

GO enrichments of biological processes and molecular functions in mouse gene clusters in figure 2b. In addition to enriched GO terms (GO id and Term), tables include total numbers of annotated genes for a given GO id, number of genes per cluster belong to the listed GO id (Sign. genes), expected number by random distribution (Expected), p-value, and p-value corrected for mutple testing (Adj. P-value). Each page contains a list for a given gene cluster (see headings).

Enrichments of biological processes mouse cluster 1

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0071826	ribonucleoprotein complex subunit organi...	168	12	2.60	0.000011	0.0011
GO:0022618	ribonucleoprotein complex assembly	161	11	2.49	0.000040	0.0014
GO:0022613	ribonucleoprotein complex biogenesis	328	16	5.07	0.000049	0.0014
GO:0000377	RNA splicing, via transesterification re...	174	11	2.69	0.000081	0.0014
GO:0000398	mRNA splicing, via spliceosome	174	11	2.69	0.000081	0.0014
GO:0000375	RNA splicing, via transesterification re...	175	11	2.71	0.000085	0.0014
GO:0090304	nucleic acid metabolic process	3317	75	51.30	0.000100	0.0014
GO:0032877	positive regulation of DNA endoreduplica...	2	2	0.03	0.000240	0.0030
GO:0016071	mRNA metabolic process	438	17	6.77	0.000450	0.0050
GO:0008380	RNA splicing	292	13	4.52	0.000610	0.0061
GO:0010467	gene expression	3512	75	54.31	0.000690	0.0061
GO:0006139	nucleobase-containing compound metabolic...	3697	78	57.17	0.000730	0.0061
GO:0034641	cellular nitrogen compound metabolic pro...	4262	87	65.91	0.000860	0.0066
GO:0034622	cellular macromolecular complex assembly	604	20	9.34	0.001070	0.0074
GO:0016070	RNA metabolic process	2927	64	45.26	0.001180	0.0074
GO:0006807	nitrogen compound metabolic process	4431	89	68.52	0.001250	0.0074
GO:0001825	blastocyst formation	31	4	0.48	0.001260	0.0074
GO:0031860	telomeric 3' overhang formation	4	2	0.06	0.001400	0.0074
GO:0060718	chorionic trophoblast cell differentiati...	4	2	0.06	0.001400	0.0074
GO:0006397	mRNA processing	363	14	5.61	0.001530	0.0076
GO:0046483	heterocycle metabolic process	3793	78	58.66	0.001640	0.0078
GO:0006725	cellular aromatic compound metabolic pro...	3809	78	58.90	0.001870	0.0085
GO:0032466	negative regulation of cytokinesis	5	2	0.08	0.002310	0.0091
GO:0070365	hepatocyte differentiation	5	2	0.08	0.002310	0.0091
GO:0019827	stem cell population maintenance	118	7	1.82	0.002350	0.0091
GO:0044260	cellular macromolecule metabolic process	5398	103	83.48	0.002360	0.0091
GO:0098727	maintenance of cell number	120	7	1.86	0.002590	0.0093
GO:0043170	macromolecule metabolic process	5740	108	88.77	0.002720	0.0093
GO:0006396	RNA processing	654	20	10.11	0.002740	0.0093
GO:0051171	regulation of nitrogen compound metaboli...	2734	59	42.28	0.002800	0.0093
GO:1901360	organic cyclic compound metabolic proces...	3933	79	60.82	0.003070	0.0099
GO:0060717	chorion development	6	2	0.09	0.003420	0.0101
GO:1902074	response to salt	6	2	0.09	0.003420	0.0101
GO:1903867	extraembryonic membrane development	6	2	0.09	0.003420	0.0101
GO:0000245	spliceosomal complex assembly	41	4	0.63	0.003590	0.0103
GO:0051172	negative regulation of nitrogen compound...	1077	28	16.66	0.004340	0.0118
GO:0010468	regulation of gene expression	2670	57	41.29	0.004370	0.0118
GO:0043038	amino acid activation	44	4	0.68	0.004640	0.0119
GO:0043039	tRNA aminoacylation	44	4	0.68	0.004640	0.0119
GO:0060255	regulation of macromolecule metabolic pr...	3694	74	57.13	0.004980	0.0124
GO:0009059	macromolecule biosynthetic process	3224	66	49.86	0.005370	0.0131
GO:0000086	G2/M transition of mitotic cell cycle	75	5	1.16	0.006040	0.0140
GO:0001824	blastocyst development	75	5	1.16	0.006040	0.0140
GO:0032875	regulation of DNA endoreduplication	8	2	0.12	0.006260	0.0142
GO:0044839	cell cycle G2/M phase transition	78	5	1.21	0.007120	0.0150
GO:0017148	negative regulation of translation	110	6	1.70	0.007170	0.0150
GO:0060706	cell differentiation involved in embryon...	26	3	0.40	0.007280	0.0150
GO:0034645	cellular macromolecule biosynthetic proc...	3149	64	48.70	0.007470	0.0150
GO:0002829	negative regulation of type 2 immune res...	9	2	0.14	0.007970	0.0150
GO:0042023	DNA endoreduplication	9	2	0.14	0.007970	0.0150
GO:0045056	transcytosis	9	2	0.14	0.007970	0.0150
GO:0071786	endoplasmic reticulum tubular network or...	9	2	0.14	0.007970	0.0150
GO:2000105	positive regulation of DNA-dependent DNA...	9	2	0.14	0.007970	0.0150
GO:0080090	regulation of primary metabolic process	3713	73	57.42	0.008770	0.0161
GO:0034249	negative regulation of cellular amide me...	115	6	1.78	0.008840	0.0161
GO:0031326	regulation of cellular biosynthetic proc...	2645	55	40.90	0.009120	0.0162
GO:0031327	negative regulation of cellular biosynth...	1035	26	16.01	0.009220	0.0162

Enrichments of molecular functions mouse cluster 1

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0003723	RNA binding	1384	47	21.13	7.30e−08	0.0000
GO:0044822	poly(A) RNA binding	1064	39	16.24	1.80e−07	0.0000
GO:0003676	nucleic acid binding	2634	66	40.21	8.20e−06	0.0003
GO:0019781	NEDD8 activating enzyme activity	2	2	0.03	2.30e−04	0.0058
GO:0008641	small protein activating enzyme activity	10	3	0.15	3.90e−04	0.0078
GO:0002151	G-quadruplex RNA binding	3	2	0.05	6.90e−04	0.0100
GO:1901363	heterocyclic compound binding	3990	82	60.92	7.00e−04	0.0100
GO:0097159	organic cyclic compound binding	4026	82	61.47	9.50e−04	0.0119
GO:0016877	ligase activity, forming carbon–sulfur b...	29	3	0.44	9.55e−03	0.0259

Enrichments of biological processes mouse cluster 2

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0032095	regulation of response to food	11	3	0.14	0.00033	0.0102
GO:0038108	negative regulation of appetite by lepti...	3	2	0.04	0.00050	0.0102
GO:0060252	positive regulation of glial cell prolif...	13	3	0.17	0.00055	0.0102
GO:0042462	eye photoreceptor cell development	15	3	0.19	0.00087	0.0102
GO:0008542	visual learning	35	4	0.45	0.00104	0.0102
GO:0032094	response to food	16	3	0.21	0.00106	0.0102
GO:0032774	RNA biosynthetic process	2301	46	29.81	0.00109	0.0102
GO:0007632	visual behavior	37	4	0.48	0.00128	0.0102
GO:0010468	regulation of gene expression	2670	51	34.59	0.00150	0.0102
GO:0035176	social behavior	18	3	0.23	0.00151	0.0102
GO:0051703	intraspecies interaction between organis...	18	3	0.23	0.00151	0.0102
GO:0043569	negative regulation of insulin-like grow...	5	2	0.06	0.00163	0.0102
GO:0060294	cilium movement involved in cell motilit...	5	2	0.06	0.00163	0.0102
GO:0060295	regulation of cilium movement involved i...	5	2	0.06	0.00163	0.0102
GO:0060296	regulation of cilium beat frequency invo...	5	2	0.06	0.00163	0.0102
GO:1902019	regulation of cilium-dependent cell moti...	5	2	0.06	0.00163	0.0102
GO:0097659	nucleic acid-templated transcription	2289	45	29.66	0.00179	0.0105
GO:0019438	aromatic compound biosynthetic process	2585	49	33.49	0.00229	0.0107
GO:0021955	central nervous system neuron axonogenes...	21	3	0.27	0.00239	0.0107
GO:0018130	heterocycle biosynthetic process	2594	49	33.61	0.00247	0.0107
GO:0008306	associative learning	45	4	0.58	0.00267	0.0107
GO:0034654	nucleobase-containing compound biosynthe...	2537	48	32.87	0.00270	0.0107
GO:0060251	regulation of glial cell proliferation	22	3	0.29	0.00274	0.0107
GO:0044708	single-organism behavior	227	9	2.94	0.00279	0.0107
GO:0006351	transcription, DNA-templated	2283	44	29.58	0.00304	0.0107
GO:0042461	photoreceptor cell development	23	3	0.30	0.00312	0.0107
GO:1903506	regulation of nucleic acid-templated tra...	2221	43	28.78	0.00316	0.0107
GO:2001141	regulation of RNA biosynthetic process	2226	43	28.84	0.00330	0.0107
GO:0003352	regulation of cilium movement	7	2	0.09	0.00336	0.0107
GO:0014889	muscle atrophy	7	2	0.09	0.00336	0.0107
GO:0034351	negative regulation of glial cell apopto...	7	2	0.09	0.00336	0.0107
GO:2000112	regulation of cellular macromolecule bio...	2501	47	32.40	0.00350	0.0107
GO:0001754	eye photoreceptor cell differentiation	24	3	0.31	0.00354	0.0107
GO:0001570	vasculogenesis	50	4	0.65	0.00393	0.0114
GO:0051965	positive regulation of synapse assembly	25	3	0.32	0.00398	0.0114
GO:1901362	organic cyclic compound biosynthetic pro...	2660	49	34.46	0.00420	0.0114
GO:0032099	negative regulation of appetite	8	2	0.10	0.00444	0.0114
GO:0033210	leptin-mediated signaling pathway	8	2	0.10	0.00444	0.0114
GO:0034350	regulation of glial cell apoptotic proce...	8	2	0.10	0.00444	0.0114
GO:0007611	learning or memory	120	6	1.55	0.00467	0.0117
GO:0040018	positive regulation of multicellular org...	27	3	0.35	0.00497	0.0118
GO:0006355	regulation of transcription, DNA-templat...	2215	42	28.70	0.00526	0.0118
GO:0001539	cilium or flagellum-dependent cell motil...	9	2	0.12	0.00566	0.0118
GO:0032096	negative regulation of response to food	9	2	0.12	0.00566	0.0118
GO:0043508	negative regulation of JUN kinase activi...	9	2	0.12	0.00566	0.0118
GO:0043567	regulation of insulin-like growth factor...	9	2	0.12	0.00566	0.0118
GO:0044320	cellular response to leptin stimulus	9	2	0.12	0.00566	0.0118
GO:0060285	cilium-dependent cell motility	9	2	0.12	0.00566	0.0118
GO:0010556	regulation of macromolecule biosynthetic...	2565	47	33.23	0.00578	0.0118
GO:0009791	post-embryonic development	89	5	1.15	0.00593	0.0119
GO:0048858	cell projection morphogenesis	510	14	6.61	0.00645	0.0121
GO:0072659	protein localization to plasma membrane	170	7	2.20	0.00663	0.0121
GO:0051252	regulation of RNA metabolic process	2312	43	29.96	0.00668	0.0121
GO:0014009	glial cell proliferation	30	3	0.39	0.00670	0.0121
GO:0021544	subpallium development	10	2	0.13	0.00701	0.0121
GO:0021756	striatum development	10	2	0.13	0.00701	0.0121
GO:1990778	protein localization to cell periphery	172	7	2.23	0.00706	0.0121
GO:0040014	regulation of multicellular organism gro...	59	4	0.76	0.00710	0.0121
GO:0051963	regulation of synapse assembly	31	3	0.40	0.00735	0.0121
GO:0032105	negative regulation of response to extra...	32	3	0.41	0.00804	0.0121
GO:0032108	negative regulation of response to nutri...	32	3	0.41	0.00804	0.0121
GO:0009314	response to radiation	268	9	3.47	0.00816	0.0121
GO:0007281	germ cell development	135	6	1.75	0.00820	0.0121
GO:0032098	regulation of appetite	11	2	0.14	0.00850	0.0121
GO:0044321	response to leptin	11	2	0.14	0.00850	0.0121
GO:0045945	positive regulation of transcription fro...	11	2	0.14	0.00850	0.0121
GO:0050877	neurological system process	369	11	4.78	0.00856	0.0121
GO:0009889	regulation of biosynthetic process	2688	48	34.83	0.00861	0.0121
GO:0021695	cerebellar cortex development	33	3	0.43	0.00876	0.0121
GO:0032873	negative regulation of stress-activated ...	33	3	0.43	0.00876	0.0121
GO:0046530	photoreceptor cell differentiation	33	3	0.43	0.00876	0.0121
GO:0070303	negative regulation of stress-activated ...	33	3	0.43	0.00876	0.0121
GO:0032990	cell part morphogenesis	530	14	6.87	0.00891	0.0121
GO:0009416	response to light stimulus	180	7	2.33	0.00896	0.0121
GO:0050890	cognition	138	6	1.79	0.00909	0.0121
GO:0035264	multicellular organism growth	140	6	1.81	0.00972	0.0128

Enrichments of molecular functions mouse cluster 2

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0015410	manganese-transporting ATPase activity	2	2	0.03	0.00016	0.016
GO:0005384	manganese ion transmembrane transporter ...	6	2	0.08	0.00237	0.065
GO:0005388	calcium-transporting ATPase activity	7	2	0.09	0.00329	0.065
GO:0015662	ATPase activity, coupled to transmembran...	24	3	0.31	0.00344	0.065
GO:0005154	epidermal growth factor receptor binding	28	3	0.36	0.00537	0.065

Enrichments of biological processes mouse cluster 3

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0021527	spinal cord association neuron different...	2	2	0.04	0.00039	0.0198
GO:0071280	cellular response to copper ion	3	2	0.06	0.00116	0.0198
GO:0046854	phosphatidylinositol phosphorylation	25	4	0.50	0.00137	0.0198
GO:0061512	protein localization to cilium	25	4	0.50	0.00137	0.0198
GO:0030258	lipid modification	140	9	2.77	0.00187	0.0198
GO:0021516	dorsal spinal cord development	4	2	0.08	0.00228	0.0198
GO:0060830	ciliary receptor clustering involved in ...	4	2	0.08	0.00228	0.0198
GO:0060971	embryonic heart tube left/right pattern ...	4	2	0.08	0.00228	0.0198
GO:0046834	lipid phosphorylation	29	4	0.57	0.00242	0.0198
GO:0015936	coenzyme A metabolic process	16	3	0.32	0.00355	0.0198
GO:0021522	spinal cord motor neuron differentiation	16	3	0.32	0.00355	0.0198
GO:0019087	transformation of host cell by virus	5	2	0.10	0.00376	0.0198
GO:0032484	Ral protein signal transduction	5	2	0.10	0.00376	0.0198
GO:0048842	positive regulation of axon extension in...	5	2	0.10	0.00376	0.0198
GO:1902669	positive regulation of axon guidance	5	2	0.10	0.00376	0.0198
GO:0046486	glycerolipid metabolic process	218	11	4.32	0.00413	0.0198
GO:0007033	vacuole organization	130	8	2.58	0.00431	0.0198
GO:0051188	cofactor biosynthetic process	104	7	2.06	0.00457	0.0198
GO:0042073	intraciliary transport	35	4	0.69	0.00486	0.0198
GO:0044088	regulation of vacuole organization	35	4	0.69	0.00486	0.0198
GO:0098840	protein transport along microtubule	35	4	0.69	0.00486	0.0198
GO:0021514	ventral spinal cord interneuron differen...	6	2	0.12	0.00556	0.0198
GO:0021515	cell differentiation in spinal cord	19	3	0.38	0.00588	0.0198
GO:0021517	ventral spinal cord development	19	3	0.38	0.00588	0.0198
GO:0009410	response to xenobiotic stimulus	37	4	0.73	0.00594	0.0198
GO:0033865	nucleoside bisphosphate metabolic proces...	20	3	0.40	0.00682	0.0198
GO:0033875	ribonucleoside bisphosphate metabolic pr...	20	3	0.40	0.00682	0.0198
GO:0034032	purine nucleoside bisphosphate metabolic...	20	3	0.40	0.00682	0.0198
GO:0051186	cofactor metabolic process	269	12	5.33	0.00738	0.0198
GO:0044255	cellular lipid metabolic process	633	22	12.54	0.00738	0.0198
GO:0006729	tetrahydrobiopterin biosynthetic process	7	2	0.14	0.00769	0.0198
GO:0014049	positive regulation of glutamate secreti...	7	2	0.14	0.00769	0.0198
GO:0046146	tetrahydrobiopterin metabolic process	7	2	0.14	0.00769	0.0198
GO:0070050	neuron cellular homeostasis	7	2	0.14	0.00769	0.0198
GO:0072488	ammonium transmembrane transport	7	2	0.14	0.00769	0.0198
GO:0097094	craniofacial suture morphogenesis	7	2	0.14	0.00769	0.0198
GO:0032892	positive regulation of organic acid tran...	21	3	0.42	0.00784	0.0198
GO:0021510	spinal cord development	40	4	0.79	0.00785	0.0198
GO:1903793	positive regulation of anion transport	40	4	0.79	0.00785	0.0198
GO:0031503	protein complex localization	91	6	1.80	0.00933	0.0198

Enrichments of molecular functions mouse cluster 3

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0004653	polypeptide N-acetylgalactosaminyltransf...	9	3	0.18	0.0006	0.0407
GO:0097322	7SK snRNA binding	3	2	0.06	0.0012	0.0407
GO:0004594	pantothenate kinase activity	4	2	0.08	0.0023	0.0407
GO:0042577	lipid phosphatase activity	6	2	0.12	0.0056	0.0407

Enrichments of biological processes mouse cluster 4

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0070886	positive regulation of calcineurin–NFAT ...	5	3	0.11	0.00011	0.0070
GO:0048016	inositol phosphate–mediated signaling	23	5	0.52	0.00014	0.0070
GO:0050817	coagulation	120	10	2.72	0.00039	0.0130
GO:0032102	negative regulation of response to exter...	184	12	4.17	0.00099	0.0161
GO:0007596	blood coagulation	118	9	2.67	0.00143	0.0161
GO:0007154	cell communication	3168	94	71.77	0.00157	0.0161
GO:0007599	hemostasis	120	9	2.72	0.00161	0.0161
GO:0007006	mitochondrial membrane organization	76	7	1.72	0.00163	0.0161
GO:0023052	signaling	3091	92	70.02	0.00164	0.0161
GO:0070884	regulation of calcineurin–NFAT signaling...	11	3	0.25	0.00166	0.0161
GO:0006120	mitochondrial electron transport, NADH t...	12	3	0.27	0.00217	0.0161
GO:0043588	skin development	150	10	3.40	0.00218	0.0161
GO:1903035	negative regulation of response to wound...	103	8	2.33	0.00232	0.0161
GO:0044700	single organism signaling	3084	91	69.86	0.00232	0.0161
GO:0007033	vacuole organization	130	9	2.94	0.00279	0.0161
GO:0035898	parathyroid hormone secretion	4	2	0.09	0.00298	0.0161
GO:0060684	epithelial–mesenchymal cell signaling	4	2	0.09	0.00298	0.0161
GO:0050701	interleukin–1 secretion	27	4	0.61	0.00300	0.0161
GO:0006914	autophagy	358	17	8.11	0.00328	0.0161
GO:0006937	regulation of muscle contraction	67	6	1.52	0.00402	0.0161
GO:0030168	platelet activation	67	6	1.52	0.00402	0.0161
GO:1902188	positive regulation of viral release fro...	15	3	0.34	0.00427	0.0161
GO:0071496	cellular response to external stimulus	139	9	3.15	0.00435	0.0161
GO:0032905	transforming growth factor beta1 product...	5	2	0.11	0.00489	0.0161
GO:0032908	regulation of transforming growth factor...	5	2	0.11	0.00489	0.0161
GO:0045991	carbon catabolite activation of transcri...	5	2	0.11	0.00489	0.0161
GO:1900165	negative regulation of interleukin–6 sec...	5	2	0.11	0.00489	0.0161
GO:0032692	negative regulation of interleukin–1 pro...	16	3	0.36	0.00517	0.0161
GO:0050878	regulation of body fluid levels	197	11	4.46	0.00526	0.0161
GO:0007165	signal transduction	2897	84	65.63	0.00609	0.0161
GO:0007176	regulation of epidermal growth factor–ac...	17	3	0.39	0.00618	0.0161
GO:0033173	calcineurin–NFAT signaling cascade	17	3	0.39	0.00618	0.0161
GO:0050663	cytokine secretion	121	8	2.74	0.00621	0.0161
GO:0019076	viral release from host cell	33	4	0.75	0.00629	0.0161
GO:0006936	muscle contraction	123	8	2.79	0.00684	0.0161
GO:0050728	negative regulation of inflammatory resp...	75	6	1.70	0.00698	0.0161
GO:0007220	Notch receptor processing	6	2	0.14	0.00722	0.0161
GO:0044828	negative regulation by host of viral gen...	6	2	0.14	0.00722	0.0161
GO:0045990	carbon catabolite regulation of transcri...	6	2	0.14	0.00722	0.0161
GO:0050711	negative regulation of interleukin–1 sec...	6	2	0.14	0.00722	0.0161
GO:0031670	cellular response to nutrient	18	3	0.41	0.00729	0.0161
GO:0050919	negative chemotaxis	18	3	0.41	0.00729	0.0161
GO:0032612	interleukin–1 production	54	5	1.22	0.00736	0.0161
GO:0050818	regulation of coagulation	54	5	1.22	0.00736	0.0161
GO:0060048	cardiac muscle contraction	54	5	1.22	0.00736	0.0161
GO:0042493	response to drug	151	9	3.42	0.00742	0.0161
GO:0031668	cellular response to extracellular stimu...	126	8	2.85	0.00788	0.0168
GO:0008053	mitochondrial fusion	19	3	0.43	0.00852	0.0170
GO:0044803	multi–organism membrane organization	19	3	0.43	0.00852	0.0170
GO:0050704	regulation of interleukin–1 secretion	19	3	0.43	0.00852	0.0170
GO:0050707	regulation of cytokine secretion	104	7	2.36	0.00932	0.0172
GO:0009991	response to extracellular stimulus	274	13	6.21	0.00967	0.0172
GO:0007618	mating	20	3	0.45	0.00985	0.0172
GO:0009612	response to mechanical stimulus	58	5	1.31	0.00991	0.0172
GO:0007620	copulation	7	2	0.16	0.00996	0.0172
GO:0044793	negative regulation by host of viral pro...	7	2	0.16	0.00996	0.0172
GO:1904467	regulation of tumor necrosis factor secr...	7	2	0.16	0.00996	0.0172
GO:1990774	tumor necrosis factor secretion	7	2	0.16	0.00996	0.0172

Enrichments of molecular functions mouse cluster 4

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0019166	trans-2-enoyl-CoA reductase (NADPH) acti...	3	2	0.07	0.0015	0.0291
GO:0005102	receptor binding	889	34	20.21	0.0019	0.0291
GO:0047391	alkylglycerophosphoethanolamine phosphod...	4	2	0.09	0.0030	0.0291
GO:0004190	aspartic-type endopeptidase activity	15	3	0.34	0.0043	0.0291
GO:0031683	G-protein beta/gamma-subunit complex bin...	15	3	0.34	0.0043	0.0291
GO:0070001	aspartic-type peptidase activity	15	3	0.34	0.0043	0.0291
GO:0004197	cysteine-type endopeptidase activity	57	5	1.30	0.0094	0.0291
GO:0016922	ligand-dependent nuclear receptor bindin...	20	3	0.45	0.0099	0.0291

Enrichments of biological processes mouse cluster 5

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0002376	immune system process	1490	62	25.03	3.4e-12	0e+00
GO:0006955	immune response	775	42	13.02	8.2e-12	0e+00
GO:0002250	adaptive immune response	241	21	4.05	6.3e-10	0e+00
GO:0002682	regulation of immune system process	821	38	13.79	8.4e-09	0e+00
GO:0042981	regulation of apoptotic process	1026	43	17.24	1.4e-08	0e+00
GO:0043067	regulation of programmed cell death	1040	43	17.47	2.1e-08	0e+00
GO:0001775	cell activation	620	31	10.42	4.3e-08	0e+00
GO:0010941	regulation of cell death	1120	44	18.82	6.3e-08	0e+00
GO:0006952	defense response	823	36	13.83	9.3e-08	0e+00
GO:0050776	regulation of immune response	410	24	6.89	9.7e-08	0e+00
GO:0045321	leukocyte activation	543	28	9.12	1.1e-07	0e+00
GO:0045087	innate immune response	395	23	6.64	2.0e-07	0e+00
GO:0006915	apoptotic process	1301	47	21.86	2.5e-07	0e+00
GO:0002684	positive regulation of immune system pro...	531	27	8.92	2.5e-07	0e+00
GO:0012501	programmed cell death	1323	47	22.23	4.1e-07	0e+00
GO:0002443	leukocyte mediated immunity	216	16	3.63	7.1e-07	0e+00
GO:0002460	adaptive immune response based on somati...	166	14	2.79	7.6e-07	0e+00
GO:0006954	inflammatory response	369	21	6.20	1.0e-06	0e+00
GO:0001816	cytokine production	434	23	7.29	1.0e-06	0e+00
GO:0050896	response to stimulus	4563	110	76.67	1.1e-06	0e+00
GO:0043065	positive regulation of apoptotic process	439	23	7.38	1.3e-06	0e+00
GO:0009617	response to bacterium	283	18	4.75	1.3e-06	0e+00
GO:0043068	positive regulation of programmed cell d...	443	23	7.44	1.5e-06	0e+00
GO:0002819	regulation of adaptive immune response	106	11	1.78	1.6e-06	0e+00
GO:0001817	regulation of cytokine production	385	21	6.47	2.0e-06	0e+00
GO:0006950	response to stress	2248	65	37.77	2.6e-06	0e+00
GO:0008219	cell death	1414	47	23.76	2.8e-06	0e+00
GO:0002703	regulation of leukocyte mediated immunit...	135	12	2.27	2.8e-06	0e+00
GO:0016265	death	1418	47	23.82	3.0e-06	0e+00
GO:0002366	leukocyte activation involved in immune ...	163	13	2.74	3.6e-06	0e+00
GO:0002263	cell activation involved in immune respo...	165	13	2.77	4.1e-06	0e+00
GO:0002822	regulation of adaptive immune response b...	95	10	1.60	4.2e-06	0e+00
GO:0010942	positive regulation of cell death	472	23	7.93	4.3e-06	0e+00
GO:0016337	single organismal cell-cell adhesion	508	24	8.54	4.5e-06	0e+00
GO:0050778	positive regulation of immune response	318	18	5.34	6.8e-06	0e+00
GO:0002252	immune effector process	485	23	8.15	6.8e-06	0e+00
GO:0007159	leukocyte cell-cell adhesion	357	19	6.00	9.1e-06	0e+00
GO:0001819	positive regulation of cytokine producti...	263	16	4.42	9.2e-06	0e+00
GO:0046649	lymphocyte activation	467	22	7.85	1.2e-05	0e+00
GO:0098609	cell-cell adhesion	545	24	9.16	1.5e-05	0e+00
GO:0002449	lymphocyte mediated immunity	160	12	2.69	1.6e-05	0e+00
GO:0002285	lymphocyte activation involved in immune...	111	10	1.87	1.7e-05	0e+00
GO:0098602	single organism cell adhesion	551	24	9.26	1.8e-05	0e+00
GO:0002683	negative regulation of immune system pro...	278	16	4.67	1.8e-05	0e+00
GO:0032623	interleukin-2 production	50	7	0.84	1.8e-05	0e+00
GO:0034109	homotypic cell-cell adhesion	386	19	6.49	2.7e-05	1e-04
GO:0002694	regulation of leukocyte activation	324	17	5.44	3.3e-05	1e-04
GO:0002706	regulation of lymphocyte mediated immuni...	98	9	1.65	3.9e-05	1e-04
GO:0042110	T cell activation	330	17	5.54	4.1e-05	1e-04
GO:0070489	T cell aggregation	330	17	5.54	4.1e-05	1e-04
GO:0007259	JAK-STAT cascade	99	9	1.66	4.2e-05	1e-04
GO:0097696	STAT cascade	99	9	1.66	4.2e-05	1e-04
GO:0071593	lymphocyte aggregation	331	17	5.56	4.3e-05	1e-04
GO:0002286	T cell activation involved in immune res...	57	7	0.96	4.4e-05	1e-04
GO:0097285	cell-type specific apoptotic process	367	18	6.17	4.6e-05	1e-04
GO:0002274	myeloid leukocyte activation	126	10	2.12	5.1e-05	1e-04
GO:0070486	leukocyte aggregation	337	17	5.66	5.4e-05	1e-04
GO:0042267	natural killer cell mediated cytotoxicit...	41	6	0.69	5.8e-05	1e-04
GO:0002705	positive regulation of leukocyte mediate...	81	8	1.36	6.2e-05	1e-04
GO:0007165	signal transduction	2897	73	48.67	7.3e-05	1e-04
GO:0046425	regulation of JAK-STAT cascade	83	8	1.39	7.4e-05	1e-04
GO:1904892	regulation of STAT cascade	83	8	1.39	7.4e-05	1e-04
GO:0002228	natural killer cell mediated immunity	43	6	0.72	7.6e-05	1e-04
GO:0050865	regulation of cell activation	348	17	5.85	8.0e-05	1e-04
GO:0046427	positive regulation of JAK-STAT cascade	44	6	0.74	8.7e-05	1e-04
GO:1904894	positive regulation of STAT cascade	44	6	0.74	8.7e-05	1e-04
GO:0002237	response to molecule of bacterial origin	190	12	3.19	8.7e-05	1e-04
GO:0051716	cellular response to stimulus	3830	90	64.35	9.2e-05	1e-04
GO:0042327	positive regulation of phosphorylation	613	24	10.30	9.6e-05	1e-04
GO:0002697	regulation of immune effector process	288	15	4.84	1.0e-04	1e-04
GO:0007155	cell adhesion	826	29	13.88	1.2e-04	2e-04
GO:0001934	positive regulation of protein phosphory...	583	23	9.80	1.2e-04	2e-04
GO:0042088	T-helper 1 type immune response	30	5	0.50	1.3e-04	2e-04
GO:0042269	regulation of natural killer cell mediat...	30	5	0.50	1.3e-04	2e-04
GO:0048518	positive regulation of biological proces...	3592	85	60.35	1.3e-04	2e-04
GO:0022610	biological adhesion	835	29	14.03	1.5e-04	2e-04
GO:0002715	regulation of natural killer cell mediat...	31	5	0.52	1.5e-04	2e-04
GO:0010562	positive regulation of phosphorus metabo...	672	25	11.29	1.5e-04	2e-04
GO:0045937	positive regulation of phosphate metabol...	672	25	11.29	1.5e-04	2e-04
GO:0001909	leukocyte mediated cytotoxicity	70	7	1.18	1.7e-04	2e-04
GO:0002707	negative regulation of lymphocyte mediat...	32	5	0.54	1.8e-04	2e-04
GO:0001910	regulation of leukocyte mediated cytotox...	50	6	0.84	1.8e-04	2e-04
GO:0044700	single organism signaling	3084	75	51.82	1.9e-04	2e-04
GO:0019221	cytokine-mediated signaling pathway	206	12	3.46	1.9e-04	2e-04
GO:0043403	skeletal muscle tissue regeneration	18	4	0.30	2.0e-04	2e-04
GO:0023052	signaling	3091	75	51.93	2.0e-04	2e-04
GO:0050777	negative regulation of immune response	96	8	1.61	2.1e-04	2e-04
GO:0007166	cell surface receptor signaling pathway	1389	41	23.34	2.1e-04	2e-04
GO:0048584	positive regulation of response to stimu...	1207	37	20.28	2.2e-04	2e-04
GO:0009605	response to external stimulus	1212	37	20.36	2.3e-04	3e-04
GO:0043312	neutrophil degranulation	8	3	0.13	2.5e-04	3e-04
GO:0007154	cell communication	3168	76	53.23	2.6e-04	3e-04
GO:0032612	interleukin-1 production	54	6	0.91	2.8e-04	3e-04
GO:0009611	response to wounding	424	18	7.12	2.9e-04	3e-04
GO:0048583	regulation of response to stimulus	2241	58	37.65	2.9e-04	3e-04
GO:0001906	cell killing	77	7	1.29	3.0e-04	3e-04
GO:0002685	regulation of leukocyte migration	102	8	1.71	3.1e-04	3e-04
GO:0035556	intracellular signal transduction	1613	45	27.10	3.5e-04	4e-04
GO:0050707	regulation of cytokine secretion	104	8	1.75	3.6e-04	4e-04
GO:0002699	positive regulation of immune effector p...	131	9	2.20	3.6e-04	4e-04

Enrichments of molecular functions mouse cluster 5

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0003823	antigen binding	60	6	1.03	0.00054	0.0382
GO:0003976	UDP-N-acetylglucosamine-lysosomal-enzyme...	3	2	0.05	0.00086	0.0382
GO:0016780	phosphotransferase activity, for other s...	18	3	0.31	0.00333	0.0382
GO:0005126	cytokine receptor binding	149	8	2.55	0.00408	0.0382
GO:0034987	immunoglobulin receptor binding	6	2	0.10	0.00418	0.0382
GO:0035064	methylated histone binding	40	4	0.68	0.00470	0.0382
GO:0042393	histone binding	124	7	2.12	0.00541	0.0382
GO:0005164	tumor necrosis factor receptor binding	25	3	0.43	0.00861	0.0382
GO:0042887	amide transmembrane transporter activity	9	2	0.15	0.00969	0.0382

Enrichments of biological processes mouse cluster 6

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006396	RNA processing	654	35	14.21	6.80e-07	0.0001
GO:0006397	mRNA processing	363	23	7.89	4.30e-06	0.0001
GO:0006412	translation	501	28	10.89	4.30e-06	0.0001
GO:0008380	RNA splicing	292	20	6.35	5.80e-06	0.0001
GO:0043604	amide biosynthetic process	576	30	12.52	7.90e-06	0.0001
GO:0043043	peptide biosynthetic process	518	28	11.26	8.10e-06	0.0001
GO:0016071	mRNA metabolic process	438	24	9.52	3.00e-05	0.0004
GO:0006518	peptide metabolic process	607	29	13.19	5.50e-05	0.0007
GO:0043603	cellular amide metabolic process	715	32	15.54	7.80e-05	0.0009
GO:0000377	RNA splicing, via transesterification re...	174	13	3.78	1.10e-04	0.0010
GO:0000398	mRNA splicing, via spliceosome	174	13	3.78	1.10e-04	0.0010
GO:0000375	RNA splicing, via transesterification re...	175	13	3.80	1.20e-04	0.0010
GO:0033119	negative regulation of RNA splicing	27	5	0.59	2.50e-04	0.0019
GO:0043414	macromolecule methylation	196	13	4.26	3.50e-04	0.0025
GO:0006413	translational initiation	91	8	1.98	8.00e-04	0.0053
GO:0010467	gene expression	3512	100	76.33	9.00e-04	0.0056
GO:1901566	organonitrogen compound biosynthetic pro...	896	34	19.47	1.00e-03	0.0059
GO:0032259	methylation	256	14	5.56	1.43e-03	0.0079
GO:0006807	nitrogen compound metabolic process	4431	119	96.30	2.18e-03	0.0115
GO:0034641	cellular nitrogen compound metabolic pro...	4262	115	92.63	2.34e-03	0.0117
GO:0016576	histone dephosphorylation	4	2	0.09	2.74e-03	0.0129
GO:0007067	mitotic nuclear division	368	17	8.00	2.84e-03	0.0129
GO:0000387	spliceosomal snRNP assembly	29	4	0.63	3.38e-03	0.0147
GO:0030638	polyketide metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0030647	aminoglycoside antibiotic metabolic proc...	5	2	0.11	4.51e-03	0.0154
GO:0043985	histone H4-R3 methylation	5	2	0.11	4.51e-03	0.0154
GO:0044597	daunorubicin metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0044598	doxorubicin metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0046607	positive regulation of centrosome cycle	5	2	0.11	4.51e-03	0.0154
GO:0070507	regulation of microtubule cytoskeleton o...	120	8	2.61	4.63e-03	0.0154
GO:0050686	negative regulation of mRNA processing	32	4	0.70	4.86e-03	0.0157
GO:0032071	regulation of endodeoxyribonuclease acti...	6	2	0.13	6.66e-03	0.0202
GO:0043615	astrocyte cell migration	6	2	0.13	6.66e-03	0.0202
GO:0016571	histone methylation	103	7	2.24	7.13e-03	0.0207
GO:0016570	histone modification	339	15	7.37	7.26e-03	0.0207
GO:0016070	RNA metabolic process	2927	81	63.61	7.97e-03	0.0214
GO:0006479	protein methylation	132	8	2.87	8.13e-03	0.0214
GO:0008213	protein alkylation	132	8	2.87	8.13e-03	0.0214
GO:0016569	covalent chromatin modification	345	15	7.50	8.47e-03	0.0217
GO:1903312	negative regulation of mRNA metabolic pr...	38	4	0.83	9.01e-03	0.0217
GO:0032070	regulation of deoxyribonuclease activity	7	2	0.15	9.19e-03	0.0217
GO:0034969	histone arginine methylation	7	2	0.15	9.19e-03	0.0217

Enrichments of molecular functions mouse cluster 6

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0003723	RNA binding	1384	70	29.49	1.80e-12	0.0000
GO:0044822	poly(A) RNA binding	1064	57	22.67	4.00e-11	0.0000
GO:0003676	nucleic acid binding	2634	100	56.12	2.60e-10	0.0000
GO:1901363	heterocyclic compound binding	3990	116	85.01	3.00e-05	0.0008
GO:0097159	organic cyclic compound binding	4026	116	85.78	4.70e-05	0.0009
GO:0034061	DNA polymerase activity	38	6	0.81	1.40e-04	0.0023
GO:0003887	DNA-directed DNA polymerase activity	25	5	0.53	1.60e-04	0.0023
GO:0008135	translation factor activity, RNA binding	76	8	1.62	2.10e-04	0.0026
GO:0031369	translation initiation factor binding	30	5	0.64	3.90e-04	0.0043
GO:0003743	translation initiation factor activity	47	6	1.00	4.60e-04	0.0045
GO:0003735	structural constituent of ribosome	181	12	3.86	5.00e-04	0.0045
GO:0004526	ribonuclease P activity	11	3	0.23	1.39e-03	0.0116
GO:0004521	endoribonuclease activity	40	5	0.85	1.51e-03	0.0116
GO:1990715	mRNA CDS binding	4	2	0.09	2.64e-03	0.0189
GO:0008173	RNA methyltransferase activity	89	7	1.90	2.86e-03	0.0191
GO:0016891	endoribonuclease activity, producing 5'-...	29	4	0.62	3.14e-03	0.0196
GO:0004549	tRNA-specific ribonuclease activity	15	3	0.32	3.60e-03	0.0212
GO:0017069	snRNA binding	31	4	0.66	4.03e-03	0.0224
GO:0016741	transferase activity, transferring one-c...	176	10	3.75	4.45e-03	0.0234
GO:0043021	ribonucleoprotein complex binding	99	7	2.11	5.18e-03	0.0256
GO:0005198	structural molecule activity	367	16	7.82	5.38e-03	0.0256
GO:0008175	tRNA methyltransferase activity	83	6	1.77	8.48e-03	0.0351
GO:0000182	rDNA binding	7	2	0.15	8.85e-03	0.0351
GO:0017070	U6 snRNA binding	7	2	0.15	8.85e-03	0.0351
GO:0016893	endonuclease activity, active with eithe...	39	4	0.83	9.22e-03	0.0351
GO:0016779	nucleotidyltransferase activity	111	7	2.37	9.54e-03	0.0351
GO:0008168	methyltransferase activity	168	9	3.58	9.87e-03	0.0351

Enrichments of biological processes mouse cluster 7

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0060088	auditory receptor cell stereocilium orga...	7	2	0.05	0.0012	0.0289
GO:0042402	cellular biogenic amine catabolic proces...	8	2	0.06	0.0016	0.0289
GO:0043123	positive regulation of I-kappaB kinase/N...	116	5	0.88	0.0019	0.0289
GO:0002093	auditory receptor cell morphogenesis	9	2	0.07	0.0020	0.0289
GO:0009310	amine catabolic process	9	2	0.07	0.0020	0.0289
GO:0060546	negative regulation of necroptotic proces...	10	2	0.08	0.0025	0.0289
GO:0030163	protein catabolic process	640	12	4.87	0.0032	0.0289
GO:0060117	auditory receptor cell development	12	2	0.09	0.0036	0.0289
GO:0060544	regulation of necroptotic process	12	2	0.09	0.0036	0.0289
GO:0060628	regulation of ER to Golgi vesicle-mediat...	12	2	0.09	0.0036	0.0289
GO:0060547	negative regulation of necrotic cell dea...	13	2	0.10	0.0042	0.0289
GO:0042176	regulation of protein catabolic process	285	7	2.17	0.0060	0.0289
GO:0006900	membrane budding	51	3	0.39	0.0068	0.0289
GO:0098656	anion transmembrane transport	101	4	0.77	0.0073	0.0289
GO:0001207	histone displacement	1	1	0.01	0.0076	0.0289
GO:0007174	epidermal growth factor catabolic proces...	1	1	0.01	0.0076	0.0289
GO:0015881	creatine transport	1	1	0.01	0.0076	0.0289
GO:0035508	positive regulation of myosin-light-chai...	1	1	0.01	0.0076	0.0289
GO:0048022	negative regulation of melanin biosynthe...	1	1	0.01	0.0076	0.0289
GO:0051039	positive regulation of transcription inv...	1	1	0.01	0.0076	0.0289
GO:0070142	synaptic vesicle budding	1	1	0.01	0.0076	0.0289
GO:1900377	negative regulation of secondary metabol...	1	1	0.01	0.0076	0.0289
GO:1902598	creatine transmembrane transport	1	1	0.01	0.0076	0.0289
GO:1902824	positive regulation of late endosome to ...	1	1	0.01	0.0076	0.0289
GO:1903337	positive regulation of vacuolar transpor...	1	1	0.01	0.0076	0.0289
GO:0043122	regulation of I-kappaB kinase/NF-kappaB ...	163	5	1.24	0.0080	0.0289
GO:0010939	regulation of necrotic cell death	18	2	0.14	0.0081	0.0289
GO:0009057	macromolecule catabolic process	815	13	6.20	0.0085	0.0289
GO:0060122	inner ear receptor stereocilium organiza...	20	2	0.15	0.0099	0.0289

Enrichments of molecular functions mouse cluster 7

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0071617	lysophospholipid acyltransferase activit...	12	3	0.09	0.000093	0.0070
GO:0004842	ubiquitin-protein transferase activity	314	10	2.42	0.000150	0.0070
GO:0019787	ubiquitin-like protein transferase activ...	328	10	2.53	0.000210	0.0070
GO:0042171	lysophosphatidic acid acyltransferase ac...	10	2	0.08	0.002550	0.0123
GO:0016740	transferase activity	1738	24	13.41	0.002660	0.0123
GO:0015095	magnesium ion transmembrane transporter ...	14	2	0.11	0.005050	0.0123
GO:0003950	NAD+ ADP-ribosyltransferase activity	17	2	0.13	0.007430	0.0123
GO:0001595	angiotensin receptor activity	1	1	0.01	0.007720	0.0123
GO:0004343	glucosamine 6-phosphate N-acetyltransfer...	1	1	0.01	0.007720	0.0123
GO:0004945	angiotensin type II receptor activity	1	1	0.01	0.007720	0.0123
GO:0005308	creatine transmembrane transporter activ...	1	1	0.01	0.007720	0.0123
GO:0005309	creatine:sodium symporter activity	1	1	0.01	0.007720	0.0123
GO:0018542	2,3-dihydroxy DDT 1,2-dioxygenase activi...	1	1	0.01	0.007720	0.0123
GO:0018555	phenanthrene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018556	2,2',3-trihydroxybiphenyl dioxygenase ac...	1	1	0.01	0.007720	0.0123
GO:0018557	1,2-dihydroxyfluorene 1,1-alpha-dioxygen...	1	1	0.01	0.007720	0.0123
GO:0018558	5,6-dihydroxy-3-methyl-2-oxo-1,2-dihydro...	1	1	0.01	0.007720	0.0123
GO:0018559	1,1-dichloro-2-(dihydroxy-4-chlorophenyl...	1	1	0.01	0.007720	0.0123
GO:0018560	protocatechuate 3,4-dioxygenase type II ...	1	1	0.01	0.007720	0.0123
GO:0018561	2'-aminobiphenyl-2,3-diol 1,2-dioxygenas...	1	1	0.01	0.007720	0.0123
GO:0018562	3,4-dihydroxyfluorene 4,4-alpha-dioxygen...	1	1	0.01	0.007720	0.0123
GO:0018563	2,3-dihydroxy-ethylbenzene 1,2-dioxygena...	1	1	0.01	0.007720	0.0123
GO:0018564	carbazole 1,9a-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018565	dihydroxydibenzothiophene dioxygenase ac...	1	1	0.01	0.007720	0.0123
GO:0018566	1,2-dihydroxynaphthalene-6-sulfonate 1,8...	1	1	0.01	0.007720	0.0123
GO:0018567	styrene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018568	3,4-dihydroxyphenanthrene dioxygenase ac...	1	1	0.01	0.007720	0.0123
GO:0018569	hydroquinone 1,2-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018570	p-cumate 2,3-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018571	2,3-dihydroxy-p-cumate dioxygenase activ...	1	1	0.01	0.007720	0.0123
GO:0018572	3,5-dichlorocatechol 1,2-dioxygenase act...	1	1	0.01	0.007720	0.0123
GO:0018573	2-aminophenol 1,6-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0018574	2,6-dichloro-p-hydroquinone 1,2-dioxygen...	1	1	0.01	0.007720	0.0123
GO:0018575	chlorocatechol 1,2-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0019114	catechol dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0019117	dihydroxyfluorene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0019782	ISG15 activating enzyme activity	1	1	0.01	0.007720	0.0123
GO:0034543	5-aminosalicylate dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034803	3-hydroxy-2-naphthoate 2,3-dioxygenase a...	1	1	0.01	0.007720	0.0123
GO:0034806	benzo(a)pyrene 11,12-dioxygenase activit...	1	1	0.01	0.007720	0.0123
GO:0034808	benzo(a)pyrene 4,5-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034810	4,5-dihydroxybenzo(a)pyrene dioxygenase ...	1	1	0.01	0.007720	0.0123
GO:0034811	benzo(a)pyrene 9,10-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034812	9,10-dihydroxybenzo(a)pyrene dioxygenase...	1	1	0.01	0.007720	0.0123
GO:0034813	benzo(a)pyrene 7,8-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034814	7,8-dihydroxy benzo(a)pyrene dioxygenase...	1	1	0.01	0.007720	0.0123
GO:0034827	1,2-dihydroxy-5,6,7,8-tetrahydronaphthal...	1	1	0.01	0.007720	0.0123
GO:0034834	2-mercaptobenzothiazole dioxygenase acti...	1	1	0.01	0.007720	0.0123
GO:0034895	pyridine-3,4-diol dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034920	pyrene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034922	4,5-dihydroxypyrene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034934	phenanthrene-4-carboxylate dioxygenase a...	1	1	0.01	0.007720	0.0123
GO:0034935	tetrachlorobenzene dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0034936	4,6-dichloro-3-methylcatechol 1,2-dioxyg...	1	1	0.01	0.007720	0.0123
GO:0034955	2,3-dihydroxydiphenyl ether dioxygenase ...	1	1	0.01	0.007720	0.0123
GO:0034956	diphenyl ether 1,2-dioxygenase activity	1	1	0.01	0.007720	0.0123
GO:0036403	arachidonate 8(S)-lipoxygenase activity	1	1	0.01	0.007720	0.0123
GO:0047074	4-hydroxycatechol 1,2-dioxygenase activi...	1	1	0.01	0.007720	0.0123
GO:0047166	1-alkenylglycerophosphoethanolamine O-ac...	1	1	0.01	0.007720	0.0123
GO:0052894	norspermine:oxygen oxidoreductase activi...	1	1	0.01	0.007720	0.0123
GO:0052895	N1-acetylspermine:oxygen oxidoreductase ...	1	1	0.01	0.007720	0.0123
GO:0097199	cysteine-type endopeptidase activity inv...	1	1	0.01	0.007720	0.0123
GO:1990583	phospholipase D activator activity	1	1	0.01	0.007720	0.0123
GO:0016747	transferase activity, transferring acyl ...	165	5	1.27	0.008940	0.0140