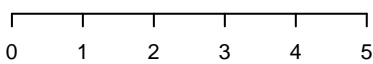


**GO:BP**

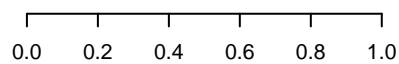
Ncol Nvec vc1.1 XM 048723292.1

fraction genes in fq and expected value

response to amyloid-beta	GO:1904645	p=4.6E-03	n=2
negative regulation of protein depolymer...	GO:1901880	p=7.6E-03	n=2
ammonium ion metabolic process	GO:0097164	p=1.1E-02	n=2
cell junction organization	GO:0034330	p=1.4E-02	n=4
positive regulation of cellular amide me...	GO:0034250	p=1.5E-02	n=2
regulation of supramolecular fiber organ...	GO:1902903	p=1.7E-02	n=3
peptide metabolic process	GO:0006518	p=1.9E-02	n=3
embryonic body morphogenesis	GO:0010172	p=2.0E-02	n=2
response to cold	GO:0009409	p=2.0E-02	n=2
supramolecular fiber organization	GO:0097435	p=2.2E-02	n=3
protein localization to plasma membrane	GO:0072659	p=2.5E-02	n=2
negative regulation of supramolecular fi...	GO:1902904	p=2.5E-02	n=2
body morphogenesis	GO:0010171	p=2.5E-02	n=2
negative regulation of cytoskeleton orga...	GO:0051494	p=2.5E-02	n=2
regulation of amyloid-beta formation	GO:1902003	p=2.9E-02	n=
positive regulation of amyloid-beta form...	GO:1902004	p=2.9E-02	n=1
ecdysone receptor-mediated signaling pat...	GO:0035076	p=2.9E-02	n=1
regulation of systemic arterial blood pr...	GO:0003025	p=2.9E-02	n=1
positive regulation of CoA-transferase a...	GO:1905920	p=2.9E-02	n=1
regulation of acetylcholine biosynthetic...	GO:1905921	p=2.9E-02	n=1
positive regulation of acetylcholine bio...	GO:1905923	p=2.9E-02	n=1
regulation of amyloid precursor protein ...	GO:1902991	p=2.9E-02	n=1
negative regulation of amyloid precursor...	GO:1902992	p=2.9E-02	n=1
positive regulation of amyloid precursor...	GO:1902993	p=2.9E-02	n=1
regulation of CoA-transferase activity	GO:1905918	p=2.9E-02	n=1
myofibroblast differentiation	GO:0036446	p=2.9E-02	n=1
positive regulation of translation in re...	GO:0032056	p=2.9E-02	n=1
positive regulation of translational ini...	GO:0032058	p=2.9E-02	n=1
amyloid-beta metabolic process	GO:0050435	p=2.9E-02	n=1
microtubule anchoring	GO:0034453	p=2.9E-02	n=1



$-\log(p)$   
n=12/46 input genes with annotations

[illegible]

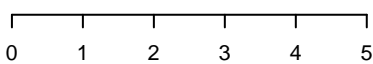
fraction

**GO:MF**

**Ncol\_Nvec\_vc1.1\_XM\_048723292.1**

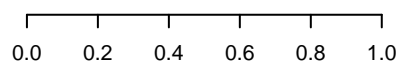
fraction genes in fg and expected value

ammonium ion binding	GO:0070405	p=3.9E-04	n=3
actin filament binding	GO:0051015	p=3.9E-04	n=3
phosphatidylcholine binding	GO:0031210	p=4.8E-03	n=2
calcium channel activity	GO:0005262	p=2.7E-02	n=2
nucleotidyltransferase activity	GO:0016779	p=3.0E-02	n=1
postsynaptic neurotransmitter receptor a...	GO:0098960	p=3.0E-02	n=1
kinetochore binding	GO:0043515	p=3.0E-02	n=1
dystroglycan binding	GO:0002162	p=3.0E-02	n=1
choline-phosphate cytidyltransferase a...	GO:0004105	p=3.0E-02	n=1
nuclear receptor coactivator activity	GO:0030374	p=3.0E-02	n=1
transmitter-gated ion channel activity i...	GO:1904315	p=3.0E-02	n=1
acetylcholine binding	GO:0042166	p=3.0E-02	n=1
misfolded protein binding	GO:0051787	p=3.0E-02	n=1
hydrolase activity, acting on carbon-nit...	GO:0016812	p=3.0E-02	n=1
5-oxoprolinase (ATP-hydrolyzing) activit...	GO:0017168	p=3.0E-02	n=1
cytidyltransferase activity	GO:0070567	p=3.0E-02	n=1
acetylcholine receptor activity	GO:0015464	p=3.0E-02	n=1
chloride channel regulator activity	GO:0017081	p=3.0E-02	n=1
toxic substance binding	GO:0015643	p=3.0E-02	n=1
neurotransmitter receptor activity invol...	GO:0099529	p=3.0E-02	n=1
acetylcholine-gated cation-selective cha...	GO:0022848	p=3.0E-02	n=1
kinase binding	GO:0019900	p=3.3E-02	n=4
protein kinase binding	GO:0019901	p=3.3E-02	n=4
calcium ion transmembrane transporter ac...	GO:0015085	p=4.6E-02	n=2
channel regulator activity	GO:0016247	p=5.4E-02	n=2
ion channel regulator activity	GO:0099106	p=5.4E-02	n=2
phosphatidylethanolamine binding	GO:0008429	p=6.0E-02	n=1
high voltage-gated calcium channel activ...	GO:0008331	p=6.0E-02	n=1
actin monomer binding	GO:0003785	p=6.0E-02	n=1
calcium-dependent phospholipid binding	GO:0005544	p=6.0E-02	n=1



-log(p)  
n=11/46 input genes with annotations

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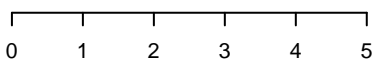
fraction

**GO:CC**

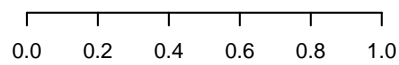
Ncol Nvec vc1.1 XM 048723292.1

fraction genes in fq and expected value

	side of membrane	GO:0098552	p=8.4E-03	n=3
	cytoplasmic microtubule plus-end	GO:1904511	p=2.7E-02	n=1
	kinetochore microtubule	GO:0005828	p=2.7E-02	n=1
	glycogen granule	GO:0042587	p=2.7E-02	n=1
	acetylcholine-gated channel complex	GO:0005892	p=2.7E-02	n=1
	kinetochore	GO:0000776	p=2.7E-02	n=1
	microtubule plus-end	GO:0035371	p=2.7E-02	n=1
	cortical microtubule plus-end	GO:1903754	p=2.7E-02	n=1
	PML body	GO:0016605	p=2.7E-02	n=1
	centrosomal corona	GO:0031592	p=2.7E-02	n=1
	cortical microtubule cytoskeleton	GO:0030981	p=2.7E-02	n=1
	cortical microtubule	GO:0055028	p=2.7E-02	n=1
	L-type voltage-gated calcium channel com...	GO:1990454	p=2.7E-02	n=1
	spindle microtubule	GO:0005876	p=2.7E-02	n=1
	extrinsic component of membrane	GO:0019898	p=3.3E-02	n=2
	cytoplasmic side of plasma membrane	GO:0009898	p=3.3E-02	n=2
	cytoplasmic side of membrane	GO:0098562	p=4.5E-02	n=1
	growth cone	GO:0030426	p=4.5E-02	n=2
	site of polarized growth	GO:0030427	p=5.2E-02	n=2
	leading edge membrane	GO:0031256	p=5.2E-02	n=2
	sarcoplasm	GO:0016528	p=5.4E-02	n=1
	sarcoplasmic reticulum	GO:0016529	p=5.4E-02	n=1
	organelle membrane contact site	GO:0044232	p=5.4E-02	n=1
	cell cortex region	GO:0099738	p=5.4E-02	n=1
	chromosome, centromeric region	GO:0000775	p=5.4E-02	n=1
	condensed chromosome, centromeric region	GO:0000779	p=5.4E-02	n=1
	microtubule end	GO:1990752	p=5.4E-02	n=1
	basal cortex	GO:0045180	p=5.4E-02	n=1
	condensed chromosome	GO:0000793	p=5.4E-02	n=1
	Cul3-RING ubiquitin liqase complex	GO:0031463	p=5.4E-02	n=1



$-\log(p)$   
n=11/46 input genes with annotations

[illegible]

fraction