

Supplementary Table 10. *Enriched pathways for genes overlapped with DMPs.* Columns are: 'path', the GO identifier of the pathway; 'desc', the pathway's short description; 'p', the number of genes simultaneously part of the pathway and in the cluster; 'm', the number of genes in the cluster; 'P', the total number of genes in the pathway; 'M', the total number of genes from all pathways; 'nrich', the enrichment ratio with value of (p/P)/(m/M); 'log2FC', the log2 value of the enrichment; 'pval', the P-value of the enrichment, from a hypergeometric test; 'fdr', the FDR-corrected P-value.

path	desc	p	m	P	M	nrich	log2FC	pval	fdr
GO:0048731	system development	222	783	3507	17583	1.42	0.51	2.9E-09	2.8E-07
GO:0031327	negative regulation of cellular biosynthetic process	117	783	1566	17583	1.68	0.75	7.0E-09	6.6E-07
GO:0009890	negative regulation of biosynthetic process	118	783	1596	17583	1.66	0.73	1.1E-08	1.0E-06
GO:0007275	multicellular organism development	238	783	3903	17583	1.37	0.45	2.0E-08	1.8E-06
GO:0010558	negative regulation of macromolecule biosynthetic process	112	783	1510	17583	1.67	0.74	2.2E-08	2.1E-06
GO:0007399	nervous system development	149	783	2189	17583	1.53	0.61	2.8E-08	2.6E-06
GO:0031324	negative regulation of cellular metabolic process	150	783	2218	17583	1.52	0.60	3.8E-08	3.5E-06
GO:0010556	regulation of macromolecule biosynthetic process	232	783	3907	17583	1.33	0.42	3.1E-07	2.8E-05
GO:0045892	negative regulation of DNA-templated transcription	96	783	1303	17583	1.65	0.73	3.2E-07	2.9E-05
GO:0010604	positive regulation of macromolecule metabolic process	211	783	3487	17583	1.36	0.44	3.3E-07	3.0E-05
GO:1903507	negative regulation of nucleic acid-templated transcription	96	783	1305	17583	1.65	0.72	3.5E-07	3.1E-05
GO:0031326	regulation of cellular biosynthetic process	239	783	4057	17583	1.32	0.40	3.6E-07	3.3E-05
GO:1902679	negative regulation of RNA biosynthetic process	96	783	1307	17583	1.65	0.72	3.7E-07	3.3E-05
GO:0009893	positive regulation of metabolic process	226	783	3796	17583	1.34	0.42	3.9E-07	3.4E-05
GO:0009889	regulation of biosynthetic process	242	783	4122	17583	1.32	0.40	3.9E-07	3.5E-05
GO:0051171	regulation of nitrogen compound metabolic process	313	783	5628	17583	1.25	0.32	6.4E-07	5.6E-05
GO:0080090	regulation of primary metabolic process	320	783	5782	17583	1.24	0.31	7.0E-07	6.1E-05
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	107	783	1541	17583	1.56	0.64	1.2E-06	1.1E-04
GO:0051253	negative regulation of RNA metabolic process	100	783	1416	17583	1.59	0.67	1.3E-06	1.1E-04
GO:0060255	regulation of macromolecule metabolic process	334	783	6147	17583	1.22	0.29	2.1E-06	1.8E-04
GO:0048856	anatomical structure development	286	783	5143	17583	1.25	0.32	2.9E-06	2.5E-04
GO:0051173	positive regulation of nitrogen compound metabolic process	187	783	3112	17583	1.35	0.43	3.1E-06	2.6E-04
GO:0031323	regulation of cellular metabolic process	305	783	5561	17583	1.23	0.30	3.8E-06	3.2E-04
GO:0051172	negative regulation of nitrogen compound metabolic process	148	783	2357	17583	1.41	0.50	4.1E-06	3.4E-04
GO:0009892	negative regulation of metabolic process	177	783	2934	17583	1.35	0.44	4.9E-06	4.1E-04
GO:0010605	negative regulation of macromolecule metabolic process	166	783	2717	17583	1.37	0.46	4.9E-06	4.1E-04

GO:0048523	negative regulation of cellular process	261	783	4675	17583	1.25	0.33	7.9E-06	6.5E-04
GO:0048519	negative regulation of biological process	288	783	5250	17583	1.23	0.30	8.8E-06	7.2E-04
GO:0032502	developmental process	308	783	5685	17583	1.22	0.28	1.0E-05	8.3E-04
GO:0019222	regulation of metabolic process	353	783	6669	17583	1.19	0.25	1.2E-05	9.9E-04
GO:0048518	positive regulation of biological process	333	783	6241	17583	1.20	0.26	1.3E-05	1.1E-03
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molec	20	783	169	17583	2.66	1.41	2.1E-05	1.6E-03
GO:0048522	positive regulation of cellular process	301	783	5593	17583	1.21	0.27	2.5E-05	1.9E-03
GO:0048934	peripheral nervous system neuron differentiation	5	783	15	17583	7.49	2.90	2.7E-05	2.1E-03
GO:0048935	peripheral nervous system neuron development	5	783	15	17583	7.49	2.90	2.7E-05	2.1E-03
GO:0031325	positive regulation of cellular metabolic process	179	783	3060	17583	1.31	0.39	2.8E-05	2.1E-03
GO:0000122	negative regulation of transcription by RNA polymerase II	69	783	959	17583	1.62	0.69	3.0E-05	2.3E-03
GO:0048513	animal organ development	170	783	2895	17583	1.32	0.40	3.7E-05	2.8E-03
GO:0010557	positive regulation of macromolecule biosynthetic process	120	783	1920	17583	1.40	0.49	4.5E-05	3.4E-03
GO:0040008	regulation of growth	48	783	609	17583	1.77	0.82	4.7E-05	3.5E-03
GO:0006355	regulation of DNA-templated transcription	195	783	3420	17583	1.28	0.36	5.3E-05	3.9E-03
GO:1903506	regulation of nucleic acid-templated transcription	195	783	3422	17583	1.28	0.36	5.5E-05	4.1E-03
GO:0014033	neural crest cell differentiation	13	783	93	17583	3.14	1.65	6.1E-05	4.5E-03
GO:2001141	regulation of RNA biosynthetic process	195	783	3431	17583	1.28	0.35	6.4E-05	4.7E-03
GO:0060562	epithelial tube morphogenesis	29	783	312	17583	2.09	1.06	6.5E-05	4.8E-03
GO:0048863	stem cell differentiation	20	783	183	17583	2.45	1.30	6.8E-05	5.0E-03
GO:0044237	cellular metabolic process	339	783	6489	17583	1.17	0.23	7.4E-05	5.4E-03
GO:0048565	digestive tract development	16	783	132	17583	2.72	1.44	7.9E-05	5.7E-03
GO:0019219	regulation of nucleobase-containing compound metabolic proce	223	783	4030	17583	1.24	0.31	9.1E-05	6.3E-03
GO:0001709	cell fate determination	8	783	43	17583	4.18	2.06	9.5E-05	6.6E-03
GO:0055075	potassium ion homeostasis	7	783	34	17583	4.62	2.21	9.7E-05	6.7E-03
GO:0010468	regulation of gene expression	260	783	4813	17583	1.21	0.28	1.0E-04	6.9E-03
GO:0009891	positive regulation of biosynthetic process	125	783	2055	17583	1.37	0.45	1.0E-04	7.2E-03
GO:0006796	phosphate-containing compound metabolic process	113	783	1826	17583	1.39	0.47	1.1E-04	7.7E-03
GO:1990573	potassium ion import across plasma membrane	8	783	44	17583	4.08	2.03	1.1E-04	7.7E-03
GO:0071695	anatomical structure maturation	22	783	218	17583	2.27	1.18	1.2E-04	7.7E-03
GO:0048754	branching morphogenesis of an epithelial tube	16	783	136	17583	2.64	1.40	1.2E-04	7.7E-03
GO:0060322	head development	59	783	826	17583	1.60	0.68	1.3E-04	8.6E-03

GO:0051252	regulation of RNA metabolic process	207	783	3724	17583	1.25	0.32	1.4E-04	9.0E-03
GO:0031328	positive regulation of cellular biosynthetic process	122	783	2016	17583	1.36	0.44	1.6E-04	1.0E-02
GO:0008219	cell death	74	783	1103	17583	1.51	0.59	1.6E-04	1.0E-02
GO:0061005	cell differentiation involved in kidney development	8	783	47	17583	3.82	1.93	2.0E-04	1.3E-02
GO:0051093	negative regulation of developmental process	63	783	911	17583	1.55	0.63	2.0E-04	1.3E-02
GO:0006793	phosphorus metabolic process	113	783	1852	17583	1.37	0.45	2.0E-04	1.3E-02
GO:0016311	dephosphorylation	23	783	242	17583	2.13	1.09	2.1E-04	1.4E-02
GO:0048469	cell maturation	18	783	171	17583	2.36	1.24	2.3E-04	1.4E-02
GO:0055123	digestive system development	16	783	144	17583	2.50	1.32	2.3E-04	1.5E-02
GO:0072012	glomerulus vasculature development	5	783	21	17583	5.35	2.42	2.3E-04	1.5E-02
GO:0030705	cytoskeleton-dependent intracellular transport	20	783	200	17583	2.25	1.17	2.4E-04	1.5E-02
GO:0048762	mesenchymal cell differentiation	18	783	173	17583	2.34	1.22	2.6E-04	1.6E-02
GO:0001558	regulation of cell growth	34	783	418	17583	1.83	0.87	2.7E-04	1.6E-02
GO:0007420	brain development	55	783	778	17583	1.59	0.67	2.7E-04	1.7E-02
GO:0012501	programmed cell death	71	783	1070	17583	1.49	0.58	2.9E-04	1.8E-02
GO:0045165	cell fate commitment	23	783	247	17583	2.09	1.06	2.9E-04	1.8E-02
GO:0048485	sympathetic nervous system development	5	783	22	17583	5.10	2.35	3.1E-04	1.9E-02
GO:0001919	regulation of receptor recycling	5	783	22	17583	5.10	2.35	3.1E-04	1.9E-02
GO:0051402	neuron apoptotic process	12	783	96	17583	2.81	1.49	3.3E-04	1.9E-02
GO:0071805	potassium ion transmembrane transport	17	783	162	17583	2.36	1.24	3.3E-04	1.9E-02
GO:0000082	G1/S transition of mitotic cell cycle	11	783	84	17583	2.94	1.56	3.3E-04	1.9E-02
GO:0045944	positive regulation of transcription by RNA polymerase II	80	783	1246	17583	1.44	0.53	3.6E-04	2.0E-02
GO:0001656	metanephros development	11	783	85	17583	2.91	1.54	3.7E-04	2.0E-02
GO:0001657	ureteric bud development	11	783	85	17583	2.91	1.54	3.7E-04	2.0E-02
GO:0098609	cell-cell adhesion	41	783	543	17583	1.70	0.76	3.7E-04	2.0E-02
GO:0006470	protein dephosphorylation	18	783	178	17583	2.27	1.18	3.8E-04	2.1E-02
GO:0061138	morphogenesis of a branching epithelium	17	783	164	17583	2.33	1.22	3.8E-04	2.1E-02
GO:0017158	regulation of calcium ion-dependent exocytosis	7	783	41	17583	3.83	1.94	3.9E-04	2.1E-02
GO:0002070	epithelial cell maturation	5	783	23	17583	4.88	2.29	4.0E-04	2.1E-02
GO:0061437	renal system vasculature development	5	783	23	17583	4.88	2.29	4.0E-04	2.1E-02
GO:0061440	kidney vasculature development	5	783	23	17583	4.88	2.29	4.0E-04	2.1E-02
GO:0021533	cell differentiation in hindbrain	5	783	23	17583	4.88	2.29	4.0E-04	2.1E-02

GO:0035162	embryonic hemopoiesis	5	783	23	17583	4.88	2.29	4.0E-04	2.1E-02
GO:0072164	mesonephric tubule development	11	783	86	17583	2.87	1.52	4.1E-04	2.2E-02
GO:0048864	stem cell development	11	783	86	17583	2.87	1.52	4.1E-04	2.2E-02
GO:0044843	cell cycle G1/S phase transition	11	783	86	17583	2.87	1.52	4.1E-04	2.2E-02
GO:0072163	mesonephric epithelium development	11	783	86	17583	2.87	1.52	4.1E-04	2.2E-02
GO:0006915	apoptotic process	68	783	1028	17583	1.49	0.57	4.2E-04	2.2E-02
GO:0031400	negative regulation of protein modification process	37	783	480	17583	1.73	0.79	4.5E-04	2.3E-02
GO:0006357	regulation of transcription by RNA polymerase II	148	783	2592	17583	1.28	0.36	4.7E-04	2.4E-02
GO:1903508	positive regulation of nucleic acid-templated transcription	103	783	1700	17583	1.36	0.44	4.9E-04	2.5E-02
GO:0045893	positive regulation of DNA-templated transcription	103	783	1700	17583	1.36	0.44	4.9E-04	2.5E-02
GO:0003254	regulation of membrane depolarization	7	783	43	17583	3.66	1.87	5.4E-04	2.8E-02
GO:0044772	mitotic cell cycle phase transition	17	783	169	17583	2.26	1.18	5.5E-04	2.8E-02
GO:1902680	positive regulation of RNA biosynthetic process	103	783	1706	17583	1.36	0.44	5.5E-04	2.8E-02
GO:0007417	central nervous system development	68	783	1041	17583	1.47	0.55	5.9E-04	3.0E-02
GO:0035295	tube development	59	783	876	17583	1.51	0.60	6.0E-04	3.0E-02
GO:0010467	gene expression	127	783	2186	17583	1.30	0.38	6.2E-04	3.1E-02
GO:0045926	negative regulation of growth	22	783	245	17583	2.02	1.01	6.3E-04	3.1E-02
GO:0001823	mesonephros development	11	783	90	17583	2.74	1.46	6.3E-04	3.1E-02
GO:0060675	ureteric bud morphogenesis	8	783	55	17583	3.27	1.71	6.6E-04	3.3E-02
GO:0051254	positive regulation of RNA metabolic process	109	783	1833	17583	1.34	0.42	6.7E-04	3.3E-02
GO:0008152	metabolic process	398	783	7967	17583	1.12	0.17	6.8E-04	3.3E-02
GO:0006813	potassium ion transport	17	783	173	17583	2.21	1.14	7.2E-04	3.5E-02
GO:0030308	negative regulation of cell growth	18	783	188	17583	2.15	1.10	7.5E-04	3.6E-02
GO:0032835	glomerulus development	8	783	56	17583	3.21	1.68	7.6E-04	3.6E-02
GO:0072171	mesonephric tubule morphogenesis	8	783	56	17583	3.21	1.68	7.6E-04	3.6E-02
GO:0001763	morphogenesis of a branching structure	17	783	174	17583	2.19	1.13	7.8E-04	3.7E-02
GO:0030182	neuron differentiation	68	783	1052	17583	1.45	0.54	7.8E-04	3.7E-02
GO:0002065	columnar/cuboidal epithelial cell differentiation	12	783	105	17583	2.57	1.36	7.8E-04	3.7E-02
GO:0035108	limb morphogenesis	15	783	146	17583	2.31	1.21	8.0E-04	3.7E-02
GO:0035107	appendage morphogenesis	15	783	146	17583	2.31	1.21	8.0E-04	3.7E-02
GO:0014032	neural crest cell development	10	783	80	17583	2.81	1.49	8.1E-04	3.7E-02
GO:0021697	cerebellar cortex formation	5	783	26	17583	4.32	2.11	8.2E-04	3.7E-02

GO:0060441	epithelial tube branching involved in lung morphogenesis	5	783	26	17583	4.32	2.11	8.2E-04	3.7E-02
GO:0086009	membrane repolarization	5	783	26	17583	4.32	2.11	8.2E-04	3.7E-02
GO:0070997	neuron death	12	783	106	17583	2.54	1.35	8.5E-04	3.8E-02
GO:0051179	localization	238	783	4502	17583	1.19	0.25	8.6E-04	3.8E-02
GO:0045596	negative regulation of cell differentiation	47	783	673	17583	1.57	0.65	8.9E-04	4.0E-02
GO:0030326	embryonic limb morphogenesis	13	783	120	17583	2.43	1.28	9.0E-04	4.0E-02
GO:0035113	embryonic appendage morphogenesis	13	783	120	17583	2.43	1.28	9.0E-04	4.0E-02
GO:0008406	gonad development	20	783	221	17583	2.03	1.02	9.1E-04	4.0E-02
GO:0071826	ribonucleoprotein complex subunit organization	19	783	207	17583	2.06	1.04	9.7E-04	4.2E-02
GO:0042733	embryonic digit morphogenesis	8	783	58	17583	3.10	1.63	9.9E-04	4.3E-02
GO:0006807	nitrogen compound metabolic process	338	783	6674	17583	1.14	0.19	1.0E-03	4.3E-02
GO:0051592	response to calcium ion	15	783	149	17583	2.26	1.18	1.0E-03	4.3E-02
GO:0016071	mRNA metabolic process	43	783	606	17583	1.59	0.67	1.0E-03	4.3E-02
GO:0042981	regulation of apoptotic process	88	783	1446	17583	1.37	0.45	1.1E-03	4.5E-02
GO:0048699	generation of neurons	71	783	1121	17583	1.42	0.51	1.1E-03	4.5E-02
GO:0010821	regulation of mitochondrion organization	15	783	150	17583	2.25	1.17	1.1E-03	4.5E-02
GO:0043068	positive regulation of programmed cell death	37	783	503	17583	1.65	0.72	1.1E-03	4.5E-02
GO:0044770	cell cycle phase transition	17	783	179	17583	2.13	1.09	1.1E-03	4.5E-02
GO:0060323	head morphogenesis	6	783	37	17583	3.64	1.86	1.1E-03	4.5E-02
GO:0048534	hematopoietic or lymphoid organ development	11	783	96	17583	2.57	1.36	1.1E-03	4.7E-02
GO:0046496	nicotinamide nucleotide metabolic process	9	783	71	17583	2.85	1.51	1.1E-03	4.7E-02
GO:0061337	cardiac conduction	9	783	71	17583	2.85	1.51	1.1E-03	4.7E-02
GO:0019362	pyridine nucleotide metabolic process	9	783	71	17583	2.85	1.51	1.1E-03	4.7E-02
GO:0021700	developmental maturation	23	783	272	17583	1.90	0.93	1.2E-03	4.7E-02
GO:0030857	negative regulation of epithelial cell differentiation	7	783	48	17583	3.27	1.71	1.2E-03	4.8E-02
GO:0044238	primary metabolic process	361	783	7194	17583	1.13	0.17	1.2E-03	4.8E-02
GO:0045137	development of primary sexual characteristics	20	783	226	17583	1.99	0.99	1.2E-03	4.9E-02
GO:0060485	mesenchyme development	21	783	242	17583	1.95	0.96	1.2E-03	4.9E-02
GO:0023051	regulation of signaling	182	783	3352	17583	1.22	0.29	1.2E-03	4.9E-02
GO:0021680	cerebellar Purkinje cell layer development	5	783	28	17583	4.01	2.00	1.2E-03	4.9E-02
GO:1903055	positive regulation of extracellular matrix organization	5	783	28	17583	4.01	2.00	1.2E-03	4.9E-02
GO:0022008	neurogenesis	79	783	1281	17583	1.38	0.47	1.3E-03	4.9E-02

GO:0003180	aortic valve morphogenesis	6	783	38	17583	3.55	1.83	1.3E-03	4.9E-02
GO:0045184	establishment of protein localization	78	783	1264	17583	1.39	0.47	1.3E-03	4.9E-02
GO:0086001	cardiac muscle cell action potential	7	783	49	17583	3.21	1.68	1.3E-03	4.9E-02
GO:0035050	embryonic heart tube development	10	783	85	17583	2.64	1.40	1.3E-03	4.9E-02
GO:0051246	regulation of protein metabolic process	140	783	2494	17583	1.26	0.33	1.4E-03	4.9E-02
GO:0043067	regulation of programmed cell death	89	783	1479	17583	1.35	0.43	1.4E-03	4.9E-02
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damag	9	783	73	17583	2.77	1.47	1.4E-03	4.9E-02
GO:0045935	positive regulation of nucleobase-containing compound metabo	117	783	2034	17583	1.29	0.37	1.5E-03	4.9E-02
GO:0001708	cell fate specification	10	783	86	17583	2.61	1.38	1.5E-03	4.9E-02
GO:0016070	RNA metabolic process	96	783	1619	17583	1.33	0.41	1.5E-03	4.9E-02
GO:0007595	lactation	6	783	39	17583	3.45	1.79	1.5E-03	4.9E-02
GO:0008088	axo-dendritic transport	9	783	74	17583	2.73	1.45	1.6E-03	4.9E-02
GO:0061458	reproductive system development	24	783	295	17583	1.83	0.87	1.6E-03	4.9E-02
GO:0043433	negative regulation of DNA-binding transcription factor activity	16	783	171	17583	2.10	1.07	1.7E-03	4.9E-02
GO:0097190	apoptotic signaling pathway	25	783	312	17583	1.80	0.85	1.7E-03	4.9E-02
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	22	783	264	17583	1.87	0.90	1.7E-03	4.9E-02
GO:0010942	positive regulation of cell death	40	783	569	17583	1.58	0.66	1.7E-03	4.9E-02
GO:0045927	positive regulation of growth	21	783	249	17583	1.89	0.92	1.8E-03	4.9E-02
GO:0001569	branching involved in blood vessel morphogenesis	5	783	30	17583	3.74	1.90	1.8E-03	4.9E-02
GO:0014741	negative regulation of muscle hypertrophy	5	783	30	17583	3.74	1.90	1.8E-03	4.9E-02
GO:0022607	cellular component assembly	135	783	2411	17583	1.26	0.33	1.8E-03	4.9E-02
GO:0010646	regulation of cell communication	181	783	3362	17583	1.21	0.27	1.9E-03	4.9E-02
GO:0099111	microtubule-based transport	18	783	204	17583	1.98	0.99	2.0E-03	4.9E-02
GO:0097193	intrinsic apoptotic signaling pathway	15	783	159	17583	2.12	1.08	2.0E-03	4.9E-02
GO:0008380	RNA splicing	28	783	366	17583	1.72	0.78	2.0E-03	4.9E-02
GO:1901700	response to oxygen-containing compound	91	783	1538	17583	1.33	0.41	2.1E-03	5.1E-02
GO:0043065	positive regulation of apoptotic process	35	783	488	17583	1.61	0.69	2.2E-03	5.3E-02
GO:0060325	face morphogenesis	5	783	31	17583	3.62	1.86	2.2E-03	5.3E-02
GO:0031057	negative regulation of histone modification	5	783	31	17583	3.62	1.86	2.2E-03	5.3E-02
GO:0002067	glandular epithelial cell differentiation	8	783	65	17583	2.76	1.47	2.2E-03	5.5E-02
GO:0019915	lipid storage	6	783	42	17583	3.21	1.68	2.3E-03	5.7E-02
GO:0003151	outflow tract morphogenesis	9	783	78	17583	2.59	1.37	2.4E-03	5.7E-02

GO:0048589	developmental growth	30	783	404	17583	1.67	0.74	2.4E-03	5.7E-02
GO:0040007	growth	30	783	404	17583	1.67	0.74	2.4E-03	5.7E-02
GO:0015031	protein transport	72	783	1176	17583	1.37	0.46	2.4E-03	5.8E-02
GO:0072006	nephron development	13	783	133	17583	2.19	1.13	2.4E-03	5.8E-02
GO:0009966	regulation of signal transduction	161	783	2966	17583	1.22	0.29	2.5E-03	6.0E-02
GO:0072078	nephron tubule morphogenesis	8	783	66	17583	2.72	1.44	2.5E-03	6.0E-02
GO:0048662	negative regulation of smooth muscle cell proliferation	7	783	54	17583	2.91	1.54	2.5E-03	6.0E-02
GO:0010970	transport along microtubule	15	783	163	17583	2.07	1.05	2.6E-03	6.1E-02
GO:0009791	post-embryonic development	10	783	92	17583	2.44	1.29	2.6E-03	6.1E-02
GO:0072524	pyridine-containing compound metabolic process	9	783	79	17583	2.56	1.36	2.6E-03	6.2E-02
GO:0009410	response to xenobiotic stimulus	31	783	424	17583	1.64	0.72	2.6E-03	6.2E-02
GO:0072001	renal system development	24	783	306	17583	1.76	0.82	2.7E-03	6.2E-02
GO:0003176	aortic valve development	6	783	43	17583	3.13	1.65	2.7E-03	6.2E-02
GO:0048663	neuron fate commitment	8	783	67	17583	2.68	1.42	2.8E-03	6.3E-02
GO:0045995	regulation of embryonic development	10	783	93	17583	2.41	1.27	2.8E-03	6.3E-02
GO:0048608	reproductive structure development	23	783	291	17583	1.77	0.83	2.8E-03	6.4E-02
GO:0044249	cellular biosynthetic process	134	783	2421	17583	1.24	0.31	2.9E-03	6.6E-02
GO:0035556	intracellular signal transduction	89	783	1517	17583	1.32	0.40	2.9E-03	6.6E-02
GO:0034641	cellular nitrogen compound metabolic process	178	783	3333	17583	1.20	0.26	3.0E-03	6.7E-02
GO:0045862	positive regulation of proteolysis	27	783	359	17583	1.69	0.76	3.0E-03	6.7E-02
GO:0007548	sex differentiation	22	783	276	17583	1.79	0.84	3.0E-03	6.8E-02
GO:0048566	embryonic digestive tract development	5	783	33	17583	3.40	1.77	3.0E-03	6.8E-02
GO:1903321	negative regulation of protein modification by small protein conj	10	783	94	17583	2.39	1.26	3.0E-03	6.8E-02
GO:0060173	limb development	16	783	181	17583	1.99	0.99	3.0E-03	6.8E-02
GO:0048736	appendage development	16	783	181	17583	1.99	0.99	3.0E-03	6.8E-02
GO:0010171	body morphogenesis	6	783	44	17583	3.06	1.61	3.1E-03	6.8E-02
GO:0072088	nephron epithelium morphogenesis	8	783	68	17583	2.64	1.40	3.1E-03	6.8E-02
GO:0070727	cellular macromolecule localization	108	783	1898	17583	1.28	0.35	3.1E-03	6.8E-02
GO:0010332	response to gamma radiation	7	783	56	17583	2.81	1.49	3.2E-03	7.1E-02
GO:0043523	regulation of neuron apoptotic process	18	783	214	17583	1.89	0.92	3.4E-03	7.4E-02
GO:0051881	regulation of mitochondrial membrane potential	8	783	69	17583	2.60	1.38	3.4E-03	7.5E-02
GO:1901698	response to nitrogen compound	65	783	1058	17583	1.38	0.46	3.4E-03	7.6E-02

GO:0030900	forebrain development	29	783	397	17583	1.64	0.71	3.4E-03	7.6E-02
GO:0051235	maintenance of location	15	783	168	17583	2.00	1.00	3.5E-03	7.6E-02
GO:0022618	ribonucleoprotein complex assembly	17	783	199	17583	1.92	0.94	3.5E-03	7.7E-02
GO:0051641	cellular localization	144	783	2639	17583	1.23	0.29	3.5E-03	7.7E-02
GO:0048701	embryonic cranial skeleton morphogenesis	6	783	45	17583	2.99	1.58	3.5E-03	7.7E-02
GO:0001658	branching involved in ureteric bud morphogenesis	6	783	45	17583	2.99	1.58	3.5E-03	7.7E-02
GO:0001822	kidney development	23	783	296	17583	1.74	0.80	3.5E-03	7.7E-02
GO:0030154	cell differentiation	188	783	3556	17583	1.19	0.25	3.5E-03	7.7E-02
GO:2000112	regulation of cellular macromolecule biosynthetic process	34	783	485	17583	1.57	0.65	3.5E-03	7.7E-02
GO:0044271	cellular nitrogen compound biosynthetic process	91	783	1567	17583	1.30	0.38	3.6E-03	7.7E-02
GO:0014743	regulation of muscle hypertrophy	7	783	57	17583	2.76	1.46	3.6E-03	7.7E-02
GO:0048869	cellular developmental process	189	783	3579	17583	1.19	0.25	3.6E-03	7.7E-02
GO:0055067	monovalent inorganic cation homeostasis	14	783	154	17583	2.04	1.03	3.7E-03	7.9E-02
GO:0035239	tube morphogenesis	44	783	667	17583	1.48	0.57	3.7E-03	7.9E-02
GO:0031397	negative regulation of protein ubiquitination	9	783	83	17583	2.43	1.28	3.7E-03	8.0E-02
GO:0009968	negative regulation of signal transduction	74	783	1236	17583	1.34	0.43	3.7E-03	8.0E-02
GO:0061333	renal tubule morphogenesis	8	783	70	17583	2.57	1.36	3.8E-03	8.0E-02
GO:0001503	ossification	22	783	281	17583	1.76	0.81	3.8E-03	8.0E-02
GO:0010243	response to organonitrogen compound	60	783	967	17583	1.39	0.48	3.8E-03	8.0E-02
GO:0014020	primary neural tube formation	10	783	97	17583	2.32	1.21	3.9E-03	8.2E-02
GO:0008104	protein localization	107	783	1892	17583	1.27	0.34	3.9E-03	8.3E-02
GO:0048660	regulation of smooth muscle cell proliferation	13	783	140	17583	2.09	1.06	3.9E-03	8.3E-02
GO:0051094	positive regulation of developmental process	78	783	1317	17583	1.33	0.41	4.0E-03	8.3E-02
GO:0021575	hindbrain morphogenesis	6	783	46	17583	2.93	1.55	4.0E-03	8.3E-02
GO:0060425	lung morphogenesis	6	783	46	17583	2.93	1.55	4.0E-03	8.3E-02
GO:1904036	negative regulation of epithelial cell apoptotic process	7	783	58	17583	2.71	1.44	4.0E-03	8.3E-02
GO:0010941	regulation of cell death	94	783	1634	17583	1.29	0.37	4.0E-03	8.3E-02
GO:0072028	nephron morphogenesis	8	783	71	17583	2.53	1.34	4.1E-03	8.3E-02
GO:0044085	cellular component biogenesis	144	783	2651	17583	1.22	0.29	4.1E-03	8.3E-02
GO:0098659	inorganic cation import across plasma membrane	10	783	98	17583	2.29	1.20	4.2E-03	8.4E-02
GO:0030048	actin filament-based movement	10	783	98	17583	2.29	1.20	4.2E-03	8.4E-02
GO:0099587	inorganic ion import across plasma membrane	10	783	98	17583	2.29	1.20	4.2E-03	8.4E-02

GO:0007389	pattern specification process	32	783	455	17583	1.58	0.66	4.2E-03	8.4E-02
GO:0051047	positive regulation of secretion	24	783	317	17583	1.70	0.77	4.2E-03	8.4E-02
GO:0051049	regulation of transport	99	783	1739	17583	1.28	0.35	4.4E-03	8.7E-02
GO:0035264	multicellular organism growth	9	783	85	17583	2.38	1.25	4.4E-03	8.7E-02
GO:1905314	semi-lunar valve development	6	783	47	17583	2.87	1.52	4.5E-03	8.8E-02
GO:0048538	thymus development	6	783	47	17583	2.87	1.52	4.5E-03	8.8E-02
GO:0000245	spliceosomal complex assembly	8	783	72	17583	2.50	1.32	4.5E-03	8.8E-02
GO:0001933	negative regulation of protein phosphorylation	24	783	319	17583	1.69	0.76	4.6E-03	8.8E-02
GO:0021696	cerebellar cortex morphogenesis	5	783	36	17583	3.12	1.64	4.7E-03	8.8E-02
GO:0035850	epithelial cell differentiation involved in kidney development	5	783	36	17583	3.12	1.64	4.7E-03	8.8E-02
GO:1902742	apoptotic process involved in development	5	783	36	17583	3.12	1.64	4.7E-03	8.8E-02
GO:0120036	plasma membrane bounded cell projection organization	67	783	1112	17583	1.35	0.44	4.8E-03	8.8E-02
GO:0051348	negative regulation of transferase activity	21	783	270	17583	1.75	0.80	4.8E-03	8.8E-02
GO:0043170	macromolecule metabolic process	291	783	5792	17583	1.13	0.17	4.8E-03	8.8E-02
GO:0061326	renal tubule development	9	783	86	17583	2.35	1.23	4.8E-03	8.8E-02
GO:0003179	heart valve morphogenesis	7	783	60	17583	2.62	1.39	4.9E-03	8.8E-02
GO:0045665	negative regulation of neuron differentiation	8	783	73	17583	2.46	1.30	5.0E-03	8.8E-02
GO:0050714	positive regulation of protein secretion	13	783	144	17583	2.03	1.02	5.0E-03	8.8E-02
GO:1901976	regulation of cell cycle checkpoint	6	783	48	17583	2.81	1.49	5.1E-03	8.8E-02
GO:0048483	autonomic nervous system development	6	783	48	17583	2.81	1.49	5.1E-03	8.8E-02
GO:0032879	regulation of localization	115	783	2073	17583	1.25	0.32	5.2E-03	8.8E-02
GO:0006469	negative regulation of protein kinase activity	17	783	207	17583	1.84	0.88	5.3E-03	8.8E-02
GO:1903532	positive regulation of secretion by cell	22	783	289	17583	1.71	0.77	5.3E-03	8.8E-02
GO:0042391	regulation of membrane potential	30	783	427	17583	1.58	0.66	5.3E-03	8.8E-02
GO:0019637	organophosphate metabolic process	57	783	926	17583	1.38	0.47	5.4E-03	8.8E-02
GO:0000377	RNA splicing, via transesterification reactions with bulged adenc	19	783	240	17583	1.78	0.83	5.4E-03	8.8E-02
GO:0000398	mRNA splicing, via spliceosome	19	783	240	17583	1.78	0.83	5.4E-03	8.8E-02
GO:0098930	axonal transport	7	783	61	17583	2.58	1.37	5.4E-03	8.8E-02
GO:0048536	spleen development	5	783	37	17583	3.03	1.60	5.5E-03	8.8E-02
GO:0031076	embryonic camera-type eye development	5	783	37	17583	3.03	1.60	5.5E-03	8.8E-02
GO:0051640	organelle localization	35	783	517	17583	1.52	0.60	5.5E-03	8.8E-02
GO:1901564	organonitrogen compound metabolic process	253	783	4982	17583	1.14	0.19	5.5E-03	8.8E-02

GO:0033036	macromolecule localization	127	783	2323	17583	1.23	0.30	5.6E-03	8.8E-02
GO:0007224	smoothened signaling pathway	9	783	88	17583	2.30	1.20	5.7E-03	8.8E-02
GO:0048546	digestive tract morphogenesis	6	783	49	17583	2.75	1.46	5.7E-03	8.8E-02
GO:0010035	response to inorganic substance	36	783	537	17583	1.51	0.59	5.8E-03	8.9E-02
GO:0031396	regulation of protein ubiquitination	17	783	209	17583	1.83	0.87	5.8E-03	8.9E-02
GO:0006397	mRNA processing	31	783	448	17583	1.55	0.64	5.9E-03	8.9E-02
GO:0006996	organelle organization	160	783	3011	17583	1.19	0.25	6.0E-03	8.9E-02
GO:0007030	Golgi organization	13	783	147	17583	1.99	0.99	6.0E-03	8.9E-02
GO:0010965	regulation of mitotic sister chromatid separation	7	783	62	17583	2.54	1.34	6.0E-03	8.9E-02
GO:0042542	response to hydrogen peroxide	10	783	103	17583	2.18	1.12	6.1E-03	9.0E-02
GO:0071704	organic substance metabolic process	369	783	7534	17583	1.10	0.14	6.1E-03	9.0E-02
GO:1901379	regulation of potassium ion transmembrane transport	9	783	89	17583	2.27	1.18	6.1E-03	9.0E-02
GO:0007029	endoplasmic reticulum organization	9	783	89	17583	2.27	1.18	6.1E-03	9.0E-02
GO:0086002	cardiac muscle cell action potential involved in contraction	5	783	38	17583	2.95	1.56	6.2E-03	9.1E-02
GO:0048667	cell morphogenesis involved in neuron differentiation	30	783	433	17583	1.56	0.64	6.5E-03	9.5E-02
GO:0000375	RNA splicing, via transesterification reactions	19	783	244	17583	1.75	0.81	6.5E-03	9.5E-02
GO:0072009	nephron epithelium development	10	783	104	17583	2.16	1.11	6.6E-03	9.6E-02
GO:0050793	regulation of developmental process	133	783	2459	17583	1.21	0.28	6.7E-03	9.7E-02
GO:0051248	negative regulation of protein metabolic process	60	783	994	17583	1.36	0.44	6.8E-03	9.9E-02
GO:0072073	kidney epithelium development	12	783	134	17583	2.01	1.01	6.8E-03	9.9E-02
GO:0045598	regulation of fat cell differentiation	12	783	134	17583	2.01	1.01	6.8E-03	9.9E-02
GO:0048568	embryonic organ development	31	783	453	17583	1.54	0.62	7.0E-03	1.0E-01
GO:1901652	response to peptide	31	783	453	17583	1.54	0.62	7.0E-03	1.0E-01
GO:0002009	morphogenesis of an epithelium	31	783	453	17583	1.54	0.62	7.0E-03	1.0E-01
GO:0023057	negative regulation of signaling	77	783	1328	17583	1.30	0.38	7.0E-03	1.0E-01
GO:0010648	negative regulation of cell communication	77	783	1328	17583	1.30	0.38	7.0E-03	1.0E-01
GO:0001841	neural tube formation	10	783	105	17583	2.14	1.10	7.1E-03	1.0E-01
GO:0030324	lung development	15	783	181	17583	1.86	0.90	7.1E-03	1.0E-01
GO:1905818	regulation of chromosome separation	8	783	77	17583	2.33	1.22	7.1E-03	1.0E-01
GO:1901983	regulation of protein acetylation	8	783	77	17583	2.33	1.22	7.1E-03	1.0E-01
GO:0051646	mitochondrion localization	6	783	51	17583	2.64	1.40	7.1E-03	1.0E-01
GO:0070286	axonemal dynein complex assembly	5	783	39	17583	2.88	1.53	7.1E-03	1.0E-01

GO:0000387	spliceosomal snRNP assembly	5	783	39	17583	2.88	1.53	7.1E-03	1.0E-01
GO:0001843	neural tube closure	9	783	91	17583	2.22	1.15	7.2E-03	1.0E-01
GO:0051239	regulation of multicellular organismal process	146	783	2734	17583	1.20	0.26	7.2E-03	1.0E-01
GO:0051234	establishment of localization	204	783	3956	17583	1.16	0.21	7.2E-03	1.0E-01
GO:0009749	response to glucose	12	783	135	17583	2.00	1.00	7.3E-03	1.0E-01
GO:0048638	regulation of developmental growth	23	783	314	17583	1.64	0.72	7.3E-03	1.0E-01
GO:0045936	negative regulation of phosphate metabolic process	29	783	419	17583	1.55	0.64	7.3E-03	1.0E-01
GO:0017157	regulation of exocytosis	16	783	198	17583	1.81	0.86	7.4E-03	1.1E-01
GO:0030856	regulation of epithelial cell differentiation	13	783	151	17583	1.93	0.95	7.6E-03	1.1E-01
GO:0010563	negative regulation of phosphorus metabolic process	29	783	420	17583	1.55	0.63	7.6E-03	1.1E-01
GO:0060606	tube closure	9	783	92	17583	2.20	1.14	7.7E-03	1.1E-01
GO:0021695	cerebellar cortex development	6	783	52	17583	2.59	1.37	7.9E-03	1.1E-01
GO:0030030	cell projection organization	68	783	1158	17583	1.32	0.40	8.0E-03	1.1E-01
GO:0042551	neuron maturation	5	783	40	17583	2.81	1.49	8.1E-03	1.1E-01
GO:0002520	immune system development	14	783	168	17583	1.87	0.90	8.2E-03	1.1E-01
GO:1902806	regulation of cell cycle G1/S phase transition	15	783	184	17583	1.83	0.87	8.2E-03	1.1E-01
GO:0046907	intracellular transport	78	783	1358	17583	1.29	0.37	8.4E-03	1.1E-01
GO:0030323	respiratory tube development	15	783	185	17583	1.82	0.86	8.6E-03	1.2E-01
GO:1903052	positive regulation of proteolysis involved in protein catabolic pr	12	783	138	17583	1.95	0.97	8.7E-03	1.2E-01
GO:0071300	cellular response to retinoic acid	7	783	66	17583	2.38	1.25	8.7E-03	1.2E-01
GO:0001541	ovarian follicle development	6	783	53	17583	2.54	1.35	8.8E-03	1.2E-01
GO:0050886	endocrine process	6	783	53	17583	2.54	1.35	8.8E-03	1.2E-01
GO:1903320	regulation of protein modification by small protein conjugation o	19	783	251	17583	1.70	0.77	8.8E-03	1.2E-01
GO:0071705	nitrogen compound transport	89	783	1581	17583	1.26	0.34	8.9E-03	1.2E-01
GO:0009058	biosynthetic process	138	783	2584	17583	1.20	0.26	8.9E-03	1.2E-01
GO:0030902	hindbrain development	13	783	154	17583	1.90	0.92	8.9E-03	1.2E-01
GO:0006139	nucleobase-containing compound metabolic process	148	783	2793	17583	1.19	0.25	9.0E-03	1.2E-01
GO:0034248	regulation of amide metabolic process	31	783	462	17583	1.51	0.59	9.2E-03	1.2E-01
GO:2000756	regulation of peptidyl-lysine acetylation	7	783	67	17583	2.35	1.23	9.6E-03	1.2E-01
GO:0010256	endomembrane system organization	36	783	555	17583	1.46	0.54	9.6E-03	1.2E-01
GO:0007507	heart development	36	783	555	17583	1.46	0.54	9.6E-03	1.2E-01
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	9	783	95	17583	2.13	1.09	9.6E-03	1.2E-01

GO:2000179	positive regulation of neural precursor cell proliferation	6	783	54	17583	2.50	1.32	9.7E-03	1.2E-01
GO:0010611	regulation of cardiac muscle hypertrophy	6	783	54	17583	2.50	1.32	9.7E-03	1.2E-01
GO:0008584	male gonad development	12	783	140	17583	1.92	0.94	9.7E-03	1.2E-01
GO:0009746	response to hexose	12	783	140	17583	1.92	0.94	9.7E-03	1.2E-01
GO:0072080	nephron tubule development	8	783	81	17583	2.22	1.15	9.8E-03	1.2E-01
GO:0001838	embryonic epithelial tube formation	11	783	125	17583	1.98	0.98	9.9E-03	1.2E-01
GO:0048639	positive regulation of developmental growth	13	783	156	17583	1.87	0.90	1.0E-02	1.2E-01
GO:0019674	NAD metabolic process	5	783	42	17583	2.67	1.42	1.0E-02	1.2E-01
GO:0086091	regulation of heart rate by cardiac conduction	5	783	42	17583	2.67	1.42	1.0E-02	1.2E-01
GO:0046546	development of primary male sexual characteristics	12	783	141	17583	1.91	0.93	1.0E-02	1.2E-01
GO:2000377	regulation of reactive oxygen species metabolic process	12	783	141	17583	1.91	0.93	1.0E-02	1.2E-01
GO:0035967	cellular response to topologically incorrect protein	9	783	96	17583	2.11	1.07	1.0E-02	1.2E-01
GO:0021537	telencephalon development	20	783	272	17583	1.65	0.72	1.0E-02	1.2E-01
GO:0034763	negative regulation of transmembrane transport	11	783	126	17583	1.96	0.97	1.1E-02	1.2E-01
GO:0009719	response to endogenous stimulus	81	783	1431	17583	1.27	0.35	1.1E-02	1.2E-01
GO:0045921	positive regulation of exocytosis	8	783	82	17583	2.19	1.13	1.1E-02	1.2E-01
GO:1901576	organic substance biosynthetic process	134	783	2515	17583	1.20	0.26	1.1E-02	1.2E-01
GO:0048585	negative regulation of response to stimulus	89	783	1593	17583	1.25	0.33	1.1E-02	1.2E-01
GO:0051046	regulation of secretion	39	783	615	17583	1.42	0.51	1.1E-02	1.2E-01
GO:0060541	respiratory system development	16	783	206	17583	1.74	0.80	1.1E-02	1.2E-01
GO:0061448	connective tissue development	17	783	223	17583	1.71	0.78	1.1E-02	1.2E-01
GO:0048592	eye morphogenesis	13	783	158	17583	1.85	0.89	1.1E-02	1.2E-01
GO:0031399	regulation of protein modification process	84	783	1495	17583	1.26	0.34	1.1E-02	1.2E-01
GO:0019538	protein metabolic process	199	783	3891	17583	1.15	0.20	1.1E-02	1.2E-01
GO:0018107	peptidyl-threonine phosphorylation	7	783	69	17583	2.28	1.19	1.1E-02	1.2E-01
GO:0070848	response to growth factor	33	783	506	17583	1.46	0.55	1.1E-02	1.2E-01
GO:0032024	positive regulation of insulin secretion	8	783	83	17583	2.16	1.11	1.1E-02	1.2E-01
GO:0021587	cerebellum morphogenesis	5	783	43	17583	2.61	1.38	1.1E-02	1.2E-01
GO:1901381	positive regulation of potassium ion transmembrane transport	5	783	43	17583	2.61	1.38	1.1E-02	1.2E-01
GO:0007409	axonogenesis	25	783	362	17583	1.55	0.63	1.2E-02	1.3E-01
GO:0021953	central nervous system neuron differentiation	14	783	175	17583	1.80	0.85	1.2E-02	1.3E-01
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	14	783	175	17583	1.80	0.85	1.2E-02	1.3E-01

GO:2000045	regulation of G1/S transition of mitotic cell cycle	13	783	159	17583	1.84	0.88	1.2E-02	1.3E-01
GO:0072132	mesenchyme morphogenesis	6	783	56	17583	2.41	1.27	1.2E-02	1.3E-01
GO:0001755	neural crest cell migration	6	783	56	17583	2.41	1.27	1.2E-02	1.3E-01
GO:0033047	regulation of mitotic sister chromatid segregation	6	783	56	17583	2.41	1.27	1.2E-02	1.3E-01
GO:0030029	actin filament-based process	38	783	600	17583	1.42	0.51	1.2E-02	1.3E-01
GO:0042326	negative regulation of phosphorylation	25	783	363	17583	1.55	0.63	1.2E-02	1.3E-01
GO:0043066	negative regulation of apoptotic process	53	783	886	17583	1.34	0.43	1.2E-02	1.3E-01
GO:2000060	positive regulation of ubiquitin-dependent protein catabolic proc	10	783	113	17583	1.99	0.99	1.2E-02	1.3E-01
GO:0051649	establishment of localization in cell	97	783	1764	17583	1.23	0.30	1.2E-02	1.3E-01
GO:0021915	neural tube development	13	783	160	17583	1.82	0.87	1.2E-02	1.3E-01
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	7	783	70	17583	2.25	1.17	1.2E-02	1.3E-01
GO:0048729	tissue morphogenesis	36	783	565	17583	1.43	0.52	1.3E-02	1.4E-01
GO:0048706	embryonic skeletal system development	11	783	129	17583	1.91	0.94	1.3E-02	1.4E-01
GO:0045664	regulation of neuron differentiation	15	783	193	17583	1.75	0.80	1.3E-02	1.4E-01
GO:0022037	metencephalon development	10	783	114	17583	1.97	0.98	1.3E-02	1.4E-01
GO:0086003	cardiac muscle cell contraction	5	783	44	17583	2.55	1.35	1.3E-02	1.4E-01
GO:0051128	regulation of cellular component organization	127	783	2384	17583	1.20	0.26	1.3E-02	1.4E-01
GO:0048732	gland development	28	783	419	17583	1.50	0.59	1.3E-02	1.4E-01
GO:0043388	positive regulation of DNA binding	6	783	57	17583	2.36	1.24	1.3E-02	1.4E-01
GO:0050433	regulation of catecholamine secretion	6	783	57	17583	2.36	1.24	1.3E-02	1.4E-01
GO:0030282	bone mineralization	6	783	57	17583	2.36	1.24	1.3E-02	1.4E-01
GO:0048666	neuron development	50	783	832	17583	1.35	0.43	1.3E-02	1.4E-01
GO:2001234	negative regulation of apoptotic signaling pathway	17	783	227	17583	1.68	0.75	1.3E-02	1.4E-01
GO:0007269	neurotransmitter secretion	8	783	85	17583	2.11	1.08	1.3E-02	1.4E-01
GO:0099643	signal release from synapse	8	783	85	17583	2.11	1.08	1.3E-02	1.4E-01
GO:0033365	protein localization to organelle	43	783	699	17583	1.38	0.47	1.3E-02	1.4E-01
GO:0048593	camera-type eye morphogenesis	11	783	130	17583	1.90	0.93	1.3E-02	1.4E-01
GO:1903305	regulation of regulated secretory pathway	11	783	130	17583	1.90	0.93	1.3E-02	1.4E-01
GO:0006810	transport	194	783	3800	17583	1.15	0.20	1.3E-02	1.4E-01
GO:0031623	receptor internalization	7	783	71	17583	2.21	1.15	1.3E-02	1.4E-01
GO:0003143	embryonic heart tube morphogenesis	7	783	71	17583	2.21	1.15	1.3E-02	1.4E-01
GO:2000036	regulation of stem cell population maintenance	7	783	71	17583	2.21	1.15	1.3E-02	1.4E-01

GO:0071453	cellular response to oxygen levels	12	783	146	17583	1.85	0.88	1.4E-02	1.4E-01
GO:0016331	morphogenesis of embryonic epithelium	12	783	146	17583	1.85	0.88	1.4E-02	1.4E-01
GO:0030307	positive regulation of cell growth	13	783	162	17583	1.80	0.85	1.4E-02	1.4E-01
GO:0010038	response to metal ion	25	783	367	17583	1.53	0.61	1.4E-02	1.4E-01
GO:0045597	positive regulation of cell differentiation	52	783	873	17583	1.34	0.42	1.4E-02	1.4E-01
GO:0006417	regulation of translation	27	783	403	17583	1.50	0.59	1.4E-02	1.4E-01
GO:0016043	cellular component organization	273	783	5509	17583	1.11	0.15	1.4E-02	1.4E-01
GO:1901701	cellular response to oxygen-containing compound	61	783	1050	17583	1.30	0.38	1.4E-02	1.4E-01
GO:0000904	cell morphogenesis involved in differentiation	35	783	551	17583	1.43	0.51	1.4E-02	1.4E-01
GO:0090497	mesenchymal cell migration	6	783	58	17583	2.32	1.22	1.4E-02	1.4E-01
GO:0035065	regulation of histone acetylation	6	783	58	17583	2.32	1.22	1.4E-02	1.4E-01
GO:0008089	anterograde axonal transport	5	783	45	17583	2.50	1.32	1.4E-02	1.4E-01
GO:2000378	negative regulation of reactive oxygen species metabolic process	5	783	45	17583	2.50	1.32	1.4E-02	1.4E-01
GO:0046661	male sex differentiation	13	783	163	17583	1.79	0.84	1.4E-02	1.4E-01
GO:0007219	Notch signaling pathway	10	783	116	17583	1.94	0.95	1.4E-02	1.4E-01
GO:1904888	cranial skeletal system development	7	783	72	17583	2.18	1.13	1.4E-02	1.4E-01
GO:0043434	response to peptide hormone	25	783	369	17583	1.52	0.61	1.4E-02	1.4E-01
GO:0001508	action potential	9	783	101	17583	2.00	1.00	1.4E-02	1.4E-01
GO:0006412	translation	25	783	370	17583	1.52	0.60	1.5E-02	1.4E-01
GO:0034284	response to monosaccharide	12	783	148	17583	1.82	0.86	1.5E-02	1.4E-01
GO:0071277	cellular response to calcium ion	8	783	87	17583	2.06	1.05	1.5E-02	1.4E-01
GO:1901800	positive regulation of proteasomal protein catabolic process	10	783	117	17583	1.92	0.94	1.5E-02	1.4E-01
GO:0009117	nucleotide metabolic process	33	783	517	17583	1.43	0.52	1.5E-02	1.4E-01
GO:0033673	negative regulation of kinase activity	17	783	231	17583	1.65	0.72	1.5E-02	1.4E-01
GO:0046483	heterocycle metabolic process	154	783	2966	17583	1.17	0.22	1.6E-02	1.4E-01
GO:0003170	heart valve development	7	783	73	17583	2.15	1.11	1.6E-02	1.4E-01
GO:0007589	body fluid secretion	7	783	73	17583	2.15	1.11	1.6E-02	1.4E-01
GO:0072175	epithelial tube formation	11	783	133	17583	1.86	0.89	1.6E-02	1.4E-01
GO:0017156	calcium-ion regulated exocytosis	5	783	46	17583	2.44	1.29	1.6E-02	1.4E-01
GO:0051784	negative regulation of nuclear division	5	783	46	17583	2.44	1.29	1.6E-02	1.4E-01
GO:0042789	mRNA transcription by RNA polymerase II	5	783	46	17583	2.44	1.29	1.6E-02	1.4E-01
GO:1901861	regulation of muscle tissue development	5	783	46	17583	2.44	1.29	1.6E-02	1.4E-01

GO:0009888	tissue development	94	783	1720	17583	1.23	0.30	1.6E-02	1.4E-01
GO:0030004	cellular monovalent inorganic cation homeostasis	10	783	118	17583	1.90	0.93	1.6E-02	1.4E-01
GO:0043009	chordate embryonic development	40	783	651	17583	1.38	0.46	1.6E-02	1.4E-01
GO:0021675	nerve development	8	783	88	17583	2.04	1.03	1.6E-02	1.4E-01
GO:0043412	macromolecule modification	149	783	2865	17583	1.17	0.22	1.6E-02	1.4E-01
GO:0006725	cellular aromatic compound metabolic process	156	783	3013	17583	1.16	0.22	1.6E-02	1.4E-01
GO:0000302	response to reactive oxygen species	13	783	166	17583	1.76	0.81	1.7E-02	1.4E-01
GO:0043271	negative regulation of ion transport	12	783	150	17583	1.80	0.85	1.7E-02	1.4E-01
GO:0090398	cellular senescence	6	783	60	17583	2.25	1.17	1.7E-02	1.4E-01
GO:0021545	cranial nerve development	6	783	60	17583	2.25	1.17	1.7E-02	1.4E-01
GO:1903530	regulation of secretion by cell	35	783	558	17583	1.41	0.49	1.7E-02	1.4E-01
GO:0010822	positive regulation of mitochondrion organization	7	783	74	17583	2.12	1.09	1.7E-02	1.4E-01
GO:0044782	cilium organization	24	783	356	17583	1.51	0.60	1.7E-02	1.4E-01
GO:0051668	localization within membrane	34	783	540	17583	1.41	0.50	1.7E-02	1.4E-01
GO:0007155	cell adhesion	56	783	963	17583	1.31	0.38	1.7E-02	1.4E-01
GO:0034612	response to tumor necrosis factor	15	783	200	17583	1.68	0.75	1.7E-02	1.4E-01
GO:1904951	positive regulation of establishment of protein localization	22	783	321	17583	1.54	0.62	1.7E-02	1.4E-01
GO:1903307	positive regulation of regulated secretory pathway	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0046173	polyol biosynthetic process	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0042073	intraciliary transport	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0048286	lung alveolus development	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0045668	negative regulation of osteoblast differentiation	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0090199	regulation of release of cytochrome c from mitochondria	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:1902459	positive regulation of stem cell population maintenance	5	783	47	17583	2.39	1.26	1.7E-02	1.4E-01
GO:0060993	kidney morphogenesis	8	783	89	17583	2.02	1.01	1.7E-02	1.4E-01
GO:0031503	protein-containing complex localization	12	783	151	17583	1.78	0.84	1.7E-02	1.4E-01
GO:0043266	regulation of potassium ion transport	9	783	104	17583	1.94	0.96	1.7E-02	1.4E-01
GO:1901796	regulation of signal transduction by p53 class mediator	9	783	104	17583	1.94	0.96	1.7E-02	1.4E-01
GO:0019751	polyol metabolic process	9	783	104	17583	1.94	0.96	1.7E-02	1.4E-01
GO:0060429	epithelium development	61	783	1063	17583	1.29	0.37	1.8E-02	1.4E-01
GO:0048646	anatomical structure formation involved in morphogenesis	55	783	945	17583	1.31	0.39	1.8E-02	1.4E-01

GO:0010720	positive regulation of cell development	30	783	467	17583	1.44	0.53	1.8E-02	1.4E-01
GO:0065008	regulation of biological quality	145	783	2788	17583	1.17	0.22	1.8E-02	1.4E-01
GO:0007049	cell cycle	72	783	1283	17583	1.26	0.33	1.8E-02	1.4E-01
GO:0043933	protein-containing complex organization	78	783	1404	17583	1.25	0.32	1.8E-02	1.4E-01
GO:0072359	circulatory system development	53	783	907	17583	1.31	0.39	1.8E-02	1.4E-01
GO:0006119	oxidative phosphorylation	10	783	120	17583	1.87	0.90	1.8E-02	1.4E-01
GO:1901360	organic cyclic compound metabolic process	167	783	3255	17583	1.15	0.20	1.8E-02	1.4E-01
GO:0032990	cell part morphogenesis	32	783	505	17583	1.42	0.51	1.8E-02	1.4E-01
GO:0051222	positive regulation of protein transport	21	783	305	17583	1.55	0.63	1.8E-02	1.4E-01
GO:0016079	synaptic vesicle exocytosis	6	783	61	17583	2.21	1.14	1.8E-02	1.4E-01
GO:0031331	positive regulation of cellular catabolic process	27	783	413	17583	1.47	0.55	1.8E-02	1.4E-01
GO:0090304	nucleic acid metabolic process	119	783	2247	17583	1.19	0.25	1.8E-02	1.4E-01
GO:0032869	cellular response to insulin stimulus	12	783	152	17583	1.77	0.83	1.8E-02	1.4E-01
GO:0043069	negative regulation of programmed cell death	53	783	908	17583	1.31	0.39	1.8E-02	1.4E-01
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	14	783	185	17583	1.70	0.76	1.9E-02	1.4E-01
GO:0071495	cellular response to endogenous stimulus	66	783	1166	17583	1.27	0.35	1.9E-02	1.4E-01
GO:0071840	cellular component organization or biogenesis	281	783	5719	17583	1.10	0.14	1.9E-02	1.4E-01
GO:0006753	nucleoside phosphate metabolic process	33	783	525	17583	1.41	0.50	1.9E-02	1.4E-01
GO:0072657	protein localization to membrane	29	783	451	17583	1.44	0.53	1.9E-02	1.4E-01
GO:0043524	negative regulation of neuron apoptotic process	12	783	153	17583	1.76	0.82	1.9E-02	1.4E-01
GO:0034620	cellular response to unfolded protein	7	783	76	17583	2.07	1.05	2.0E-02	1.4E-01
GO:0034502	protein localization to chromosome	7	783	76	17583	2.07	1.05	2.0E-02	1.4E-01
GO:0051301	cell division	32	783	508	17583	1.41	0.50	2.0E-02	1.4E-01
GO:0051090	regulation of DNA-binding transcription factor activity	28	783	434	17583	1.45	0.53	2.0E-02	1.4E-01
GO:0009653	anatomical structure morphogenesis	118	783	2232	17583	1.19	0.25	2.0E-02	1.4E-01
GO:0008285	negative regulation of cell population proliferation	42	783	698	17583	1.35	0.43	2.0E-02	1.4E-01
GO:0051205	protein insertion into membrane	6	783	62	17583	2.17	1.12	2.0E-02	1.4E-01
GO:0032663	regulation of interleukin-2 production	6	783	62	17583	2.17	1.12	2.0E-02	1.4E-01
GO:0051240	positive regulation of multicellular organismal process	82	783	1492	17583	1.23	0.30	2.0E-02	1.4E-01
GO:0060021	roof of mouth development	8	783	91	17583	1.97	0.98	2.0E-02	1.4E-01
GO:0001654	eye development	25	783	380	17583	1.48	0.56	2.0E-02	1.4E-01
GO:0046434	organophosphate catabolic process	12	783	154	17583	1.75	0.81	2.0E-02	1.4E-01

GO:0055082	cellular chemical homeostasis	34	783	547	17583	1.40	0.48	2.0E-02	1.4E-01
GO:0046887	positive regulation of hormone secretion	11	783	138	17583	1.79	0.84	2.0E-02	1.4E-01
GO:0007346	regulation of mitotic cell cycle	31	783	491	17583	1.42	0.50	2.0E-02	1.4E-01
GO:0019438	aromatic compound biosynthetic process	61	783	1072	17583	1.28	0.35	2.1E-02	1.4E-01
GO:1901653	cellular response to peptide	21	783	309	17583	1.53	0.61	2.1E-02	1.4E-01
GO:0033045	regulation of sister chromatid segregation	9	783	107	17583	1.89	0.92	2.1E-02	1.4E-01
GO:0032006	regulation of TOR signaling	9	783	107	17583	1.89	0.92	2.1E-02	1.4E-01
GO:1901990	regulation of mitotic cell cycle phase transition	22	783	327	17583	1.51	0.60	2.1E-02	1.4E-01
GO:0048599	oocyte development	5	783	49	17583	2.29	1.20	2.1E-02	1.4E-01
GO:0035094	response to nicotine	5	783	49	17583	2.29	1.20	2.1E-02	1.4E-01
GO:2000026	regulation of multicellular organismal development	76	783	1374	17583	1.24	0.31	2.1E-02	1.4E-01
GO:0034249	negative regulation of amide metabolic process	14	783	188	17583	1.67	0.74	2.1E-02	1.4E-01
GO:0006396	RNA processing	51	783	876	17583	1.31	0.39	2.1E-02	1.4E-01
GO:0030071	regulation of mitotic metaphase/anaphase transition	8	783	92	17583	1.95	0.97	2.1E-02	1.4E-01
GO:0065003	protein-containing complex assembly	70	783	1254	17583	1.25	0.33	2.1E-02	1.4E-01
GO:0071456	cellular response to hypoxia	10	783	123	17583	1.83	0.87	2.1E-02	1.4E-01
GO:0009894	regulation of catabolic process	57	783	995	17583	1.29	0.36	2.1E-02	1.4E-01
GO:0032507	maintenance of protein location in cell	6	783	63	17583	2.14	1.10	2.2E-02	1.4E-01
GO:1990778	protein localization to cell periphery	17	783	240	17583	1.59	0.67	2.2E-02	1.4E-01
GO:0061564	axon development	26	783	401	17583	1.46	0.54	2.2E-02	1.4E-01
GO:0048812	neuron projection morphogenesis	30	783	475	17583	1.42	0.50	2.2E-02	1.4E-01
GO:0071363	cellular response to growth factor stimulus	30	783	475	17583	1.42	0.50	2.2E-02	1.4E-01
GO:0048562	embryonic organ morphogenesis	20	783	293	17583	1.53	0.62	2.2E-02	1.4E-01
GO:1901566	organonitrogen compound biosynthetic process	73	783	1317	17583	1.24	0.32	2.2E-02	1.4E-01
GO:0050852	T cell receptor signaling pathway	9	783	108	17583	1.87	0.90	2.2E-02	1.4E-01
GO:0006644	phospholipid metabolic process	24	783	365	17583	1.48	0.56	2.2E-02	1.4E-01
GO:0023056	positive regulation of signaling	91	783	1684	17583	1.21	0.28	2.2E-02	1.4E-01
GO:0043269	regulation of ion transport	42	783	704	17583	1.34	0.42	2.2E-02	1.4E-01
GO:0022402	cell cycle process	52	783	899	17583	1.30	0.38	2.2E-02	1.4E-01
GO:1901568	fatty acid derivative metabolic process	7	783	78	17583	2.02	1.01	2.3E-02	1.4E-01
GO:1902807	negative regulation of cell cycle G1/S phase transition	7	783	78	17583	2.02	1.01	2.3E-02	1.4E-01
GO:0043502	regulation of muscle adaptation	7	783	78	17583	2.02	1.01	2.3E-02	1.4E-01

GO:0042773	ATP synthesis coupled electron transport	8	783	93	17583	1.93	0.95	2.3E-02	1.4E-01
GO:0042775	mitochondrial ATP synthesis coupled electron transport	8	783	93	17583	1.93	0.95	2.3E-02	1.4E-01
GO:0150063	visual system development	25	783	384	17583	1.46	0.55	2.3E-02	1.4E-01
GO:0043268	positive regulation of potassium ion transport	5	783	50	17583	2.25	1.17	2.3E-02	1.4E-01
GO:0030968	endoplasmic reticulum unfolded protein response	5	783	50	17583	2.25	1.17	2.3E-02	1.4E-01
GO:0002064	epithelial cell development	14	783	190	17583	1.65	0.73	2.3E-02	1.4E-01
GO:0042776	proton motive force-driven mitochondrial ATP synthesis	6	783	64	17583	2.11	1.07	2.3E-02	1.4E-01
GO:0030888	regulation of B cell proliferation	6	783	64	17583	2.11	1.07	2.3E-02	1.4E-01
GO:0032526	response to retinoic acid	9	783	109	17583	1.85	0.89	2.3E-02	1.4E-01
GO:0036211	protein modification process	137	783	2645	17583	1.16	0.22	2.4E-02	1.4E-01
GO:0048705	skeletal system morphogenesis	16	783	225	17583	1.60	0.68	2.4E-02	1.4E-01
GO:0009199	ribonucleoside triphosphate metabolic process	14	783	191	17583	1.65	0.72	2.4E-02	1.4E-01
GO:0006163	purine nucleotide metabolic process	29	783	460	17583	1.42	0.50	2.4E-02	1.4E-01
GO:0035304	regulation of protein dephosphorylation	8	783	94	17583	1.91	0.93	2.4E-02	1.4E-01
GO:0018210	peptidyl-threonine modification	7	783	79	17583	1.99	0.99	2.4E-02	1.4E-01
GO:0043604	amide biosynthetic process	32	783	517	17583	1.39	0.48	2.5E-02	1.4E-01
GO:0009743	response to carbohydrate	13	783	175	17583	1.67	0.74	2.5E-02	1.4E-01
GO:0032543	mitochondrial translation	9	783	110	17583	1.84	0.88	2.5E-02	1.4E-01
GO:0120039	plasma membrane bounded cell projection morphogenesis	30	783	480	17583	1.40	0.49	2.5E-02	1.4E-01
GO:0021515	cell differentiation in spinal cord	5	783	51	17583	2.20	1.14	2.5E-02	1.4E-01
GO:1902895	positive regulation of miRNA transcription	5	783	51	17583	2.20	1.14	2.5E-02	1.4E-01
GO:0009299	mRNA transcription	5	783	51	17583	2.20	1.14	2.5E-02	1.4E-01
GO:0001947	heart looping	6	783	65	17583	2.07	1.05	2.5E-02	1.4E-01
GO:0009790	embryo development	59	783	1044	17583	1.27	0.34	2.5E-02	1.4E-01
GO:0045595	regulation of cell differentiation	85	783	1570	17583	1.22	0.28	2.5E-02	1.4E-01
GO:0070925	organelle assembly	48	783	827	17583	1.30	0.38	2.5E-02	1.4E-01
GO:0046034	ATP metabolic process	12	783	159	17583	1.69	0.76	2.6E-02	1.4E-01
GO:0008585	female gonad development	8	783	95	17583	1.89	0.92	2.6E-02	1.4E-01
GO:0000723	telomere maintenance	8	783	95	17583	1.89	0.92	2.6E-02	1.4E-01
GO:0019882	antigen processing and presentation	8	783	95	17583	1.89	0.92	2.6E-02	1.4E-01
GO:0051247	positive regulation of protein metabolic process	79	783	1449	17583	1.22	0.29	2.6E-02	1.4E-01
GO:0006366	transcription by RNA polymerase II	23	783	352	17583	1.47	0.55	2.6E-02	1.4E-01

GO:0030162	regulation of proteolysis	42	783	711	17583	1.33	0.41	2.6E-02	1.4E-01
GO:0045333	cellular respiration	14	783	193	17583	1.63	0.70	2.6E-02	1.4E-01
GO:0006399	tRNA metabolic process	14	783	193	17583	1.63	0.70	2.6E-02	1.4E-01
GO:0010212	response to ionizing radiation	11	783	143	17583	1.73	0.79	2.6E-02	1.4E-01
GO:0009792	embryo development ending in birth or egg hatching	40	783	673	17583	1.33	0.42	2.6E-02	1.4E-01
GO:0007015	actin filament organization	18	783	263	17583	1.54	0.62	2.7E-02	1.4E-01
GO:0097485	neuron projection guidance	16	783	228	17583	1.58	0.66	2.7E-02	1.4E-01
GO:0007411	axon guidance	16	783	228	17583	1.58	0.66	2.7E-02	1.4E-01
GO:0003002	regionalization	22	783	335	17583	1.47	0.56	2.7E-02	1.4E-01
GO:0048880	sensory system development	25	783	390	17583	1.44	0.53	2.7E-02	1.4E-01
GO:0010660	regulation of muscle cell apoptotic process	6	783	66	17583	2.04	1.03	2.7E-02	1.4E-01
GO:0008654	phospholipid biosynthetic process	17	783	246	17583	1.55	0.63	2.7E-02	1.4E-01
GO:0001678	cellular glucose homeostasis	8	783	96	17583	1.87	0.90	2.7E-02	1.4E-01
GO:0060548	negative regulation of cell death	57	783	1009	17583	1.27	0.34	2.7E-02	1.4E-01
GO:0032007	negative regulation of TOR signaling	5	783	52	17583	2.16	1.11	2.7E-02	1.4E-01
GO:2000677	regulation of transcription regulatory region DNA binding	5	783	52	17583	2.16	1.11	2.7E-02	1.4E-01
GO:0060324	face development	5	783	52	17583	2.16	1.11	2.7E-02	1.4E-01
GO:0030855	epithelial cell differentiation	37	783	617	17583	1.35	0.43	2.7E-02	1.4E-01
GO:0032774	RNA biosynthetic process	37	783	617	17583	1.35	0.43	2.7E-02	1.4E-01
GO:0008344	adult locomotory behavior	7	783	81	17583	1.94	0.96	2.8E-02	1.4E-01
GO:2001021	negative regulation of response to DNA damage stimulus	7	783	81	17583	1.94	0.96	2.8E-02	1.4E-01
GO:1903050	regulation of proteolysis involved in protein catabolic process	16	783	229	17583	1.57	0.65	2.8E-02	1.4E-01
GO:0009725	response to hormone	45	783	773	17583	1.31	0.39	2.8E-02	1.4E-01
GO:0009060	aerobic respiration	12	783	161	17583	1.67	0.74	2.8E-02	1.4E-01
GO:1901991	negative regulation of mitotic cell cycle phase transition	12	783	161	17583	1.67	0.74	2.8E-02	1.4E-01
GO:0048858	cell projection morphogenesis	30	783	485	17583	1.39	0.47	2.8E-02	1.4E-01
GO:0031056	regulation of histone modification	11	783	145	17583	1.70	0.77	2.9E-02	1.4E-01
GO:0009887	animal organ morphogenesis	56	783	992	17583	1.27	0.34	2.9E-02	1.4E-01
GO:0045600	positive regulation of fat cell differentiation	6	783	67	17583	2.01	1.01	2.9E-02	1.4E-01
GO:1901607	alpha-amino acid biosynthetic process	6	783	67	17583	2.01	1.01	2.9E-02	1.4E-01
GO:0007006	mitochondrial membrane organization	9	783	113	17583	1.79	0.84	2.9E-02	1.4E-01
GO:1901214	regulation of neuron death	21	783	320	17583	1.47	0.56	2.9E-02	1.4E-01

GO:0070887	cellular response to chemical stimulus	122	783	2350	17583	1.17	0.22	2.9E-02	1.4E-01
GO:0048545	response to steroid hormone	19	783	284	17583	1.50	0.59	2.9E-02	1.4E-01
GO:0043086	negative regulation of catalytic activity	38	783	640	17583	1.33	0.42	3.0E-02	1.4E-01
GO:0009994	oocyte differentiation	5	783	53	17583	2.12	1.08	3.0E-02	1.4E-01
GO:0010647	positive regulation of cell communication	90	783	1685	17583	1.20	0.26	3.0E-02	1.4E-01
GO:0098662	inorganic cation transmembrane transport	36	783	602	17583	1.34	0.43	3.0E-02	1.4E-01
GO:0048598	embryonic morphogenesis	35	783	583	17583	1.35	0.43	3.0E-02	1.4E-01
GO:0031329	regulation of cellular catabolic process	46	783	797	17583	1.30	0.37	3.0E-02	1.4E-01
GO:0051952	regulation of amine transport	8	783	98	17583	1.83	0.87	3.1E-02	1.4E-01
GO:1904035	regulation of epithelial cell apoptotic process	8	783	98	17583	1.83	0.87	3.1E-02	1.4E-01
GO:0009142	nucleoside triphosphate biosynthetic process	9	783	114	17583	1.77	0.83	3.1E-02	1.4E-01
GO:0048844	artery morphogenesis	6	783	68	17583	1.98	0.99	3.1E-02	1.4E-01
GO:0070252	actin-mediated cell contraction	6	783	68	17583	1.98	0.99	3.1E-02	1.4E-01
GO:0002062	chondrocyte differentiation	7	783	83	17583	1.89	0.92	3.1E-02	1.4E-01
GO:0048661	positive regulation of smooth muscle cell proliferation	7	783	83	17583	1.89	0.92	3.1E-02	1.4E-01
GO:0042176	regulation of protein catabolic process	23	783	359	17583	1.44	0.52	3.2E-02	1.4E-01
GO:0010959	regulation of metal ion transport	25	783	396	17583	1.42	0.50	3.2E-02	1.4E-01
GO:0036294	cellular response to decreased oxygen levels	10	783	131	17583	1.71	0.78	3.2E-02	1.4E-01
GO:0045599	negative regulation of fat cell differentiation	5	783	54	17583	2.08	1.06	3.2E-02	1.4E-01
GO:0046545	development of primary female sexual characteristics	8	783	99	17583	1.81	0.86	3.2E-02	1.4E-01
GO:0071901	negative regulation of protein serine/threonine kinase activity	9	783	115	17583	1.76	0.81	3.2E-02	1.4E-01
GO:0010608	post-transcriptional regulation of gene expression	30	783	491	17583	1.37	0.46	3.2E-02	1.4E-01
GO:0006351	DNA-templated transcription	36	783	606	17583	1.33	0.42	3.3E-02	1.4E-01
GO:0035148	tube formation	11	783	148	17583	1.67	0.74	3.3E-02	1.4E-01
GO:0098771	inorganic ion homeostasis	32	783	530	17583	1.36	0.44	3.3E-02	1.4E-01
GO:0003007	heart morphogenesis	17	783	252	17583	1.51	0.60	3.3E-02	1.4E-01
GO:0097659	nucleic acid-templated transcription	36	783	607	17583	1.33	0.41	3.3E-02	1.4E-01
GO:0032989	cellular component morphogenesis	36	783	607	17583	1.33	0.41	3.3E-02	1.4E-01
GO:1902893	regulation of miRNA transcription	6	783	69	17583	1.95	0.97	3.3E-02	1.4E-01
GO:0032868	response to insulin	15	783	217	17583	1.55	0.63	3.4E-02	1.4E-01
GO:0009896	positive regulation of catabolic process	31	783	512	17583	1.36	0.44	3.4E-02	1.4E-01
GO:0045639	positive regulation of myeloid cell differentiation	8	783	100	17583	1.80	0.85	3.4E-02	1.4E-01

GO:0071773	cellular response to BMP stimulus	8	783	100	17583	1.80	0.85	3.4E-02	1.4E-01
GO:0071772	response to BMP	8	783	100	17583	1.80	0.85	3.4E-02	1.4E-01
GO:0043043	peptide biosynthetic process	25	783	399	17583	1.41	0.49	3.4E-02	1.4E-01
GO:0022904	respiratory electron transport chain	9	783	116	17583	1.74	0.80	3.4E-02	1.4E-01
GO:0017148	negative regulation of translation	12	783	166	17583	1.62	0.70	3.5E-02	1.4E-01
GO:0006518	peptide metabolic process	32	783	532	17583	1.35	0.43	3.5E-02	1.4E-01
GO:0003006	developmental process involved in reproduction	53	783	944	17583	1.26	0.33	3.5E-02	1.4E-01
GO:0006873	cellular ion homeostasis	27	783	438	17583	1.38	0.47	3.6E-02	1.4E-01
GO:0001501	skeletal system development	31	783	514	17583	1.35	0.44	3.6E-02	1.4E-01
GO:0006886	intracellular protein transport	40	783	688	17583	1.31	0.38	3.6E-02	1.4E-01
GO:0046470	phosphatidylcholine metabolic process	6	783	70	17583	1.92	0.94	3.6E-02	1.4E-01
GO:0061371	determination of heart left/right asymmetry	6	783	70	17583	1.92	0.94	3.6E-02	1.4E-01
GO:0009205	purine ribonucleoside triphosphate metabolic process	13	783	184	17583	1.59	0.67	3.6E-02	1.4E-01
GO:0010628	positive regulation of gene expression	62	783	1127	17583	1.24	0.30	3.6E-02	1.4E-01
GO:0055080	cation homeostasis	31	783	515	17583	1.35	0.43	3.6E-02	1.4E-01
GO:0018193	peptidyl-amino acid modification	47	783	828	17583	1.27	0.35	3.7E-02	1.4E-01
GO:0051241	negative regulation of multicellular organismal process	57	783	1028	17583	1.25	0.32	3.7E-02	1.4E-01
GO:0048878	chemical homeostasis	51	783	908	17583	1.26	0.33	3.7E-02	1.4E-01
GO:0009059	macromolecule biosynthetic process	79	783	1476	17583	1.20	0.27	3.7E-02	1.4E-01
GO:0030901	midbrain development	7	783	86	17583	1.83	0.87	3.8E-02	1.4E-01
GO:0008589	regulation of smoothened signaling pathway	7	783	86	17583	1.83	0.87	3.8E-02	1.4E-01
GO:0035019	somatic stem cell population maintenance	5	783	56	17583	2.00	1.00	3.8E-02	1.4E-01
GO:0007088	regulation of mitotic nuclear division	9	783	118	17583	1.71	0.78	3.8E-02	1.4E-01
GO:0006812	cation transport	48	783	849	17583	1.27	0.34	3.8E-02	1.4E-01
GO:0009201	ribonucleoside triphosphate biosynthetic process	8	783	102	17583	1.76	0.82	3.8E-02	1.4E-01
GO:0045833	negative regulation of lipid metabolic process	8	783	102	17583	1.76	0.82	3.8E-02	1.4E-01
GO:0003208	cardiac ventricle morphogenesis	6	783	71	17583	1.90	0.92	3.8E-02	1.4E-01
GO:0032922	circadian regulation of gene expression	6	783	71	17583	1.90	0.92	3.8E-02	1.4E-01
GO:0019725	cellular homeostasis	38	783	653	17583	1.31	0.39	3.9E-02	1.4E-01
GO:0007018	microtubule-based movement	24	783	385	17583	1.40	0.49	3.9E-02	1.4E-01
GO:0006468	protein phosphorylation	41	783	712	17583	1.29	0.37	3.9E-02	1.4E-01
GO:0022900	electron transport chain	12	783	169	17583	1.59	0.67	3.9E-02	1.4E-01

GO:0051961	negative regulation of nervous system development	11	783	152	17583	1.63	0.70	3.9E-02	1.4E-01
GO:0007612	learning	11	783	152	17583	1.63	0.70	3.9E-02	1.4E-01
GO:0034654	nucleobase-containing compound biosynthetic process	55	783	991	17583	1.25	0.32	3.9E-02	1.4E-01
GO:0071310	cellular response to organic substance	91	783	1728	17583	1.18	0.24	3.9E-02	1.4E-01
GO:1901654	response to ketone	14	783	204	17583	1.54	0.62	4.0E-02	1.4E-01
GO:0031398	positive regulation of protein ubiquitination	9	783	119	17583	1.70	0.76	4.0E-02	1.4E-01
GO:0000956	nuclear-transcribed mRNA catabolic process	8	783	103	17583	1.74	0.80	4.0E-02	1.4E-01
GO:0002244	hematopoietic progenitor cell differentiation	8	783	103	17583	1.74	0.80	4.0E-02	1.4E-01
GO:0051098	regulation of binding	23	783	368	17583	1.40	0.49	4.0E-02	1.4E-01
GO:2000630	positive regulation of miRNA metabolic process	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:1903053	regulation of extracellular matrix organization	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:0031060	regulation of histone methylation	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:0002763	positive regulation of myeloid leukocyte differentiation	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:0002707	negative regulation of lymphocyte mediated immunity	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:0048168	regulation of neuronal synaptic plasticity	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:1902808	positive regulation of cell cycle G1/S phase transition	5	783	57	17583	1.97	0.98	4.0E-02	1.4E-01
GO:0003281	ventricular septum development	6	783	72	17583	1.87	0.90	4.1E-02	1.4E-01
GO:1901987	regulation of cell cycle phase transition	26	783	425	17583	1.37	0.46	4.1E-02	1.4E-01
GO:0055065	metal ion homeostasis	26	783	425	17583	1.37	0.46	4.1E-02	1.4E-01
GO:0043010	camera-type eye development	21	783	332	17583	1.42	0.51	4.2E-02	1.4E-01
GO:0051101	regulation of DNA binding	9	783	120	17583	1.68	0.75	4.2E-02	1.4E-01
GO:0046777	protein autophosphorylation	13	783	188	17583	1.55	0.63	4.2E-02	1.4E-01
GO:2000177	regulation of neural precursor cell proliferation	7	783	88	17583	1.79	0.84	4.2E-02	1.4E-01
GO:0019217	regulation of fatty acid metabolic process	7	783	88	17583	1.79	0.84	4.2E-02	1.4E-01
GO:0051591	response to cAMP	7	783	88	17583	1.79	0.84	4.2E-02	1.4E-01
GO:0019646	aerobic electron transport chain	7	783	88	17583	1.79	0.84	4.2E-02	1.4E-01
GO:0006885	regulation of pH	8	783	104	17583	1.73	0.79	4.2E-02	1.4E-01
GO:0021549	cerebellum development	8	783	104	17583	1.73	0.79	4.2E-02	1.4E-01
GO:0045727	positive regulation of translation	10	783	137	17583	1.64	0.71	4.2E-02	1.4E-01
GO:0008277	regulation of G protein-coupled receptor signaling pathway	10	783	137	17583	1.64	0.71	4.2E-02	1.4E-01
GO:0001764	neuron migration	10	783	137	17583	1.64	0.71	4.2E-02	1.4E-01
GO:0033043	regulation of organelle organization	65	783	1199	17583	1.22	0.28	4.3E-02	1.4E-01

GO:0006091	generation of precursor metabolites and energy	25	783	408	17583	1.38	0.46	4.3E-02	1.4E-01
GO:0050801	ion homeostasis	32	783	542	17583	1.33	0.41	4.3E-02	1.4E-01
GO:0090407	organophosphate biosynthetic process	32	783	542	17583	1.33	0.41	4.3E-02	1.4E-01
GO:0045786	negative regulation of cell cycle	22	783	352	17583	1.40	0.49	4.3E-02	1.4E-01
GO:0016310	phosphorylation	50	783	897	17583	1.25	0.32	4.3E-02	1.4E-01
GO:0009144	purine nucleoside triphosphate metabolic process	13	783	189	17583	1.54	0.63	4.3E-02	1.4E-01
GO:0071479	cellular response to ionizing radiation	6	783	73	17583	1.85	0.88	4.3E-02	1.4E-01
GO:0071333	cellular response to glucose stimulus	6	783	73	17583	1.85	0.88	4.3E-02	1.4E-01
GO:0015986	proton motive force-driven ATP synthesis	6	783	73	17583	1.85	0.88	4.3E-02	1.4E-01
GO:0060350	endochondral bone morphogenesis	5	783	58	17583	1.94	0.95	4.4E-02	1.4E-01
GO:0051438	regulation of ubiquitin-protein transferase activity	5	783	58	17583	1.94	0.95	4.4E-02	1.4E-01
GO:0034762	regulation of transmembrane transport	34	783	582	17583	1.31	0.39	4.4E-02	1.4E-01
GO:0050680	negative regulation of epithelial cell proliferation	10	783	138	17583	1.63	0.70	4.4E-02	1.4E-01
GO:0032200	telomere organization	8	783	105	17583	1.71	0.77	4.5E-02	1.4E-01
GO:0034101	erythrocyte homeostasis	8	783	105	17583	1.71	0.77	4.5E-02	1.4E-01
GO:0045185	maintenance of protein location	7	783	89	17583	1.77	0.82	4.5E-02	1.4E-01
GO:0071322	cellular response to carbohydrate stimulus	7	783	89	17583	1.77	0.82	4.5E-02	1.4E-01
GO:0140694	non-membrane-bounded organelle assembly	21	783	335	17583	1.41	0.49	4.5E-02	1.4E-01
GO:0009141	nucleoside triphosphate metabolic process	14	783	208	17583	1.51	0.60	4.6E-02	1.4E-01
GO:0045930	negative regulation of mitotic cell cycle	14	783	208	17583	1.51	0.60	4.6E-02	1.4E-01
GO:0007610	behavior	35	783	603	17583	1.30	0.38	4.6E-02	1.4E-01
GO:0007613	memory	9	783	122	17583	1.66	0.73	4.6E-02	1.4E-01
GO:0071375	cellular response to peptide hormone stimulus	16	783	244	17583	1.47	0.56	4.6E-02	1.4E-01
GO:0048468	cell development	111	783	2160	17583	1.15	0.21	4.6E-02	1.4E-01
GO:0140029	exocytic process	6	783	74	17583	1.82	0.86	4.6E-02	1.4E-01
GO:0001649	osteoblast differentiation	10	783	139	17583	1.62	0.69	4.6E-02	1.4E-01
GO:0070228	regulation of lymphocyte apoptotic process	5	783	59	17583	1.90	0.93	4.7E-02	1.4E-01
GO:0140115	export across plasma membrane	5	783	59	17583	1.90	0.93	4.7E-02	1.4E-01
GO:0009948	anterior/posterior axis specification	5	783	59	17583	1.90	0.93	4.7E-02	1.4E-01
GO:0018130	heterocycle biosynthetic process	58	783	1063	17583	1.23	0.29	4.7E-02	1.4E-01
GO:0030001	metal ion transport	36	783	624	17583	1.30	0.37	4.7E-02	1.4E-01
GO:1902017	regulation of cilium assembly	7	783	90	17583	1.75	0.80	4.7E-02	1.4E-01

GO:0045732	positive regulation of protein catabolic process	14	783	209	17583	1.50	0.59	4.7E-02	1.4E-01
GO:0000902	cell morphogenesis	40	783	703	17583	1.28	0.35	4.7E-02	1.4E-01
GO:0061136	regulation of proteasomal protein catabolic process	13	783	192	17583	1.52	0.60	4.8E-02	1.4E-01
GO:0001701	in utero embryonic development	24	783	394	17583	1.37	0.45	4.8E-02	1.4E-01
GO:0065009	regulation of molecular function	131	783	2588	17583	1.14	0.18	4.9E-02	1.4E-01
GO:1902532	negative regulation of intracellular signal transduction	30	783	509	17583	1.32	0.40	4.9E-02	1.4E-01
GO:0072521	purine-containing compound metabolic process	29	783	490	17583	1.33	0.41	4.9E-02	1.5E-01
GO:0071331	cellular response to hexose stimulus	6	783	75	17583	1.80	0.85	4.9E-02	1.5E-01
GO:0008333	endosome to lysosome transport	6	783	75	17583	1.80	0.85	4.9E-02	1.5E-01
GO:0008652	amino acid biosynthetic process	6	783	75	17583	1.80	0.85	4.9E-02	1.5E-01
GO:0061387	regulation of extent of cell growth	8	783	107	17583	1.68	0.75	4.9E-02	1.5E-01
GO:0090277	positive regulation of peptide hormone secretion	8	783	107	17583	1.68	0.75	4.9E-02	1.5E-01
GO:0071356	cellular response to tumor necrosis factor	12	783	175	17583	1.54	0.62	4.9E-02	1.5E-01
GO:0031175	neuron projection development	38	783	666	17583	1.28	0.36	4.9E-02	1.5E-01
GO:0007423	sensory organ development	33	783	568	17583	1.30	0.38	4.9E-02	1.5E-01
GO:0048583	regulation of response to stimulus	197	783	4008	17583	1.10	0.14	5.0E-02	1.5E-01
GO:0003231	cardiac ventricle development	9	783	124	17583	1.63	0.70	5.0E-02	1.5E-01
GO:0003206	cardiac chamber morphogenesis	9	783	124	17583	1.63	0.70	5.0E-02	1.5E-01
GO:0044265	cellular macromolecule catabolic process	44	783	786	17583	1.26	0.33	5.0E-02	1.5E-01
GO:0030177	positive regulation of Wnt signaling pathway	10	783	141	17583	1.59	0.67	5.0E-02	1.5E-01
GO:0140053	mitochondrial gene expression	10	783	141	17583	1.59	0.67	5.0E-02	1.5E-01
GO:0008283	cell population proliferation	40	783	707	17583	1.27	0.35	5.1E-02	1.5E-01
GO:0048024	regulation of mRNA splicing, via spliceosome	8	783	108	17583	1.66	0.73	5.2E-02	1.5E-01
GO:0042593	glucose homeostasis	13	783	194	17583	1.50	0.59	5.2E-02	1.5E-01
GO:0090150	establishment of protein localization to membrane	14	783	212	17583	1.48	0.57	5.2E-02	1.5E-01
GO:0030516	regulation of axon extension	7	783	92	17583	1.71	0.77	5.2E-02	1.5E-01
GO:0051384	response to glucocorticoid	10	783	142	17583	1.58	0.66	5.3E-02	1.5E-01
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic	10	783	142	17583	1.58	0.66	5.3E-02	1.5E-01
GO:0032501	multicellular organismal process	303	783	6337	17583	1.07	0.10	5.3E-02	1.5E-01
GO:0007517	muscle organ development	19	783	304	17583	1.40	0.49	5.3E-02	1.6E-01
GO:1901016	regulation of potassium ion transmembrane transporter activity	5	783	61	17583	1.84	0.88	5.4E-02	1.6E-01
GO:0033500	carbohydrate homeostasis	13	783	195	17583	1.50	0.58	5.4E-02	1.6E-01

GO:0060271	cilium assembly	20	783	323	17583	1.39	0.48	5.4E-02	1.6E-01
GO:1902115	regulation of organelle assembly	15	783	231	17583	1.46	0.54	5.4E-02	1.6E-01
GO:0002793	positive regulation of peptide secretion	8	783	109	17583	1.65	0.72	5.4E-02	1.6E-01
GO:0030534	adult behavior	10	783	143	17583	1.57	0.65	5.5E-02	1.6E-01
GO:0021987	cerebral cortex development	9	783	126	17583	1.60	0.68	5.5E-02	1.6E-01
GO:0030879	mammary gland development	9	783	126	17583	1.60	0.68	5.5E-02	1.6E-01
GO:0010948	negative regulation of cell cycle process	17	783	268	17583	1.42	0.51	5.5E-02	1.6E-01
GO:0030512	negative regulation of transforming growth factor beta receptor s	7	783	93	17583	1.69	0.76	5.5E-02	1.6E-01
GO:0070664	negative regulation of leukocyte proliferation	7	783	93	17583	1.69	0.76	5.5E-02	1.6E-01
GO:1904063	negative regulation of cation transmembrane transport	7	783	93	17583	1.69	0.76	5.5E-02	1.6E-01
GO:0060047	heart contraction	7	783	93	17583	1.69	0.76	5.5E-02	1.6E-01
GO:0048709	oligodendrocyte differentiation	6	783	77	17583	1.75	0.81	5.5E-02	1.6E-01
GO:0071326	cellular response to monosaccharide stimulus	6	783	77	17583	1.75	0.81	5.5E-02	1.6E-01
GO:0003015	heart process	8	783	110	17583	1.63	0.71	5.7E-02	1.6E-01
GO:0035966	response to topologically incorrect protein	10	783	144	17583	1.56	0.64	5.7E-02	1.6E-01
GO:0050994	regulation of lipid catabolic process	5	783	62	17583	1.81	0.86	5.7E-02	1.6E-01
GO:0032720	negative regulation of tumor necrosis factor production	5	783	62	17583	1.81	0.86	5.7E-02	1.6E-01
GO:2001233	regulation of apoptotic signaling pathway	22	783	363	17583	1.36	0.44	5.7E-02	1.6E-01
GO:1901215	negative regulation of neuron death	14	783	215	17583	1.46	0.55	5.8E-02	1.6E-01
GO:0061061	muscle structure development	29	783	498	17583	1.31	0.39	5.8E-02	1.7E-01
GO:0090596	sensory organ morphogenesis	17	783	270	17583	1.41	0.50	5.8E-02	1.7E-01
GO:0008593	regulation of Notch signaling pathway	7	783	94	17583	1.67	0.74	5.8E-02	1.7E-01
GO:0048477	oogenesis	7	783	94	17583	1.67	0.74	5.8E-02	1.7E-01
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein c	7	783	94	17583	1.67	0.74	5.8E-02	1.7E-01
GO:0009967	positive regulation of signal transduction	79	783	1511	17583	1.17	0.23	5.8E-02	1.7E-01
GO:0055086	nucleobase-containing small molecule metabolic process	34	783	596	17583	1.28	0.36	5.8E-02	1.7E-01
GO:0034765	regulation of ion transmembrane transport	29	783	499	17583	1.31	0.38	5.9E-02	1.7E-01
GO:0098655	cation transmembrane transport	38	783	677	17583	1.26	0.33	6.0E-02	1.7E-01
GO:0018212	peptidyl-tyrosine modification	11	783	163	17583	1.52	0.60	6.1E-02	1.7E-01
GO:0034250	positive regulation of amide metabolic process	11	783	163	17583	1.52	0.60	6.1E-02	1.7E-01
GO:0006879	cellular iron ion homeostasis	5	783	63	17583	1.78	0.83	6.1E-02	1.7E-01
GO:0051651	maintenance of location in cell	7	783	95	17583	1.65	0.73	6.1E-02	1.7E-01

GO:0048704	embryonic skeletal system morphogenesis	7	783	95	17583	1.65	0.73	6.1E-02	1.7E-01
GO:0043603	amide metabolic process	44	783	798	17583	1.24	0.31	6.1E-02	1.7E-01
GO:0072659	protein localization to plasma membrane	13	783	199	17583	1.47	0.55	6.2E-02	1.7E-01
GO:0071248	cellular response to metal ion	13	783	199	17583	1.47	0.55	6.2E-02	1.7E-01
GO:0050768	negative regulation of neurogenesis	10	783	146	17583	1.54	0.62	6.2E-02	1.7E-01
GO:0051783	regulation of nuclear division	10	783	146	17583	1.54	0.62	6.2E-02	1.7E-01
GO:0071702	organic substance transport	100	783	1956	17583	1.15	0.20	6.2E-02	1.7E-01
GO:2000628	regulation of miRNA metabolic process	6	783	79	17583	1.71	0.77	6.2E-02	1.7E-01
GO:0007422	peripheral nervous system development	6	783	79	17583	1.71	0.77	6.2E-02	1.7E-01
GO:0001101	response to acid chemical	9	783	129	17583	1.57	0.65	6.2E-02	1.8E-01
GO:0010629	negative regulation of gene expression	49	783	900	17583	1.22	0.29	6.2E-02	1.8E-01
GO:0007611	learning or memory	17	783	273	17583	1.40	0.48	6.3E-02	1.8E-01
GO:1902107	positive regulation of leukocyte differentiation	12	783	182	17583	1.48	0.57	6.3E-02	1.8E-01
GO:1903708	positive regulation of hemopoiesis	12	783	182	17583	1.48	0.57	6.3E-02	1.8E-01
GO:0008016	regulation of heart contraction	13	783	200	17583	1.46	0.55	6.4E-02	1.8E-01
GO:0120161	regulation of cold-induced thermogenesis	10	783	147	17583	1.53	0.61	6.4E-02	1.8E-01
GO:0030218	erythrocyte differentiation	7	783	96	17583	1.64	0.71	6.4E-02	1.8E-01
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	7	783	96	17583	1.64	0.71	6.4E-02	1.8E-01
GO:0009798	axis specification	7	783	96	17583	1.64	0.71	6.4E-02	1.8E-01
GO:0040014	regulation of multicellular organism growth	5	783	64	17583	1.75	0.81	6.5E-02	1.8E-01
GO:0099518	vesicle cytoskeletal trafficking	5	783	64	17583	1.75	0.81	6.5E-02	1.8E-01
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine	5	783	64	17583	1.75	0.81	6.5E-02	1.8E-01
GO:0050891	multicellular organismal water homeostasis	5	783	64	17583	1.75	0.81	6.5E-02	1.8E-01
GO:0042440	pigment metabolic process	5	783	64	17583	1.75	0.81	6.5E-02	1.8E-01
GO:0030335	positive regulation of cell migration	30	783	523	17583	1.29	0.37	6.5E-02	1.8E-01
GO:0046916	cellular transition metal ion homeostasis	8	783	113	17583	1.59	0.67	6.5E-02	1.8E-01
GO:0071559	response to transforming growth factor beta	11	783	165	17583	1.50	0.58	6.5E-02	1.8E-01
GO:2000142	regulation of DNA-templated transcription initiation	6	783	80	17583	1.68	0.75	6.5E-02	1.8E-01
GO:0048872	homeostasis of number of cells	16	783	256	17583	1.40	0.49	6.6E-02	1.8E-01
GO:0014070	response to organic cyclic compound	47	783	864	17583	1.22	0.29	6.7E-02	1.8E-01
GO:0009145	purine nucleoside triphosphate biosynthetic process	7	783	97	17583	1.62	0.70	6.7E-02	1.8E-01
GO:0031960	response to corticosteroid	11	783	166	17583	1.49	0.57	6.8E-02	1.8E-01

GO:0008033	tRNA processing	9	783	131	17583	1.54	0.63	6.8E-02	1.8E-01
GO:0007368	determination of left/right symmetry	9	783	131	17583	1.54	0.63	6.8E-02	1.8E-01
GO:0046660	female sex differentiation	8	783	114	17583	1.58	0.66	6.8E-02	1.8E-01
GO:0043200	response to amino acid	8	783	114	17583	1.58	0.66	6.8E-02	1.8E-01
GO:0035051	cardiocyte differentiation	8	783	114	17583	1.58	0.66	6.8E-02	1.8E-01
GO:0048857	neural nucleus development	5	783	65	17583	1.73	0.79	6.9E-02	1.8E-01
GO:0014910	regulation of smooth muscle cell migration	5	783	65	17583	1.73	0.79	6.9E-02	1.8E-01
GO:0070936	protein K48-linked ubiquitination	5	783	65	17583	1.73	0.79	6.9E-02	1.8E-01
GO:0051926	negative regulation of calcium ion transport	5	783	65	17583	1.73	0.79	6.9E-02	1.8E-01
GO:0050890	cognition	19	783	314	17583	1.36	0.44	6.9E-02	1.8E-01
GO:0051051	negative regulation of transport	25	783	429	17583	1.31	0.39	7.0E-02	1.8E-01
GO:0019693	ribose phosphate metabolic process	24	783	410	17583	1.31	0.39	7.0E-02	1.8E-01
GO:0022613	ribonucleoprotein complex biogenesis	26	783	449	17583	1.30	0.38	7.0E-02	1.8E-01
GO:0051168	nuclear export	9	783	132	17583	1.53	0.61	7.0E-02	1.8E-01
GO:0051962	positive regulation of nervous system development	17	783	277	17583	1.38	0.46	7.1E-02	1.8E-01
GO:0060349	bone morphogenesis	7	783	98	17583	1.60	0.68	7.1E-02	1.8E-01
GO:0050000	chromosome localization	6	783	82	17583	1.64	0.72	7.3E-02	1.8E-01
GO:0072384	organelle transport along microtubule	6	783	82	17583	1.64	0.72	7.3E-02	1.8E-01
GO:0010033	response to organic substance	122	783	2439	17583	1.12	0.17	7.3E-02	1.8E-01
GO:0018105	peptidyl-serine phosphorylation	12	783	186	17583	1.45	0.53	7.3E-02	1.8E-01
GO:0031100	animal organ regeneration	5	783	66	17583	1.70	0.77	7.3E-02	1.8E-01
GO:2000379	positive regulation of reactive oxygen species metabolic process	5	783	66	17583	1.70	0.77	7.3E-02	1.8E-01
GO:0051983	regulation of chromosome segregation	9	783	133	17583	1.52	0.60	7.3E-02	1.8E-01
GO:1901362	organic cyclic compound biosynthetic process	63	783	1199	17583	1.18	0.24	7.4E-02	1.8E-01
GO:0030278	regulation of ossification	8	783	116	17583	1.55	0.63	7.4E-02	1.8E-01
GO:0050767	regulation of neurogenesis	22	783	374	17583	1.32	0.40	7.4E-02	1.8E-01
GO:0050678	regulation of epithelial cell proliferation	22	783	374	17583	1.32	0.40	7.4E-02	1.8E-01
GO:0016579	protein deubiquitination	10	783	151	17583	1.49	0.57	7.5E-02	1.8E-01
GO:0031099	regeneration	10	783	151	17583	1.49	0.57	7.5E-02	1.8E-01
GO:0046474	glycerophospholipid biosynthetic process	13	783	205	17583	1.42	0.51	7.5E-02	1.8E-01
GO:0050673	epithelial cell proliferation	11	783	169	17583	1.46	0.55	7.5E-02	1.8E-01
GO:0070646	protein modification by small protein removal	11	783	169	17583	1.46	0.55	7.5E-02	1.8E-01

GO:1903047	mitotic cell cycle process	30	783	531	17583	1.27	0.34	7.6E-02	1.8E-01
GO:0070647	protein modification by small protein conjugation or removal	48	783	893	17583	1.21	0.27	7.6E-02	1.8E-01
GO:0002028	regulation of sodium ion transport	6	783	83	17583	1.62	0.70	7.6E-02	1.8E-01
GO:0007292	female gamete generation	10	783	152	17583	1.48	0.56	7.7E-02	1.8E-01
GO:0061351	neural precursor cell proliferation	7	783	100	17583	1.57	0.65	7.8E-02	1.8E-01
GO:0010498	proteasomal protein catabolic process	22	783	376	17583	1.31	0.39	7.8E-02	1.8E-01
GO:0050878	regulation of body fluid levels	22	783	376	17583	1.31	0.39	7.8E-02	1.8E-01
GO:0022603	regulation of anatomical structure morphogenesis	49	783	915	17583	1.20	0.27	7.8E-02	1.8E-01
GO:0015980	energy derivation by oxidation of organic compounds	16	783	262	17583	1.37	0.46	7.8E-02	1.8E-01
GO:0051960	regulation of nervous system development	26	783	454	17583	1.29	0.36	7.8E-02	1.8E-01
GO:0060284	regulation of cell development	46	783	856	17583	1.21	0.27	8.0E-02	1.8E-01
GO:0006511	ubiquitin-dependent protein catabolic process	32	783	574	17583	1.25	0.32	8.0E-02	1.8E-01
GO:0099537	trans-synaptic signaling	25	783	436	17583	1.29	0.36	8.1E-02	1.8E-01
GO:0034766	negative regulation of ion transmembrane transport	7	783	101	17583	1.56	0.64	8.1E-02	1.8E-01
GO:2000144	positive regulation of DNA-templated transcription initiation	5	783	68	17583	1.65	0.72	8.2E-02	1.8E-01
GO:0006413	translational initiation	5	783	68	17583	1.65	0.72	8.2E-02	1.8E-01
GO:0046854	phosphatidylinositol phosphate biosynthetic process	5	783	68	17583	1.65	0.72	8.2E-02	1.8E-01
GO:0007623	circadian rhythm	9	783	136	17583	1.49	0.57	8.2E-02	1.8E-01
GO:0030003	cellular cation homeostasis	24	783	418	17583	1.29	0.37	8.3E-02	1.8E-01
GO:0045931	positive regulation of mitotic cell cycle	8	783	119	17583	1.51	0.59	8.4E-02	1.8E-01
GO:0006754	ATP biosynthetic process	6	783	85	17583	1.59	0.66	8.4E-02	1.8E-01
GO:0050672	negative regulation of lymphocyte proliferation	6	783	85	17583	1.59	0.66	8.4E-02	1.8E-01
GO:1901292	nucleoside phosphate catabolic process	6	783	85	17583	1.59	0.66	8.4E-02	1.8E-01
GO:0002709	regulation of T cell mediated immunity	6	783	85	17583	1.59	0.66	8.4E-02	1.8E-01
GO:0031647	regulation of protein stability	19	783	322	17583	1.33	0.41	8.4E-02	1.8E-01
GO:0030510	regulation of BMP signaling pathway	7	783	102	17583	1.54	0.62	8.5E-02	1.8E-01
GO:0098916	anterograde trans-synaptic signaling	24	783	419	17583	1.29	0.36	8.5E-02	1.8E-01
GO:0007268	chemical synaptic transmission	24	783	419	17583	1.29	0.36	8.5E-02	1.8E-01
GO:1903322	positive regulation of protein modification by small protein conju	9	783	137	17583	1.48	0.56	8.5E-02	1.8E-01
GO:0009855	determination of bilateral symmetry	9	783	137	17583	1.48	0.56	8.5E-02	1.8E-01
GO:0098739	import across plasma membrane	10	783	155	17583	1.45	0.53	8.6E-02	1.8E-01
GO:1903522	regulation of blood circulation	15	783	247	17583	1.36	0.45	8.6E-02	1.8E-01

GO:0030104	water homeostasis	5	783	69	17583	1.63	0.70	8.6E-02	1.8E-01
GO:0002704	negative regulation of leukocyte mediated immunity	5	783	69	17583	1.63	0.70	8.6E-02	1.8E-01
GO:0014823	response to activity	5	783	69	17583	1.63	0.70	8.6E-02	1.8E-01
GO:0051050	positive regulation of transport	48	783	902	17583	1.19	0.26	8.6E-02	1.8E-01
GO:0009259	ribonucleotide metabolic process	23	783	401	17583	1.29	0.37	8.8E-02	1.8E-01
GO:0030036	actin cytoskeleton organization	30	783	539	17583	1.25	0.32	8.8E-02	1.8E-01
GO:0071241	cellular response to inorganic substance	14	783	229	17583	1.37	0.46	8.8E-02	1.8E-01
GO:0006164	purine nucleotide biosynthetic process	14	783	229	17583	1.37	0.46	8.8E-02	1.8E-01
GO:0034504	protein localization to nucleus	12	783	192	17583	1.40	0.49	8.8E-02	1.8E-01
GO:0032945	negative regulation of mononuclear cell proliferation	6	783	86	17583	1.57	0.65	8.8E-02	1.8E-01
GO:0009150	purine ribonucleotide metabolic process	22	783	382	17583	1.29	0.37	8.8E-02	1.8E-01
GO:0009799	specification of symmetry	9	783	138	17583	1.46	0.55	8.9E-02	1.8E-01
GO:0042127	regulation of cell population proliferation	84	783	1654	17583	1.14	0.19	8.9E-02	1.8E-01
GO:1903311	regulation of mRNA metabolic process	18	783	306	17583	1.32	0.40	9.1E-02	1.9E-01
GO:0001570	vasculogenesis	5	783	70	17583	1.60	0.68	9.1E-02	1.9E-01
GO:0008286	insulin receptor signaling pathway	5	783	70	17583	1.60	0.68	9.1E-02	1.9E-01
GO:0060411	cardiac septum morphogenesis	5	783	70	17583	1.60	0.68	9.1E-02	1.9E-01
GO:1903201	regulation of oxidative stress-induced cell death	5	783	70	17583	1.60	0.68	9.1E-02	1.9E-01
GO:0001666	response to hypoxia	16	783	268	17583	1.34	0.42	9.1E-02	1.9E-01
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic pro	20	783	345	17583	1.30	0.38	9.2E-02	1.9E-01
GO:0050821	protein stabilization	13	783	212	17583	1.38	0.46	9.2E-02	1.9E-01
GO:0051726	regulation of cell cycle	58	783	1113	17583	1.17	0.23	9.2E-02	1.9E-01
GO:0030509	BMP signaling pathway	6	783	87	17583	1.55	0.63	9.3E-02	1.9E-01
GO:0055072	iron ion homeostasis	6	783	87	17583	1.55	0.63	9.3E-02	1.9E-01
GO:0120031	plasma membrane bounded cell projection assembly	24	783	424	17583	1.27	0.35	9.4E-02	1.9E-01
GO:0002698	negative regulation of immune effector process	8	783	122	17583	1.47	0.56	9.4E-02	1.9E-01
GO:0009306	protein secretion	8	783	122	17583	1.47	0.56	9.4E-02	1.9E-01
GO:0006986	response to unfolded protein	8	783	122	17583	1.47	0.56	9.4E-02	1.9E-01
GO:0002832	negative regulation of response to biotic stimulus	8	783	122	17583	1.47	0.56	9.4E-02	1.9E-01
GO:0051099	positive regulation of binding	11	783	176	17583	1.40	0.49	9.5E-02	1.9E-01
GO:0009451	RNA modification	11	783	176	17583	1.40	0.49	9.5E-02	1.9E-01
GO:0060348	bone development	13	783	213	17583	1.37	0.45	9.5E-02	1.9E-01

GO:0007163	establishment or maintenance of cell polarity	13	783	213	17583	1.37	0.45	9.5E-02	1.9E-01
GO:0060537	muscle tissue development	19	783	327	17583	1.30	0.38	9.5E-02	1.9E-01
GO:0099536	synaptic signaling	26	783	464	17583	1.26	0.33	9.5E-02	2.0E-01
GO:0071560	cellular response to transforming growth factor beta stimulus	10	783	158	17583	1.42	0.51	9.5E-02	2.0E-01
GO:0062013	positive regulation of small molecule metabolic process	9	783	140	17583	1.44	0.53	9.5E-02	2.0E-01
GO:0002573	myeloid leukocyte differentiation	9	783	140	17583	1.44	0.53	9.5E-02	2.0E-01
GO:0001568	blood vessel development	28	783	504	17583	1.25	0.32	9.6E-02	2.0E-01
GO:0019941	modification-dependent protein catabolic process	32	783	584	17583	1.23	0.30	9.6E-02	2.0E-01
GO:0046637	regulation of alpha-beta T cell differentiation	5	783	71	17583	1.58	0.66	9.6E-02	2.0E-01
GO:0007626	locomotory behavior	12	783	195	17583	1.38	0.47	9.6E-02	2.0E-01
GO:0090263	positive regulation of canonical Wnt signaling pathway	7	783	105	17583	1.50	0.58	9.6E-02	2.0E-01
GO:0003279	cardiac septum development	7	783	105	17583	1.50	0.58	9.6E-02	2.0E-01
GO:0030148	sphingolipid biosynthetic process	7	783	105	17583	1.50	0.58	9.6E-02	2.0E-01
GO:1901890	positive regulation of cell junction assembly	7	783	105	17583	1.50	0.58	9.6E-02	2.0E-01
GO:0018958	phenol-containing compound metabolic process	6	783	88	17583	1.53	0.61	9.7E-02	2.0E-01
GO:0051453	regulation of intracellular pH	6	783	88	17583	1.53	0.61	9.7E-02	2.0E-01
GO:0031058	positive regulation of histone modification	6	783	88	17583	1.53	0.61	9.7E-02	2.0E-01
GO:0001578	microtubule bundle formation	8	783	123	17583	1.46	0.55	9.8E-02	2.0E-01
GO:0035592	establishment of protein localization to extracellular region	8	783	123	17583	1.46	0.55	9.8E-02	2.0E-01
GO:0033044	regulation of chromosome organization	15	783	252	17583	1.34	0.42	9.8E-02	2.0E-01
GO:0032984	protein-containing complex disassembly	9	783	141	17583	1.43	0.52	9.9E-02	2.0E-01
GO:0044057	regulation of system process	31	783	566	17583	1.23	0.30	9.9E-02	2.0E-01
GO:2000147	positive regulation of cell motility	30	783	546	17583	1.23	0.30	9.9E-02	2.0E-01