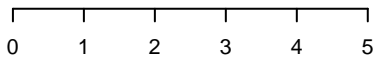


GO:BP

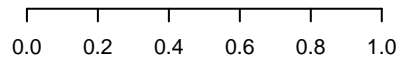
Ncol_Nvec_vc1.1_XM_032384126.2

fraction genes in fg and expected value

2-oxoglutarate metabolic process	GO:00061103	p=1.7E-02	n=1
peptide catabolic process	GO:0043171	p=1.7E-02	n=1
glutathione catabolic process	GO:0006751	p=1.7E-02	n=1
negative regulation of determination of ...	GO:2000016	p=1.7E-02	n=1
regulation of response to food	GO:0032095	p=1.7E-02	n=1
negative regulation of response to food	GO:0032096	p=1.7E-02	n=1
regulation of appetite	GO:0032098	p=1.7E-02	n=1
negative regulation of appetite	GO:0032099	p=1.7E-02	n=1
negative regulation of protein maturati...	GO:1903318	p=1.7E-02	n=1
tyrosine metabolic process	GO:0006570	p=1.7E-02	n=1
tyrosine catabolic process	GO:0006572	p=1.7E-02	n=1
determination of ventral identity	GO:0048264	p=1.7E-02	n=1
sulfur compound catabolic process	GO:0044273	p=1.7E-02	n=1
regulation of response to extracellular ...	GO:0032104	p=1.7E-02	n=1
negative regulation of response to extra...	GO:0032105	p=1.7E-02	n=1
regulation of response to nutrient level...	GO:0032107	p=1.7E-02	n=1
negative regulation of response to nutri...	GO:0032108	p=1.7E-02	n=1
negative regulation of protein processin...	GO:0010955	p=1.7E-02	n=1
neurotransmitter secretion	GO:0007269	p=2.1E-02	n=2
signal release from synapse	GO:0099643	p=2.1E-02	n=2
phospholipid catabolic process	GO:0009395	p=3.4E-02	n=1
aromatic amino acid family metabolic pro...	GO:0009072	p=3.4E-02	n=1
aromatic amino acid family catabolic pro...	GO:0009074	p=3.4E-02	n=1
regulation of determination of dorsal id...	GO:2000015	p=3.4E-02	n=1
N-acylethanolamine metabolic process	GO:0070291	p=3.4E-02	n=1
negative regulation of JUN kinase activi...	GO:0043508	p=3.4E-02	n=1
glycerophospholipid catabolic process	GO:0046475	p=3.4E-02	n=1
response to food	GO:0032094	p=3.4E-02	n=1
ethanolamine-containing compound metabol...	GO:0042439	p=3.4E-02	n=1
L-phenylalanine metabolic process	GO:0006558	p=3.4E-02	n=1

 $-\log(p)$

n=7/28 input genes with annotations

[illegible]

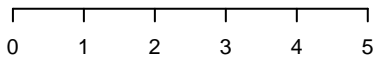
fraction

GO:MF

Ncol_Nvec_vc1.1_XM_032384126.2

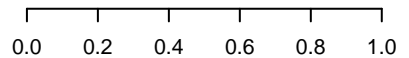
fraction genes in fg and expected value

	anion binding	GO:0043168	p=1.2E-02	n=4
	Notch binding	GO:0005112	p=1.9E-02	n=1
glycerophosphoinositol	glycerophosphodite...	GO:0047395	p=1.9E-02	n=1
	growth factor activity	GO:0008083	p=1.9E-02	n=1
	transaminase activity	GO:0008483	p=1.9E-02	n=1
gamma-glutamylcyclotransferase	activity	GO:0003839	p=1.9E-02	n=1
L-tyrosine	aminotransferase activity	GO:0070547	p=1.9E-02	n=1
glycerophosphodiester	phosphodiesterase ...	GO:0008889	p=1.9E-02	n=1
L-tyrosine:2-oxoglutarate	aminotransfera...	GO:0004838	p=1.9E-02	n=1
intracellular sodium	activated potassium...	GO:0005228	p=1.9E-02	n=1
	phosphatidylinositol binding	GO:0035091	p=3.3E-02	n=2
	signaling receptor regulator activity	GO:0030545	p=3.8E-02	n=1
	signaling receptor activator activity	GO:0030546	p=3.8E-02	n=1
calcium-dependent	phospholipid binding	GO:0005544	p=3.8E-02	n=1
calcium-activated	potassium channel acti...	GO:0015269	p=3.8E-02	n=1
	transferase activity, transferring nitro...	GO:0016769	p=3.8E-02	n=1
	carbon-nitrogen lyase activity	GO:0016840	p=3.8E-02	n=1
	amidase-lyase activity	GO:0016842	p=3.8E-02	n=1
phosphatidylethanolamine	binding	GO:0008429	p=3.8E-02	n=1
	receptor ligand activity	GO:0048018	p=3.8E-02	n=1
	ion binding	GO:0043167	p=4.1E-02	n=4
	lysophospholipase activity	GO:0004622	p=7.5E-02	n=1
calcium activated	cation channel activit...	GO:0005227	p=7.5E-02	n=1
quaternary ammonium	group binding	GO:0050997	p=7.5E-02	n=1
	phosphatidylcholine binding	GO:0031210	p=7.5E-02	n=1
	phospholipid binding	GO:0005543	p=8.3E-02	n=2
	amino acid binding	GO:0016597	p=9.3E-02	n=1
	lipid binding	GO:0008289	p=1.1E-01	n=2
	ammonium ion binding	GO:0070405	p=1.1E-01	n=1
	carboxylic acid binding	GO:0031406	p=1.1E-01	n=1

 $-\log(p)$

n=7/28 input genes with annotations

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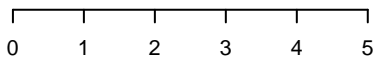
fraction

GO:CC

Ncol_Nvec_vc1.1_XM_032384126.2

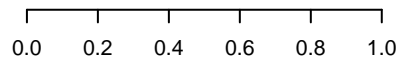
fraction genes in fg and expected value

organelle membrane contact site	GO:0044232	p=3.5E-02	n=1
extrinsic component of cytoplasmic side ...	GO:0031234	p=6.8E-02	n=3
integral component of plasma membrane	GO:0005887	p=6.8E-02	n=3
intrinsic component of plasma membrane	GO:0031226	p=8.4E-02	n=3
extrinsic component of plasma membrane	GO:0019897	p=8.4E-02	n=1
voltage-gated potassium channel complex	GO:0008076	p=1.3E-01	n=1
potassium channel complex	GO:0034705	p=1.3E-01	n=1
integral component of endoplasmic reticu...	GO:0030176	p=1.8E-01	n=1
extrinsic component of membrane	GO:0019898	p=1.8E-01	n=1
cytoplasmic side of plasma membrane	GO:0009898	p=1.8E-01	n=1
intrinsic component of endoplasmic retic...	GO:0031227	p=1.8E-01	n=1
extracellular space	GO:0005615	p=2.1E-01	n=1
trans-Golgi network	GO:0005802	p=2.1E-01	n=1
cytoplasmic side of membrane	GO:0098562	p=2.1E-01	n=1
cation channel complex	GO:0034703	p=2.3E-01	n=1
synaptic vesicle	GO:0008021	p=2.3E-01	n=1
integral component of membrane	GO:0016021	p=2.4E-01	n=3
transmembrane transporter complex	GO:1902495	p=2.5E-01	n=1
ion channel complex	GO:0034702	p=2.5E-01	n=1
transporter complex	GO:1990351	p=2.5E-01	n=1
exocytic vesicle	GO:0070382	p=2.5E-01	n=1
organelle subcompartment	GO:0031984	p=2.6E-01	n=2
side of membrane	GO:0098552	p=2.6E-01	n=1
intrinsic component of membrane	GO:0031224	p=2.7E-01	n=3
intrinsic component of organelle membran...	GO:0031300	p=2.8E-01	n=1
integral component of organelle membrane	GO:0031301	p=2.8E-01	n=1
transport vesicle	GO:0030133	p=3.0E-01	n=1
membrane	GO:0016020	p=3.1E-01	n=5
plasma membrane protein complex	GO:0098797	p=3.3E-01	n=1
extracellular region	GO:0005576	p=3.8E-01	n=1

 $-\log(p)$

n=7/28 input genes with annotations

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fraction