

caecal_day4_bic vs caecal_day4_wt, down:328

Gene to GO-BP conditional test for over-representation

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006334	2.3e-19	15.8	2.37	25	85	nucleosome assembly
GO:0006323	2.0e-17	11.0	3.37	27	121	DNA packaging
GO:0006333	5.7e-17	11.1	3.21	26	115	chromatin assembly or disassembly
GO:0065003	3.8e-11	4.8	7.78	31	279	macromolecular complex assembly
GO:0051276	7.6e-10	4.4	7.75	29	278	chromosome organization and biogenesis
GO:0006955	3.0e-08	4.3	6.49	24	239	immune response
GO:0002504	1.8e-06	23.7	0.42	6	15	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0048534	7.6e-06	3.6	5.94	19	213	hemopoietic or lymphoid organ development
GO:0019886	2.6e-05	19.7	0.39	5	14	antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0046649	6.0e-05	3.6	4.63	15	166	lymphocyte activation
GO:0001775	1.2e-04	3.2	5.49	16	197	cell activation
GO:0019884	2.3e-04	11.1	0.59	5	21	antigen processing and presentation of exogenous antigen
GO:0030217	2.7e-04	5.4	1.70	8	61	T cell differentiation
GO:0050863	3.0e-04	5.3	1.73	8	62	regulation of T cell activation
GO:0007067	4.4e-04	3.5	3.82	12	137	mitosis
GO:0042100	5.5e-04	8.9	0.70	5	25	B cell proliferation
GO:0002521	5.5e-04	3.6	3.37	11	121	leukocyte differentiation
GO:0032943	5.7e-04	4.8	1.90	8	68	mononuclear cell proliferation
GO:0048002	6.6e-04	8.4	0.72	5	26	antigen processing and presentation of peptide antigen
GO:0051301	6.8e-04	2.8	5.77	15	207	cell division
GO:0002684	7.7e-04	3.4	3.51	11	126	positive regulation of immune system process
GO:0002694	1.3e-03	4.7	1.66	7	60	regulation of leukocyte activation
GO:0002429	1.3e-03	7.1	0.84	5	30	immune response-activating cell surface receptor signaling pathway
GO:0045619	1.5e-03	6.8	0.86	5	31	regulation of lymphocyte differentiation
GO:0051251	1.6e-03	4.5	1.73	7	62	positive regulation of lymphocyte activation
GO:0050670	1.8e-03	5.2	1.31	6	47	regulation of lymphocyte proliferation
GO:0050867	1.9e-03	4.4	1.78	7	64	positive regulation of cell activation
GO:0006954	2.0e-03	2.8	4.54	12	163	inflammatory response
GO:0002376	2.3e-03	2.8	4.61	12	183	immune system process
GO:0000278	2.3e-03	2.7	5.24	13	188	mitotic cell cycle
GO:0050776	2.6e-03	3.7	2.38	8	86	regulation of immune response
GO:0006935	3.1e-03	3.6	2.45	8	88	chemotaxis
GO:0030574	5.0e-03	10.6	0.36	3	13	collagen catabolic process
GO:0044243	5.0e-03	10.6	0.36	3	13	multicellular organismal catabolic process
GO:0044256	5.0e-03	10.6	0.36	3	13	protein digestion
GO:0044266	5.0e-03	10.6	0.36	3	13	multicellular organismal macromolecule catabolic process
GO:0044268	5.0e-03	10.6	0.36	3	13	multicellular organismal protein metabolic process
GO:0009605	5.6e-03	2.0	10.01	19	359	response to external stimulus
GO:0000279	5.9e-03	2.5	5.19	12	186	M phase
GO:0030890	6.2e-03	9.6	0.39	3	14	positive regulation of B cell proliferation
GO:0006260	6.3e-03	2.9	3.35	9	120	DNA replication
GO:0022402	6.4e-03	2.2	7.28	15	261	cell cycle process
GO:0006220	1.3e-02	7.0	0.50	3	18	pyrimidine nucleotide metabolic process
GO:0032946	1.4e-02	4.7	0.95	4	34	positive regulation of mononuclear cell proliferation
GO:0045582	1.5e-02	6.6	0.53	3	19	positive regulation of T cell differentiation
GO:0051239	1.9e-02	2.0	6.78	13	245	regulation of multicellular organismal process
GO:0048584	2.0e-02	2.7	2.76	7	99	positive regulation of response to stimulus
GO:0007265	2.6e-02	2.2	4.24	9	152	Ras protein signal transduction
GO:0051130	2.7e-02	3.8	1.14	4	41	positive regulation of cellular component organization and biogenesis
GO:0030155	2.8e-02	5.1	0.67	3	24	regulation of cell adhesion
GO:0002253	2.9e-02	3.1	1.73	5	62	activation of immune response
GO:0019882	2.9e-02	8.9	0.27	2	10	antigen processing and presentation
GO:0009220	3.0e-02	8.8	0.28	2	10	pyrimidine ribonucleotide biosynthetic process
GO:0051056	3.1e-02	2.3	3.68	8	132	regulation of small GTPase mediated signal transduction
GO:0002695	3.1e-02	4.8	0.70	3	25	negative regulation of leukocyte activation
GO:0030099	3.6e-02	2.6	2.45	6	88	myeloid cell differentiation
GO:0006911	3.6e-02	7.8	0.31	2	11	phagocytosis, engulfment
GO:0007051	3.6e-02	7.8	0.31	2	11	spindle organization and biogenesis
GO:0007159	3.6e-02	7.8	0.31	2	11	leukocyte adhesion
GO:0043331	3.6e-02	7.8	0.31	2	11	response to dsRNA
GO:0045191	3.6e-02	7.8	0.31	2	11	regulation of isotype switching
GO:0050869	3.6e-02	7.8	0.31	2	11	negative regulation of B cell activation
GO:0001776	3.8e-02	4.4	0.75	3	27	leukocyte homeostasis
GO:0006270	4.3e-02	7.0	0.33	2	12	DNA replication initiation
GO:0006541	4.3e-02	7.0	0.33	2	12	glutamine metabolic process
GO:0050766	4.3e-02	7.0	0.33	2	12	positive regulation of phagocytosis
GO:0050798	4.3e-02	7.0	0.33	2	12	activated T cell proliferation
GO:0051085	4.3e-02	7.0	0.33	2	12	chaperone cofactor-dependent protein folding
GO:0009617	4.3e-02	2.8	1.92	5	69	response to bacterium
GO:0022610	4.4e-02	1.6	12.44	19	446	biological adhesion
GO:0001817	4.6e-02	4.1	0.81	3	29	regulation of cytokine production
GO:0032615	4.9e-02	6.4	0.36	2	13	interleukin-12 production
GO:0045785	4.9e-02	6.4	0.36	2	13	positive regulation of cell adhesion
GO:0050777	4.9e-02	6.4	0.36	2	13	negative regulation of immune response
GO:0009607	5.0e-02	2.1	4.04	8	145	response to biotic stimulus