

term	tot	exp	obs	pValue	description	annotation
GO:0006355	426	13	21	1.88E-002	regulation of transcription, DNA-dependent	GO_BP
GO:0001701	118	4	10	3.04E-003	in utero embryonic development	GO_BP
GO:0007399	128	4	8	4.09E-002	nervous system development	GO_BP
GO:0030324	62	2	7	2.59E-003	lung development	GO_BP
GO:0007507	97	3	7	2.79E-002	heart development	GO_BP
GO:0032355	75	2	6	2.61E-002	response to estradiol stimulus	GO_BP
GO:0001889	66	2	5	4.98E-002	liver development	GO_BP
GO:0030100	9	0	4	9.31E-005	regulation of endocytosis	GO_BP
GO:0048839	14	0	4	6.56E-004	inner ear development	GO_BP
GO:0007492	20	1	4	2.75E-003	endoderm development	GO_BP
GO:0001558	30	1	4	1.23E-002	regulation of cell growth	GO_BP
GO:0009611	38	1	4	2.74E-002	response to wounding	GO_BP
GO:0003151	8	0	3	1.39E-003	outflow tract morphogenesis	GO_BP
GO:0030902	11	0	3	3.83E-003	hindbrain development	GO_BP
GO:0035050	12	0	3	4.99E-003	embryonic heart tube development	GO_BP
GO:0007205	21	1	3	2.47E-002	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	GO_BP
GO:0048146	22	1	3	2.79E-002	positive regulation of fibroblast proliferation	GO_BP
GO:0048705	23	1	3	3.14E-002	skeletal system morphogenesis	GO_BP
GO:0034261	3	0	2	2.71E-003	negative regulation of Ras GTPase activity	GO_BP
GO:0007529	3	0	2	2.71E-003	establishment of synaptic specificity at neuromuscular junction	GO_BP
GO:0048617	4	0	2	5.31E-003	embryonic foregut morphogenesis	GO_BP
GO:0015904	4	0	2	5.31E-003	tetracycline transport	GO_BP
GO:0042063	4	0	2	5.31E-003	gliogenesis	GO_BP
GO:0051024	5	0	2	8.68E-003	positive regulation of immunoglobulin secretion	GO_BP
GO:0001759	5	0	2	8.68E-003	organ induction	GO_BP
GO:0035414	5	0	2	8.68E-003	negative regulation of catenin import into nucleus	GO_BP
GO:0008610	8	0	2	2.29E-002	lipid biosynthetic process	GO_BP
GO:0048873	8	0	2	2.29E-002	homeostasis of number of cells within a tissue	GO_BP
GO:0048771	8	0	2	2.29E-002	tissue remodeling	GO_BP
GO:0010718	9	0	2	2.88E-002	positive regulation of epithelial to mesenchymal transition	GO_BP
GO:0010634	9	0	2	2.88E-002	positive regulation of epithelial cell migration	GO_BP
GO:0051928	9	0	2	2.88E-002	positive regulation of calcium ion transport	GO_BP
GO:0001944	9	0	2	2.88E-002	vasculature development	GO_BP
GO:0046580	9	0	2	2.88E-002	negative regulation of Ras protein signal transduction	GO_BP
GO:0071356	10	0	2	3.53E-002	cellular response to tumor necrosis factor	GO_BP
GO:0006471	11	0	2	4.23E-002	protein ADP-ribosylation	GO_BP
GO:0017148	11	0	2	4.23E-002	negative regulation of translation	GO_BP
GO:0030878	11	0	2	4.23E-002	thyroid gland development	GO_BP
GO:0048701	12	0	2	4.98E-002	embryonic cranial skeleton morphogenesis	GO_BP

GO:0045596	12	0	2	4.98E-002	negative regulation of cell differentiation	GO_BP
GO:0001755	12	0	2	4.98E-002	neural crest cell migration	GO_BP
GO:0002009	12	0	2	4.98E-002	morphogenesis of an epithelium	GO_BP
GO:0030032	12	0	2	4.98E-002	lamellipodium assembly	GO_BP
GO:0045907	12	0	2	4.98E-002	positive regulation of vasoconstriction	GO_BP
GO:0014068	12	0	2	4.98E-002	positive regulation of phosphatidylinositol 3-kinase cascade	GO_BP
GO:0009743	12	0	2	4.98E-002	response to carbohydrate stimulus	GO_BP
GO:0006710	1	0	1	3.04E-002	androgen catabolic process	GO_BP
GO:0048298	1	0	1	3.04E-002	positive regulation of isotype switching to IgA isotypes	GO_BP
GO:0002426	1	0	1	3.04E-002	immunoglobulin production in mucosal tissue	GO_BP
GO:0010608	1	0	1	3.04E-002	posttranscriptional regulation of gene expression	GO_BP
GO:0007509	1	0	1	3.04E-002	mesoderm migration involved in gastrulation	GO_BP
GO:0080009	1	0	1	3.04E-002	mRNA methylation	GO_BP
GO:0002686	1	0	1	3.04E-002	negative regulation of leukocyte migration	GO_BP
GO:0002830	1	0	1	3.04E-002	positive regulation of type 2 immune response	GO_BP
GO:0051025	1	0	1	3.04E-002	negative regulation of immunoglobulin secretion	GO_BP
GO:0070267	1	0	1	3.04E-002	oncosis	GO_BP
GO:0042984	1	0	1	3.04E-002	regulation of amyloid precursor protein biosynthetic process	GO_BP
GO:0017000	1	0	1	3.04E-002	antibiotic biosynthetic process	GO_BP
GO:0019477	1	0	1	3.04E-002	L-lysine catabolic process	GO_BP
GO:0032235	1	0	1	3.04E-002	negative regulation of calcium ion transport via store-operated calcium channel activity	GO_BP
GO:0000244	1	0	1	3.04E-002	assembly of spliceosomal tri-snRNP	GO_BP
GO:0071000	1	0	1	3.04E-002	response to magnetism	GO_BP
GO:0048729	1	0	1	3.04E-002	tissue morphogenesis	GO_BP
GO:0048327	1	0	1	3.04E-002	axial mesodermal cell fate specification	GO_BP
GO:0002085	1	0	1	3.04E-002	inhibition of neuroepithelial cell differentiation	GO_BP
GO:0033505	1	0	1	3.04E-002	floor plate morphogenesis	GO_BP
GO:0090010	1	0	1	3.04E-002	transforming growth factor beta receptor signaling pathway involved in primitive streak formation	GO_BP
GO:0060802	1	0	1	3.04E-002	epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification	GO_BP
GO:0048859	1	0	1	3.04E-002	formation of anatomical boundary	GO_BP
GO:0003215	1	0	1	3.04E-002	cardiac right ventricle morphogenesis	GO_BP
GO:0050651	1	0	1	3.04E-002	dermatan sulfate proteoglycan biosynthetic process	GO_BP
GO:0035110	1	0	1	3.04E-002	leg morphogenesis	GO_BP
GO:0060913	1	0	1	3.04E-002	cardiac cell fate determination	GO_BP
GO:0050655	1	0	1	3.04E-002	dermatan sulfate proteoglycan metabolic process	GO_BP
GO:0006543	1	0	1	3.04E-002	glutamine catabolic process	GO_BP
GO:0021956	1	0	1	3.04E-002	central nervous system interneuron axonogenesis	GO_BP
GO:0042663	1	0	1	3.04E-002	regulation of endodermal cell fate specification	GO_BP
GO:0072179	1	0	1	3.04E-002	nephric duct formation	GO_BP
GO:0072095	1	0	1	3.04E-002	regulation of branch elongation involved in ureteric bud branching	GO_BP

GO:0001714	1	0	1	3.04E-002	endodermal cell fate specification	GO_BP
GO:0072176	1	0	1	3.04E-002	nephric duct development	GO_BP
GO:0060677	1	0	1	3.04E-002	ureteric bud elongation	GO_BP
GO:0051915	1	0	1	3.04E-002	induction of synaptic plasticity by chemical substance	GO_BP
GO:0021700	1	0	1	3.04E-002	developmental maturation	GO_BP
GO:0032387	1	0	1	3.04E-002	negative regulation of intracellular transport	GO_BP
GO:0061162	1	0	1	3.04E-002	establishment of monopolar cell polarity	GO_BP
GO:0060748	1	0	1	3.04E-002	tertiary branching involved in mammary gland duct morphogenesis	GO_BP
GO:0031638	1	0	1	3.04E-002	zymogen activation	GO_BP
GO:0010002	1	0	1	3.04E-002	cardioblast differentiation	GO_BP
GO:0010693	1	0	1	3.04E-002	negative regulation of alkaline phosphatase activity	GO_BP
GO:0051280	1	0	1	3.04E-002	negative regulation of release of sequestered calcium ion into cytosol	GO_BP
GO:0045726	1	0	1	3.04E-002	positive regulation of integrin biosynthetic process	GO_BP
GO:0051795	1	0	1	3.04E-002	positive regulation of catagen	GO_BP
GO:0009912	1	0	1	3.04E-002	auditory receptor cell fate commitment	GO_BP
GO:0060594	1	0	1	3.04E-002	mammary gland specification	GO_BP
GO:0030505	1	0	1	3.04E-002	inorganic diphosphate transport	GO_BP
GO:0045591	1	0	1	3.04E-002	positive regulation of regulatory T cell differentiation	GO_BP
GO:0006203	1	0	1	3.04E-002	dGTP catabolic process	GO_BP
GO:0042262	1	0	1	3.04E-002	DNA protection	GO_BP
GO:0006195	1	0	1	3.04E-002	purine nucleotide catabolic process	GO_BP
GO:0002223	1	0	1	3.04E-002	stimulatory C-type lectin receptor signaling pathway	GO_BP
GO:0071364	1	0	1	3.04E-002	cellular response to epidermal growth factor stimulus	GO_BP
GO:0055096	1	0	1	3.04E-002	low-density lipoprotein particle mediated signaling	GO_BP
GO:0042058	1	0	1	3.04E-002	regulation of epidermal growth factor receptor signaling pathway	GO_BP
GO:0045917	1	0	1	3.04E-002	positive regulation of complement activation	GO_BP
GO:0001970	1	0	1	3.04E-002	positive regulation of activation of membrane attack complex	GO_BP
GO:0005887	132	4	9	2.26E-002	integral to plasma membrane	GO_CC
GO:0005667	92	3	7	2.50E-002	transcription factor complex	GO_CC
GO:0005923	41	1	4	3.85E-002	tight junction	GO_CC
GO:0030131	16	1	3	1.26E-002	clathrin adaptor complex	GO_CC
GO:0005912	22	1	3	3.02E-002	adherens junction	GO_CC
GO:0000118	11	0	2	4.47E-002	histone deacetylase complex	GO_CC
GO:0045271	1	0	1	3.14E-002	respiratory chain complex I	GO_CC
GO:0046540	1	0	1	3.14E-002	U4/U6 x U5 tri-snRNP complex	GO_CC
GO:0031011	1	0	1	3.14E-002	Ino80 complex	GO_CC
GO:0030530	1	0	1	3.14E-002	heterogeneous nuclear ribonucleoprotein complex	GO_CC

GO:0016563	182	5	10	4.45E-002	transcription activator activity	GO_MF
GO:0016301	98	3	7	2.63E-002	kinase activity	GO_MF
GO:0008083	60	2	5	3.23E-002	growth factor activity	GO_MF
GO:0030674	21	1	3	2.32E-002	protein binding, bridging	GO_MF
GO:0030414	21	1	3	2.32E-002	peptidase inhibitor activity	GO_MF
GO:0003705	24	1	3	3.32E-002	sequence-specific enhancer binding RNA polymerase II transcription factor activity	GO_MF
GO:0003953	3	0	2	2.59E-003	NAD+ nucleosidase activity	GO_MF
GO:0030371	4	0	2	5.08E-003	translation repressor activity	GO_MF
GO:0015520	4	0	2	5.08E-003	tetracycline:hydrogen antiporter activity	GO_MF
GO:0003956	5	0	2	8.30E-003	NAD(P)+-protein-arginine ADP-ribosyltransferase activity	GO_MF
GO:0035257	5	0	2	8.30E-003	nuclear hormone receptor binding	GO_MF
GO:0042288	6	0	2	1.22E-002	MHC class I protein binding	GO_MF
GO:0042974	6	0	2	1.22E-002	retinoic acid receptor binding	GO_MF
GO:0016922	6	0	2	1.22E-002	ligand-dependent nuclear receptor binding	GO_MF
GO:0005099	7	0	2	1.68E-002	Ras GTPase activator activity	GO_MF
GO:0048407	7	0	2	1.68E-002	platelet-derived growth factor binding	GO_MF
GO:0016747	8	0	2	2.19E-002	transferase activity, transferring acyl groups other than amino-acyl groups	GO_MF
GO:0004198	8	0	2	2.19E-002	calcium-dependent cysteine-type endopeptidase activity	GO_MF
GO:0005234	10	0	2	3.39E-002	extracellular-glutamate-gated ion channel activity	GO_MF
GO:0004483	1	0	1	2.97E-002	mRNA (nucleoside-2'-O-)-methyltransferase activity	GO_MF
GO:0016651	1	0	1	2.97E-002	oxidoreductase activity, acting on NADH or NADPH	GO_MF
GO:0047130	1	0	1	2.97E-002	saccharopine dehydrogenase (NADP+, L-lysine-forming) activity	GO_MF
GO:0047131	1	0	1	2.97E-002	saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity	GO_MF
GO:0070990	1	0	1	2.97E-002	snRNP binding	GO_MF
GO:0019780	1	0	1	2.97E-002	FAT10 activating enzyme activity	GO_MF
GO:0002166	1	0	1	2.97E-002	beta-dystroglycan binding	GO_MF
GO:0004349	1	0	1	2.97E-002	glutamate 5-kinase activity	GO_MF
GO:0004350	1	0	1	2.97E-002	glutamate-5-semialdehyde dehydrogenase activity	GO_MF
GO:0051033	1	0	1	2.97E-002	RNA transmembrane transporter activity	GO_MF
GO:0004971	1	0	1	2.97E-002	alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	GO_MF
GO:0005018	1	0	1	2.97E-002	platelet-derived growth factor alpha-receptor activity	GO_MF
GO:0030345	1	0	1	2.97E-002	structural constituent of tooth enamel	GO_MF
GO:0004564	1	0	1	2.97E-002	beta-fructofuranosidase activity	GO_MF
GO:0004575	1	0	1	2.97E-002	sucrose alpha-glucosidase activity	GO_MF
GO:0004574	1	0	1	2.97E-002	oligo-1,6-glucosidase activity	GO_MF
GO:0030504	1	0	1	2.97E-002	inorganic diphosphate transmembrane transporter activity	GO_MF
GO:0031851	1	0	1	2.97E-002	kappa-type opioid receptor binding	GO_MF
GO:0005134	1	0	1	2.97E-002	interleukin-2 receptor binding	GO_MF
GO:0008413	1	0	1	2.97E-002	8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity	GO_MF

GO:0035539	1	0	1	2.97E-002	8-oxo-7,8-dihydrodeoxyguanosine triphosphate pyrophosphatase activity	GO_MF
GO:0032394	1	0	1	2.97E-002	MHC class Ib receptor activity	GO_MF
GO:0045233	1	0	1	2.97E-002	natural killer cell receptor activity	GO_MF
GO:0055100	1	0	1	2.97E-002	adiponectin binding	GO_MF
04810	108	3	8	1.74E-002	Regulation of actin cytoskeleton	KEGG
04110	78	2	7	9.60E-003	Cell cycle	KEGG
05146	49	2	5	1.67E-002	Amoebiasis	KEGG
04630	64	2	5	4.64E-002	Jak-STAT signaling pathway	KEGG
04623	24	1	3	3.64E-002	Cytosolic DNA-sensing pathway	KEGG