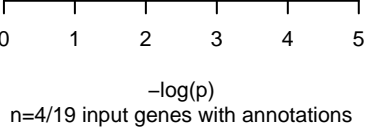
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GO:CC
Fox_Nvec_vc1.1_XM_001624941.3

presynaptic active zone membrane	GO:0048787
cytosol	GO:0005829
cAMP-dependent protein kinase complex	GO:0005952
germinal vesicle	GO:0042585
female germ cell nucleus	GO:0001674
nucleotide-activated protein kinase comp...	GO:0031588
germ cell nucleus	GO:0043073
protein kinase complex	GO:1902911
ficolin-1-rich granule lumen	GO:1904813
secretory vesicle	GO:0099503
fibrillar center	GO:0001650
ficolin-1-rich granule	GO:0101002
ciliary base	GO:0097546
T-tubule	GO:0030315
sarcolemma	GO:0042383
transferase complex, transferring phosph...	GO:0061695
synaptic vesicle membrane	GO:0030672
vesicle lumen	GO:0031983
secretory granule lumen	GO:0034774
mitochondrial inner membrane	GO:0005743
cytoplasmic vesicle lumen	GO:0060205
dendritic shaft	GO:0043198
organelle inner membrane	GO:0019866
exocytic vesicle membrane	GO:0099501
plasma membrane raft	GO:0044853
transport vesicle membrane	GO:0030658
centrosome	GO:0005813
mitochondrial membrane	GO:0031966
synaptic vesicle	GO:0008021
mitochondrial envelope	GO:0005740

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p=1.5E-02	n=4
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fraction genes in fg and expected value

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