

term	tot	exp	obs	pValue	description	annotation
GO:0055085	276	17	28	7.01E-003	transmembrane transport	GO_BP
GO:0045944	242	15	23	2.78E-002	positive regulation of transcription from RNA polymerase II promoter	GO_BP
GO:0007420	105	7	13	1.32E-002	brain development	GO_BP
GO:0016192	89	6	10	4.95E-002	vesicle-mediated transport	GO_BP
GO:0007156	59	4	8	2.90E-002	homophilic cell adhesion	GO_BP
GO:0070588	31	2	7	2.49E-003	calcium ion transmembrane transport	GO_BP
GO:0009611	38	2	7	8.18E-003	response to wounding	GO_BP
GO:0006816	51	3	7	3.76E-002	calcium ion transport	GO_BP
GO:0042755	15	1	4	1.18E-002	eating behavior	GO_BP
GO:0048477	6	0	3	4.19E-003	oogenesis	GO_BP
GO:0009312	7	0	3	6.99E-003	oligosaccharide biosynthetic process	GO_BP
GO:0060749	8	0	3	1.07E-002	mammary gland alveolus development	GO_BP
GO:0051272	9	1	3	1.53E-002	positive regulation of cellular component movement	GO_BP
GO:0001101	10	1	3	2.08E-002	response to acid	GO_BP
GO:0031290	11	1	3	2.73E-002	retinal ganglion cell axon guidance	GO_BP
GO:0030902	11	1	3	2.73E-002	hindbrain development	GO_BP
GO:0006826	12	1	3	3.48E-002	iron ion transport	GO_BP
GO:0050770	12	1	3	3.48E-002	regulation of axonogenesis	GO_BP
GO:0016197	12	1	3	3.48E-002	endosome transport	GO_BP
GO:0015807	12	1	3	3.48E-002	L-amino acid transport	GO_BP
GO:0040007	13	1	3	4.32E-002	growth	GO_BP
GO:0051865	13	1	3	4.32E-002	protein autoubiquitination	GO_BP
GO:0010740	2	0	2	3.89E-003	positive regulation of intracellular protein kinase cascade	GO_BP
GO:0010807	2	0	2	3.89E-003	regulation of synaptic vesicle priming	GO_BP
GO:0045088	3	0	2	1.12E-002	regulation of innate immune response	GO_BP
GO:0007617	3	0	2	1.12E-002	mating behavior	GO_BP
GO:0010907	3	0	2	1.12E-002	positive regulation of glucose metabolic process	GO_BP
GO:0060055	3	0	2	1.12E-002	angiogenesis involved in wound healing	GO_BP
GO:0060046	3	0	2	1.12E-002	regulation of acrosome reaction	GO_BP
GO:0008088	3	0	2	1.12E-002	axon cargo transport	GO_BP
GO:0045176	4	0	2	2.14E-002	apical protein localization	GO_BP
GO:0009072	4	0	2	2.14E-002	aromatic amino acid family metabolic process	GO_BP
GO:0043011	4	0	2	2.14E-002	myeloid dendritic cell differentiation	GO_BP
GO:0050881	4	0	2	2.14E-002	musculoskeletal movement	GO_BP
GO:0002675	4	0	2	2.14E-002	positive regulation of acute inflammatory response	GO_BP
GO:0061036	4	0	2	2.14E-002	positive regulation of cartilage development	GO_BP
GO:0051938	4	0	2	2.14E-002	L-glutamate import	GO_BP
GO:0021680	5	0	2	3.42E-002	cerebellar Purkinje cell layer development	GO_BP
GO:0032456	5	0	2	3.42E-002	endocytic recycling	GO_BP

GO:0032229	5	0	2	3.42E-002	negative regulation of synaptic transmission, GABAergic	GO_BP
GO:0015813	5	0	2	3.42E-002	L-glutamate transport	GO_BP
GO:0006839	5	0	2	3.42E-002	mitochondrial transport	GO_BP
GO:0006270	6	0	2	4.93E-002	DNA-dependent DNA replication initiation	GO_BP
GO:0030111	6	0	2	4.93E-002	regulation of Wnt receptor signaling pathway	GO_BP
GO:0048745	6	0	2	4.93E-002	smooth muscle tissue development	GO_BP
GO:0003009	6	0	2	4.93E-002	skeletal muscle contraction	GO_BP
GO:0018022	6	0	2	4.93E-002	peptidyl-lysine methylation	GO_BP
GO:0045056	6	0	2	4.93E-002	transcytosis	GO_BP
GO:0005624	261	16	24	3.23E-002	membrane fraction	GO_CC
GO:0019717	90	6	11	2.23E-002	synaptosome	GO_CC
GO:0031307	7	0	3	6.82E-003	integral to mitochondrial outer membrane	GO_CC
GO:0001518	10	1	3	2.03E-002	voltage-gated sodium channel complex	GO_CC
GO:0032045	3	0	2	1.10E-002	guanyl-nucleotide exchange factor complex	GO_CC
GO:0033270	4	0	2	2.11E-002	paranode region of axon	GO_CC
GO:0016602	4	0	2	2.11E-002	CCAAT-binding factor complex	GO_CC
GO:0005641	5	0	2	3.37E-002	nuclear envelope lumen	GO_CC
GO:0033180	5	0	2	3.37E-002	proton-transporting V-type ATPase, V1 domain	GO_CC
GO:0008385	5	0	2	3.37E-002	IkappaB kinase complex	GO_CC
GO:0000145	5	0	2	3.37E-002	exocyst	GO_CC
GO:0033268	5	0	2	3.37E-002	node of Ranvier	GO_CC
GO:0005216	92	6	11	2.91E-002	ion channel activity	GO_MF
GO:0016597	19	1	4	2.83E-002	amino acid binding	GO_MF
GO:0016881	19	1	4	2.83E-002	acid-amino acid ligase activity	GO_MF
GO:0005262	22	1	4	4.61E-002	calcium channel activity	GO_MF
GO:0031402	8	1	3	1.10E-002	sodium ion binding	GO_MF
GO:0005248	11	1	3	2.81E-002	voltage-gated sodium channel activity	GO_MF
GO:0043022	12	1	3	3.57E-002	ribosome binding	GO_MF
GO:0003829	2	0	2	3.96E-003	beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltra	GO_MF
GO:0005250	2	0	2	3.96E-003	A-type (transient outward) potassium channel activity	GO_MF
GO:0008401	3	0	2	1.14E-002	retinoic acid 4-hydroxylase activity	GO_MF
GO:0008384	3	0	2	1.14E-002	IkappaB kinase activity	GO_MF
GO:0017016	4	0	2	2.18E-002	Ras GTPase binding	GO_MF
GO:0005313	4	0	2	2.18E-002	L-glutamate transmembrane transporter activity	GO_MF
GO:0031490	5	0	2	3.49E-002	chromatin DNA binding	GO_MF

4722	73	5	9	3.87E-002 Neurotrophin signaling pathway	KEGG
512	16	1	4	1.55E-002 Mucin type O-Glycan biosynthesis	KEGG