

term	tot	exp	obs	pValue	description	annotation
GO:0006810	140	25	35	2.62E-002	transport	GO_BP
GO:0001701	118	21	31	1.80E-002	in utero embryonic development	GO_BP
GO:0030335	57	10	17	2.19E-002	positive regulation of cell migration	GO_BP
GO:0050790	60	11	17	3.54E-002	regulation of catalytic activity	GO_BP
GO:0001822	52	9	16	1.91E-002	kidney development	GO_BP
GO:0009636	49	9	14	4.99E-002	response to toxin	GO_BP
GO:0006897	41	7	13	2.59E-002	endocytosis	GO_BP
GO:0006464	33	6	12	1.03E-002	protein modification process	GO_BP
GO:0032526	40	7	12	4.75E-002	response to retinoic acid	GO_BP
GO:0018108	28	5	11	7.20E-003	peptidyl-tyrosine phosphorylation	GO_BP
GO:0000902	30	5	11	1.29E-002	cell morphogenesis	GO_BP
GO:0031175	36	7	11	5.00E-002	neuron projection development	GO_BP
GO:0006006	27	5	10	1.62E-002	glucose metabolic process	GO_BP
GO:0007179	30	5	10	3.43E-002	transforming growth factor beta receptor signaling pathway	GO_BP
GO:0002756	31	6	10	4.27E-002	MyD88-independent toll-like receptor signaling pathway	GO_BP
GO:0007492	20	4	9	5.20E-003	endoderm development	GO_BP
GO:0006936	21	4	9	7.65E-003	muscle contraction	GO_BP
GO:0001657	25	5	9	2.67E-002	ureteric bud development	GO_BP
GO:0007610	13	2	8	6.35E-004	behavior	GO_BP
GO:0032313	19	3	8	1.33E-002	regulation of Rab GTPase activity	GO_BP
GO:0007205	21	4	8	2.55E-002	activation of protein kinase C activity by G-protein coupled receptor protein signalir	GO_BP
GO:0048705	23	4	8	4.39E-002	skeletal system morphogenesis	GO_BP
GO:0001656	14	3	7	6.77E-003	metanephros development	GO_BP
GO:0043407	15	3	7	1.07E-002	negative regulation of MAP kinase activity	GO_BP
GO:0043010	18	3	7	3.21E-002	camera-type eye development	GO_BP
GO:0048646	9	2	6	1.83E-003	anatomical structure formation involved in morphogenesis	GO_BP
GO:0034605	12	2	6	1.22E-002	cellular response to heat	GO_BP
GO:0048168	13	2	6	1.92E-002	regulation of neuronal synaptic plasticity	GO_BP
GO:0048538	13	2	6	1.92E-002	thymus development	GO_BP
GO:0045785	14	3	6	2.86E-002	positive regulation of cell adhesion	GO_BP
GO:0048839	14	3	6	2.86E-002	inner ear development	GO_BP
GO:0006098	6	1	5	1.01E-003	pentose-phosphate shunt	GO_BP
GO:0048856	7	1	5	3.00E-003	anatomical structure development	GO_BP
GO:0034504	8	1	5	6.81E-003	protein localization to nucleus	GO_BP
GO:0051928	9	2	5	1.30E-002	positive regulation of calcium ion transport	GO_BP
GO:0043280	9	2	5	1.30E-002	positive regulation of caspase activity	GO_BP
GO:0030100	9	2	5	1.30E-002	regulation of endocytosis	GO_BP
GO:0048147	9	2	5	1.30E-002	negative regulation of fibroblast proliferation	GO_BP
GO:0030168	9	2	5	1.30E-002	platelet activation	GO_BP

GO:0071347	9	2	5	1.30E-002	cellular response to interleukin-1	GO_BP
GO:0014911	10	2	5	2.22E-002	positive regulation of smooth muscle cell migration	GO_BP
GO:0019835	10	2	5	2.22E-002	cytolysis	GO_BP
GO:0001958	11	2	5	3.48E-002	endochondral ossification	GO_BP
GO:0007369	11	2	5	3.48E-002	gastrulation	GO_BP
GO:0030902	11	2	5	3.48E-002	hindbrain development	GO_BP
GO:0007162	11	2	5	3.48E-002	negative regulation of cell adhesion	GO_BP
GO:0001841	4	1	4	1.09E-003	neural tube formation	GO_BP
GO:0030104	5	1	4	4.67E-003	water homeostasis	GO_BP
GO:0001759	5	1	4	4.67E-003	organ induction	GO_BP
GO:0048745	6	1	4	1.20E-002	smooth muscle tissue development	GO_BP
GO:0035024	6	1	4	1.20E-002	negative regulation of Rho protein signal transduction	GO_BP
GO:0060173	6	1	4	1.20E-002	limb development	GO_BP
GO:0043401	6	1	4	1.20E-002	steroid hormone mediated signaling pathway	GO_BP
GO:0006972	6	1	4	1.20E-002	hyperosmotic response	GO_BP
GO:0045022	7	1	4	2.40E-002	early endosome to late endosome transport	GO_BP
GO:0042771	7	1	4	2.40E-002	DNA damage response, signal transduction by p53 class mediator resulting in induc	GO_BP
GO:0033261	7	1	4	2.40E-002	regulation of S phase	GO_BP
GO:0051281	7	1	4	2.40E-002	positive regulation of release of sequestered calcium ion into cytosol	GO_BP
GO:0007249	8	1	4	4.11E-002	I-kappaB kinase/NF-kappaB cascade	GO_BP
GO:0007026	8	1	4	4.11E-002	negative regulation of microtubule depolymerization	GO_BP
GO:0009948	8	1	4	4.11E-002	anterior/posterior axis specification	GO_BP
GO:0003151	8	1	4	4.11E-002	outflow tract morphogenesis	GO_BP
GO:0016265	8	1	4	4.11E-002	death	GO_BP
GO:0009653	8	1	4	4.11E-002	anatomical structure morphogenesis	GO_BP
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GO:0051966	4	1	3	2.08E-002	regulation of synaptic transmission, glutamatergic	GO_BP
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GO:0001953	4	1	3	2.08E-002	negative regulation of cell-matrix adhesion	GO_BP
GO:0048566	4	1	3	2.08E-002	embryonic digestive tract development	GO_BP
GO:0032228	4	1	3	2.08E-002	regulation of synaptic transmission, GABAergic	GO_BP
GO:0060291	4	1	3	2.08E-002	long-term synaptic potentiation	GO_BP
GO:0001952	4	1	3	2.08E-002	regulation of cell-matrix adhesion	GO_BP
GO:0031214	5	1	3	4.50E-002	biomineral tissue development	GO_BP
GO:0032331	5	1	3	4.50E-002	negative regulation of chondrocyte differentiation	GO_BP
GO:0034616	5	1	3	4.50E-002	response to laminar fluid shear stress	GO_BP
GO:0046879	5	1	3	4.50E-002	hormone secretion	GO_BP
GO:0048747	5	1	3	4.50E-002	muscle fiber development	GO_BP
GO:0001655	5	1	3	4.50E-002	urogenital system development	GO_BP

GO:0006402	5	1	3	4.50E-002 mRNA catabolic process	GO_BP
GO:0035414	5	1	3	4.50E-002 negative regulation of catenin import into nucleus	GO_BP
GO:0043149	5	1	3	4.50E-002 stress fiber assembly	GO_BP
GO:0021904	5	1	3	4.50E-002 dorsal/ventral neural tube patterning	GO_BP
GO:0032456	5	1	3	4.50E-002 endocytic recycling	GO_BP
GO:0032229	5	1	3	4.50E-002 negative regulation of synaptic transmission, GABAergic	GO_BP
GO:0090190	5	1	3	4.50E-002 positive regulation of branching involved in ureteric bud morphogenesis	GO_BP
GO:0060389	5	1	3	4.50E-002 pathway-restricted SMAD protein phosphorylation	GO_BP
GO:0060292	5	1	3	4.50E-002 long term synaptic depression	GO_BP
GO:0030194	5	1	3	4.50E-002 positive regulation of blood coagulation	GO_BP
GO:0032525	2	0	2	3.31E-002 somite rostral/caudal axis specification	GO_BP
GO:0009052	2	0	2	3.31E-002 pentose-phosphate shunt, non-oxidative branch	GO_BP
GO:0015014	2	0	2	3.31E-002 heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	GO_BP
GO:0060676	2	0	2	3.31E-002 ureteric bud formation	GO_BP
GO:0042035	2	0	2	3.31E-002 regulation of cytokine biosynthetic process	GO_BP
GO:0000083	2	0	2	3.31E-002 regulation of transcription involved in G1/S phase of mitotic cell cycle	GO_BP
GO:0002829	2	0	2	3.31E-002 negative regulation of type 2 immune response	GO_BP
GO:0001831	2	0	2	3.31E-002 trophoblast cellular morphogenesis	GO_BP
GO:0051451	2	0	2	3.31E-002 myoblast migration	GO_BP
GO:0072181	2	0	2	3.31E-002 mesonephric duct formation	GO_BP
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GO:0072164	2	0	2	3.31E-002 mesonephric tubule development	GO_BP
GO:0007382	2	0	2	3.31E-002 specification of segmental identity, maxillary segment	GO_BP
GO:0060513	2	0	2	3.31E-002 prostatic bud formation	GO_BP
GO:0010506	2	0	2	3.31E-002 regulation of autophagy	GO_BP
GO:0033004	2	0	2	3.31E-002 negative regulation of mast cell activation	GO_BP
GO:0021871	2	0	2	3.31E-002 forebrain regionalization	GO_BP
GO:0045839	2	0	2	3.31E-002 negative regulation of mitosis	GO_BP
GO:0046929	2	0	2	3.31E-002 negative regulation of neurotransmitter secretion	GO_BP
GO:0035021	2	0	2	3.31E-002 negative regulation of Rac protein signal transduction	GO_BP
GO:0021533	2	0	2	3.31E-002 cell differentiation in hindbrain	GO_BP
GO:0060487	2	0	2	3.31E-002 lung epithelial cell differentiation	GO_BP
GO:0006288	2	0	2	3.31E-002 base-excision repair, DNA ligation	GO_BP
GO:0061017	2	0	2	3.31E-002 hepatoblast differentiation	GO_BP
GO:0048599	2	0	2	3.31E-002 oocyte development	GO_BP
GO:0031558	2	0	2	3.31E-002 induction of apoptosis in response to chemical stimulus	GO_BP
GO:0051895	2	0	2	3.31E-002 negative regulation of focal adhesion assembly	GO_BP
GO:0019805	2	0	2	3.31E-002 quinolinate biosynthetic process	GO_BP

GO:0005789	252	46	59	1.95E-002	endoplasmic reticulum membrane	GO_CC
GO:0005856	219	40	50	4.49E-002	cytoskeleton	GO_CC
GO:0005887	132	24	33	2.97E-002	integral to plasma membrane	GO_CC
GO:0014069	61	11	18	2.05E-002	postsynaptic density	GO_CC
GO:0043209	14	3	7	6.71E-003	myelin sheath	GO_CC
GO:0000932	10	2	5	2.21E-002	cytoplasmic mRNA processing body	GO_CC
GO:0005680	11	2	5	3.46E-002	anaphase-promoting complex	GO_CC
GO:0031463	6	1	4	1.19E-002	Cul3-RING ubiquitin ligase complex	GO_CC
GO:0044445	6	1	4	1.19E-002	cytosolic part	GO_CC
GO:0005868	8	1	4	4.09E-002	cytoplasmic dynein complex	GO_CC
GO:0005579	3	1	3	5.99E-003	membrane attack complex	GO_CC
GO:0016327	4	1	3	2.07E-002	apicolateral plasma membrane	GO_CC
GO:0000137	5	1	3	4.48E-002	Golgi cis cisterna	GO_CC
GO:0033180	5	1	3	4.48E-002	proton-transporting V-type ATPase, V1 domain	GO_CC
GO:0001940	2	0	2	3.30E-002	male pronucleus	GO_CC
GO:0045244	2	0	2	3.30E-002	succinate-CoA ligase complex (GDP-forming)	GO_CC
GO:0071204	2	0	2	3.30E-002	histone pre-mRNA 3'end processing complex	GO_CC

GO:0008270	813	148	185	3.13E-004	zinc ion binding	GO_MF
GO:0004872	435	79	93	4.80E-002	receptor activity	GO_MF
GO:0005509	293	53	69	1.17E-002	calcium ion binding	GO_MF
GO:0003779	102	19	28	1.37E-002	actin binding	GO_MF
GO:0004221	33	6	14	1.08E-003	ubiquitin thiolesterase activity	GO_MF
GO:0008234	26	5	9	3.50E-002	cysteine-type peptidase activity	GO_MF
GO:0005097	22	4	8	3.44E-002	Rab GTPase activator activity	GO_MF
GO:0046332	18	3	7	3.26E-002	SMAD binding	GO_MF
GO:0016881	19	3	7	4.37E-002	acid-amino acid ligase activity	GO_MF
GO:0070491	10	2	5	2.25E-002	repressing transcription factor binding	GO_MF
GO:0004703	4	1	4	1.10E-003	G-protein coupled receptor kinase activity	GO_MF
GO:0004708	5	1	4	4.72E-003	MAP kinase kinase activity	GO_MF
GO:0042974	6	1	4	1.21E-002	retinoic acid receptor binding	GO_MF
GO:0042975	6	1	4	1.21E-002	peroxisome proliferator activated receptor binding	GO_MF
GO:0016922	6	1	4	1.21E-002	ligand-dependent nuclear receptor binding	GO_MF
GO:0050431	6	1	4	1.21E-002	transforming growth factor beta binding	GO_MF
GO:0005160	7	1	4	2.42E-002	transforming growth factor beta receptor binding	GO_MF
GO:0016229	3	1	3	6.06E-003	steroid dehydrogenase activity	GO_MF
GO:0048155	3	1	3	6.06E-003	S100 alpha binding	GO_MF
GO:0050786	3	1	3	6.06E-003	RAGE receptor binding	GO_MF
GO:0004045	4	1	3	2.09E-002	aminoacyl-tRNA hydrolase activity	GO_MF

GO:0008301	4	1	3	2.09E-002 DNA bending activity	GO_MF
GO:0004983	5	1	3	4.53E-002 neuropeptide Y receptor activity	GO_MF
GO:0005161	5	1	3	4.53E-002 platelet-derived growth factor receptor binding	GO_MF
GO:0030506	5	1	3	4.53E-002 ankyrin binding	GO_MF
GO:0004427	2	0	2	3.33E-002 inorganic diphosphatase activity	GO_MF
GO:0004776	2	0	2	3.33E-002 succinate-CoA ligase (GDP-forming) activity	GO_MF
GO:0001641	2	0	2	3.33E-002 group II metabotropic glutamate receptor activity	GO_MF
GO:0004345	2	0	2	3.33E-002 glucose-6-phosphate dehydrogenase activity	GO_MF
GO:0009922	2	0	2	3.33E-002 fatty acid elongase activity	GO_MF
GO:0004949	2	0	2	3.33E-002 cannabinoid receptor activity	GO_MF
GO:0004568	2	0	2	3.33E-002 chitinase activity	GO_MF
GO:0005250	2	0	2	3.33E-002 A-type (transient outward) potassium channel activity	GO_MF
4110	78	14	25	1.87E-003 Cell cycle	KEGG
4914	47	9	15	1.53E-002 Progesterone-mediated oocyte maturation	KEGG
5215	47	9	15	1.53E-002 Prostate cancer	KEGG
4115	48	9	14	4.04E-002 p53 signaling pathway	KEGG
4350	49	9	14	4.75E-002 TGF-beta signaling pathway	KEGG
5218	28	5	10	2.03E-002 Melanoma	KEGG
5020	17	3	7	2.25E-002 Prion diseases	KEGG
592	12	2	5	4.98E-002 alpha-Linolenic acid metabolism	KEGG