

term	tot	exp	obs	pValue	description	annotation
GO:0001701	118	10	17	0.01926	in utero embryonic development	GO_BP
GO:0035556	120	10	16	0.04293	intracellular signal transduction	GO_BP
GO:0006916	86	7	13	0.02662	anti-apoptosis	GO_BP
GO:0000165	27	2	6	0.02218	MAPKKK cascade	GO_BP
GO:0007267	30	3	6	0.03594	cell-cell signaling	GO_BP
GO:0046928	11	1	5	0.00125	regulation of neurotransmitter secretion	GO_BP
GO:0019432	18	2	5	0.01409	triglyceride biosynthetic process	GO_BP
GO:0045768	18	2	5	0.01409	positive regulation of anti-apoptosis	GO_BP
GO:0048705	23	2	5	0.03907	skeletal system morphogenesis	GO_BP
GO:0006182	9	1	4	0.00443	cGMP biosynthetic process	GO_BP
GO:0046627	12	1	4	0.01419	negative regulation of insulin receptor signaling pathway	GO_BP
GO:0002026	12	1	4	0.01419	regulation of the force of heart contraction	GO_BP
GO:0030521	13	1	4	0.01917	androgen receptor signaling pathway	GO_BP
GO:0016079	16	1	4	0.03990	synaptic vesicle exocytosis	GO_BP
GO:0003007	16	1	4	0.03990	heart morphogenesis	GO_BP
GO:0010642	3	0	3	0.00059	negative regulation of platelet-derived growth factor receptor signaling pathway	GO_BP
GO:0006857	3	0	3	0.00059	oligopeptide transport	GO_BP
GO:0000090	4	0	3	0.00222	mitotic anaphase	GO_BP
GO:0046085	5	0	3	0.00520	adenosine metabolic process	GO_BP
GO:0030431	5	0	3	0.00520	sleep	GO_BP
GO:0008589	6	1	3	0.00976	regulation of smoothened signaling pathway	GO_BP
GO:0048813	8	1	3	0.02406	dendrite morphogenesis	GO_BP
GO:0046854	8	1	3	0.02406	phosphatidylinositol phosphorylation	GO_BP
GO:0035115	9	1	3	0.03387	embryonic forelimb morphogenesis	GO_BP
GO:0042113	9	1	3	0.03387	B cell activation	GO_BP
GO:0030100	9	1	3	0.03387	regulation of endocytosis	GO_BP
GO:0035108	9	1	3	0.03387	limb morphogenesis	GO_BP
GO:0045648	9	1	3	0.03387	positive regulation of erythrocyte differentiation	GO_BP
GO:0030518	10	1	3	0.04543	steroid hormone receptor signaling pathway	GO_BP
GO:0032006	2	0	2	0.00706	regulation of TOR signaling cascade	GO_BP
GO:0015074	2	0	2	0.00706	DNA integration	GO_BP

GO:0046548	2	0	2	0.00706 retinal rod cell development	GO_BP
GO:0019367	2	0	2	0.00706 fatty acid elongation saturated fatty acid	GO_BP
GO:0015988	2	0	2	0.00706 energy coupled proton transport against electrochemical gradient	GO_BP
GO:0016081	3	0	2	0.02001 synaptic vesicle docking involved in exocytosis	GO_BP
GO:0042723	3	0	2	0.02001 thiamine-containing compound metabolic process	GO_BP
GO:0033089	3	0	2	0.02001 positive regulation of T cell differentiation in thymus	GO_BP
GO:0051000	3	0	2	0.02001 positive regulation of nitric-oxide synthase activity	GO_BP
GO:0030643	3	0	2	0.02001 cellular phosphate ion homeostasis	GO_BP
GO:0031110	3	0	2	0.02001 regulation of microtubule polymerization or depolymerization	GO_BP
GO:0042761	3	0	2	0.02001 very long-chain fatty acid biosynthetic process	GO_BP
GO:0014033	3	0	2	0.02001 neural crest cell differentiation	GO_BP
GO:0033962	3	0	2	0.02001 cytoplasmic mRNA processing body assembly	GO_BP
GO:0010107	3	0	2	0.02001 potassium ion import	GO_BP
GO:0006688	3	0	2	0.02001 glycosphingolipid biosynthetic process	GO_BP
GO:0060346	3	0	2	0.02001 bone trabecula formation	GO_BP
GO:0001957	3	0	2	0.02001 intramembranous ossification	GO_BP
GO:0010614	3	0	2	0.02001 negative regulation of cardiac muscle hypertrophy	GO_BP
GO:0043589	4	0	2	0.03780 skin morphogenesis	GO_BP
GO:0017158	4	0	2	0.03780 regulation of calcium ion-dependent exocytosis	GO_BP
GO:0034614	4	0	2	0.03780 cellular response to reactive oxygen species	GO_BP
GO:0060174	4	0	2	0.03780 limb bud formation	GO_BP
GO:0032465	4	0	2	0.03780 regulation of cytokinesis	GO_BP
GO:0001841	4	0	2	0.03780 neural tube formation	GO_BP
GO:0050435	4	0	2	0.03780 beta-amyloid metabolic process	GO_BP
GO:0043353	4	0	2	0.03780 enucleate erythrocyte differentiation	GO_BP
GO:0045078	4	0	2	0.03780 positive regulation of interferon-gamma biosynthetic process	GO_BP
GO:0002031	4	0	2	0.03780 G-protein coupled receptor internalization	GO_BP
GO:0001956	4	0	2	0.03780 positive regulation of neurotransmitter secretion	GO_BP
GO:0005886	1204	98	115	0.03104 plasma membrane	GO_CC
GO:0005626	34	3	7	0.01785 insoluble fraction	GO_CC

GO:0016604	16	1	5	0.00724 nuclear body	GO_CC
GO:0016592	23	2	5	0.03477 mediator complex	GO_CC
GO:0042598	6	0	4	0.00057 vesicular fraction	GO_CC
GO:0000118	11	1	4	0.00907 histone deacetylase complex	GO_CC
GO:0017053	17	1	4	0.04428 transcriptional repressor complex	GO_CC
GO:0005922	7	1	3	0.01471 connexon complex	GO_CC
GO:0034361	7	1	3	0.01471 very-low-density lipoprotein particle	GO_CC
GO:0005942	7	1	3	0.01471 phosphatidylinositol 3-kinase complex	GO_CC
GO:0016235	7	1	3	0.01471 aggresome	GO_CC
GO:0043229	8	1	3	0.02213 intracellular organelle	GO_CC
GO:0000777	10	1	3	0.04195 condensed chromosome kinetochore	GO_CC
GO:0000015	2	0	2	0.00664 phosphopyruvate hydratase complex	GO_CC
GO:0071204	2	0	2	0.00664 histone pre-mRNA 3'end processing complex	GO_CC
GO:0042584	3	0	2	0.01883 chromaffin granule membrane	GO_CC
GO:0034366	3	0	2	0.01883 spherical high-density lipoprotein particle	GO_CC
GO:0032045	3	0	2	0.01883 guanyl-nucleotide exchange factor complex	GO_CC
GO:0044306	3	0	2	0.01883 neuron projection terminus	GO_CC
GO:0005744	4	0	2	0.03563 mitochondrial inner membrane presequence translocase complex	GO_CC
GO:0070032	4	0	2	0.03563 synaptobrevin 2-SNAP-25-syntaxin-1a-complexin I complex	GO_CC
GO:0070044	4	0	2	0.03563 synaptobrevin 2-SNAP-25-syntaxin-1a complex	GO_CC
GO:0042393	27	2	8	0.00108 histone binding	GO_MF
GO:0019900	26	2	7	0.00402 kinase binding	GO_MF
GO:0003729	22	2	6	0.00715 mRNA binding	GO_MF
GO:0005507	27	2	6	0.01998 copper ion binding	GO_MF
GO:0046966	19	2	5	0.01624 thyroid hormone receptor binding	GO_MF
GO:0005080	19	2	5	0.01624 protein kinase C binding	GO_MF
GO:0016455	20	2	5	0.02022 RNA polymerase II transcription mediator activity	GO_MF
GO:0005243	7	1	4	0.00129 gap junction channel activity	GO_MF
GO:0005246	13	1	4	0.01771 calcium channel regulator activity	GO_MF
GO:0000149	13	1	4	0.01771 SNARE binding	GO_MF

GO:0004428	5	0	3	0.00487 inositol or phosphatidylinositol kinase activity	GO_MF
GO:0043295	6	0	3	0.00914 glutathione binding	GO_MF
GO:0043008	7	1	3	0.01503 ATP-dependent protein binding	GO_MF
GO:0016303	7	1	3	0.01503 1-phosphatidylinositol-3-kinase activity	GO_MF
GO:0017134	8	1	3	0.02260 fibroblast growth factor binding	GO_MF
GO:0005391	8	1	3	0.02260 sodium:potassium-exchanging ATPase activity	GO_MF
GO:0046873	10	1	3	0.04281 metal ion transmembrane transporter activity	GO_MF
GO:0005070	10	1	3	0.04281 SH3/SH2 adaptor activity	GO_MF
GO:0001641	2	0	2	0.00674 group II metabotropic glutamate receptor activity	GO_MF
GO:0004720	2	0	2	0.00674 protein-lysine 6-oxidase activity	GO_MF
GO:0050700	2	0	2	0.00674 CARD domain binding	GO_MF
GO:0004634	2	0	2	0.00674 phosphopyruvate hydratase activity	GO_MF
GO:0008489	2	0	2	0.00674 UDP-galactose:glucosylceramide beta-1.4-galactosyltransferase activity	GO_MF
GO:0019870	3	0	2	0.01912 potassium channel inhibitor activity	GO_MF
GO:0003865	3	0	2	0.01912 3-oxo-5-alpha-steroid 4-dehydrogenase activity	GO_MF
GO:0008253	3	0	2	0.01912 5'-nucleotidase activity	GO_MF
GO:0046934	3	0	2	0.01912 phosphatidylinositol-4.5-bisphosphate 3-kinase activity	GO_MF
GO:0005523	4	0	2	0.03617 tropomyosin binding	GO_MF
GO:0015276	4	0	2	0.03617 ligand-gated ion channel activity	GO_MF
GO:0017016	4	0	2	0.03617 Ras GTPase binding	GO_MF
GO:0004445	4	0	2	0.03617 inositol-polyphosphate 5-phosphatase activity	GO_MF
03040	79	6	13	0.00990 Spliceosome	KEGG
04070	50	4	9	0.01726 Phosphatidylinositol signaling system	KEGG
04973	24	2	8	0.00039 Carbohydrate digestion and absorption	KEGG
00562	35	3	8	0.00573 Inositol phosphate metabolism	KEGG
05210	30	2	6	0.03044 Colorectal cancer	KEGG
04960	30	2	6	0.03044 Aldosterone-regulated sodium reabsorption	KEGG
00561	31	3	6	0.03528 Glycerolipid metabolism	KEGG
00100	11	1	5	0.00104 Steroid biosynthesis	KEGG