

## OVEREXP DMI03

Term	Tot	Exp	Obs	p Value	Description	Annotation
GO:0035556	120	8	15	1.15E-002	intracellular signal transduction	GO_BP
GO:0006281	61	4	9	1.71E-002	DNA repair	GO_BP
GO:0006816	51	3	7	4.73E-002	calcium ion transport	GO_BP
GO:0007596	32	2	6	1.62E-002	blood coagulation	GO_BP
GO:0002755	34	2	6	2.16E-002	MyD88-dependent toll-like receptor signaling pathway	GO_BP
GO:0031175	36	2	6	2.80E-002	neuron projection development	GO_BP
GO:0007409	39	3	6	3.98E-002	axonogenesis	GO_BP
GO:0006885	12	1	4	5.93E-003	regulation of pH	GO_BP
GO:0030890	18	1	4	2.68E-002	positive regulation of B cell proliferation	GO_BP
GO:0006310	19	1	4	3.22E-002	DNA recombination	GO_BP
GO:0040008	20	1	4	3.83E-002	regulation of growth	GO_BP
GO:0006301	3	0	3	2.81E-004	postreplication repair	GO_BP
GO:0006744	7	0	3	8.05E-003	ubiquinone biosynthetic process	GO_BP
GO:0035162	8	1	3	1.23E-002	embryonic hemopoiesis	GO_BP
GO:0050930	9	1	3	1.75E-002	induction of positive chemotaxis	GO_BP
GO:0051928	9	1	3	1.75E-002	positive regulation of calcium ion transport	GO_BP
GO:0010942	9	1	3	1.75E-002	positive regulation of cell death	GO_BP
GO:0031532	10	1	3	2.38E-002	actin cytoskeleton reorganization	GO_BP
GO:0019835	10	1	3	2.38E-002	cytolysis	GO_BP
GO:0008272	11	1	3	3.12E-002	sulfate transport	GO_BP
GO:0000724	13	1	3	4.90E-002	double-strand break repair via homologous recombination	GO_BP
GO:0007598	2	0	2	4.30E-003	blood coagulation extrinsic pathway	GO_BP
GO:0006112	2	0	2	4.30E-003	energy reserve metabolic process	GO_BP
GO:0021884	2	0	2	4.30E-003	forebrain neuron development	GO_BP
GO:0006027	2	0	2	4.30E-003	glycosaminoglycan catabolic process	GO_BP
GO:0045639	2	0	2	4.30E-003	positive regulation of myeloid cell differentiation	GO_BP
GO:0006290	2	0	2	4.30E-003	pyrimidine dimer repair	GO_BP
GO:0050663	3	0	2	1.23E-002	cytokine secretion	GO_BP
GO:0048312	3	0	2	1.23E-002	intracellular distribution of mitochondria	GO_BP
GO:0006111	3	0	2	1.23E-002	regulation of gluconeogenesis	GO_BP

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GO:0007090	3	0	2	1.23E-002	regulation of S phase of mitotic cell cycle	GO_BP
GO:0045921	4	0	2	2.36E-002	positive regulation of exocytosis	GO_BP
GO:0001841	4	0	2	2.36E-002	neural tube formation	GO_BP
GO:0032465	4	0	2	2.36E-002	regulation of cytokinesis	GO_BP
GO:0019222	4	0	2	2.36E-002	regulation of metabolic process	GO_BP
GO:0001667	4	0	2	2.36E-002	ameboidal cell migration	GO_BP
GO:0060710	4	0	2	2.36E-002	chorio-allantoic fusion	GO_BP
GO:0060555	4	0	2	2.36E-002	induction of necroptosis by extracellular signals	GO_BP
GO:0045663	4	0	2	2.36E-002	positive regulation of myoblast differentiation	GO_BP
GO:0015701	5	0	2	3.76E-002	bicarbonate transport	GO_BP
GO:0021707	5	0	2	3.76E-002	cerebellar granule cell differentiation	GO_BP
GO:0009062	5	0	2	3.76E-002	fatty acid catabolic process	GO_BP
GO:0007076	5	0	2	3.76E-002	mitotic chromosome condensation	GO_BP
GO:0033673	5	0	2	3.76E-002	negative regulation of kinase activity	GO_BP
GO:0034214	5	0	2	3.76E-002	protein hexamerization	GO_BP
GO:0043488	5	0	2	3.76E-002	regulation of mRNA stability	GO_BP
GO:0005886	1204	76	93	1.98E-002	plasma membrane	GO_CC
GO:0045177	44	3	7	1.96E-002	apical part of cell	GO_CC
GO:0017053	17	1	4	1.96E-002	transcriptional repressor complex	GO_CC
GO:0000794	12	1	3	3.63E-002	condensed nuclear chromosome	GO_CC
GO:0017119	5	0	2	3.53E-002	Golgi transport complex	GO_CC
GO:0008385	5	0	2	3.53E-002	IkappaB kinase complex	GO_CC
GO:0031224	5	0	2	3.53E-002	intrinsic to membrane	GO_CC
GO:0008270	813	52	67	1.60E-002	zinc ion binding	GO_MF
GO:0004674	182	12	18	4.29E-002	protein serine/threonine kinase activity	GO_MF
GO:0005125	39	2	6	3.60E-002	cytokine activity	GO_MF
GO:0008415	41	3	6	4.46E-002	acyltransferase activity	GO_MF

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GO:0015297	18	1	5	4.50E-003	antiporter activity	GO_MF
GO:0004177	16	1	4	1.63E-002	aminopeptidase activity	GO_MF
GO:0043130	16	1	4	1.63E-002	ubiquitin binding	GO_MF
GO:0005154	10	1	3	2.23E-002	epidermal growth factor receptor binding	GO_MF
GO:0035064	10	1	3	2.23E-002	methylated histone residue binding	GO_MF
GO:0003887	11	1	3	2.93E-002	DNA-directed DNA polymerase activity	GO_MF
GO:0043566	2	0	2	4.10E-003	structure-specific DNA binding	GO_MF
GO:0015108	3	0	2	1.18E-002	chloride transmembrane transporter activity	GO_MF
GO:0055077	3	0	2	1.18E-002	gap junction hemi-channel activity	GO_MF
GO:0015116	3	0	2	1.18E-002	sulfate transmembrane transporter activity	GO_MF
GO:0005149	4	0	2	2.25E-002	interleukin-1 receptor binding	GO_MF
GO:0031702	4	0	2	2.25E-002	type 1 angiotensin receptor binding	GO_MF
GO:0008499	4	0	2	2.25E-002	UDP-galactose:beta-N-acetylglucosamine beta-1.3-galactosyltransferase activity	GO_MF
GO:0003810	5	0	2	3.60E-002	protein-glutamine gamma-glutamyltransferase activity	GO_MF
GO:0015385	5	0	2	3.60E-002	sodium:hydrogen antiporter activity	GO_MF
04650	59	4	12	3.31E-004	Natural killer cell mediated cytotoxicity	KEGG
04310	85	6	10	4.93E-002	Wnt signaling pathway	KEGG
04380	69	5	9	3.45E-002	Osteoclast differentiation	KEGG
04670	72	5	9	4.37E-002	Leukocyte transendothelial migration	KEGG
04664	45	3	7	2.54E-002	Fc epsilon RI signaling pathway	KEGG
04620	50	3	7	4.25E-002	Toll-like receptor signaling pathway	KEGG
05214	37	2	6	3.12E-002	Glioma	KEGG
05140	39	3	6	3.94E-002	Leishmaniasis	KEGG
00071	30	2	5	4.31E-002	Fatty acid metabolism	KEGG
00410	16	1	4	1.76E-002	beta-Alanine metabolism	KEGG