

OVEREXP DMI07

Term	Tot	Exp	Obs	p Value	Description	Annotation
GO:0001701	118	16	23	3.20E-002	in utero embryonic development	GO_BP
GO:0001822	52	7	12	3.40E-002	kidney development	GO_BP
GO:0006874	36	5	11	4.99E-003	cellular calcium ion homeostasis	GO_BP
GO:0000165	27	4	10	1.48E-003	MAPKKK cascade	GO_BP
GO:0006200	42	6	10	4.17E-002	ATP catabolic process	GO_BP
GO:0007267	30	4	9	1.22E-002	cell-cell signaling	GO_BP
GO:0016311	32	4	9	1.88E-002	dephosphorylation	GO_BP
GO:0090090	37	5	9	4.60E-002	negative regulation of canonical Wnt receptor signaling pathway	GO_BP
GO:0045768	18	2	8	1.11E-003	positive regulation of anti-apoptosis	GO_BP
GO:0006006	27	4	8	1.92E-002	glucose metabolic process	GO_BP
GO:0070588	31	4	8	4.25E-002	calcium ion transmembrane transport	GO_BP
GO:0001756	21	3	7	1.44E-002	somitogenesis	GO_BP
GO:0051781	20	3	6	3.85E-002	positive regulation of cell division	GO_BP
GO:0000082	21	3	6	4.81E-002	G1/S transition of mitotic cell cycle	GO_BP
GO:0006869	21	3	6	4.81E-002	lipid transport	GO_BP
GO:0033344	11	1	5	9.02E-003	cholesterol efflux	GO_BP
GO:0046928	11	1	5	9.02E-003	regulation of neurotransmitter secretion	GO_BP
GO:0010165	11	1	5	9.02E-003	response to X-ray	GO_BP
GO:0015807	12	2	5	1.38E-002	L-amino acid transport	GO_BP
GO:0002026	12	2	5	1.38E-002	regulation of the force of heart contraction	GO_BP
GO:0017156	14	2	5	2.79E-002	calcium ion-dependent exocytosis	GO_BP
GO:0030199	14	2	5	2.79E-002	collagen fibril organization	GO_BP
GO:0001707	15	2	5	3.75E-002	mesoderm formation	GO_BP
GO:0051966	4	1	4	2.96E-004	regulation of synaptic transmission glutamatergic	GO_BP
GO:0048598	6	1	4	3.56E-003	embryonic morphogenesis	GO_BP
GO:0042113	9	1	4	2.16E-002	B cell activation	GO_BP
GO:0006182	9	1	4	2.16E-002	cGMP biosynthetic process	GO_BP
GO:0045648	9	1	4	2.16E-002	positive regulation of erythrocyte differentiation	GO_BP
GO:0050768	10	1	4	3.23E-002	negative regulation of neurogenesis	GO_BP
GO:0006829	10	1	4	3.23E-002	zinc ion transport	GO_BP

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GO:0048844	11	1	4	4.56E-002	artery morphogenesis	GO_BP
GO:0051028	11	1	4	4.56E-002	mRNA transport	GO_BP
GO:0010951	11	1	4	4.56E-002	negative regulation of endopeptidase activity	GO_BP
GO:0035121	11	1	4	4.56E-002	tail morphogenesis	GO_BP
GO:0033962	3	0	3	2.26E-003	cytoplasmic mRNA processing body assembly	GO_BP
GO:0010642	3	0	3	2.26E-003	negative regulation of platelet-derived growth factor receptor signi	GO_BP
GO:0006857	3	0	3	2.26E-003	oligopeptide transport	GO_BP
GO:0010107	3	0	3	2.26E-003	potassium ion import	GO_BP
GO:0000103	3	0	3	2.26E-003	sulfate assimilation	GO_BP
GO:0060291	4	1	3	8.16E-003	long-term synaptic potentiation	GO_BP
GO:0000090	4	1	3	8.16E-003	mitotic anaphase	GO_BP
GO:0001953	4	1	3	8.16E-003	negative regulation of cell-matrix adhesion	GO_BP
GO:0010766	4	1	3	8.16E-003	negative regulation of sodium ion transport	GO_BP
GO:0001841	4	1	3	8.16E-003	neural tube formation	GO_BP
GO:0001952	4	1	3	8.16E-003	regulation of cell-matrix adhesion	GO_BP
GO:0032228	4	1	3	8.16E-003	regulation of synaptic transmission GABAergic	GO_BP
GO:0046085	5	1	3	1.84E-002	adenosine metabolic process	GO_BP
GO:0009950	5	1	3	1.84E-002	dorsal/ventral axis specification	GO_BP
GO:0030431	5	1	3	1.84E-002	sleep	GO_BP
GO:0051480	6	1	3	3.32E-002	cytosolic calcium ion homeostasis	GO_BP
GO:0035024	6	1	3	3.32E-002	negative regulation of Rho protein signal transduction	GO_BP
GO:0008589	6	1	3	3.32E-002	regulation of smoothened signaling pathway	GO_BP
GO:0034405	6	1	3	3.32E-002	response to fluid shear stress	GO_BP
GO:0019413	2	0	2	1.72E-002	acetate biosynthetic process	GO_BP
GO:0015074	2	0	2	1.72E-002	DNA integration	GO_BP
GO:0015988	2	0	2	1.72E-002	energy coupled proton transport against electrochemical gradient	GO_BP
GO:0019367	2	0	2	1.72E-002	fatty acid elongation saturated fatty acid	GO_BP
GO:0006895	2	0	2	1.72E-002	Golgi to endosome transport	GO_BP
GO:0042628	2	0	2	1.72E-002	mating plug formation	GO_BP
GO:0006851	2	0	2	1.72E-002	mitochondrial calcium ion transport	GO_BP
GO:0045796	2	0	2	1.72E-002	negative regulation of intestinal cholesterol absorption	GO_BP

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GO:0010949	2	0	2	1.72E-002	negative regulation of intestinal phytosterol absorption	GO_BP
GO:0033004	2	0	2	1.72E-002	negative regulation of mast cell activation	GO_BP
GO:0046929	2	0	2	1.72E-002	negative regulation of neurotransmitter secretion	GO_BP
GO:0032463	2	0	2	1.72E-002	negative regulation of protein homooligomerization	GO_BP
GO:0042660	2	0	2	1.72E-002	positive regulation of cell fate specification	GO_BP
GO:0002842	2	0	2	1.72E-002	positive regulation of T cell mediated immune response to tumor cells	GO_BP
GO:0002329	2	0	2	1.72E-002	pre-B cell differentiation	GO_BP
GO:0019542	2	0	2	1.72E-002	propionate biosynthetic process	GO_BP
GO:0032006	2	0	2	1.72E-002	regulation of TOR signaling cascade	GO_BP
GO:0046548	2	0	2	1.72E-002	retinal rod cell development	GO_BP
GO:0071173	2	0	2	1.72E-002	spindle assembly checkpoint	GO_BP
GO:0060346	3	0	2	4.72E-002	bone trabecula formation	GO_BP
GO:0030643	3	0	2	4.72E-002	cellular phosphate ion homeostasis	GO_BP
GO:0019348	3	0	2	4.72E-002	dolichol metabolic process	GO_BP
GO:0060059	3	0	2	4.72E-002	embryonic retina morphogenesis in camera-type eye	GO_BP
GO:0006688	3	0	2	4.72E-002	glycosphingolipid biosynthetic process	GO_BP
GO:0048312	3	0	2	4.72E-002	intracellular distribution of mitochondria	GO_BP
GO:0001957	3	0	2	4.72E-002	intramembranous ossification	GO_BP
GO:0042490	3	0	2	4.72E-002	mechanoreceptor differentiation	GO_BP
GO:0045759	3	0	2	4.72E-002	negative regulation of action potential	GO_BP
GO:0010614	3	0	2	4.72E-002	negative regulation of cardiac muscle hypertrophy	GO_BP
GO:0014033	3	0	2	4.72E-002	neural crest cell differentiation	GO_BP
GO:0001504	3	0	2	4.72E-002	neurotransmitter uptake	GO_BP
GO:0019800	3	0	2	4.72E-002	peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	GO_BP
GO:0032727	3	0	2	4.72E-002	positive regulation of interferon-alpha production	GO_BP
GO:0051000	3	0	2	4.72E-002	positive regulation of nitric-oxide synthase activity	GO_BP
GO:0033089	3	0	2	4.72E-002	positive regulation of T cell differentiation in thymus	GO_BP
GO:0014048	3	0	2	4.72E-002	regulation of glutamate secretion	GO_BP
GO:0030300	3	0	2	4.72E-002	regulation of intestinal cholesterol absorption	GO_BP
GO:0031110	3	0	2	4.72E-002	regulation of microtubule polymerization or depolymerization	GO_BP
GO:0007090	3	0	2	4.72E-002	regulation of S phase of mitotic cell cycle	GO_BP

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GO:0015918	3	0	2	4.72E-002	sterol transport	GO_BP
GO:0016081	3	0	2	4.72E-002	synaptic vesicle docking involved in exocytosis	GO_BP
GO:0042723	3	0	2	4.72E-002	thiamine-containing compound metabolic process	GO_BP
GO:0042761	3	0	2	4.72E-002	very long-chain fatty acid biosynthetic process	GO_BP
GO:0016050	3	0	2	4.72E-002	vesicle organization	GO_BP
GO:0016021	1589	205	233	1.07E-002	integral to membrane	GO_CC
GO:0005622	743	96	111	4.80E-002	intracellular	GO_CC
GO:0005789	252	33	42	4.68E-002	endoplasmic reticulum membrane	GO_CC
GO:0005792	199	26	35	3.34E-002	microsome	GO_CC
GO:0005768	116	15	22	3.94E-002	endosome	GO_CC
GO:0019717	90	12	18	3.71E-002	synaptosome	GO_CC
GO:0042734	21	3	7	1.32E-002	presynaptic membrane	GO_CC
GO:0005793	23	3	7	2.21E-002	ER-Golgi intermediate compartment	GO_CC
GO:0016459	16	2	6	1.16E-002	myosin complex	GO_CC
GO:0016604	16	2	5	4.57E-002	nuclear body	GO_CC
GO:0042598	6	1	4	3.34E-003	vesicular fraction	GO_CC
GO:0016235	7	1	4	7.00E-003	aggresome	GO_CC
GO:0043229	8	1	4	1.26E-002	intracellular organelle	GO_CC
GO:0005671	11	1	4	4.32E-002	Ada2/Gcn5/Ada3 transcription activator complex	GO_CC
GO:0000118	11	1	4	4.32E-002	histone deacetylase complex	GO_CC
GO:0060170	5	1	3	1.75E-002	cilium membrane	GO_CC
GO:0000145	5	1	3	1.75E-002	exocyst	GO_CC
GO:0031463	6	1	3	3.17E-002	Cul3-RING ubiquitin ligase complex	GO_CC
GO:0048786	6	1	3	3.17E-002	presynaptic active zone	GO_CC
GO:0008282	2	0	2	1.67E-002	ATP-sensitive potassium channel complex	GO_CC
GO:0071204	2	0	2	1.67E-002	histone pre-mRNA 3'end processing complex	GO_CC
GO:0000015	2	0	2	1.67E-002	phosphopyruvate hydratase complex	GO_CC
GO:0043190	3	0	2	4.57E-002	ATP-binding cassette (ABC) transporter complex	GO_CC
GO:0042584	3	0	2	4.57E-002	chromaffin granule membrane	GO_CC

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GO:0032045	3	0	2	4.57E-002	guanyl-nucleotide exchange factor complex	GO_CC
GO:0044306	3	0	2	4.57E-002	neuron projection terminus	GO_CC
GO:0034366	3	0	2	4.57E-002	spherical high-density lipoprotein particle	GO_CC
GO:0005515	603	78	95	1.80E-002	protein binding	GO_MF
GO:0003700	402	52	66	2.01E-002	sequence-specific DNA binding transcription factor activity	GO_MF
GO:0043565	270	35	48	1.15E-002	sequence-specific DNA binding	GO_MF
GO:0042393	27	3	8	1.72E-002	histone binding	GO_MF
GO:0003729	22	3	7	1.71E-002	mRNA binding	GO_MF
GO:0019900	26	3	7	4.17E-002	kinase binding	GO_MF
GO:0046332	18	2	6	2.12E-002	SMAD binding	GO_MF
GO:0046966	19	2	6	2.77E-002	thyroid hormone receptor binding	GO_MF
GO:0016773	20	3	6	3.54E-002	phosphotransferase activity alcohol group as acceptor	GO_MF
GO:0005246	13	2	5	1.86E-002	calcium channel regulator activity	GO_MF
GO:0000149	13	2	5	1.86E-002	SNARE binding	GO_MF
GO:0015631	13	2	5	1.86E-002	tubulin binding	GO_MF
GO:0017147	13	2	5	1.86E-002	Wnt-protein binding	GO_MF
GO:0005243	7	1	4	6.94E-003	gap junction channel activity	GO_MF
GO:0004437	10	1	4	3.03E-002	inositol or phosphatidylinositol phosphatase activity	GO_MF
GO:0046873	10	1	4	3.03E-002	metal ion transmembrane transporter activity	GO_MF
GO:0005083	11	1	4	4.29E-002	small GTPase regulator activity	GO_MF
GO:0004445	4	1	3	7.71E-003	inositol-polyphosphate 5-phosphatase activity	GO_MF
GO:0017016	4	1	3	7.71E-003	Ras GTPase binding	GO_MF
GO:0004428	5	1	3	1.74E-002	inositol or phosphatidylinositol kinase activity	GO_MF
GO:0043295	6	1	3	3.16E-002	glutathione binding	GO_MF
GO:0015179	6	1	3	3.16E-002	L-amino acid transmembrane transporter activity	GO_MF
GO:0005041	6	1	3	3.16E-002	low-density lipoprotein receptor activity	GO_MF
GO:0004020	2	0	2	1.66E-002	adenylylsulfate kinase activity	GO_MF
GO:0004949	2	0	2	1.66E-002	cannabinoid receptor activity	GO_MF
GO:0050700	2	0	2	1.66E-002	CARD domain binding	GO_MF

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GO:0008821	2	0	2	1.66E-002	crossover junction endodeoxyribonuclease activity	GO_MF
GO:0001641	2	0	2	1.66E-002	group II metabotropic glutamate receptor activity	GO_MF
GO:0004634	2	0	2	1.66E-002	phosphopyruvate hydratase activity	GO_MF
GO:0004720	2	0	2	1.66E-002	protein-lysine 6-oxidase activity	GO_MF
GO:0004781	2	0	2	1.66E-002	sulfate adenylyltransferase (ATP) activity	GO_MF
GO:0008489	2	0	2	1.66E-002	UDP-galactose:glucosylceramide beta-1.4-galactosyltransferase acti	GO_MF
GO:0003865	3	0	2	4.55E-002	3-oxo-5-alpha-steroid 4-dehydrogenase activity	GO_MF
GO:0008253	3	0	2	4.55E-002	5'-nucleotidase activity	GO_MF
GO:0031698	3	0	2	4.55E-002	beta-2 adrenergic receptor binding	GO_MF
GO:0015108	3	0	2	4.55E-002	chloride transmembrane transporter activity	GO_MF
GO:0070290	3	0	2	4.55E-002	NAPE-specific phospholipase D activity	GO_MF
GO:0046934	3	0	2	4.55E-002	phosphatidylinositol-4.5-bisphosphate 3-kinase activity	GO_MF
GO:0019870	3	0	2	4.55E-002	potassium channel inhibitor activity	GO_MF
04110	78	10	16	2.79E-002	Cell cycle	KEGG
03040	79	10	16	3.12E-002	Spliceosome	KEGG
04662	45	6	10	4.60E-002	B cell receptor signaling pathway	KEGG
04520	35	4	9	2.39E-002	Adherens junction	KEGG
05214	37	5	9	3.37E-002	Glioma	KEGG
04973	24	3	8	6.48E-003	Carbohydrate digestion and absorption	KEGG
05210	30	4	8	2.64E-002	Colorectal cancer	KEGG
05219	23	3	7	1.82E-002	Bladder cancer	KEGG
00600	27	3	7	4.26E-002	Sphingolipid metabolism	KEGG
00450	11	1	5	7.12E-003	Selenocompound metabolism	KEGG
00100	11	1	5	7.12E-003	Steroid biosynthesis	KEGG