

OVEREXP FLX03

term	tot	exp	obs	pValue	description	annotation
GO:0001701	118	9	15	3.84E-002	in utero embryonic development	GO_BP
GO:0009791	42	3	9	4.16E-003	post-embryonic development	GO_BP
GO:0006974	51	4	9	1.53E-002	response to DNA damage stimulus	GO_BP
GO:0032869	40	3	8	1.04E-002	cellular response to insulin stimulus	GO_BP
GO:0010468	35	3	6	4.99E-002	regulation of gene expression	GO_BP
GO:0050853	13	1	5	2.09E-003	B cell receptor signaling pathway	GO_BP
GO:0009395	8	1	4	1.94E-003	phospholipid catabolic process	GO_BP
GO:0007610	13	1	4	1.45E-002	behavior	GO_BP
GO:0045785	14	1	4	1.91E-002	positive regulation of cell adhesion	GO_BP
GO:0006333	16	1	4	3.07E-002	chromatin assembly or disassembly	GO_BP
GO:0043010	18	1	4	4.57E-002	camera-type eye development	GO_BP
GO:0030890	18	1	4	4.57E-002	positive regulation of B cell proliferation	GO_BP
GO:0060292	5	0	3	4.12E-003	long term synaptic depression	GO_BP
GO:0045089	6	0	3	7.76E-003	positive regulation of innate immune response	GO_BP
GO:0030278	6	0	3	7.76E-003	regulation of ossification	GO_BP
GO:0001782	7	1	3	1.28E-002	B cell homeostasis	GO_BP
GO:0021542	7	1	3	1.28E-002	dentate gyrus development	GO_BP
GO:0035329	8	1	3	1.93E-002	hippo signaling cascade	GO_BP
GO:0045579	8	1	3	1.93E-002	positive regulation of B cell differentiation	GO_BP
GO:0030539	9	1	3	2.73E-002	male genitalia development	GO_BP
GO:0035265	9	1	3	2.73E-002	organ growth	GO_BP
GO:0032728	10	1	3	3.69E-002	positive regulation of interferon-beta production	GO_BP
GO:0030833	10	1	3	3.69E-002	regulation of actin filament polymerization	GO_BP
GO:0006909	11	1	3	4.78E-002	phagocytosis	GO_BP
GO:0043085	11	1	3	4.78E-002	positive regulation of catalytic activity	GO_BP
GO:0050727	11	1	3	4.78E-002	regulation of inflammatory response	GO_BP
GO:0015867	2	0	2	6.00E-003	ATP transport	GO_BP
GO:0051026	2	0	2	6.00E-003	chiasma assembly	GO_BP
GO:0009410	2	0	2	6.00E-003	response to xenobiotic stimulus	GO_BP
GO:0006419	3	0	2	1.71E-002	alanyl-tRNA aminoacylation	GO_BP

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GO:0001825	3	0	2	1.71E-002	blastocyst formation	GO_BP
GO:0035284	3	0	2	1.71E-002	brain segmentation	GO_BP
GO:0015872	3	0	2	1.71E-002	dopamine transport	GO_BP
GO:0010216	3	0	2	1.71E-002	maintenance of DNA methylation	GO_BP
GO:0045916	3	0	2	1.71E-002	negative regulation of complement activation	GO_BP
GO:0033089	3	0	2	1.71E-002	positive regulation of T cell differentiation in thymus	GO_BP
GO:0031620	3	0	2	1.71E-002	regulation of fever generation	GO_BP
GO:0000103	3	0	2	1.71E-002	sulfate assimilation	GO_BP
GO:0042723	3	0	2	1.71E-002	thiamine-containing compound metabolic process	GO_BP
GO:0006085	4	0	2	3.24E-002	acetyl-CoA biosynthetic process	GO_BP
GO:0071875	4	0	2	3.24E-002	adrenergic receptor signaling pathway	GO_BP
GO:0050435	4	0	2	3.24E-002	beta-amyloid metabolic process	GO_BP
GO:0021853	4	0	2	3.24E-002	cerebral cortex GABAergic interneuron migration	GO_BP
GO:0006534	4	0	2	3.24E-002	cysteine metabolic process	GO_BP
GO:0016458	4	0	2	3.24E-002	gene silencing	GO_BP
GO:0006750	4	0	2	3.24E-002	glutathione biosynthetic process	GO_BP
GO:0060174	4	0	2	3.24E-002	limb bud formation	GO_BP
GO:0060291	4	0	2	3.24E-002	long-term synaptic potentiation	GO_BP
GO:0045670	4	0	2	3.24E-002	regulation of osteoclast differentiation	GO_BP
GO:0070723	4	0	2	3.24E-002	response to cholesterol	GO_BP
GO:0046653	4	0	2	3.24E-002	tetrahydrofolate metabolic process	GO_BP
GO:0043039	4	0	2	3.24E-002	tRNA aminoacylation	GO_BP
GO:0030424	110	9	14	4.65E-002	axon	GO_CC
GO:0080008	6	0	3	7.92E-003	CUL4 RING ubiquitin ligase complex	GO_CC
GO:0032154	9	1	3	2.79E-002	cleavage furrow	GO_CC
GO:0045120	9	1	3	2.79E-002	pronucleus	GO_CC
GO:0000932	10	1	3	3.76E-002	cytoplasmic mRNA processing body	GO_CC
GO:0005657	10	1	3	3.76E-002	replication fork	GO_CC
GO:0032587	11	1	3	4.87E-002	ruffle membrane	GO_CC

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GO:0005847	2	0	2	6.09E-003	mRNA cleavage and polyadenylation specificity factor complex	GO_CC
GO:0033017	4	0	2	3.29E-002	sarcoplasmic reticulum membrane	GO_CC
GO:0003677	548	43	57	1.22E-002	DNA binding	GO_MF
GO:0005509	293	23	35	6.43E-003	calcium ion binding	GO_MF
GO:0005085	48	4	9	1.04E-002	guanyl-nucleotide exchange factor activity	GO_MF
GO:0035091	38	3	7	2.49E-002	phosphatidylinositol binding	GO_MF
GO:0030742	9	1	4	3.30E-003	GTP-dependent protein binding	GO_MF
GO:0048155	3	0	3	4.65E-004	S100 alpha binding	GO_MF
GO:0004630	5	0	3	4.13E-003	phospholipase D activity	GO_MF
GO:0005388	6	0	3	7.78E-003	calcium-transporting ATPase activity	GO_MF
GO:0051020	10	1	3	3.70E-002	GTPase binding	GO_MF
GO:0004813	3	0	2	1.71E-002	alanine-tRNA ligase activity	GO_MF
GO:0051379	3	0	2	1.71E-002	epinephrine binding	GO_MF
GO:0003951	3	0	2	1.71E-002	NAD+ kinase activity	GO_MF
GO:0070290	3	0	2	1.71E-002	NAPE-specific phospholipase D activity	GO_MF
GO:0030676	3	0	2	1.71E-002	Rac guanyl-nucleotide exchange factor activity	GO_MF
GO:0030215	3	0	2	1.71E-002	semaphorin receptor binding	GO_MF
GO:0035240	4	0	2	3.25E-002	dopamine binding	GO_MF
GO:0004308	4	0	2	3.25E-002	exo-alpha-sialidase activity	GO_MF
GO:0019209	4	0	2	3.25E-002	kinase activator activity	GO_MF
GO:0070063	4	0	2	3.25E-002	RNA polymerase binding	GO_MF
GO:0050733	4	0	2	3.25E-002	RS domain binding	GO_MF
GO:0008483	4	0	2	3.25E-002	transaminase activity	GO_MF
04144	127	10	19	5.12E-003	Endocytosis	KEGG
04810	108	9	14	4.70E-002	Regulation of actin cytoskeleton	KEGG
04020	95	8	13	3.75E-002	Calcium signaling pathway	KEGG
04666	62	5	11	9.00E-003	Fc gamma R-mediated phagocytosis	KEGG

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04972	56	4	9	3.18E-002	Pancreatic secretion	KEGG
04623	24	2	6	9.79E-003	Cytosolic DNA-sensing pathway	KEGG
00232	8	1	3	2.10E-002	Caffeine metabolism	KEGG
00511	9	1	3	2.97E-002	Other glycan degradation	KEGG
00471	3	0	2	1.82E-002	D-Glutamine and D-glutamate metabolism	KEGG