

Supplementary Table 12. *Enriched pathways of Pattern I genes* . Columns are the same as Table S10.

path	desc	p	m	P	M	nrich	log2FC	pval	fdr
GO:0031327	negative regulation of cellular biosynthetic process	111	703	1566	17583	1.77	0.83	6.95E-10	6.86E-08
GO:0009890	negative regulation of biosynthetic process	112	703	1596	17583	1.76	0.81	1.04E-09	1.02E-07
GO:0010558	negative regulation of macromolecule biosynthetic process	106	703	1510	17583	1.76	0.81	3.00E-09	2.92E-07
GO:0007399	nervous system development	139	703	2189	17583	1.59	0.67	6.81E-09	6.60E-07
GO:0048731	system development	201	703	3507	17583	1.43	0.52	7.79E-09	7.50E-07
GO:0045892	negative regulation of DNA-templated transcription	92	703	1303	17583	1.77	0.82	2.69E-08	2.58E-06
GO:0031324	negative regulation of cellular metabolic process	138	703	2218	17583	1.56	0.64	2.82E-08	2.68E-06
GO:1903507	negative regulation of nucleic acid-templated transcription	92	703	1305	17583	1.76	0.82	2.90E-08	2.74E-06
GO:1902679	negative regulation of RNA biosynthetic process	92	703	1307	17583	1.76	0.82	3.12E-08	2.93E-06
GO:0031326	regulation of cellular biosynthetic process	223	703	4057	17583	1.37	0.46	3.18E-08	2.97E-06
GO:0007275	multicellular organism development	216	703	3903	17583	1.38	0.47	3.35E-08	3.12E-06
GO:0009889	regulation of biosynthetic process	225	703	4122	17583	1.37	0.45	4.85E-08	4.48E-06
GO:0010556	regulation of macromolecule biosynthetic process	215	703	3907	17583	1.38	0.46	5.89E-08	5.40E-06
GO:0051253	negative regulation of RNA metabolic process	95	703	1416	17583	1.68	0.75	1.83E-07	1.67E-05
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	100	703	1541	17583	1.62	0.70	4.21E-07	3.82E-05
GO:0000122	negative regulation of transcription by RNA polymerase II	69	703	959	17583	1.80	0.85	7.44E-07	6.71E-05
GO:0009893	positive regulation of metabolic process	203	703	3796	17583	1.34	0.42	1.41E-06	1.26E-04
GO:0010604	positive regulation of macromolecule metabolic process	188	703	3487	17583	1.35	0.43	2.38E-06	2.13E-04

GO:0010605	negative regulation of macromolecule metabolic process	153	703	2717	17583	1.41	0.49	2.43E-06	2.15E-04
GO:0031323	regulation of cellular metabolic process	278	703	5561	17583	1.25	0.32	2.47E-06	2.18E-04
GO:0048856	anatomical structure development	260	703	5143	17583	1.26	0.34	2.70E-06	2.34E-04
GO:0048518	positive regulation of biological process	306	703	6241	17583	1.23	0.29	3.04E-06	2.62E-04
GO:0051171	regulation of nitrogen compound metabolic process	280	703	5628	17583	1.24	0.32	3.39E-06	2.90E-04
GO:0006355	regulation of DNA-templated transcription	184	703	3420	17583	1.35	0.43	3.66E-06	3.12E-04
GO:0009892	negative regulation of metabolic process	162	703	2934	17583	1.38	0.47	3.74E-06	3.17E-04
GO:1903506	regulation of nucleic acid-templated transcription	184	703	3422	17583	1.34	0.43	3.80E-06	3.20E-04
GO:0014033	neural crest cell differentiation	14	703	93	17583	3.77	1.91	3.95E-06	3.31E-04
GO:0080090	regulation of primary metabolic process	286	703	5782	17583	1.24	0.31	4.06E-06	3.39E-04
GO:0051172	negative regulation of nitrogen compound metabolic process	135	703	2357	17583	1.43	0.52	4.46E-06	3.71E-04
GO:2001141	regulation of RNA biosynthetic process	184	703	3431	17583	1.34	0.42	4.50E-06	3.72E-04
GO:0048523	negative regulation of cellular process	237	703	4675	17583	1.27	0.34	8.25E-06	6.78E-04
GO:0010557	positive regulation of macromolecule biosynthetic process	113	703	1920	17583	1.47	0.56	8.77E-06	7.16E-04
GO:0060255	regulation of macromolecule metabolic process	299	703	6147	17583	1.22	0.28	9.28E-06	7.54E-04
GO:0048519	negative regulation of biological process	261	703	5250	17583	1.24	0.31	1.02E-05	8.25E-04
GO:0051252	regulation of RNA metabolic process	195	703	3724	17583	1.31	0.39	1.03E-05	8.25E-04
GO:0048522	positive regulation of cellular process	275	703	5593	17583	1.23	0.30	1.23E-05	9.67E-04
GO:0061005	cell differentiation involved in kidney development	9	703	47	17583	4.79	2.26	1.33E-05	1.04E-03
GO:0051173	positive regulation of nitrogen compound metabolic process	167	703	3112	17583	1.34	0.42	1.39E-05	1.08E-03
GO:0048863	stem cell differentiation	20	703	183	17583	2.73	1.45	1.41E-05	1.10E-03
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	19	703	169	17583	2.81	1.49	1.43E-05	1.10E-03

GO:0048934	peripheral nervous system neuron differentiation	5	703	15	17583	8.34	3.06	1.47E-05	1.12E-03
GO:0048935	peripheral nervous system neuron development	5	703	15	17583	8.34	3.06	1.47E-05	1.12E-03
GO:0014032	neural crest cell development	12	703	80	17583	3.75	1.91	1.59E-05	1.21E-03
GO:0009891	positive regulation of biosynthetic process	118	703	2055	17583	1.44	0.52	1.72E-05	1.30E-03
GO:0019219	regulation of nucleobase-containing compound metabolic process	207	703	4030	17583	1.28	0.36	1.78E-05	1.34E-03
GO:0002065	columnar/cuboidal epithelial cell differentiation	14	703	105	17583	3.33	1.74	1.80E-05	1.35E-03
GO:0031328	positive regulation of cellular biosynthetic process	116	703	2016	17583	1.44	0.53	1.86E-05	1.39E-03
GO:0048565	digestive tract development	16	703	132	17583	3.03	1.60	2.06E-05	1.53E-03
GO:0060562	epithelial tube morphogenesis	28	703	312	17583	2.24	1.17	2.31E-05	1.70E-03
GO:0032502	developmental process	277	703	5685	17583	1.22	0.29	2.35E-05	1.72E-03
GO:0006357	regulation of transcription by RNA polymerase II	142	703	2592	17583	1.37	0.45	2.55E-05	1.86E-03
GO:0040008	regulation of growth	45	703	609	17583	1.85	0.89	2.74E-05	1.99E-03
GO:0019222	regulation of metabolic process	317	703	6669	17583	1.19	0.25	3.20E-05	2.31E-03
GO:0048864	stem cell development	12	703	86	17583	3.49	1.80	3.52E-05	2.53E-03
GO:0031325	positive regulation of cellular metabolic process	162	703	3060	17583	1.32	0.41	4.08E-05	2.92E-03
GO:0001709	cell fate determination	8	703	43	17583	4.65	2.22	4.12E-05	2.94E-03
GO:0002067	glandular epithelial cell differentiation	10	703	65	17583	3.85	1.94	4.82E-05	3.41E-03
GO:0010468	regulation of gene expression	238	703	4813	17583	1.24	0.31	4.82E-05	3.41E-03
GO:0072202	cell differentiation involved in metanephros development	5	703	18	17583	6.95	2.80	4.91E-05	3.43E-03
GO:1903508	positive regulation of nucleic acid-templated transcription	99	703	1700	17583	1.46	0.54	4.93E-05	3.43E-03
GO:0045893	positive regulation of DNA-templated transcription	99	703	1700	17583	1.46	0.54	4.93E-05	3.43E-03

GO:0045944	positive regulation of transcription by RNA polymerase II	77	703	1246	17583	1.55	0.63	4.95E-05	3.43E-03
GO:1902680	positive regulation of RNA biosynthetic process	99	703	1706	17583	1.45	0.54	5.66E-05	3.90E-03
GO:0055123	digestive system development	16	703	144	17583	2.78	1.47	6.36E-05	4.23E-03
GO:0048762	mesenchymal cell differentiation	18	703	173	17583	2.60	1.38	6.55E-05	4.33E-03
GO:0051254	positive regulation of RNA metabolic process	104	703	1833	17583	1.42	0.50	9.01E-05	5.88E-03
GO:0051093	negative regulation of developmental process	59	703	911	17583	1.62	0.70	9.83E-05	6.39E-03
GO:0030857	negative regulation of epithelial cell differentiation	8	703	48	17583	4.17	2.06	1.03E-04	6.64E-03
GO:0048754	branching morphogenesis of an epithelial tube	15	703	136	17583	2.76	1.46	1.08E-04	6.96E-03
GO:0072012	glomerulus vasculature development	5	703	21	17583	5.96	2.57	1.30E-04	8.32E-03
GO:0001656	metanephros development	11	703	85	17583	3.24	1.69	1.38E-04	8.76E-03
GO:0035050	embryonic heart tube development	11	703	85	17583	3.24	1.69	1.38E-04	8.76E-03
GO:0045596	negative regulation of cell differentiation	46	703	673	17583	1.71	0.77	1.50E-04	9.48E-03
GO:0030705	cytoskeleton-dependent intracellular transport	19	703	200	17583	2.38	1.25	1.57E-04	9.72E-03
GO:0008088	axo-dendritic transport	10	703	74	17583	3.38	1.76	1.62E-04	1.00E-02
GO:0048513	animal organ development	151	703	2895	17583	1.30	0.38	1.64E-04	1.01E-02
GO:0048485	sympathetic nervous system development	5	703	22	17583	5.68	2.51	1.72E-04	1.05E-02
GO:0001919	regulation of receptor recycling	5	703	22	17583	5.68	2.51	1.72E-04	1.05E-02
GO:0017158	regulation of calcium ion-dependent exocytosis	7	703	41	17583	4.27	2.09	1.86E-04	1.13E-02
GO:0022008	neurogenesis	76	703	1281	17583	1.48	0.57	2.03E-04	1.23E-02
GO:0001763	morphogenesis of a branching structure	17	703	174	17583	2.44	1.29	2.16E-04	1.29E-02
GO:0061437	renal system vasculature development	5	703	23	17583	5.44	2.44	2.25E-04	1.34E-02
GO:0061440	kidney vasculature development	5	703	23	17583	5.44	2.44	2.25E-04	1.34E-02
GO:2000179	positive regulation of neural precursor cell proliferation	8	703	54	17583	3.71	1.89	2.63E-04	1.47E-02
GO:0060322	head development	53	703	826	17583	1.60	0.68	2.63E-04	1.47E-02
GO:0060485	mesenchyme development	21	703	242	17583	2.17	1.12	2.97E-04	1.65E-02

	plasma membrane bounded cell projection								
GO:0120036	organization	67	703	1112	17583	1.51	0.59	3.01E-04	1.66E-02
GO:0060675	ureteric bud morphogenesis	8	703	55	17583	3.64	1.86	3.03E-04	1.66E-02
GO:0030182	neuron differentiation	64	703	1052	17583	1.52	0.61	3.10E-04	1.68E-02
GO:0030900	forebrain development	30	703	397	17583	1.89	0.92	3.11E-04	1.68E-02
GO:0098609	cell-cell adhesion	38	703	543	17583	1.75	0.81	3.11E-04	1.68E-02
GO:0051592	response to calcium ion	15	703	149	17583	2.52	1.33	3.13E-04	1.68E-02
GO:0061138	morphogenesis of a branching epithelium	16	703	164	17583	2.44	1.29	3.13E-04	1.68E-02
GO:0055075	potassium ion homeostasis	6	703	34	17583	4.41	2.14	3.32E-04	1.77E-02
GO:0030030	cell projection organization	69	703	1158	17583	1.49	0.58	3.41E-04	1.81E-02
GO:0001755	neural crest cell migration	8	703	56	17583	3.57	1.84	3.49E-04	1.84E-02
GO:0072171	mesonephric tubule morphogenesis	8	703	56	17583	3.57	1.84	3.49E-04	1.84E-02
GO:0072088	nephron epithelium morphogenesis	9	703	68	17583	3.31	1.73	3.50E-04	1.84E-02
GO:0010467	gene expression	117	703	2186	17583	1.34	0.42	3.63E-04	1.91E-02
	positive regulation of nucleobase-containing								
GO:0045935	compound metabolic process	110	703	2034	17583	1.35	0.44	3.72E-04	1.95E-02
GO:0048699	generation of neurons	67	703	1121	17583	1.49	0.58	3.77E-04	1.97E-02
GO:0022607	cellular component assembly	127	703	2411	17583	1.32	0.40	3.90E-04	2.03E-02
GO:0045165	cell fate commitment	21	703	247	17583	2.13	1.09	3.95E-04	2.05E-02
GO:0050433	regulation of catecholamine secretion	8	703	57	17583	3.51	1.81	3.99E-04	2.06E-02
GO:0045927	positive regulation of growth	21	703	249	17583	2.11	1.08	4.41E-04	2.23E-02
GO:0051047	positive regulation of secretion	25	703	317	17583	1.97	0.98	4.44E-04	2.24E-02
GO:0009410	response to xenobiotic stimulus	31	703	424	17583	1.83	0.87	4.55E-04	2.28E-02
GO:0042733	embryonic digit morphogenesis	8	703	58	17583	3.45	1.79	4.56E-04	2.28E-02
GO:0090497	mesenchymal cell migration	8	703	58	17583	3.45	1.79	4.56E-04	2.28E-02
	epithelial tube branching involved in lung								
GO:0060441	morphogenesis	5	703	26	17583	4.81	2.27	4.64E-04	2.30E-02
GO:0086009	membrane repolarization	5	703	26	17583	4.81	2.27	4.64E-04	2.30E-02
	epithelial cell differentiation involved in kidney								
GO:0035850	development	6	703	36	17583	4.17	2.06	4.80E-04	2.38E-02
GO:0071695	anatomical structure maturation	19	703	218	17583	2.18	1.12	4.90E-04	2.42E-02

GO:0009968	negative regulation of signal transduction	72	703	1236	17583	1.46	0.54	4.96E-04	2.43E-02
GO:0046496	nicotinamide nucleotide metabolic process	9	703	71	17583	3.17	1.66	4.99E-04	2.43E-02
GO:0072028	nephron morphogenesis	9	703	71	17583	3.17	1.66	4.99E-04	2.43E-02
GO:0019362	pyridine nucleotide metabolic process	9	703	71	17583	3.17	1.66	4.99E-04	2.43E-02
GO:0001657	ureteric bud development	10	703	85	17583	2.94	1.56	5.57E-04	2.70E-02
GO:0099111	microtubule-based transport	18	703	204	17583	2.21	1.14	5.57E-04	2.70E-02
GO:0023057	negative regulation of signaling	76	703	1328	17583	1.43	0.52	5.97E-04	2.75E-02
GO:0010648	negative regulation of cell communication	76	703	1328	17583	1.43	0.52	5.97E-04	2.75E-02
GO:1903532	positive regulation of secretion by cell	23	703	289	17583	1.99	0.99	6.09E-04	2.79E-02
GO:0072164	mesonephric tubule development	10	703	86	17583	2.91	1.54	6.16E-04	2.80E-02
GO:0072163	mesonephric epithelium development	10	703	86	17583	2.91	1.54	6.16E-04	2.80E-02
GO:0035295	tube development	54	703	876	17583	1.54	0.62	6.17E-04	2.80E-02
GO:0007420	brain development	49	703	778	17583	1.58	0.66	6.50E-04	2.94E-02
GO:0048667	cell morphogenesis involved in neuron differentiation	31	703	433	17583	1.79	0.84	6.52E-04	2.94E-02
GO:0007417	central nervous system development	62	703	1041	17583	1.49	0.57	6.56E-04	2.94E-02
GO:0008219	cell death	65	703	1103	17583	1.47	0.56	6.60E-04	2.94E-02
GO:0098930	axonal transport	8	703	61	17583	3.28	1.71	6.68E-04	2.94E-02
GO:0003180	aortic valve morphogenesis	6	703	38	17583	3.95	1.98	6.77E-04	2.98E-02
GO:0023051	regulation of signaling	167	703	3352	17583	1.25	0.32	6.87E-04	3.01E-02
GO:1903055	positive regulation of extracellular matrix organization	5	703	28	17583	4.47	2.16	7.09E-04	3.10E-02
GO:0012501	programmed cell death	63	703	1070	17583	1.47	0.56	8.04E-04	3.49E-02
GO:0010970	transport along microtubule	15	703	163	17583	2.30	1.20	8.47E-04	3.67E-02
GO:0072006	nephron development	13	703	133	17583	2.44	1.29	8.87E-04	3.83E-02
GO:0072009	nephron epithelium development	11	703	104	17583	2.65	1.40	9.07E-04	3.90E-02
GO:0001823	mesonephros development	10	703	90	17583	2.78	1.47	9.07E-04	3.90E-02
GO:0044249	cellular biosynthetic process	125	703	2421	17583	1.29	0.37	9.51E-04	4.04E-02
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	21	703	264	17583	1.99	0.99	9.65E-04	4.08E-02
GO:0044085	cellular component biogenesis	135	703	2651	17583	1.27	0.35	1.03E-03	4.10E-02

GO:0014741	negative regulation of muscle hypertrophy	5	703	30	17583	4.17	2.06	1.04E-03	4.10E-02
GO:0003151	outflow tract morphogenesis	9	703	78	17583	2.89	1.53	1.06E-03	4.10E-02
GO:0032879	regulation of localization	109	703	2073	17583	1.32	0.40	1.08E-03	4.10E-02
GO:0032990	cell part morphogenesis	34	703	505	17583	1.68	0.75	1.17E-03	4.10E-02
GO:0072524	pyridine-containing compound metabolic process	9	703	79	17583	2.85	1.51	1.17E-03	4.10E-02
GO:0072078	nephron tubule morphogenesis	8	703	66	17583	3.03	1.60	1.19E-03	4.10E-02
GO:0019915	lipid storage	6	703	42	17583	3.57	1.84	1.26E-03	4.10E-02
GO:0019674	NAD metabolic process	6	703	42	17583	3.57	1.84	1.26E-03	4.10E-02
GO:0051239	regulation of multicellular organismal process	138	703	2734	17583	1.26	0.34	1.29E-03	4.10E-02
GO:0006915	apoptotic process	60	703	1028	17583	1.46	0.55	1.29E-03	4.10E-02
GO:0035304	regulation of protein dephosphorylation	10	703	94	17583	2.66	1.41	1.30E-03	4.10E-02
GO:0048469	cell maturation	15	703	171	17583	2.19	1.13	1.41E-03	4.10E-02
GO:0021537	telencephalon development	21	703	272	17583	1.93	0.95	1.42E-03	4.10E-02
GO:0003176	aortic valve development	6	703	43	17583	3.49	1.80	1.46E-03	4.10E-02
GO:0006796	phosphate-containing compound metabolic process	97	703	1826	17583	1.33	0.41	1.46E-03	4.10E-02
GO:0007409	axonogenesis	26	703	362	17583	1.80	0.85	1.46E-03	4.10E-02
GO:0010646	regulation of cell communication	165	703	3362	17583	1.23	0.30	1.47E-03	4.10E-02
GO:0051049	regulation of transport	93	703	1739	17583	1.34	0.42	1.47E-03	4.10E-02
GO:0007389	pattern specification process	31	703	455	17583	1.70	0.77	1.47E-03	4.10E-02
GO:0000904	cell morphogenesis involved in differentiation	36	703	551	17583	1.63	0.71	1.50E-03	4.10E-02
GO:0001558	regulation of cell growth	29	703	418	17583	1.74	0.80	1.50E-03	4.10E-02
GO:0048812	neuron projection morphogenesis	32	703	475	17583	1.68	0.75	1.53E-03	4.10E-02
GO:0051402	neuron apoptotic process	10	703	96	17583	2.61	1.38	1.55E-03	4.10E-02
GO:0048732	gland development	29	703	419	17583	1.73	0.79	1.56E-03	4.10E-02
GO:0045921	positive regulation of exocytosis	9	703	82	17583	2.75	1.46	1.56E-03	4.10E-02
GO:0044237	cellular metabolic process	296	703	6489	17583	1.14	0.19	1.67E-03	4.28E-02
GO:1990573	potassium ion import across plasma membrane	6	703	44	17583	3.41	1.77	1.67E-03	4.28E-02

	ribonucleoprotein complex subunit								
GO:0071826	organization	17	703	207	17583	2.05	1.04	1.69E-03	4.32E-02
GO:0072210	metanephric nephron development	5	703	33	17583	3.79	1.92	1.76E-03	4.48E-02
GO:0048566	embryonic digestive tract development	5	703	33	17583	3.79	1.92	1.76E-03	4.48E-02
GO:0010035	response to inorganic substance	35	703	537	17583	1.63	0.71	1.77E-03	4.52E-02
GO:0010038	response to metal ion	26	703	367	17583	1.77	0.83	1.78E-03	4.53E-02
	negative regulation of protein modification								
GO:0031400	process	32	703	480	17583	1.67	0.74	1.81E-03	4.59E-02
	plasma membrane bounded cell projection								
GO:0120039	morphogenesis	32	703	480	17583	1.67	0.74	1.81E-03	4.59E-02
GO:0061333	renal tubule morphogenesis	8	703	70	17583	2.86	1.52	1.82E-03	4.61E-02
GO:0014743	regulation of muscle hypertrophy	7	703	57	17583	3.07	1.62	1.83E-03	4.62E-02
GO:0008089	anterograde axonal transport	6	703	45	17583	3.33	1.74	1.91E-03	4.74E-02
GO:0048701	embryonic cranial skeleton morphogenesis	6	703	45	17583	3.33	1.74	1.91E-03	4.74E-02
	branching involved in ureteric bud								
GO:0001658	morphogenesis	6	703	45	17583	3.33	1.74	1.91E-03	4.74E-02
GO:0048706	embryonic skeletal system development	12	703	129	17583	2.33	1.22	1.99E-03	4.78E-02
GO:1901700	response to oxygen-containing compound	83	703	1538	17583	1.35	0.43	1.99E-03	4.78E-02
GO:0003143	embryonic heart tube morphogenesis	8	703	71	17583	2.82	1.49	2.01E-03	4.82E-02
GO:0061337	cardiac conduction	8	703	71	17583	2.82	1.49	2.01E-03	4.82E-02
GO:0035264	multicellular organism growth	9	703	85	17583	2.65	1.41	2.05E-03	4.90E-02
GO:0045926	negative regulation of growth	19	703	245	17583	1.94	0.96	2.06E-03	4.91E-02
GO:0048858	cell projection morphogenesis	32	703	485	17583	1.65	0.72	2.14E-03	5.10E-02
GO:0019637	organophosphate metabolic process	54	703	926	17583	1.46	0.54	2.16E-03	5.14E-02
GO:0071805	potassium ion transmembrane transport	14	703	162	17583	2.16	1.11	2.17E-03	5.14E-02
GO:0035108	limb morphogenesis	13	703	146	17583	2.23	1.16	2.17E-03	5.14E-02
GO:0035107	appendage morphogenesis	13	703	146	17583	2.23	1.16	2.17E-03	5.14E-02
GO:0017156	calcium-ion regulated exocytosis	6	703	46	17583	3.26	1.71	2.18E-03	5.14E-02
GO:0021575	hindbrain morphogenesis	6	703	46	17583	3.26	1.71	2.18E-03	5.14E-02
GO:0060425	lung morphogenesis	6	703	46	17583	3.26	1.71	2.18E-03	5.14E-02
GO:0061326	renal tubule development	9	703	86	17583	2.62	1.39	2.24E-03	5.26E-02

GO:0001708	cell fate specification	9	703	86	17583	2.62	1.39	2.24E-03	5.26E-02
GO:0006793	phosphorus metabolic process	97	703	1852	17583	1.31	0.39	2.26E-03	5.30E-02
GO:0007219	Notch signaling pathway	11	703	116	17583	2.37	1.25	2.34E-03	5.48E-02
GO:0070925	organelle assembly	49	703	827	17583	1.48	0.57	2.37E-03	5.55E-02
GO:0016071	mRNA metabolic process	38	703	606	17583	1.57	0.65	2.42E-03	5.62E-02
GO:0048585	negative regulation of response to stimulus	85	703	1593	17583	1.33	0.42	2.44E-03	5.64E-02
GO:0045665	negative regulation of neuron differentiation	8	703	73	17583	2.74	1.45	2.45E-03	5.64E-02
GO:0016043	cellular component organization	254	703	5509	17583	1.15	0.21	2.47E-03	5.68E-02
	positive regulation of regulated secretory pathway								
GO:1903307	pathway	6	703	47	17583	3.19	1.67	2.47E-03	5.68E-02
GO:1905314	semi-lunar valve development	6	703	47	17583	3.19	1.67	2.47E-03	5.68E-02
GO:0032989	cellular component morphogenesis	38	703	607	17583	1.57	0.65	2.49E-03	5.70E-02
GO:1901698	response to nitrogen compound	60	703	1058	17583	1.42	0.50	2.52E-03	5.76E-02
	positive regulation of establishment of protein localization								
GO:1904951	localization	23	703	321	17583	1.79	0.84	2.54E-03	5.79E-02
GO:0003179	heart valve morphogenesis	7	703	60	17583	2.92	1.54	2.56E-03	5.83E-02
GO:0017157	regulation of exocytosis	16	703	198	17583	2.02	1.02	2.56E-03	5.84E-02
GO:1901652	response to peptide	30	703	453	17583	1.66	0.73	2.64E-03	5.99E-02
GO:0002009	morphogenesis of an epithelium	30	703	453	17583	1.66	0.73	2.64E-03	5.99E-02
GO:0007224	smoothened signaling pathway	9	703	88	17583	2.56	1.36	2.66E-03	6.02E-02
GO:2000177	regulation of neural precursor cell proliferation	9	703	88	17583	2.56	1.36	2.66E-03	6.02E-02
GO:0051094	positive regulation of developmental process	72	703	1317	17583	1.37	0.45	2.71E-03	6.13E-02
GO:0051222	positive regulation of protein transport	22	703	305	17583	1.80	0.85	2.77E-03	6.19E-02
GO:0072073	kidney epithelium development	12	703	134	17583	2.24	1.16	2.78E-03	6.20E-02
GO:0045598	regulation of fat cell differentiation	12	703	134	17583	2.24	1.16	2.78E-03	6.20E-02
GO:0021696	cerebellar cortex morphogenesis	5	703	36	17583	3.47	1.80	2.79E-03	6.20E-02
GO:1902742	apoptotic process involved in development	5	703	36	17583	3.47	1.80	2.79E-03	6.20E-02
GO:0010821	regulation of mitochondrion organization	13	703	150	17583	2.17	1.12	2.79E-03	6.20E-02
GO:0048483	autonomic nervous system development	6	703	48	17583	3.13	1.64	2.80E-03	6.20E-02
GO:0016079	synaptic vesicle exocytosis	7	703	61	17583	2.87	1.52	2.84E-03	6.29E-02
GO:0072001	renal system development	22	703	306	17583	1.80	0.85	2.89E-03	6.38E-02

GO:0060993	kidney morphogenesis	9	703	89	17583	2.53	1.34	2.89E-03	6.38E-02
GO:0045936	negative regulation of phosphate metabolic process	28	703	419	17583	1.67	0.74	3.03E-03	6.45E-02
GO:0051235	maintenance of location	14	703	168	17583	2.08	1.06	3.09E-03	6.49E-02
GO:0030326	embryonic limb morphogenesis	11	703	120	17583	2.29	1.20	3.11E-03	6.50E-02
GO:0035113	embryonic appendage morphogenesis	11	703	120	17583	2.29	1.20	3.11E-03	6.50E-02
GO:0061564	axon development	27	703	401	17583	1.68	0.75	3.14E-03	6.50E-02
GO:0010563	negative regulation of phosphorus metabolic process	28	703	420	17583	1.67	0.74	3.14E-03	6.50E-02
GO:0021700	developmental maturation	20	703	272	17583	1.84	0.88	3.15E-03	6.52E-02
GO:0086001	cardiac muscle cell action potential	6	703	49	17583	3.06	1.61	3.15E-03	6.52E-02
GO:0009117	nucleotide metabolic process	33	703	517	17583	1.60	0.67	3.19E-03	6.58E-02
GO:0060323	head morphogenesis	5	703	37	17583	3.38	1.76	3.22E-03	6.63E-02
GO:0031076	embryonic camera-type eye development	5	703	37	17583	3.38	1.76	3.22E-03	6.63E-02
GO:0014059	regulation of dopamine secretion	5	703	37	17583	3.38	1.76	3.22E-03	6.63E-02
GO:0044772	mitotic cell cycle phase transition	14	703	169	17583	2.07	1.05	3.26E-03	6.70E-02
GO:0009888	tissue development	90	703	1720	17583	1.31	0.39	3.27E-03	6.71E-02
GO:0006163	purine nucleotide metabolic process	30	703	460	17583	1.63	0.71	3.32E-03	6.76E-02
GO:0010243	response to organonitrogen compound	55	703	967	17583	1.42	0.51	3.40E-03	6.92E-02
GO:0070997	neuron death	10	703	106	17583	2.36	1.24	3.42E-03	6.94E-02
GO:0009966	regulation of signal transduction	145	703	2966	17583	1.22	0.29	3.43E-03	6.95E-02
GO:0008380	RNA splicing	25	703	366	17583	1.71	0.77	3.45E-03	6.98E-02
GO:0048589	developmental growth	27	703	404	17583	1.67	0.74	3.48E-03	7.03E-02
GO:0040007	growth	27	703	404	17583	1.67	0.74	3.48E-03	7.03E-02
GO:0021536	diencephalon development	8	703	77	17583	2.60	1.38	3.53E-03	7.13E-02
GO:0048562	embryonic organ morphogenesis	21	703	293	17583	1.79	0.84	3.56E-03	7.17E-02
GO:0030308	negative regulation of cell growth	15	703	188	17583	2.00	1.00	3.68E-03	7.17E-02
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	18	703	240	17583	1.88	0.91	3.69E-03	7.17E-02
GO:0000398	mRNA splicing, via spliceosome	18	703	240	17583	1.88	0.91	3.69E-03	7.17E-02

GO:0086002	cardiac muscle cell action potential involved in contraction	5	703	38	17583	3.29	1.72	3.70E-03	7.17E-02
GO:0071840	cellular component organization or biogenesis	261	703	5719	17583	1.14	0.19	3.75E-03	7.17E-02
GO:0009058	biosynthetic process	128	703	2584	17583	1.24	0.31	3.80E-03	7.17E-02
GO:0000902	cell morphogenesis	42	703	703	17583	1.49	0.58	3.80E-03	7.17E-02
GO:0043502	regulation of muscle adaptation	8	703	78	17583	2.57	1.36	3.85E-03	7.17E-02
GO:0030154	cell differentiation	170	703	3556	17583	1.20	0.26	3.86E-03	7.17E-02
GO:0061458	reproductive system development	21	703	295	17583	1.78	0.83	3.87E-03	7.17E-02
GO:0048638	regulation of developmental growth	22	703	314	17583	1.75	0.81	3.97E-03	7.17E-02
GO:0051646	mitochondrion localization	6	703	51	17583	2.94	1.56	3.97E-03	7.17E-02
GO:0048639	positive regulation of developmental growth	13	703	156	17583	2.08	1.06	3.99E-03	7.17E-02
GO:0051179	localization	210	703	4502	17583	1.17	0.22	3.99E-03	7.17E-02
GO:0001822	kidney development	21	703	296	17583	1.77	0.83	4.02E-03	7.17E-02
GO:0006469	negative regulation of protein kinase activity	16	703	207	17583	1.93	0.95	4.05E-03	7.17E-02
GO:0006753	nucleoside phosphate metabolic process	33	703	525	17583	1.57	0.65	4.05E-03	7.17E-02
GO:0006813	potassium ion transport	14	703	173	17583	2.02	1.02	4.07E-03	7.17E-02
GO:0002064	epithelial cell development	15	703	190	17583	1.97	0.98	4.08E-03	7.17E-02
GO:0007595	lactation	5	703	39	17583	3.21	1.68	4.23E-03	7.17E-02
GO:0001947	heart looping	7	703	65	17583	2.69	1.43	4.24E-03	7.17E-02
GO:0035239	tube morphogenesis	40	703	667	17583	1.50	0.58	4.27E-03	7.17E-02
GO:0060429	epithelium development	59	703	1063	17583	1.39	0.47	4.33E-03	7.17E-02
GO:0003002	regionalization	23	703	335	17583	1.72	0.78	4.36E-03	7.17E-02
GO:0034641	cellular nitrogen compound metabolic process	160	703	3333	17583	1.20	0.26	4.36E-03	7.17E-02
GO:0008152	metabolic process	352	703	7967	17583	1.11	0.14	4.38E-03	7.17E-02
GO:0000375	RNA splicing, via transesterification reactions	18	703	244	17583	1.85	0.88	4.41E-03	7.17E-02
GO:0021695	cerebellar cortex development	6	703	52	17583	2.89	1.53	4.43E-03	7.17E-02
GO:0001503	ossification	20	703	281	17583	1.78	0.83	4.59E-03	7.17E-02
GO:0072657	protein localization to membrane	29	703	451	17583	1.61	0.69	4.61E-03	7.17E-02
GO:0021987	cerebral cortex development	11	703	126	17583	2.18	1.13	4.62E-03	7.17E-02

GO:0044782	cilium organization	24	703	356	17583	1.69	0.75	4.73E-03	7.26E-02
GO:0043009	chordate embryonic development	39	703	651	17583	1.50	0.58	4.77E-03	7.31E-02
GO:0097485	neuron projection guidance	17	703	228	17583	1.86	0.90	4.77E-03	7.31E-02
GO:0007411	axon guidance	17	703	228	17583	1.86	0.90	4.77E-03	7.31E-02
GO:0001933	negative regulation of protein phosphorylation	22	703	319	17583	1.72	0.79	4.80E-03	7.36E-02
GO:0032570	response to progesterone	5	703	40	17583	3.13	1.64	4.81E-03	7.36E-02
GO:0007155	cell adhesion	54	703	963	17583	1.40	0.49	4.89E-03	7.48E-02
GO:0072080	nephron tubule development	8	703	81	17583	2.47	1.30	4.96E-03	7.55E-02
GO:0021915	neural tube development	13	703	160	17583	2.03	1.02	4.99E-03	7.59E-02
GO:0048534	hematopoietic or lymphoid organ development	9	703	96	17583	2.34	1.23	5.00E-03	7.59E-02
GO:0048869	cellular developmental process	170	703	3579	17583	1.19	0.25	5.03E-03	7.63E-02
GO:1901576	organic substance biosynthetic process	124	703	2515	17583	1.23	0.30	5.10E-03	7.73E-02
GO:0048663	neuron fate commitment	7	703	67	17583	2.61	1.39	5.11E-03	7.73E-02
GO:0050714	positive regulation of protein secretion	12	703	144	17583	2.08	1.06	5.16E-03	7.80E-02
GO:0035270	endocrine system development	11	703	128	17583	2.15	1.10	5.24E-03	7.92E-02
GO:0014020	primary neural tube formation	9	703	97	17583	2.32	1.21	5.38E-03	8.11E-02
GO:0010256	endomembrane system organization	34	703	555	17583	1.53	0.62	5.40E-03	8.12E-02
GO:0016070	RNA metabolic process	84	703	1619	17583	1.30	0.38	5.46E-03	8.20E-02
GO:0010611	regulation of cardiac muscle hypertrophy	6	703	54	17583	2.78	1.47	5.48E-03	8.22E-02
GO:0044770	cell cycle phase transition	14	703	179	17583	1.96	0.97	5.57E-03	8.35E-02
GO:0030855	epithelial cell differentiation	37	703	617	17583	1.50	0.58	5.64E-03	8.45E-02
GO:0030048	actin filament-based movement	9	703	98	17583	2.30	1.20	5.78E-03	8.64E-02
GO:0051952	regulation of amine transport	9	703	98	17583	2.30	1.20	5.78E-03	8.64E-02
GO:0016331	morphogenesis of embryonic epithelium	12	703	146	17583	2.06	1.04	5.79E-03	8.64E-02
GO:1903530	regulation of secretion by cell	34	703	558	17583	1.52	0.61	5.86E-03	8.75E-02
GO:1903305	regulation of regulated secretory pathway	11	703	130	17583	2.12	1.08	5.93E-03	8.83E-02
GO:0051240	positive regulation of multicellular organismal process	78	703	1492	17583	1.31	0.39	5.96E-03	8.87E-02
GO:1901566	organonitrogen compound biosynthetic process	70	703	1317	17583	1.33	0.41	5.98E-03	8.88E-02

GO:0050793	regulation of developmental process	121	703	2459	17583	1.23	0.30	6.02E-03	8.88E-02
GO:0042326	negative regulation of phosphorylation	24	703	363	17583	1.65	0.73	6.03E-03	8.88E-02
GO:0009653	anatomical structure morphogenesis	111	703	2232	17583	1.24	0.31	6.08E-03	8.88E-02
GO:0021983	pituitary gland development	5	703	42	17583	2.98	1.57	6.15E-03	8.88E-02
GO:0060173	limb development	14	703	181	17583	1.93	0.95	6.16E-03	8.88E-02
GO:0048736	appendage development	14	703	181	17583	1.93	0.95	6.16E-03	8.88E-02
GO:0030324	lung development	14	703	181	17583	1.93	0.95	6.16E-03	8.88E-02
GO:0051668	localization within membrane	33	703	540	17583	1.53	0.61	6.20E-03	8.89E-02
GO:0006807	nitrogen compound metabolic process	298	703	6674	17583	1.12	0.16	6.25E-03	8.94E-02
GO:0000082	G1/S transition of mitotic cell cycle	8	703	84	17583	2.38	1.25	6.30E-03	9.00E-02
GO:0022618	ribonucleoprotein complex assembly	15	703	199	17583	1.89	0.91	6.35E-03	9.06E-02
GO:0034248	regulation of amide metabolic process	29	703	462	17583	1.57	0.65	6.44E-03	9.18E-02
GO:1901653	cellular response to peptide	21	703	309	17583	1.70	0.77	6.63E-03	9.43E-02
GO:0061371	determination of heart left/right asymmetry	7	703	70	17583	2.50	1.32	6.66E-03	9.48E-02
GO:0048598	embryonic morphogenesis	35	703	583	17583	1.50	0.59	6.67E-03	9.48E-02
GO:0051168	nuclear export	11	703	132	17583	2.08	1.06	6.68E-03	9.49E-02
GO:0032835	glomerulus development	6	703	56	17583	2.68	1.42	6.70E-03	9.50E-02
GO:0072132	mesenchyme morphogenesis	6	703	56	17583	2.68	1.42	6.70E-03	9.50E-02
GO:0048608	reproductive structure development	20	703	291	17583	1.72	0.78	6.79E-03	9.61E-02
GO:0044271	cellular nitrogen compound biosynthetic process	81	703	1567	17583	1.29	0.37	6.86E-03	9.70E-02
GO:0021587	cerebellum morphogenesis	5	703	43	17583	2.91	1.54	6.91E-03	9.75E-02
GO:0050805	negative regulation of synaptic transmission	5	703	43	17583	2.91	1.54	6.91E-03	9.75E-02
GO:0048666	neuron development	47	703	832	17583	1.41	0.50	6.92E-03	9.76E-02
GO:0031175	neuron projection development	39	703	666	17583	1.46	0.55	6.93E-03	9.77E-02
GO:0048729	tissue morphogenesis	34	703	565	17583	1.51	0.59	7.07E-03	9.96E-02
GO:2000112	regulation of cellular macromolecule biosynthetic process	30	703	485	17583	1.55	0.63	7.08E-03	9.96E-02
GO:0032922	circadian regulation of gene expression	7	703	71	17583	2.47	1.30	7.25E-03	1.01E-01
GO:0044843	cell cycle G1/S phase transition	8	703	86	17583	2.33	1.22	7.34E-03	1.02E-01
GO:0008589	regulation of smoothened signaling pathway	8	703	86	17583	2.33	1.22	7.34E-03	1.02E-01

GO:0043434	response to peptide hormone	24	703	369	17583	1.63	0.70	7.37E-03	1.02E-01
GO:1903053	regulation of extracellular matrix organization	6	703	57	17583	2.63	1.40	7.38E-03	1.02E-01
GO:0030282	bone mineralization	6	703	57	17583	2.63	1.40	7.38E-03	1.02E-01
GO:0097190	apoptotic signaling pathway	21	703	312	17583	1.68	0.75	7.39E-03	1.02E-01
GO:0030323	respiratory tube development	14	703	185	17583	1.89	0.92	7.50E-03	1.03E-01
GO:0006397	mRNA processing	28	703	448	17583	1.56	0.64	7.62E-03	1.03E-01
GO:0030856	regulation of epithelial cell differentiation	12	703	151	17583	1.99	0.99	7.63E-03	1.03E-01
GO:0051241	negative regulation of multicellular organismal process	56	703	1028	17583	1.36	0.45	7.67E-03	1.03E-01
GO:0051641	cellular localization	128	703	2639	17583	1.21	0.28	7.68E-03	1.03E-01
GO:0008406	gonad development	16	703	221	17583	1.81	0.86	7.70E-03	1.03E-01
GO:0006584	catecholamine metabolic process	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:0009712	catechol-containing compound metabolic process	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:0009154	purine ribonucleotide catabolic process	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:1902692	regulation of neuroblast proliferation	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:0086003	cardiac muscle cell contraction	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:0010171	body morphogenesis	5	703	44	17583	2.84	1.51	7.73E-03	1.03E-01
GO:0000245	spliceosomal complex assembly	7	703	72	17583	2.43	1.28	7.88E-03	1.03E-01
GO:1904888	cranial skeletal system development	7	703	72	17583	2.43	1.28	7.88E-03	1.03E-01
GO:0071277	cellular response to calcium ion	8	703	87	17583	2.30	1.20	7.90E-03	1.03E-01
GO:0009749	response to glucose	11	703	135	17583	2.04	1.03	7.95E-03	1.03E-01
GO:0051050	positive regulation of transport	50	703	902	17583	1.39	0.47	7.97E-03	1.03E-01
GO:1901654	response to ketone	15	703	204	17583	1.84	0.88	8.00E-03	1.03E-01
GO:1990778	protein localization to cell periphery	17	703	240	17583	1.77	0.83	8.01E-03	1.03E-01
GO:0032869	cellular response to insulin stimulus	12	703	152	17583	1.97	0.98	8.05E-03	1.03E-01
GO:0035065	regulation of histone acetylation	6	703	58	17583	2.59	1.37	8.11E-03	1.03E-01
GO:0072521	purine-containing compound metabolic process	30	703	490	17583	1.53	0.61	8.15E-03	1.03E-01
GO:0009792	embryo development ending in birth or egg hatching	39	703	673	17583	1.45	0.54	8.19E-03	1.03E-01

GO:0046907	intracellular transport	71	703	1358	17583	1.31	0.39	8.27E-03	1.03E-01
GO:0061448	connective tissue development	16	703	223	17583	1.79	0.84	8.39E-03	1.03E-01
GO:0021675	nerve development	8	703	88	17583	2.27	1.19	8.50E-03	1.03E-01
GO:0043933	protein-containing complex organization	73	703	1404	17583	1.30	0.38	8.54E-03	1.03E-01
GO:0003170	heart valve development	7	703	73	17583	2.40	1.26	8.55E-03	1.03E-01
GO:0043266	regulation of potassium ion transport	9	703	104	17583	2.16	1.11	8.72E-03	1.03E-01
GO:0048568	embryonic organ development	28	703	453	17583	1.55	0.63	8.82E-03	1.03E-01
	negative regulation of DNA-binding								
GO:0043433	transcription factor activity	13	703	171	17583	1.90	0.93	8.84E-03	1.03E-01
GO:0001764	neuron migration	11	703	137	17583	2.01	1.01	8.90E-03	1.03E-01
GO:0055067	monovalent inorganic cation homeostasis	12	703	154	17583	1.95	0.96	8.94E-03	1.03E-01
GO:0070727	cellular macromolecule localization	95	703	1898	17583	1.25	0.32	8.95E-03	1.03E-01
GO:0051046	regulation of secretion	36	703	615	17583	1.46	0.55	8.95E-03	1.03E-01
GO:0048705	skeletal system morphogenesis	16	703	225	17583	1.78	0.83	9.13E-03	1.04E-01
	regulation of potassium ion transmembrane								
GO:1901379	transport	8	703	89	17583	2.25	1.17	9.13E-03	1.04E-01
GO:0007029	endoplasmic reticulum organization	8	703	89	17583	2.25	1.17	9.13E-03	1.04E-01
GO:0033365	protein localization to organelle	40	703	699	17583	1.43	0.52	9.26E-03	1.05E-01
GO:0001841	neural tube formation	9	703	105	17583	2.14	1.10	9.30E-03	1.05E-01
GO:0034101	erythrocyte homeostasis	9	703	105	17583	2.14	1.10	9.30E-03	1.05E-01
	negative regulation of epithelial cell								
GO:0050680	proliferation	11	703	138	17583	1.99	1.00	9.40E-03	1.06E-01
GO:0046887	positive regulation of hormone secretion	11	703	138	17583	1.99	1.00	9.40E-03	1.06E-01
GO:0048167	regulation of synaptic plasticity	14	703	190	17583	1.84	0.88	9.48E-03	1.07E-01
GO:0045137	development of primary sexual characteristics	16	703	226	17583	1.77	0.82	9.52E-03	1.07E-01
GO:0042789	mRNA transcription by RNA polymerase II	5	703	46	17583	2.72	1.44	9.60E-03	1.08E-01
GO:0021545	cranial nerve development	6	703	60	17583	2.50	1.32	9.73E-03	1.10E-01
GO:0051169	nuclear transport	17	703	246	17583	1.73	0.79	1.02E-02	1.15E-01
GO:0008654	phospholipid biosynthetic process	17	703	246	17583	1.73	0.79	1.02E-02	1.15E-01
GO:0006913	nucleocytoplasmic transport	17	703	246	17583	1.73	0.79	1.02E-02	1.15E-01
GO:0043269	regulation of ion transport	40	703	704	17583	1.42	0.51	1.04E-02	1.16E-01

GO:0048660	regulation of smooth muscle cell proliferation	11	703	140	17583	1.97	0.97	1.05E-02	1.16E-01
GO:0009746	response to hexose	11	703	140	17583	1.97	0.97	1.05E-02	1.16E-01
GO:0001843	neural tube closure	8	703	91	17583	2.20	1.14	1.05E-02	1.16E-01
GO:0032006	regulation of TOR signaling	9	703	107	17583	2.10	1.07	1.06E-02	1.16E-01
GO:0048468	cell development	106	703	2160	17583	1.23	0.30	1.06E-02	1.16E-01
	negative regulation of I-kappaB kinase/NF-kappaB signaling	5	703	47	17583	2.66	1.41	1.06E-02	1.16E-01
GO:0043124	intraciliary transport	5	703	47	17583	2.66	1.41	1.06E-02	1.16E-01
GO:0021953	central nervous system neuron differentiation	13	703	175	17583	1.86	0.89	1.07E-02	1.16E-01
GO:0034620	cellular response to unfolded protein	7	703	76	17583	2.30	1.20	1.08E-02	1.17E-01
GO:0045664	regulation of neuron differentiation	14	703	193	17583	1.81	0.86	1.09E-02	1.18E-01
GO:0033036	macromolecule localization	113	703	2323	17583	1.22	0.28	1.09E-02	1.19E-01
GO:0009791	post-embryonic development	8	703	92	17583	2.17	1.12	1.12E-02	1.22E-01
GO:0060606	tube closure	8	703	92	17583	2.17	1.12	1.12E-02	1.22E-01
GO:0046034	ATP metabolic process	12	703	159	17583	1.89	0.92	1.15E-02	1.22E-01
GO:0006417	regulation of translation	25	703	403	17583	1.55	0.63	1.16E-02	1.22E-01
GO:0032663	regulation of interleukin-2 production	6	703	62	17583	2.42	1.28	1.16E-02	1.22E-01
GO:0001838	embryonic epithelial tube formation	10	703	125	17583	2.00	1.00	1.16E-02	1.22E-01
GO:0001666	response to hypoxia	18	703	268	17583	1.68	0.75	1.16E-02	1.22E-01
GO:1901983	regulation of protein acetylation	7	703	77	17583	2.27	1.19	1.17E-02	1.22E-01
GO:0033673	negative regulation of kinase activity	16	703	231	17583	1.73	0.79	1.17E-02	1.22E-01
GO:0042981	regulation of apoptotic process	74	703	1446	17583	1.28	0.36	1.17E-02	1.22E-01
GO:0008542	visual learning	5	703	48	17583	2.61	1.38	1.18E-02	1.22E-01
GO:0032388	positive regulation of intracellular transport	14	703	195	17583	1.80	0.84	1.19E-02	1.22E-01
GO:0032526	response to retinoic acid	9	703	109	17583	2.07	1.05	1.19E-02	1.22E-01
GO:0045995	regulation of embryonic development	8	703	93	17583	2.15	1.11	1.20E-02	1.22E-01
	nucleobase-containing compound metabolic process	133	703	2793	17583	1.19	0.25	1.20E-02	1.22E-01
GO:0006139	primary metabolic process	316	703	7194	17583	1.10	0.14	1.21E-02	1.22E-01
GO:0007018	microtubule-based movement	24	703	385	17583	1.56	0.64	1.22E-02	1.22E-01
GO:0060341	regulation of cellular localization	51	703	946	17583	1.35	0.43	1.24E-02	1.22E-01

GO:0051649	establishment of localization in cell	88	703	1764	17583	1.25	0.32	1.25E-02	1.22E-01
GO:0032507	maintenance of protein location in cell	6	703	63	17583	2.38	1.25	1.26E-02	1.22E-01
GO:0032543	mitochondrial translation	9	703	110	17583	2.05	1.03	1.27E-02	1.22E-01
GO:0003007	heart morphogenesis	17	703	252	17583	1.69	0.75	1.28E-02	1.22E-01
	positive regulation of protein								
GO:0035307	dephosphorylation	5	703	49	17583	2.55	1.35	1.30E-02	1.22E-01
GO:0048546	digestive tract morphogenesis	5	703	49	17583	2.55	1.35	1.30E-02	1.22E-01
GO:0035094	response to nicotine	5	703	49	17583	2.55	1.35	1.30E-02	1.22E-01
GO:0010720	positive regulation of cell development	28	703	467	17583	1.50	0.58	1.30E-02	1.22E-01
GO:0065003	protein-containing complex assembly	65	703	1254	17583	1.30	0.37	1.31E-02	1.22E-01
GO:0006996	organelle organization	142	703	3011	17583	1.18	0.24	1.32E-02	1.22E-01
GO:0051301	cell division	30	703	508	17583	1.48	0.56	1.32E-02	1.22E-01
	negative regulation of intracellular signal								
GO:1902532	transduction	30	703	509	17583	1.47	0.56	1.35E-02	1.22E-01
GO:0040014	regulation of multicellular organism growth	6	703	64	17583	2.34	1.23	1.37E-02	1.22E-01
GO:0019882	antigen processing and presentation	8	703	95	17583	2.11	1.07	1.37E-02	1.22E-01
GO:0048704	embryonic skeletal system morphogenesis	8	703	95	17583	2.11	1.07	1.37E-02	1.22E-01
GO:0006412	translation	23	703	370	17583	1.55	0.64	1.40E-02	1.22E-01
GO:0045595	regulation of cell differentiation	79	703	1570	17583	1.26	0.33	1.40E-02	1.22E-01
GO:0071248	cellular response to metal ion	14	703	199	17583	1.76	0.82	1.41E-02	1.22E-01
GO:0009261	ribonucleotide catabolic process	5	703	50	17583	2.50	1.32	1.42E-02	1.22E-01
	endoplasmic reticulum unfolded protein								
GO:0030968	response	5	703	50	17583	2.50	1.32	1.42E-02	1.22E-01
GO:0071453	cellular response to oxygen levels	11	703	146	17583	1.88	0.91	1.43E-02	1.22E-01
GO:0006518	peptide metabolic process	31	703	532	17583	1.46	0.54	1.44E-02	1.22E-01
	cellular response to topologically incorrect								
GO:0035967	protein	8	703	96	17583	2.08	1.06	1.46E-02	1.22E-01
GO:0009798	axis specification	8	703	96	17583	2.08	1.06	1.46E-02	1.22E-01
GO:0034612	response to tumor necrosis factor	14	703	200	17583	1.75	0.81	1.47E-02	1.22E-01
GO:0048872	homeostasis of number of cells	17	703	256	17583	1.66	0.73	1.49E-02	1.22E-01

	nucleobase-containing small molecule								
GO:0055086	metabolic process	34	703	596	17583	1.43	0.51	1.52E-02	1.22E-01
GO:0008104	protein localization	93	703	1892	17583	1.23	0.30	1.52E-02	1.22E-01
GO:0009790	embryo development	55	703	1044	17583	1.32	0.40	1.52E-02	1.22E-01
GO:0007548	sex differentiation	18	703	276	17583	1.63	0.71	1.54E-02	1.22E-01
GO:0090307	mitotic spindle assembly	5	703	51	17583	2.45	1.29	1.56E-02	1.22E-01
GO:1902895	positive regulation of miRNA transcription	5	703	51	17583	2.45	1.29	1.56E-02	1.22E-01
GO:0016925	protein sumoylation	5	703	51	17583	2.45	1.29	1.56E-02	1.22E-01
GO:0009299	mRNA transcription	5	703	51	17583	2.45	1.29	1.56E-02	1.22E-01
GO:0043392	negative regulation of DNA binding	5	703	51	17583	2.45	1.29	1.56E-02	1.22E-01
GO:0051960	regulation of nervous system development	27	703	454	17583	1.49	0.57	1.57E-02	1.22E-01
GO:0034284	response to monosaccharide	11	703	148	17583	1.86	0.89	1.58E-02	1.22E-01
GO:0050767	regulation of neurogenesis	23	703	374	17583	1.54	0.62	1.58E-02	1.22E-01
	regulation of DNA-binding transcription factor								
GO:0051090	activity	26	703	434	17583	1.50	0.58	1.58E-02	1.22E-01
GO:0045597	positive regulation of cell differentiation	47	703	873	17583	1.35	0.43	1.58E-02	1.22E-01
	positive regulation of nervous system								
GO:0051962	development	18	703	277	17583	1.63	0.70	1.60E-02	1.22E-01
GO:0022037	metencephalon development	9	703	114	17583	1.97	0.98	1.60E-02	1.22E-01
GO:0071300	cellular response to retinoic acid	6	703	66	17583	2.27	1.19	1.60E-02	1.22E-01
GO:0021543	pallium development	13	703	184	17583	1.77	0.82	1.61E-02	1.22E-01
GO:1902806	regulation of cell cycle G1/S phase transition	13	703	184	17583	1.77	0.82	1.61E-02	1.22E-01
GO:0051246	regulation of protein metabolic process	119	703	2494	17583	1.19	0.26	1.61E-02	1.22E-01
GO:0043604	amide biosynthetic process	30	703	517	17583	1.45	0.54	1.65E-02	1.22E-01
	inorganic cation import across plasma								
GO:0098659	membrane	8	703	98	17583	2.04	1.03	1.65E-02	1.22E-01
GO:0099587	inorganic ion import across plasma membrane	8	703	98	17583	2.04	1.03	1.65E-02	1.22E-01
GO:0006405	RNA export from nucleus	7	703	82	17583	2.14	1.09	1.66E-02	1.22E-01
GO:0006396	RNA processing	47	703	876	17583	1.34	0.42	1.67E-02	1.22E-01

GO:2000113	negative regulation of cellular macromolecule biosynthetic process	13	703	185	17583	1.76	0.81	1.68E-02	1.22E-01
GO:1901701	cellular response to oxygen-containing compound	55	703	1050	17583	1.31	0.39	1.69E-02	1.22E-01
GO:0032007	negative regulation of TOR signaling	5	703	52	17583	2.40	1.27	1.71E-02	1.22E-01
GO:2000677	regulation of transcription regulatory region DNA binding	5	703	52	17583	2.40	1.27	1.71E-02	1.22E-01
GO:0035556	intracellular signal transduction	76	703	1517	17583	1.25	0.33	1.72E-02	1.22E-01
GO:0045600	positive regulation of fat cell differentiation	6	703	67	17583	2.24	1.16	1.73E-02	1.22E-01
GO:2000756	regulation of peptidyl-lysine acetylation	6	703	67	17583	2.24	1.16	1.73E-02	1.22E-01
GO:0002520	immune system development	12	703	168	17583	1.79	0.84	1.75E-02	1.22E-01
GO:0072175	epithelial tube formation	10	703	133	17583	1.88	0.91	1.78E-02	1.22E-01
GO:0002062	chondrocyte differentiation	7	703	83	17583	2.11	1.08	1.78E-02	1.22E-01
GO:0048661	positive regulation of smooth muscle cell proliferation	7	703	83	17583	2.11	1.08	1.78E-02	1.22E-01
GO:0032024	positive regulation of insulin secretion	7	703	83	17583	2.11	1.08	1.78E-02	1.22E-01
GO:0009719	response to endogenous stimulus	72	703	1431	17583	1.26	0.33	1.81E-02	1.22E-01
GO:0045862	positive regulation of proteolysis	22	703	359	17583	1.53	0.62	1.82E-02	1.22E-01
GO:0009059	macromolecule biosynthetic process	74	703	1476	17583	1.25	0.33	1.82E-02	1.22E-01
GO:0031503	protein-containing complex localization	11	703	151	17583	1.82	0.87	1.82E-02	1.22E-01
GO:0036293	response to decreased oxygen levels	18	703	281	17583	1.60	0.68	1.83E-02	1.22E-01
GO:0050673	epithelial cell proliferation	12	703	169	17583	1.78	0.83	1.83E-02	1.22E-01
GO:0070252	actin-mediated cell contraction	6	703	68	17583	2.21	1.14	1.86E-02	1.22E-01
GO:0006195	purine nucleotide catabolic process	5	703	53	17583	2.36	1.24	1.86E-02	1.22E-01
GO:0050886	endocrine process	5	703	53	17583	2.36	1.24	1.86E-02	1.22E-01
GO:0045639	positive regulation of myeloid cell differentiation	8	703	100	17583	2.00	1.00	1.86E-02	1.22E-01
GO:0061351	neural precursor cell proliferation	8	703	100	17583	2.00	1.00	1.86E-02	1.22E-01
GO:0035303	regulation of dephosphorylation	10	703	134	17583	1.87	0.90	1.87E-02	1.22E-01
GO:0060541	respiratory system development	14	703	206	17583	1.70	0.77	1.87E-02	1.22E-01
GO:0043067	regulation of programmed cell death	74	703	1479	17583	1.25	0.32	1.90E-02	1.22E-01

GO:0034249	negative regulation of amide metabolic process	13	703	188	17583	1.73	0.79	1.90E-02	1.22E-01
GO:0071375	cellular response to peptide hormone stimulus	16	703	244	17583	1.64	0.71	1.91E-02	1.22E-01
GO:0051961	negative regulation of nervous system development	11	703	152	17583	1.81	0.86	1.91E-02	1.22E-01
GO:0009887	animal organ morphogenesis	52	703	992	17583	1.31	0.39	1.92E-02	1.22E-01
GO:1901564	organonitrogen compound metabolic process	223	703	4982	17583	1.12	0.16	1.97E-02	1.22E-01
GO:0001508	action potential	8	703	101	17583	1.98	0.99	1.98E-02	1.22E-01
GO:1902893	regulation of miRNA transcription	6	703	69	17583	2.17	1.12	2.00E-02	1.22E-01
GO:0060271	cilium assembly	20	703	323	17583	1.55	0.63	2.01E-02	1.22E-01
GO:0048545	response to steroid hormone	18	703	284	17583	1.59	0.66	2.02E-02	1.22E-01
GO:0010628	positive regulation of gene expression	58	703	1127	17583	1.29	0.36	2.02E-02	1.22E-01
GO:1901292	nucleoside phosphate catabolic process	7	703	85	17583	2.06	1.04	2.02E-02	1.22E-01
GO:0007269	neurotransmitter secretion	7	703	85	17583	2.06	1.04	2.02E-02	1.22E-01
GO:0099643	signal release from synapse	7	703	85	17583	2.06	1.04	2.02E-02	1.22E-01
GO:0007632	visual behavior	5	703	54	17583	2.32	1.21	2.03E-02	1.22E-01
GO:0048662	negative regulation of smooth muscle cell proliferation	5	703	54	17583	2.32	1.21	2.03E-02	1.22E-01
GO:0045599	negative regulation of fat cell differentiation	5	703	54	17583	2.32	1.21	2.03E-02	1.22E-01
GO:0007623	circadian rhythm	10	703	136	17583	1.84	0.88	2.06E-02	1.22E-01
GO:0046434	organophosphate catabolic process	11	703	154	17583	1.79	0.84	2.09E-02	1.22E-01
GO:0030902	hindbrain development	11	703	154	17583	1.79	0.84	2.09E-02	1.22E-01
GO:0051234	establishment of localization	180	703	3956	17583	1.14	0.19	2.09E-02	1.22E-01
GO:0045833	negative regulation of lipid metabolic process	8	703	102	17583	1.96	0.97	2.09E-02	1.22E-01
GO:0009199	ribonucleoside triphosphate metabolic process	13	703	191	17583	1.70	0.77	2.15E-02	1.22E-01
GO:0045184	establishment of protein localization	64	703	1264	17583	1.27	0.34	2.15E-02	1.22E-01
GO:0046470	phosphatidylcholine metabolic process	6	703	70	17583	2.14	1.10	2.15E-02	1.22E-01
GO:0045727	positive regulation of translation	10	703	137	17583	1.83	0.87	2.16E-02	1.22E-01

GO:0006725	cellular aromatic compound metabolic process	140	703	3013	17583	1.16	0.22	2.19E-02	1.22E-01
GO:0071241	cellular response to inorganic substance	15	703	229	17583	1.64	0.71	2.20E-02	1.22E-01
GO:0007405	neuroblast proliferation	5	703	55	17583	2.27	1.19	2.20E-02	1.22E-01
GO:0051101	regulation of DNA binding	9	703	120	17583	1.88	0.91	2.21E-02	1.22E-01
GO:0006119	oxidative phosphorylation	9	703	120	17583	1.88	0.91	2.21E-02	1.22E-01
GO:0042542	response to hydrogen peroxide	8	703	103	17583	1.94	0.96	2.21E-02	1.22E-01
GO:0071705	nitrogen compound transport	78	703	1581	17583	1.23	0.30	2.23E-02	1.22E-01
GO:2000036	regulation of stem cell population maintenance	6	703	71	17583	2.11	1.08	2.31E-02	1.22E-01
GO:0070482	response to oxygen levels	19	703	308	17583	1.54	0.63	2.32E-02	1.22E-01
GO:0006399	tRNA metabolic process	13	703	193	17583	1.68	0.75	2.32E-02	1.22E-01
GO:0021549	cerebellum development	8	703	104	17583	1.92	0.94	2.34E-02	1.22E-01
GO:0090150	establishment of protein localization to membrane	14	703	212	17583	1.65	0.72	2.35E-02	1.22E-01
GO:0001649	osteoblast differentiation	10	703	139	17583	1.80	0.85	2.38E-02	1.22E-01
GO:0010608	post-transcriptional regulation of gene expression	28	703	491	17583	1.43	0.51	2.38E-02	1.22E-01
GO:0010332	response to gamma radiation	5	703	56	17583	2.23	1.16	2.38E-02	1.22E-01
GO:0051348	negative regulation of transferase activity	17	703	270	17583	1.57	0.66	2.40E-02	1.22E-01
GO:0019217	regulation of fatty acid metabolic process	7	703	88	17583	1.99	0.99	2.44E-02	1.22E-01
GO:0019693	ribose phosphate metabolic process	24	703	410	17583	1.46	0.55	2.45E-02	1.22E-01
GO:0007507	heart development	31	703	555	17583	1.40	0.48	2.47E-02	1.22E-01
GO:0008584	male gonad development	10	703	140	17583	1.79	0.84	2.49E-02	1.22E-01
GO:0001501	skeletal system development	29	703	514	17583	1.41	0.50	2.51E-02	1.22E-01
GO:0009952	anterior/posterior pattern specification	14	703	214	17583	1.64	0.71	2.53E-02	1.22E-01
GO:0071456	cellular response to hypoxia	9	703	123	17583	1.83	0.87	2.57E-02	1.22E-01
GO:2000630	positive regulation of miRNA metabolic process	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01
GO:0043388	positive regulation of DNA binding	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01
GO:0031060	regulation of histone methylation	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01

GO:0002763	positive regulation of myeloid leukocyte differentiation	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01
GO:0048168	regulation of neuronal synaptic plasticity	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01
GO:1902808	positive regulation of cell cycle G1/S phase transition	5	703	57	17583	2.19	1.13	2.58E-02	1.22E-01
GO:1900542	regulation of purine nucleotide metabolic process	7	703	89	17583	1.97	0.98	2.59E-02	1.22E-01
GO:2000045	regulation of G1/S transition of mitotic cell cycle	11	703	159	17583	1.73	0.79	2.60E-02	1.22E-01
GO:0097193	intrinsic apoptotic signaling pathway	11	703	159	17583	1.73	0.79	2.60E-02	1.22E-01
GO:0046546	development of primary male sexual characteristics	10	703	141	17583	1.77	0.83	2.61E-02	1.22E-01
GO:0140053	mitochondrial gene expression	10	703	141	17583	1.77	0.83	2.61E-02	1.22E-01
GO:0071495	cellular response to endogenous stimulus	59	703	1166	17583	1.27	0.34	2.63E-02	1.22E-01
GO:0030029	actin filament-based process	33	703	600	17583	1.38	0.46	2.63E-02	1.22E-01
GO:0043010	camera-type eye development	20	703	332	17583	1.51	0.59	2.63E-02	1.22E-01
GO:0031016	pancreas development	6	703	73	17583	2.06	1.04	2.64E-02	1.22E-01
GO:0034103	regulation of tissue remodeling	6	703	73	17583	2.06	1.04	2.64E-02	1.22E-01
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	6	703	73	17583	2.06	1.04	2.64E-02	1.22E-01
GO:0007589	body fluid secretion	6	703	73	17583	2.06	1.04	2.64E-02	1.22E-01
GO:0008283	cell population proliferation	38	703	707	17583	1.34	0.43	2.65E-02	1.22E-01
GO:0048583	regulation of response to stimulus	181	703	4008	17583	1.13	0.18	2.68E-02	1.22E-01
GO:0003206	cardiac chamber morphogenesis	9	703	124	17583	1.82	0.86	2.70E-02	1.22E-01
GO:0001667	ameboidal-type cell migration	13	703	197	17583	1.65	0.72	2.71E-02	1.22E-01
GO:0051236	establishment of RNA localization	11	703	160	17583	1.72	0.78	2.72E-02	1.22E-01
GO:0009725	response to hormone	41	703	773	17583	1.33	0.41	2.73E-02	1.22E-01
GO:0001701	in utero embryonic development	23	703	394	17583	1.46	0.55	2.74E-02	1.22E-01
GO:0006140	regulation of nucleotide metabolic process	7	703	90	17583	1.95	0.96	2.75E-02	1.22E-01
GO:0061387	regulation of extent of cell growth	8	703	107	17583	1.87	0.90	2.75E-02	1.22E-01

GO:0090277	positive regulation of peptide hormone secretion	8	703	107	17583	1.87	0.90	2.75E-02	1.22E-01
GO:0050678	regulation of epithelial cell proliferation	22	703	374	17583	1.47	0.56	2.76E-02	1.22E-01
GO:0046483	heterocycle metabolic process	137	703	2966	17583	1.16	0.21	2.76E-02	1.22E-01
GO:1904036	negative regulation of epithelial cell apoptotic process	5	703	58	17583	2.16	1.11	2.78E-02	1.22E-01
GO:0061061	muscle structure development	28	703	498	17583	1.41	0.49	2.80E-02	1.22E-01
GO:0032868	response to insulin	14	703	217	17583	1.61	0.69	2.82E-02	1.22E-01
GO:0010822	positive regulation of mitochondrion organization	6	703	74	17583	2.03	1.02	2.82E-02	1.22E-01
GO:0007049	cell cycle	64	703	1283	17583	1.25	0.32	2.83E-02	1.22E-01
GO:0009060	aerobic respiration	11	703	161	17583	1.71	0.77	2.83E-02	1.22E-01
GO:0006810	transport	172	703	3800	17583	1.13	0.18	2.85E-02	1.22E-01
GO:0010212	response to ionizing radiation	10	703	143	17583	1.75	0.81	2.86E-02	1.22E-01
GO:0030534	adult behavior	10	703	143	17583	1.75	0.81	2.86E-02	1.22E-01
GO:0051223	regulation of protein transport	28	703	499	17583	1.40	0.49	2.87E-02	1.22E-01
GO:2000026	regulation of multicellular organismal development	68	703	1374	17583	1.24	0.31	2.87E-02	1.22E-01
GO:0010959	regulation of metal ion transport	23	703	396	17583	1.45	0.54	2.88E-02	1.22E-01
GO:0043603	amide metabolic process	42	703	798	17583	1.32	0.40	2.89E-02	1.22E-01
GO:0050852	T cell receptor signaling pathway	8	703	108	17583	1.85	0.89	2.90E-02	1.22E-01
GO:0060021	roof of mouth development	7	703	91	17583	1.92	0.94	2.91E-02	1.22E-01
GO:0072659	protein localization to plasma membrane	13	703	199	17583	1.63	0.71	2.92E-02	1.22E-01
GO:0090407	organophosphate biosynthetic process	30	703	542	17583	1.38	0.47	2.94E-02	1.22E-01
GO:0030307	positive regulation of cell growth	11	703	162	17583	1.70	0.76	2.95E-02	1.22E-01
GO:0034763	negative regulation of transmembrane transport	9	703	126	17583	1.79	0.84	2.97E-02	1.22E-01
GO:0030879	mammary gland development	9	703	126	17583	1.79	0.84	2.97E-02	1.22E-01
GO:0071704	organic substance metabolic process	325	703	7534	17583	1.08	0.11	2.97E-02	1.22E-01
GO:0072523	purine-containing compound catabolic process	5	703	59	17583	2.12	1.08	2.99E-02	1.22E-01

	regulation of phosphoprotein phosphatase activity	5	703	59	17583	2.12	1.08	2.99E-02	1.22E-01
GO:0043666	activity	5	703	59	17583	2.12	1.08	2.99E-02	1.22E-01
GO:0140115	export across plasma membrane	5	703	59	17583	2.12	1.08	2.99E-02	1.22E-01
GO:0009948	anterior/posterior axis specification	5	703	59	17583	2.12	1.08	2.99E-02	1.22E-01
GO:0006403	RNA localization	12	703	181	17583	1.66	0.73	3.01E-02	1.22E-01
GO:0015031	protein transport	59	703	1176	17583	1.25	0.33	3.04E-02	1.22E-01
GO:1903829	positive regulation of protein localization	26	703	460	17583	1.41	0.50	3.04E-02	1.22E-01
GO:0002793	positive regulation of peptide secretion	8	703	109	17583	1.84	0.88	3.06E-02	1.22E-01
GO:0030335	positive regulation of cell migration	29	703	523	17583	1.39	0.47	3.07E-02	1.22E-01
GO:0046661	male sex differentiation	11	703	163	17583	1.69	0.76	3.08E-02	1.22E-01
GO:0034250	positive regulation of amide metabolic process	11	703	163	17583	1.69	0.76	3.08E-02	1.22E-01
GO:0030516	regulation of axon extension	7	703	92	17583	1.90	0.93	3.08E-02	1.22E-01
GO:0043043	peptide biosynthetic process	23	703	399	17583	1.44	0.53	3.11E-02	1.22E-01
GO:0031056	regulation of histone modification	10	703	145	17583	1.72	0.79	3.12E-02	1.22E-01
GO:0044057	regulation of system process	31	703	566	17583	1.37	0.45	3.12E-02	1.22E-01
GO:0043068	positive regulation of programmed cell death	28	703	503	17583	1.39	0.48	3.14E-02	1.22E-01
GO:0070201	regulation of establishment of protein localization	29	703	524	17583	1.38	0.47	3.14E-02	1.22E-01
GO:0009166	nucleotide catabolic process	6	703	76	17583	1.97	0.98	3.20E-02	1.22E-01
GO:0050796	regulation of insulin secretion	11	703	164	17583	1.68	0.75	3.21E-02	1.22E-01
GO:0090398	cellular senescence	5	703	60	17583	2.08	1.06	3.22E-02	1.22E-01
GO:0001654	eye development	22	703	380	17583	1.45	0.53	3.23E-02	1.22E-01
GO:0050708	regulation of protein secretion	16	703	260	17583	1.54	0.62	3.26E-02	1.22E-01
GO:0050768	negative regulation of neurogenesis	10	703	146	17583	1.71	0.78	3.26E-02	1.22E-01
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	7	703	93	17583	1.88	0.91	3.26E-02	1.22E-01
GO:0042773	ATP synthesis coupled electron transport	7	703	93	17583	1.88	0.91	3.26E-02	1.22E-01
GO:0042775	mitochondrial ATP synthesis coupled electron transport	7	703	93	17583	1.88	0.91	3.26E-02	1.22E-01
GO:0099177	regulation of trans-synaptic signaling	26	703	463	17583	1.40	0.49	3.26E-02	1.22E-01

GO:0051028	mRNA transport	9	703	128	17583	1.76	0.81	3.27E-02	1.22E-01
GO:0009259	ribonucleotide metabolic process	23	703	401	17583	1.43	0.52	3.27E-02	1.22E-01
GO:0010941	regulation of cell death	79	703	1634	17583	1.21	0.27	3.28E-02	1.22E-01
GO:0010942	positive regulation of cell death	31	703	569	17583	1.36	0.45	3.33E-02	1.22E-01
GO:0018193	peptidyl-amino acid modification	43	703	828	17583	1.30	0.38	3.34E-02	1.22E-01
GO:0030334	regulation of cell migration	47	703	916	17583	1.28	0.36	3.35E-02	1.22E-01
GO:0009205	purine ribonucleoside triphosphate metabolic process	12	703	184	17583	1.63	0.71	3.37E-02	1.22E-01
GO:1901989	positive regulation of cell cycle phase transition	8	703	111	17583	1.80	0.85	3.38E-02	1.22E-01
GO:0009150	purine ribonucleotide metabolic process	22	703	382	17583	1.44	0.53	3.39E-02	1.22E-01
GO:0120161	regulation of cold-induced thermogenesis	10	703	147	17583	1.70	0.77	3.40E-02	1.22E-01
GO:0007030	Golgi organization	10	703	147	17583	1.70	0.77	3.40E-02	1.22E-01
GO:0048709	oligodendrocyte differentiation	6	703	77	17583	1.95	0.96	3.41E-02	1.22E-01
GO:0023056	positive regulation of signaling	81	703	1684	17583	1.20	0.27	3.45E-02	1.22E-01
GO:1901016	regulation of potassium ion transmembrane transporter activity	5	703	61	17583	2.05	1.04	3.45E-02	1.22E-01
GO:0051148	negative regulation of muscle cell differentiation	5	703	61	17583	2.05	1.04	3.45E-02	1.22E-01
GO:0032963	collagen metabolic process	5	703	61	17583	2.05	1.04	3.45E-02	1.22E-01
GO:0120031	plasma membrane bounded cell projection assembly	24	703	424	17583	1.42	0.50	3.46E-02	1.22E-01
GO:0017148	negative regulation of translation	11	703	166	17583	1.66	0.73	3.47E-02	1.22E-01
GO:0034645	cellular macromolecule biosynthetic process	40	703	765	17583	1.31	0.39	3.48E-02	1.22E-01
GO:0035148	tube formation	10	703	148	17583	1.69	0.76	3.54E-02	1.22E-01
GO:0098771	inorganic ion homeostasis	29	703	530	17583	1.37	0.45	3.57E-02	1.22E-01
GO:0150063	visual system development	22	703	384	17583	1.43	0.52	3.57E-02	1.22E-01
GO:0007015	actin filament organization	16	703	263	17583	1.52	0.61	3.57E-02	1.22E-01
GO:0048593	camera-type eye morphogenesis	9	703	130	17583	1.73	0.79	3.58E-02	1.22E-01
GO:0043065	positive regulation of apoptotic process	27	703	488	17583	1.38	0.47	3.58E-02	1.22E-01
GO:1901568	fatty acid derivative metabolic process	6	703	78	17583	1.92	0.94	3.62E-02	1.22E-01

GO:0001942	hair follicle development	6	703	78	17583	1.92	0.94	3.62E-02	1.22E-01
GO:0046474	glycerophospholipid biosynthetic process	13	703	205	17583	1.59	0.67	3.62E-02	1.22E-01
GO:0051651	maintenance of location in cell	7	703	95	17583	1.84	0.88	3.63E-02	1.22E-01
GO:0051128	regulation of cellular component organization	111	703	2384	17583	1.16	0.22	3.65E-02	1.22E-01
GO:0007517	muscle organ development	18	703	304	17583	1.48	0.57	3.69E-02	1.22E-01
GO:0050994	regulation of lipid catabolic process	5	703	62	17583	2.02	1.01	3.70E-02	1.22E-01
GO:0051205	protein insertion into membrane	5	703	62	17583	2.02	1.01	3.70E-02	1.22E-01
GO:0006644	phospholipid metabolic process	21	703	365	17583	1.44	0.53	3.71E-02	1.22E-01
GO:0007006	mitochondrial membrane organization	8	703	113	17583	1.77	0.82	3.73E-02	1.22E-01
GO:0046916	cellular transition metal ion homeostasis	8	703	113	17583	1.77	0.82	3.73E-02	1.22E-01
GO:0036294	cellular response to decreased oxygen levels	9	703	131	17583	1.72	0.78	3.74E-02	1.22E-01
GO:0007368	determination of left/right symmetry	9	703	131	17583	1.72	0.78	3.74E-02	1.22E-01
	anatomical structure formation involved in								
GO:0048646	morphogenesis	48	703	945	17583	1.27	0.35	3.74E-02	1.22E-01
GO:0030218	erythrocyte differentiation	7	703	96	17583	1.82	0.87	3.83E-02	1.22E-01
GO:2000628	regulation of miRNA metabolic process	6	703	79	17583	1.90	0.93	3.84E-02	1.22E-01
GO:0007422	peripheral nervous system development	6	703	79	17583	1.90	0.93	3.84E-02	1.22E-01
GO:0009100	glycoprotein metabolic process	20	703	346	17583	1.45	0.53	3.85E-02	1.22E-01
GO:0043271	negative regulation of ion transport	10	703	150	17583	1.67	0.74	3.85E-02	1.22E-01
GO:0032501	multicellular organismal process	275	703	6337	17583	1.09	0.12	3.85E-02	1.22E-01
	generation of precursor metabolites and								
GO:0006091	energy	23	703	408	17583	1.41	0.50	3.88E-02	1.22E-01
GO:0002262	myeloid cell homeostasis	9	703	132	17583	1.71	0.77	3.91E-02	1.22E-01
GO:0035051	cardiocyte differentiation	8	703	114	17583	1.76	0.81	3.91E-02	1.22E-01
GO:0006879	cellular iron ion homeostasis	5	703	63	17583	1.99	0.99	3.96E-02	1.22E-01
GO:0006406	mRNA export from nucleus	5	703	63	17583	1.99	0.99	3.96E-02	1.22E-01
GO:0097305	response to alcohol	15	703	247	17583	1.52	0.60	4.01E-02	1.22E-01
GO:1903522	regulation of blood circulation	15	703	247	17583	1.52	0.60	4.01E-02	1.22E-01
	negative regulation of protein metabolic								
GO:0051248	process	50	703	994	17583	1.26	0.33	4.01E-02	1.22E-01
GO:0009141	nucleoside triphosphate metabolic process	13	703	208	17583	1.56	0.64	4.02E-02	1.22E-01

GO:0009144	purine nucleoside triphosphate metabolic process	12	703	189	17583	1.59	0.67	4.05E-02	1.23E-01
GO:0055080	cation homeostasis	28	703	515	17583	1.36	0.44	4.06E-02	1.24E-01
GO:0061053	somite development	6	703	80	17583	1.88	0.91	4.07E-02	1.24E-01
GO:0071901	negative regulation of protein serine/threonine kinase activity	8	703	115	17583	1.74	0.80	4.10E-02	1.25E-01
GO:0021761	limbic system development	8	703	115	17583	1.74	0.80	4.10E-02	1.25E-01
GO:0072359	circulatory system development	46	703	907	17583	1.27	0.34	4.13E-02	1.26E-01
GO:1901135	carbohydrate derivative metabolic process	50	703	996	17583	1.26	0.33	4.13E-02	1.26E-01
GO:0048880	sensory system development	22	703	390	17583	1.41	0.50	4.14E-02	1.26E-01
GO:0098662	inorganic cation transmembrane transport	32	703	602	17583	1.33	0.41	4.19E-02	1.27E-01
GO:0010001	glial cell differentiation	12	703	190	17583	1.58	0.66	4.20E-02	1.28E-01
GO:0032386	regulation of intracellular transport	19	703	329	17583	1.44	0.53	4.20E-02	1.28E-01
GO:0014070	response to organic cyclic compound	44	703	864	17583	1.27	0.35	4.21E-02	1.28E-01
GO:0050769	positive regulation of neurogenesis	14	703	229	17583	1.53	0.61	4.22E-02	1.28E-01
GO:0099518	vesicle cytoskeletal trafficking	5	703	64	17583	1.95	0.97	4.23E-02	1.28E-01
GO:0042776	proton motive force-driven mitochondrial ATP synthesis	5	703	64	17583	1.95	0.97	4.23E-02	1.28E-01
GO:0035306	positive regulation of dephosphorylation	5	703	64	17583	1.95	0.97	4.23E-02	1.28E-01
GO:1905330	regulation of morphogenesis of an epithelium	5	703	64	17583	1.95	0.97	4.23E-02	1.28E-01
GO:0030888	regulation of B cell proliferation	5	703	64	17583	1.95	0.97	4.23E-02	1.28E-01
GO:0051640	organelle localization	28	703	517	17583	1.35	0.44	4.23E-02	1.28E-01
GO:0007610	behavior	32	703	603	17583	1.33	0.41	4.27E-02	1.30E-01
GO:0008344	adult locomotory behavior	6	703	81	17583	1.85	0.89	4.31E-02	1.31E-01
GO:0034762	regulation of transmembrane transport	31	703	582	17583	1.33	0.41	4.31E-02	1.31E-01
GO:1901360	organic cyclic compound metabolic process	147	703	3255	17583	1.13	0.18	4.43E-02	1.33E-01
GO:1902115	regulation of organelle assembly	14	703	231	17583	1.52	0.60	4.50E-02	1.36E-01
GO:0034504	protein localization to nucleus	12	703	192	17583	1.56	0.64	4.50E-02	1.36E-01
GO:0070936	protein K48-linked ubiquitination	5	703	65	17583	1.92	0.94	4.51E-02	1.36E-01
GO:0051926	negative regulation of calcium ion transport	5	703	65	17583	1.92	0.94	4.51E-02	1.36E-01

GO:0090316	positive regulation of intracellular protein transport	10	703	154	17583	1.62	0.70	4.52E-02	1.36E-01
GO:0006351	DNA-templated transcription	32	703	606	17583	1.32	0.40	4.52E-02	1.36E-01
GO:0034765	regulation of ion transmembrane transport	27	703	499	17583	1.35	0.44	4.53E-02	1.36E-01
GO:0022404	molting cycle process	6	703	82	17583	1.83	0.87	4.56E-02	1.37E-01
GO:0072384	organelle transport along microtubule	6	703	82	17583	1.83	0.87	4.56E-02	1.37E-01
GO:0022405	hair cycle process	6	703	82	17583	1.83	0.87	4.56E-02	1.37E-01
GO:0050801	ion homeostasis	29	703	542	17583	1.34	0.42	4.56E-02	1.37E-01
GO:0010647	positive regulation of cell communication	80	703	1685	17583	1.19	0.25	4.57E-02	1.37E-01
GO:0097659	nucleic acid-templated transcription	32	703	607	17583	1.32	0.40	4.61E-02	1.38E-01
GO:0045333	cellular respiration	12	703	193	17583	1.56	0.64	4.66E-02	1.40E-01
GO:0030031	cell projection assembly	24	703	437	17583	1.37	0.46	4.67E-02	1.40E-01
GO:0019438	aromatic compound biosynthetic process	53	703	1072	17583	1.24	0.31	4.70E-02	1.40E-01
GO:0030004	cellular monovalent inorganic cation homeostasis	8	703	118	17583	1.70	0.76	4.70E-02	1.40E-01
GO:0006873	cellular ion homeostasis	24	703	438	17583	1.37	0.45	4.77E-02	1.41E-01
GO:0031100	animal organ regeneration	5	703	66	17583	1.89	0.92	4.80E-02	1.41E-01
GO:0002028	regulation of sodium ion transport	6	703	83	17583	1.81	0.85	4.81E-02	1.42E-01
GO:0098773	skin epidermis development	6	703	83	17583	1.81	0.85	4.81E-02	1.42E-01
GO:0009855	determination of bilateral symmetry	9	703	137	17583	1.64	0.72	4.83E-02	1.42E-01
GO:0050890	cognition	18	703	314	17583	1.43	0.52	4.84E-02	1.42E-01
GO:0050878	regulation of body fluid levels	21	703	376	17583	1.40	0.48	4.86E-02	1.43E-01
GO:0009743	response to carbohydrate	11	703	175	17583	1.57	0.65	4.87E-02	1.43E-01
GO:0071356	cellular response to tumor necrosis factor	11	703	175	17583	1.57	0.65	4.87E-02	1.43E-01
GO:0043523	regulation of neuron apoptotic process	13	703	214	17583	1.52	0.60	4.89E-02	1.44E-01
GO:0140694	non-membrane-bounded organelle assembly	19	703	335	17583	1.42	0.50	4.90E-02	1.44E-01
GO:0045931	positive regulation of mitotic cell cycle	8	703	119	17583	1.68	0.75	4.92E-02	1.44E-01
GO:2000147	positive regulation of cell motility	29	703	546	17583	1.33	0.41	4.93E-02	1.45E-01
GO:0006836	neurotransmitter transport	9	703	138	17583	1.63	0.71	5.03E-02	1.46E-01
GO:0009799	specification of symmetry	9	703	138	17583	1.63	0.71	5.03E-02	1.46E-01
GO:0055082	cellular chemical homeostasis	29	703	547	17583	1.33	0.41	5.03E-02	1.46E-01

GO:0009451	RNA modification	11	703	176	17583	1.56	0.64	5.04E-02	1.47E-01
GO:0140014	mitotic nuclear division	11	703	176	17583	1.56	0.64	5.04E-02	1.47E-01
GO:0050804	modulation of chemical synaptic transmission	25	703	462	17583	1.35	0.44	5.07E-02	1.48E-01
GO:1901607	alpha-amino acid biosynthetic process	5	703	67	17583	1.87	0.90	5.10E-02	1.48E-01
GO:1901699	cellular response to nitrogen compound	33	703	635	17583	1.30	0.38	5.17E-02	1.50E-01
GO:0043170	macromolecule metabolic process	251	703	5792	17583	1.08	0.12	5.21E-02	1.51E-01
GO:0070848	response to growth factor	27	703	506	17583	1.33	0.42	5.22E-02	1.52E-01
GO:0060284	regulation of cell development	43	703	856	17583	1.26	0.33	5.25E-02	1.52E-01
GO:0050657	nucleic acid transport	10	703	158	17583	1.58	0.66	5.26E-02	1.53E-01
GO:0048592	eye morphogenesis	10	703	158	17583	1.58	0.66	5.26E-02	1.53E-01
GO:0050658	RNA transport	10	703	158	17583	1.58	0.66	5.26E-02	1.53E-01
GO:0033993	response to lipid	42	703	834	17583	1.26	0.33	5.26E-02	1.53E-01
GO:0040011	locomotion	28	703	528	17583	1.33	0.41	5.28E-02	1.53E-01
GO:0016050	vesicle organization	19	703	338	17583	1.41	0.49	5.28E-02	1.53E-01
GO:0006470	protein dephosphorylation	11	703	178	17583	1.55	0.63	5.41E-02	1.57E-01
GO:0042127	regulation of cell population proliferation	78	703	1654	17583	1.18	0.24	5.41E-02	1.57E-01
GO:0048844	artery morphogenesis	5	703	68	17583	1.84	0.88	5.41E-02	1.57E-01
GO:2000144	positive regulation of DNA-templated transcription initiation	5	703	68	17583	1.84	0.88	5.41E-02	1.57E-01
GO:0046854	phosphatidylinositol phosphate biosynthetic process	5	703	68	17583	1.84	0.88	5.41E-02	1.57E-01
GO:0000956	nuclear-transcribed mRNA catabolic process	7	703	103	17583	1.70	0.77	5.41E-02	1.57E-01
GO:0062013	positive regulation of small molecule metabolic process	9	703	140	17583	1.61	0.69	5.45E-02	1.58E-01
GO:0032774	RNA biosynthetic process	32	703	617	17583	1.30	0.38	5.53E-02	1.60E-01
GO:0031399	regulation of protein modification process	71	703	1495	17583	1.19	0.25	5.56E-02	1.61E-01
GO:0007613	memory	8	703	122	17583	1.64	0.71	5.59E-02	1.61E-01
GO:0006986	response to unfolded protein	8	703	122	17583	1.64	0.71	5.59E-02	1.61E-01
GO:0002832	negative regulation of response to biotic stimulus	8	703	122	17583	1.64	0.71	5.59E-02	1.61E-01
GO:0009894	regulation of catabolic process	49	703	995	17583	1.23	0.30	5.63E-02	1.62E-01

GO:0021766	hippocampus development	6	703	86	17583	1.74	0.80	5.63E-02	1.62E-01
GO:0030901	midbrain development	6	703	86	17583	1.74	0.80	5.63E-02	1.62E-01
GO:0099504	synaptic vesicle cycle	9	703	141	17583	1.60	0.67	5.66E-02	1.63E-01
	regulation of reactive oxygen species								
GO:2000377	metabolic process	9	703	141	17583	1.60	0.67	5.66E-02	1.63E-01
GO:0032984	protein-containing complex disassembly	9	703	141	17583	1.60	0.67	5.66E-02	1.63E-01
	regulation of signal transduction by p53 class								
GO:1901796	mediator	7	703	104	17583	1.68	0.75	5.67E-02	1.63E-01
GO:0019751	polyol metabolic process	7	703	104	17583	1.68	0.75	5.67E-02	1.63E-01
GO:0032880	regulation of protein localization	42	703	839	17583	1.25	0.32	5.68E-02	1.63E-01
GO:0055065	metal ion homeostasis	23	703	425	17583	1.35	0.44	5.69E-02	1.64E-01
	regulation of mitochondrial membrane								
GO:0051881	potential	5	703	69	17583	1.81	0.86	5.73E-02	1.64E-01
GO:0014823	response to activity	5	703	69	17583	1.81	0.86	5.73E-02	1.64E-01
GO:2000145	regulation of cell motility	48	703	974	17583	1.23	0.30	5.75E-02	1.64E-01
GO:0071417	cellular response to organonitrogen compound	30	703	576	17583	1.30	0.38	5.78E-02	1.64E-01
GO:0008016	regulation of heart contraction	12	703	200	17583	1.50	0.59	5.86E-02	1.65E-01
GO:0055076	transition metal ion homeostasis	9	703	142	17583	1.59	0.66	5.88E-02	1.65E-01
GO:0043066	negative regulation of apoptotic process	44	703	886	17583	1.24	0.31	5.89E-02	1.65E-01
	positive regulation of cell population								
GO:0008284	proliferation	46	703	931	17583	1.24	0.31	5.90E-02	1.65E-01
GO:0008610	lipid biosynthetic process	31	703	599	17583	1.29	0.37	5.91E-02	1.65E-01
GO:0055072	iron ion homeostasis	6	703	87	17583	1.72	0.79	5.93E-02	1.65E-01
GO:0003279	cardiac septum development	7	703	105	17583	1.67	0.74	5.93E-02	1.65E-01
GO:0030148	sphingolipid biosynthetic process	7	703	105	17583	1.67	0.74	5.93E-02	1.65E-01
GO:1901890	positive regulation of cell junction assembly	7	703	105	17583	1.67	0.74	5.93E-02	1.65E-01
GO:0042391	regulation of membrane potential	23	703	427	17583	1.35	0.43	5.94E-02	1.65E-01
GO:0090304	nucleic acid metabolic process	103	703	2247	17583	1.15	0.20	5.97E-02	1.65E-01
GO:0007017	microtubule-based process	41	703	821	17583	1.25	0.32	6.06E-02	1.65E-01
GO:0001570	vasculogenesis	5	703	70	17583	1.79	0.84	6.07E-02	1.65E-01

GO:0008286	insulin receptor signaling pathway	5	703	70	17583	1.79	0.84	6.07E-02	1.65E-01
GO:0060411	cardiac septum morphogenesis	5	703	70	17583	1.79	0.84	6.07E-02	1.65E-01
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	5	703	70	17583	1.79	0.84	6.07E-02	1.65E-01
	regulation of oxidative stress-induced cell death								
GO:1903201	cardiac ventricle development	8	703	124	17583	1.61	0.69	6.08E-02	1.65E-01
GO:0045787	positive regulation of cell cycle	19	703	344	17583	1.38	0.47	6.10E-02	1.65E-01
GO:0010033	response to organic substance	111	703	2439	17583	1.14	0.19	6.16E-02	1.65E-01
GO:1902107	positive regulation of leukocyte differentiation	11	703	182	17583	1.51	0.60	6.19E-02	1.65E-01
GO:1903708	positive regulation of hemopoiesis	11	703	182	17583	1.51	0.60	6.19E-02	1.65E-01
GO:0031023	microtubule organizing center organization	7	703	106	17583	1.65	0.72	6.21E-02	1.65E-01
GO:0018958	phenol-containing compound metabolic process	6	703	88	17583	1.71	0.77	6.23E-02	1.65E-01
GO:0097553	calcium ion transmembrane import into cytosol	6	703	88	17583	1.71	0.77	6.23E-02	1.65E-01
GO:0031058	positive regulation of histone modification	6	703	88	17583	1.71	0.77	6.23E-02	1.65E-01
GO:0051591	response to cAMP	6	703	88	17583	1.71	0.77	6.23E-02	1.65E-01
GO:0019646	aerobic electron transport chain	6	703	88	17583	1.71	0.77	6.23E-02	1.65E-01
GO:0016311	dephosphorylation	14	703	242	17583	1.45	0.53	6.23E-02	1.65E-01
GO:0061025	membrane fusion	10	703	163	17583	1.53	0.62	6.29E-02	1.65E-01
GO:0045055	regulated exocytosis	9	703	144	17583	1.56	0.64	6.35E-02	1.65E-01
GO:0035966	response to topologically incorrect protein	9	703	144	17583	1.56	0.64	6.35E-02	1.65E-01
GO:0007033	vacuole organization	11	703	183	17583	1.50	0.59	6.40E-02	1.65E-01
GO:0031623	receptor internalization	5	703	71	17583	1.76	0.82	6.42E-02	1.65E-01
GO:0003208	cardiac ventricle morphogenesis	5	703	71	17583	1.76	0.82	6.42E-02	1.65E-01
GO:1903578	regulation of ATP metabolic process	5	703	71	17583	1.76	0.82	6.42E-02	1.65E-01
	regulation of anatomical structure morphogenesis								
GO:0022603	cellular response to chemical stimulus	45	703	915	17583	1.23	0.30	6.47E-02	1.65E-01
GO:0070887	positive regulation of locomotion	107	703	2350	17583	1.14	0.19	6.47E-02	1.65E-01
GO:0040017		29	703	561	17583	1.29	0.37	6.53E-02	1.65E-01

GO:1901216	positive regulation of neuron death	6	703	89	17583	1.69	0.75	6.54E-02	1.65E-01
GO:0045185	maintenance of protein location	6	703	89	17583	1.69	0.75	6.54E-02	1.65E-01
GO:0051098	regulation of binding	20	703	368	17583	1.36	0.44	6.54E-02	1.65E-01
GO:0070555	response to interleukin-1	8	703	126	17583	1.59	0.67	6.59E-02	1.65E-01
GO:0006812	cation transport	42	703	849	17583	1.24	0.31	6.59E-02	1.65E-01
GO:0071363	cellular response to growth factor stimulus	25	703	475	17583	1.32	0.40	6.61E-02	1.65E-01
GO:0003205	cardiac chamber development	10	703	165	17583	1.52	0.60	6.74E-02	1.65E-01
GO:0001960	negative regulation of cytokine-mediated signaling pathway	5	703	72	17583	1.74	0.80	6.78E-02	1.65E-01
GO:0003281	ventricular septum development	5	703	72	17583	1.74	0.80	6.78E-02	1.65E-01
GO:0045017	glycerolipid biosynthetic process	13	703	225	17583	1.45	0.53	6.83E-02	1.65E-01
GO:0010565	regulation of cellular ketone metabolic process	8	703	127	17583	1.58	0.66	6.85E-02	1.65E-01
GO:1902017	regulation of cilium assembly	6	703	90	17583	1.67	0.74	6.86E-02	1.65E-01
GO:0006029	proteoglycan metabolic process	6	703	90	17583	1.67	0.74	6.86E-02	1.65E-01
GO:0031331	positive regulation of cellular catabolic process	22	703	413	17583	1.33	0.41	6.92E-02	1.65E-01
GO:0000302	response to reactive oxygen species	10	703	166	17583	1.51	0.59	6.97E-02	1.65E-01
GO:0019725	cellular homeostasis	33	703	653	17583	1.26	0.34	7.03E-02	1.65E-01
GO:0061640	cytoskeleton-dependent cytokinesis	7	703	109	17583	1.61	0.68	7.07E-02	1.65E-01
GO:0007416	synapse assembly	7	703	109	17583	1.61	0.68	7.07E-02	1.65E-01
GO:0060538	skeletal muscle organ development	9	703	147	17583	1.53	0.61	7.08E-02	1.65E-01
GO:0022402	cell cycle process	44	703	899	17583	1.22	0.29	7.09E-02	1.65E-01
GO:0008285	negative regulation of cell population proliferation	35	703	698	17583	1.25	0.33	7.11E-02	1.65E-01
GO:0071479	cellular response to ionizing radiation	5	703	73	17583	1.71	0.78	7.15E-02	1.65E-01
GO:0071333	cellular response to glucose stimulus	5	703	73	17583	1.71	0.78	7.15E-02	1.65E-01
GO:0015986	proton motive force-driven ATP synthesis	5	703	73	17583	1.71	0.78	7.15E-02	1.65E-01
GO:0042063	gliogenesis	14	703	247	17583	1.42	0.50	7.16E-02	1.65E-01
GO:0010629	negative regulation of gene expression	44	703	900	17583	1.22	0.29	7.18E-02	1.65E-01
GO:0043648	dicarboxylic acid metabolic process	6	703	91	17583	1.65	0.72	7.19E-02	1.65E-01

GO:0051247	positive regulation of protein metabolic process	68	703	1449	17583	1.17	0.23	7.21E-02	1.65E-01
GO:0034654	nucleobase-containing compound biosynthetic process	48	703	991	17583	1.21	0.28	7.24E-02	1.65E-01
GO:0042692	muscle cell differentiation	15	703	268	17583	1.40	0.49	7.25E-02	1.65E-01
GO:0006366	transcription by RNA polymerase II	19	703	352	17583	1.35	0.43	7.33E-02	1.65E-01
GO:0090287	regulation of cellular response to growth factor stimulus	17	703	310	17583	1.37	0.46	7.34E-02	1.65E-01
GO:0009628	response to abiotic stimulus	53	703	1106	17583	1.20	0.26	7.36E-02	1.65E-01
GO:0003015	heart process	7	703	110	17583	1.59	0.67	7.37E-02	1.65E-01
GO:0021782	glial cell development	7	703	110	17583	1.59	0.67	7.37E-02	1.65E-01
GO:0060560	developmental growth involved in morphogenesis	8	703	129	17583	1.55	0.63	7.40E-02	1.65E-01
GO:0001101	response to acid chemical	8	703	129	17583	1.55	0.63	7.40E-02	1.65E-01
GO:0010950	positive regulation of endopeptidase activity	10	703	168	17583	1.49	0.57	7.45E-02	1.65E-01
GO:0031345	negative regulation of cell projection organization	11	703	188	17583	1.46	0.55	7.49E-02	1.65E-01
GO:0140029	exocytic process	5	703	74	17583	1.69	0.76	7.53E-02	1.65E-01
GO:0030003	cellular cation homeostasis	22	703	418	17583	1.32	0.40	7.66E-02	1.65E-01
GO:0000910	cytokinesis	7	703	111	17583	1.58	0.66	7.68E-02	1.65E-01
GO:0006661	phosphatidylinositol biosynthetic process	8	703	130	17583	1.54	0.62	7.68E-02	1.65E-01
GO:0070646	protein modification by small protein removal	10	703	169	17583	1.48	0.57	7.70E-02	1.65E-01
GO:0022900	electron transport chain	10	703	169	17583	1.48	0.57	7.70E-02	1.65E-01
GO:0071466	cellular response to xenobiotic stimulus	11	703	189	17583	1.46	0.54	7.73E-02	1.65E-01
GO:0040012	regulation of locomotion	49	703	1019	17583	1.20	0.27	7.76E-02	1.65E-01
GO:0099003	vesicle-mediated transport in synapse	9	703	150	17583	1.50	0.59	7.86E-02	1.66E-01
GO:0070664	negative regulation of leukocyte proliferation	6	703	93	17583	1.61	0.69	7.87E-02	1.66E-01
GO:1904063	negative regulation of cation transmembrane transport	6	703	93	17583	1.61	0.69	7.87E-02	1.66E-01
GO:0060047	heart contraction	6	703	93	17583	1.61	0.69	7.87E-02	1.66E-01
GO:0071331	cellular response to hexose stimulus	5	703	75	17583	1.67	0.74	7.92E-02	1.67E-01

GO:0008333	endosome to lysosome transport	5	703	75	17583	1.67	0.74	7.92E-02	1.67E-01
GO:0009185	ribonucleoside diphosphate metabolic process	5	703	75	17583	1.67	0.74	7.92E-02	1.67E-01
GO:0008652	amino acid biosynthetic process	5	703	75	17583	1.67	0.74	7.92E-02	1.67E-01
GO:0046883	regulation of hormone secretion	14	703	251	17583	1.40	0.48	7.96E-02	1.67E-01
GO:0043467	regulation of generation of precursor metabolites and energy	8	703	131	17583	1.53	0.61	7.97E-02	1.67E-01
GO:0008033	tRNA processing	8	703	131	17583	1.53	0.61	7.97E-02	1.67E-01
GO:0048878	chemical homeostasis	44	703	908	17583	1.21	0.28	8.01E-02	1.67E-01
GO:0043069	negative regulation of programmed cell death	44	703	908	17583	1.21	0.28	8.01E-02	1.67E-01
GO:0016579	protein deubiquitination	9	703	151	17583	1.49	0.58	8.14E-02	1.69E-01
GO:0090068	positive regulation of cell cycle process	14	703	252	17583	1.39	0.47	8.17E-02	1.69E-01
GO:0006875	cellular metal ion homeostasis	18	703	336	17583	1.34	0.42	8.22E-02	1.70E-01
GO:0042060	wound healing	18	703	336	17583	1.34	0.42	8.22E-02	1.70E-01
GO:0007611	learning or memory	15	703	273	17583	1.37	0.46	8.22E-02	1.70E-01
GO:0008593	regulation of Notch signaling pathway	6	703	94	17583	1.60	0.67	8.23E-02	1.70E-01
GO:0032465	regulation of cytokinesis	6	703	94	17583	1.60	0.67	8.23E-02	1.70E-01
GO:0050806	positive regulation of synaptic transmission	8	703	132	17583	1.52	0.60	8.27E-02	1.71E-01
GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	7	703	113	17583	1.55	0.63	8.32E-02	1.72E-01
GO:1903047	mitotic cell cycle process	27	703	531	17583	1.27	0.35	8.32E-02	1.72E-01
GO:0060761	negative regulation of response to cytokine stimulus	5	703	76	17583	1.65	0.72	8.33E-02	1.72E-01
GO:0060048	cardiac muscle contraction	5	703	76	17583	1.65	0.72	8.33E-02	1.72E-01
GO:0034502	protein localization to chromosome	5	703	76	17583	1.65	0.72	8.33E-02	1.72E-01
GO:0072594	establishment of protein localization to organelle	18	703	337	17583	1.34	0.42	8.40E-02	1.73E-01
GO:0019538	protein metabolic process	170	703	3891	17583	1.09	0.13	8.41E-02	1.73E-01
GO:0007612	learning	9	703	152	17583	1.48	0.57	8.42E-02	1.73E-01
GO:0042633	hair cycle	6	703	95	17583	1.58	0.66	8.60E-02	1.77E-01
GO:0000723	telomere maintenance	6	703	95	17583	1.58	0.66	8.60E-02	1.77E-01

GO:0042303	molting cycle	6	703	95	17583	1.58	0.66	8.60E-02	1.77E-01
	transmembrane receptor protein tyrosine								
GO:0007169	kinase signaling pathway	22	703	424	17583	1.30	0.38	8.62E-02	1.77E-01
GO:0065008	regulation of biological quality	124	703	2788	17583	1.11	0.15	8.63E-02	1.77E-01
GO:0060348	bone development	12	703	213	17583	1.41	0.49	8.63E-02	1.77E-01
GO:0007163	establishment or maintenance of cell polarity	12	703	213	17583	1.41	0.49	8.63E-02	1.77E-01
GO:0007272	ensheathment of neurons	7	703	114	17583	1.54	0.62	8.65E-02	1.78E-01
GO:0009142	nucleoside triphosphate biosynthetic process	7	703	114	17583	1.54	0.62	8.65E-02	1.78E-01
GO:0043200	response to amino acid	7	703	114	17583	1.54	0.62	8.65E-02	1.78E-01
GO:0008366	axon ensheathment	7	703	114	17583	1.54	0.62	8.65E-02	1.78E-01
GO:0090276	regulation of peptide hormone secretion	11	703	193	17583	1.43	0.51	8.71E-02	1.79E-01
GO:0070588	calcium ion transmembrane transport	11	703	193	17583	1.43	0.51	8.71E-02	1.79E-01
GO:0030500	regulation of bone mineralization	5	703	77	17583	1.62	0.70	8.74E-02	1.79E-01
GO:0009880	embryonic pattern specification	5	703	77	17583	1.62	0.70	8.74E-02	1.79E-01
GO:0071326	cellular response to monosaccharide stimulus	5	703	77	17583	1.62	0.70	8.74E-02	1.79E-01
GO:0009101	glycoprotein biosynthetic process	15	703	276	17583	1.36	0.44	8.84E-02	1.81E-01
GO:0007519	skeletal muscle tissue development	8	703	134	17583	1.49	0.58	8.89E-02	1.82E-01
GO:0007346	regulation of mitotic cell cycle	25	703	491	17583	1.27	0.35	8.90E-02	1.83E-01
GO:0042593	glucose homeostasis	11	703	194	17583	1.42	0.50	8.96E-02	1.84E-01
GO:0001678	cellular glucose homeostasis	6	703	96	17583	1.56	0.64	8.97E-02	1.84E-01
GO:0030001	metal ion transport	31	703	624	17583	1.24	0.31	8.98E-02	1.84E-01
GO:0006606	protein import into nucleus	7	703	115	17583	1.52	0.61	8.99E-02	1.84E-01
GO:0071310	cellular response to organic substance	79	703	1728	17583	1.14	0.19	9.10E-02	1.87E-01
GO:0060548	negative regulation of cell death	48	703	1009	17583	1.19	0.25	9.11E-02	1.87E-01
GO:0009612	response to mechanical stimulus	12	703	215	17583	1.40	0.48	9.12E-02	1.87E-01
GO:0009123	nucleoside monophosphate metabolic process	5	703	78	17583	1.60	0.68	9.17E-02	1.87E-01
	negative regulation of cell cycle G1/S phase								
GO:1902807	transition	5	703	78	17583	1.60	0.68	9.17E-02	1.87E-01
GO:0022613	ribonucleoprotein complex biogenesis	23	703	449	17583	1.28	0.36	9.18E-02	1.87E-01
GO:0061008	hepaticobiliary system development	8	703	135	17583	1.48	0.57	9.20E-02	1.88E-01

GO:0007626	locomotory behavior	11	703	195	17583	1.41	0.50	9.22E-02	1.88E-01
GO:0033500	carbohydrate homeostasis	11	703	195	17583	1.41	0.50	9.22E-02	1.88E-01
GO:0022904	respiratory electron transport chain	7	703	116	17583	1.51	0.59	9.34E-02	1.88E-01
GO:0006006	glucose metabolic process	7	703	116	17583	1.51	0.59	9.34E-02	1.88E-01
GO:0016310	phosphorylation	43	703	897	17583	1.20	0.26	9.35E-02	1.88E-01
GO:0048870	cell motility	50	703	1057	17583	1.18	0.24	9.35E-02	1.88E-01
GO:0007229	integrin-mediated signaling pathway	6	703	97	17583	1.55	0.63	9.35E-02	1.88E-01
GO:0007052	mitotic spindle organization	6	703	97	17583	1.55	0.63	9.35E-02	1.88E-01
GO:0015931	nucleobase-containing compound transport	12	703	216	17583	1.39	0.47	9.37E-02	1.89E-01
GO:0140352	export from cell	24	703	472	17583	1.27	0.35	9.37E-02	1.89E-01
GO:0002791	regulation of peptide secretion	11	703	196	17583	1.40	0.49	9.49E-02	1.91E-01
GO:0045637	regulation of myeloid cell differentiation	11	703	196	17583	1.40	0.49	9.49E-02	1.91E-01
GO:0051604	protein maturation	15	703	279	17583	1.34	0.43	9.50E-02	1.91E-01
GO:0003006	developmental process involved in reproduction	45	703	944	17583	1.19	0.25	9.52E-02	1.92E-01
GO:0002088	lens development in camera-type eye	5	703	79	17583	1.58	0.66	9.61E-02	1.93E-01
GO:0007492	endoderm development	5	703	79	17583	1.58	0.66	9.61E-02	1.93E-01
GO:1904892	regulation of receptor signaling pathway via STAT	5	703	79	17583	1.58	0.66	9.61E-02	1.93E-01
GO:0051966	regulation of synaptic transmission, glutamatergic	5	703	79	17583	1.58	0.66	9.61E-02	1.93E-01
GO:0016477	cell migration	43	703	900	17583	1.19	0.26	9.72E-02	1.95E-01
GO:0120162	positive regulation of cold-induced thermogenesis	6	703	98	17583	1.53	0.61	9.75E-02	1.96E-01
GO:0006672	ceramide metabolic process	6	703	98	17583	1.53	0.61	9.75E-02	1.96E-01
GO:0060349	bone morphogenesis	6	703	98	17583	1.53	0.61	9.75E-02	1.96E-01
GO:0043279	response to alkaloid	6	703	98	17583	1.53	0.61	9.75E-02	1.96E-01
GO:1902600	proton transmembrane transport	8	703	137	17583	1.46	0.55	9.86E-02	1.98E-01
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	8	703	137	17583	1.46	0.55	9.86E-02	1.98E-01
GO:0019058	viral life cycle	10	703	177	17583	1.41	0.50	9.86E-02	1.98E-01

GO:0090066	regulation of anatomical structure size	25	703	497	17583	1.26	0.33	9.89E-02	1.98E-01
GO:0051701	biological process involved in interaction with host	9	703	157	17583	1.43	0.52	9.90E-02	1.99E-01
GO:0006665	sphingolipid metabolic process	9	703	157	17583	1.43	0.52	9.90E-02	1.99E-01
GO:0090087	regulation of peptide transport	11	703	198	17583	1.39	0.47	1.00E-01	2.00E-01
GO:0016485	protein processing	11	703	198	17583	1.39	0.47	1.00E-01	2.00E-01
GO:0018130	heterocycle biosynthetic process	50	703	1063	17583	1.18	0.23	1.00E-01	2.00E-01
GO:2000142	regulation of DNA-templated transcription initiation	5	703	80	17583	1.56	0.64	1.01E-01	2.00E-01
GO:0043413	macromolecule glycosylation	12	703	219	17583	1.37	0.45	1.01E-01	2.00E-01
GO:0006486	protein glycosylation	12	703	219	17583	1.37	0.45	1.01E-01	2.00E-01
GO:0031214	biomineral tissue development	6	703	99	17583	1.52	0.60	1.01E-01	2.00E-01
GO:0110020	regulation of actomyosin structure organization	6	703	99	17583	1.52	0.60	1.01E-01	2.00E-01
GO:0007040	lysosome organization	6	703	99	17583	1.52	0.60	1.01E-01	2.00E-01
GO:0080171	lytic vacuole organization	6	703	99	17583	1.52	0.60	1.01E-01	2.00E-01
GO:0010952	positive regulation of peptidase activity	10	703	178	17583	1.41	0.49	1.02E-01	2.00E-01
GO:0006790	sulfur compound metabolic process	18	703	346	17583	1.30	0.38	1.02E-01	2.00E-01
GO:0098655	cation transmembrane transport	33	703	677	17583	1.22	0.29	1.02E-01	2.00E-01
GO:1903052	positive regulation of proteolysis involved in protein catabolic process	8	703	138	17583	1.45	0.54	1.02E-01	2.00E-01
GO:0000280	nuclear division	17	703	325	17583	1.31	0.39	1.03E-01	2.00E-01
GO:0002761	regulation of myeloid leukocyte differentiation	7	703	119	17583	1.47	0.56	1.04E-01	2.00E-01
GO:0031398	positive regulation of protein ubiquitination	7	703	119	17583	1.47	0.56	1.04E-01	2.00E-01
GO:0006352	DNA-templated transcription initiation	7	703	119	17583	1.47	0.56	1.04E-01	2.00E-01
GO:0015980	energy derivation by oxidation of organic compounds	14	703	262	17583	1.34	0.42	1.04E-01	2.00E-01
GO:0006887	exocytosis	13	703	241	17583	1.35	0.43	1.04E-01	2.00E-01
GO:1900407	regulation of cellular response to oxidative stress	5	703	81	17583	1.54	0.63	1.05E-01	2.00E-01

	negative regulation of response to DNA								
GO:2001021	damage stimulus	5	703	81	17583	1.54	0.63	1.05E-01	2.00E-01
GO:0021510	spinal cord development	6	703	100	17583	1.50	0.59	1.06E-01	2.00E-01
GO:0071773	cellular response to BMP stimulus	6	703	100	17583	1.50	0.59	1.06E-01	2.00E-01
GO:0071772	response to BMP	6	703	100	17583	1.50	0.59	1.06E-01	2.00E-01
GO:0007423	sensory organ development	28	703	568	17583	1.23	0.30	1.06E-01	2.00E-01
GO:0060537	muscle tissue development	17	703	327	17583	1.30	0.38	1.07E-01	2.00E-01
GO:0051648	vesicle localization	10	703	180	17583	1.39	0.47	1.08E-01	2.00E-01
GO:0009967	positive regulation of signal transduction	69	703	1511	17583	1.14	0.19	1.08E-01	2.00E-01
GO:1902531	regulation of intracellular signal transduction	77	703	1699	17583	1.13	0.18	1.08E-01	2.00E-01
GO:0099537	trans-synaptic signaling	22	703	436	17583	1.26	0.34	1.08E-01	2.00E-01
GO:0051170	import into nucleus	7	703	120	17583	1.46	0.54	1.08E-01	2.00E-01
GO:0006898	receptor-mediated endocytosis	9	703	160	17583	1.41	0.49	1.09E-01	2.00E-01
GO:1904062	regulation of cation transmembrane transport	19	703	371	17583	1.28	0.36	1.09E-01	2.00E-01
GO:0002573	myeloid leukocyte differentiation	8	703	140	17583	1.43	0.52	1.09E-01	2.00E-01
	negative regulation of neuron projection								
GO:0010977	development	8	703	140	17583	1.43	0.52	1.09E-01	2.00E-01
	nucleobase-containing compound catabolic								
GO:0034655	process	15	703	285	17583	1.32	0.40	1.09E-01	2.00E-01
GO:0014013	regulation of gliogenesis	6	703	101	17583	1.49	0.57	1.10E-01	2.00E-01
	negative regulation of ion transmembrane								
GO:0034766	transport	6	703	101	17583	1.49	0.57	1.10E-01	2.00E-01
GO:1902117	positive regulation of organelle assembly	5	703	82	17583	1.53	0.61	1.10E-01	2.00E-01
GO:0048285	organelle fission	18	703	350	17583	1.29	0.36	1.10E-01	2.00E-01
GO:0008361	regulation of cell size	10	703	181	17583	1.38	0.47	1.11E-01	2.00E-01
GO:0001568	blood vessel development	25	703	504	17583	1.24	0.31	1.11E-01	2.00E-01
GO:0033157	regulation of intracellular protein transport	12	703	223	17583	1.35	0.43	1.12E-01	2.00E-01
	regulation of transforming growth factor beta								
GO:0017015	receptor signaling pathway	8	703	141	17583	1.42	0.50	1.12E-01	2.00E-01
	ribonucleoside triphosphate biosynthetic								
GO:0009201	process	6	703	102	17583	1.47	0.56	1.14E-01	2.00E-01

GO:0006906	vesicle fusion	6	703	102	17583	1.47	0.56	1.14E-01	2.00E-01
GO:0009953	dorsal/ventral pattern formation	5	703	83	17583	1.51	0.59	1.15E-01	2.00E-01
GO:0032410	negative regulation of transporter activity	5	703	83	17583	1.51	0.59	1.15E-01	2.00E-01
	transcription initiation at RNA polymerase II promoter								
GO:0006367		5	703	83	17583	1.51	0.59	1.15E-01	2.00E-01
