

Supplementary Table 6. *Gene set enrichment analyses in Gene Ontology's biological processes for genes in the "V" cluster.* 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:0070647	protein modification by small protein conjugation or removal	36	305	893	17583	2.3	1.22	8.3E-07	2.8E-04
GO:0043170	macromolecule metabolic process	137	305	5792	17583	1.4	0.45	4.3E-06	1.4E-03
GO:0019219	regulation of nucleobase-containing compound metabolic process	103	305	4030	17583	1.5	0.56	4.9E-06	1.6E-03
GO:0036211	protein modification process	74	305	2645	17583	1.6	0.69	7.3E-06	2.3E-03
GO:0016071	mRNA metabolic process	26	305	606	17583	2.5	1.31	7.7E-06	2.4E-03
GO:0010468	regulation of gene expression	116	305	4813	17583	1.4	0.47	1.7E-05	5.2E-03
GO:0032446	protein modification by small protein conjugation	29	305	751	17583	2.2	1.15	2.0E-05	5.8E-03
GO:0043412	macromolecule modification	77	305	2865	17583	1.5	0.63	2.0E-05	5.8E-03
GO:0060255	regulation of macromolecule metabolic process	140	305	6147	17583	1.3	0.39	2.8E-05	7.6E-03
GO:0051171	regulation of nitrogen compound metabolic process	130	305	5628	17583	1.3	0.41	3.4E-05	9.2E-03
GO:0051252	regulation of RNA metabolic process	93	305	3724	17583	1.4	0.53	4.5E-05	1.2E-02
GO:0031323	regulation of cellular metabolic process	128	305	5561	17583	1.3	0.41	5.0E-05	1.2E-02

GO:0016567	protein ubiquitination	26	305	681	17583	2.2	1.14	5.9E-05	1.4E-02
	cellular macromolecule								
GO:0044260	metabolic process	67	305	2498	17583	1.5	0.63	8.2E-05	1.9E-02
	proteasome-mediated								
	ubiquitin-dependent protein								
GO:0043161	catabolic process	16	305	345	17583	2.7	1.42	1.2E-04	2.7E-02
	regulation of metabolic								
GO:0019222	process	146	305	6669	17583	1.3	0.34	1.4E-04	3.1E-02
	negative regulation of								
GO:0017148	translation	10	305	166	17583	3.5	1.80	1.6E-04	3.1E-02
	regulation of								
GO:0010556	macromolecule biosynthetic	94	305	3907	17583	1.4	0.47	1.7E-04	3.1E-02
	regulation of primary								
GO:0080090	metabolic process	129	305	5782	17583	1.3	0.36	2.1E-04	3.1E-02
	nucleic acid metabolic								
GO:0090304	process	60	305	2247	17583	1.5	0.62	2.2E-04	3.1E-02
	regulation of transcription by								
GO:0006357	RNA polymerase II	67	305	2592	17583	1.5	0.58	2.5E-04	3.1E-02
GO:0007030	Golgi organization	9	305	147	17583	3.5	1.82	2.5E-04	3.1E-02
	macromolecule catabolic								
GO:0009057	process	32	305	992	17583	1.9	0.90	2.6E-04	3.1E-02
	cellular macromolecule								
GO:0044265	catabolic process	27	305	786	17583	2.0	0.99	2.6E-04	3.1E-02
GO:0043484	regulation of RNA splicing	10	305	179	17583	3.2	1.69	3.0E-04	3.1E-02
	regulation of biosynthetic								
GO:0009889	process	97	305	4122	17583	1.4	0.44	3.0E-04	3.1E-02
	regulation of mRNA								
GO:1903311	metabolic process	14	305	306	17583	2.6	1.40	3.1E-04	3.2E-02
	proteasomal protein								
GO:0010498	catabolic process	16	305	376	17583	2.5	1.29	3.2E-04	3.3E-02
	regulation of centrosome								
GO:0046605	cycle	5	305	54	17583	5.3	2.42	3.3E-04	3.4E-02

GO:0016482	cytosolic transport	9	305	154	17583	3.4	1.75	3.6E-04	3.7E-02
GO:0007265	Ras protein signal transduction	10	305	185	17583	3.1	1.64	4.0E-04	3.9E-02
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	10	305	185	17583	3.1	1.64	4.0E-04	3.9E-02
GO:0031326	regulation of cellular biosynthetic process	95	305	4057	17583	1.3	0.43	4.2E-04	4.1E-02
GO:0000956	nuclear-transcribed mRNA catabolic process	7	305	103	17583	3.9	1.97	4.3E-04	4.1E-02
GO:0034249	negative regulation of amide metabolic process	10	305	188	17583	3.1	1.62	4.6E-04	4.4E-02
GO:0030433	ubiquitin-dependent ERAD pathway	6	305	80	17583	4.3	2.11	4.7E-04	4.5E-02
GO:0034976	response to endoplasmic reticulum stress	11	305	220	17583	2.9	1.53	4.8E-04	4.6E-02
GO:0006807	nitrogen compound metabolic process	143	305	6674	17583	1.2	0.30	5.5E-04	5.1E-02
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	5	305	61	17583	4.7	2.24	6.5E-04	6.0E-02
GO:0001824	blastocyst development	7	305	110	17583	3.7	1.88	6.6E-04	6.0E-02
GO:0000209	protein polyubiquitination	11	305	232	17583	2.7	1.45	7.7E-04	6.0E-02
GO:0006903	vesicle targeting	5	305	63	17583	4.6	2.19	7.7E-04	6.0E-02
GO:0035966	response to topologically incorrect protein	8	305	144	17583	3.2	1.68	9.3E-04	6.2E-02
GO:0010629	negative regulation of gene expression	28	305	900	17583	1.8	0.84	1.0E-03	6.7E-02
GO:0016070	RNA metabolic process	44	305	1619	17583	1.6	0.65	1.1E-03	6.8E-02
GO:2001020	regulation of response to DNA damage stimulus	13	305	311	17583	2.4	1.27	1.1E-03	7.3E-02

GO:1903312	negative regulation of mRNA metabolic process	6	305	94	17583	3.7	1.88	1.2E-03	7.7E-02
GO:0016579	protein deubiquitination response to unfolded protein	8	305	151	17583	3.1	1.61	1.3E-03	7.7E-02
GO:0006986	primary metabolic process	7	305	122	17583	3.3	1.73	1.3E-03	7.7E-02
GO:0044238	regulation of DNA-templated transcription	150	305	7194	17583	1.2	0.27	1.4E-03	7.7E-02
GO:0006355	regulation of nucleic acid-templated transcription	80	305	3420	17583	1.3	0.43	1.4E-03	7.7E-02
GO:1903506	protein metabolic process	80	305	3422	17583	1.3	0.43	1.4E-03	7.7E-02
GO:0019538	integrin-mediated signaling pathway	89	305	3891	17583	1.3	0.40	1.5E-03	7.7E-02
GO:0007229	regulation of RNA biosynthetic process	6	305	97	17583	3.6	1.83	1.5E-03	7.7E-02
GO:2001141	ERAD pathway	80	305	3431	17583	1.3	0.43	1.6E-03	7.7E-02
GO:0036503	mRNA catabolic process	6	305	98	17583	3.5	1.82	1.6E-03	7.7E-02
GO:0006402	small GTPase mediated signal transduction	7	305	127	17583	3.2	1.67	1.7E-03	7.7E-02
GO:0007264	organic substance metabolic process	11	305	256	17583	2.5	1.31	1.8E-03	7.7E-02
GO:0071704	mRNA processing	155	305	7534	17583	1.2	0.25	2.0E-03	7.7E-02
GO:0006397	erythrocyte homeostasis	16	305	448	17583	2.1	1.04	2.2E-03	7.7E-02
GO:0034101	ubiquitin-dependent protein catabolic process	6	305	105	17583	3.3	1.72	2.4E-03	7.7E-02
GO:0006511	establishment of vesicle localization	19	305	574	17583	1.9	0.93	2.5E-03	7.7E-02
GO:0051650	regulation of mRNA splicing, via spliceosome	8	305	167	17583	2.8	1.47	2.6E-03	7.7E-02
GO:0048024	protein modification by small protein removal	6	305	108	17583	3.2	1.68	2.8E-03	7.7E-02
GO:0070646	DNA repair	8	305	169	17583	2.7	1.45	2.8E-03	7.7E-02
GO:0006281		17	305	499	17583	2.0	0.97	2.9E-03	7.7E-02

GO:0007049	cell cycle regulation of mRNA	35	305	1283	17583	1.6	0.65	2.9E-03	7.7E-02
GO:0050684	processing modification-dependent	7	305	139	17583	2.9	1.54	3.0E-03	7.7E-02
GO:0019941	protein catabolic process	19	305	584	17583	1.9	0.91	3.1E-03	7.7E-02
GO:0008152	metabolic process	161	305	7967	17583	1.2	0.22	3.5E-03	7.7E-02
GO:0030163	protein catabolic process negative regulation of macromolecule metabolic	23	305	760	17583	1.7	0.80	3.5E-03	7.7E-02
GO:0010605	process in utero embryonic	64	305	2717	17583	1.4	0.44	3.7E-03	7.7E-02
GO:0001701	development modification-dependent macromolecule catabolic	14	305	394	17583	2.0	1.03	3.8E-03	7.7E-02
GO:0043632	process regulation of microtubule-	19	305	596	17583	1.8	0.88	3.9E-03	7.7E-02
GO:0032886	based process	10	305	248	17583	2.3	1.22	4.1E-03	7.7E-02
GO:0046907	intracellular transport	36	305	1358	17583	1.5	0.61	4.2E-03	7.7E-02
GO:0051648	vesicle localization proteolysis involved in	8	305	180	17583	2.6	1.36	4.3E-03	7.7E-02
GO:0051603	protein catabolic process endoplasmic reticulum	20	305	645	17583	1.8	0.84	4.4E-03	7.7E-02
GO:0007029	organization	5	305	89	17583	3.2	1.70	4.5E-03	7.7E-02
GO:0006417	regulation of translation	14	305	403	17583	2.0	1.00	4.7E-03	7.7E-02
GO:0007032	endosome organization positive regulation of mRNA	5	305	91	17583	3.2	1.66	5.0E-03	7.7E-02
GO:0061014	catabolic process post-transcriptional regulation of gene	5	305	92	17583	3.1	1.65	5.3E-03	7.7E-02
GO:0010608	expression regulation of mRNA	16	305	491	17583	1.9	0.91	5.6E-03	7.7E-02
GO:0061013	catabolic process	8	305	188	17583	2.5	1.29	5.6E-03	7.7E-02

GO:0033157	regulation of intracellular protein transport	9	305	223	17583	2.3	1.22	5.7E-03	7.7E-02
GO:0042147	retrograde transport, endosome to Golgi	5	305	94	17583	3.1	1.62	5.9E-03	7.7E-02
GO:0080135	regulation of cellular response to stress	21	305	707	17583	1.7	0.78	6.1E-03	7.7E-02
GO:1903313	positive regulation of mRNA metabolic process	6	305	125	17583	2.8	1.47	6.2E-03	7.7E-02
GO:0051726	regulation of cell cycle	30	305	1113	17583	1.6	0.64	6.3E-03	7.7E-02
GO:0016050	vesicle organization	12	305	338	17583	2.0	1.03	6.3E-03	7.7E-02
GO:0061136	regulation of proteasomal protein catabolic process	8	305	192	17583	2.4	1.26	6.5E-03	7.7E-02
GO:0035967	cellular response to topologically incorrect protein	5	305	96	17583	3.0	1.59	6.5E-03	7.7E-02
GO:0030218	erythrocyte differentiation	5	305	96	17583	3.0	1.59	6.5E-03	7.7E-02
GO:0006508	proteolysis	33	305	1258	17583	1.5	0.60	6.7E-03	7.7E-02
GO:1903050	regulation of proteolysis involved in protein catabolic process	9	305	229	17583	2.3	1.18	6.8E-03	7.7E-02
GO:0034248	regulation of amide metabolic process	15	305	462	17583	1.9	0.90	7.0E-03	7.7E-02
GO:0006139	nucleobase-containing compound metabolic process	64	305	2793	17583	1.3	0.40	7.0E-03	7.7E-02
GO:0007179	transforming growth factor beta receptor signaling pathway	5	305	98	17583	2.9	1.56	7.2E-03	7.7E-02
GO:0007040	lysosome organization	5	305	99	17583	2.9	1.54	7.6E-03	7.7E-02
GO:0080171	lytic vacuole organization	5	305	99	17583	2.9	1.54	7.6E-03	7.7E-02
GO:0006401	RNA catabolic process	7	305	163	17583	2.5	1.31	7.7E-03	7.7E-02

	positive regulation of amide								
GO:0034250	metabolic process	7	305	163	17583	2.5	1.31	7.7E-03	7.7E-02
GO:0051301	cell division	16	305	508	17583	1.8	0.86	7.7E-03	7.7E-02
GO:0016197	endosomal transport	9	305	234	17583	2.2	1.15	7.9E-03	7.7E-02
	heterocycle metabolic								
GO:0046483	process	67	305	2966	17583	1.3	0.38	8.1E-03	7.7E-02
GO:0002262	myeloid cell homeostasis	6	305	132	17583	2.6	1.39	8.2E-03	7.7E-02
	endomembrane system								
GO:0010256	organization	17	305	555	17583	1.8	0.82	8.4E-03	7.7E-02
	endoplasmic reticulum to								
	Golgi vesicle-mediated								
GO:0006888	transport	6	305	133	17583	2.6	1.38	8.6E-03	7.7E-02
GO:0044237	cellular metabolic process	132	305	6489	17583	1.2	0.23	9.0E-03	7.7E-02
	negative regulation of								
GO:0048523	cellular process	99	305	4675	17583	1.2	0.29	9.0E-03	7.7E-02
GO:0043488	regulation of mRNA stability	7	305	168	17583	2.4	1.26	9.1E-03	7.7E-02
	negative regulation of								
GO:0009892	metabolic process	66	305	2934	17583	1.3	0.37	9.4E-03	7.7E-02
GO:0033554	cellular response to stress	39	305	1576	17583	1.4	0.51	9.4E-03	7.7E-02
GO:0048588	developmental cell growth	5	305	105	17583	2.7	1.46	1.0E-02	7.7E-02
	cardiac septum								
GO:0003279	development	5	305	105	17583	2.7	1.46	1.0E-02	7.7E-02
	positive regulation of								
GO:0045727	translation	6	305	137	17583	2.5	1.34	1.0E-02	7.7E-02
	negative regulation of								
	nucleobase-containing								
	compound metabolic								
GO:0045934	process	38	305	1541	17583	1.4	0.51	1.1E-02	7.7E-02
	regulation of								
GO:0046822	nucleocytoplasmic transport	5	305	107	17583	2.7	1.43	1.1E-02	7.7E-02
GO:0016049	cell growth	5	305	107	17583	2.7	1.43	1.1E-02	7.7E-02

GO:2000112	regulation of cellular macromolecule biosynthetic process	15	305	485	17583	1.8	0.83	1.1E-02	7.7E-02
GO:0034655	nucleobase-containing compound catabolic process	10	305	285	17583	2.0	1.02	1.1E-02	7.7E-02
GO:0006996	organelle organization	67	305	3011	17583	1.3	0.36	1.1E-02	7.7E-02
GO:2000058	regulation of ubiquitin- dependent protein catabolic process	7	305	175	17583	2.3	1.21	1.1E-02	7.7E-02
GO:0006725	cellular aromatic compound metabolic process	67	305	3013	17583	1.3	0.36	1.2E-02	7.7E-02
GO:0031330	negative regulation of cellular catabolic process	9	305	248	17583	2.1	1.06	1.2E-02	7.7E-02
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	6	305	142	17583	2.4	1.28	1.2E-02	7.7E-02
GO:0032386	regulation of intracellular transport	11	305	329	17583	1.9	0.95	1.3E-02	7.7E-02
GO:0033044	regulation of chromosome organization	9	305	252	17583	2.1	1.04	1.3E-02	7.7E-02
GO:0090305	nucleic acid phosphodiester bond hydrolysis	9	305	252	17583	2.1	1.04	1.3E-02	7.7E-02
GO:0010558	negative regulation of macromolecule biosynthetic process	37	305	1510	17583	1.4	0.50	1.3E-02	7.7E-02
GO:0048193	Golgi vesicle transport	10	305	291	17583	2.0	0.99	1.3E-02	7.7E-02
GO:0015931	nucleobase-containing compound transport	8	305	216	17583	2.1	1.09	1.3E-02	7.7E-02
GO:0043487	regulation of RNA stability	7	305	180	17583	2.2	1.16	1.3E-02	7.7E-02
GO:0031324	negative regulation of cellular metabolic process	51	305	2218	17583	1.3	0.41	1.4E-02	7.7E-02

GO:0048872	homeostasis of number of cells	9	305	256	17583	2.0	1.02	1.4E-02	7.7E-02
GO:0044248	cellular catabolic process	39	305	1630	17583	1.4	0.46	1.6E-02	7.7E-02
GO:2001236	regulation of extrinsic apoptotic signaling pathway	6	305	151	17583	2.3	1.20	1.6E-02	7.7E-02
GO:0034728	nucleosome organization	5	305	118	17583	2.4	1.29	1.7E-02	7.7E-02
GO:0051056	regulation of small GTPase mediated signal transduction	10	305	303	17583	1.9	0.93	1.7E-02	7.7E-02
GO:0006259	DNA metabolic process	21	305	778	17583	1.6	0.64	1.7E-02	7.7E-02
GO:0009100	glycoprotein metabolic process	11	305	346	17583	1.8	0.87	1.8E-02	8.0E-02
GO:0006974	cellular response to DNA damage stimulus	20	305	743	17583	1.6	0.63	2.0E-02	8.7E-02
GO:0071824	protein-DNA complex subunit organization	8	305	231	17583	2.0	1.00	2.0E-02	8.7E-02
GO:0110053	regulation of actin filament organization	9	305	270	17583	1.9	0.94	2.0E-02	8.7E-02
GO:0071560	cellular response to transforming growth factor beta stimulus	6	305	158	17583	2.2	1.13	2.0E-02	9.0E-02
GO:0030099	myeloid cell differentiation	9	305	273	17583	1.9	0.93	2.1E-02	9.2E-02
GO:0051253	negative regulation of RNA metabolic process	34	305	1416	17583	1.4	0.47	2.1E-02	9.2E-02
GO:0051649	establishment of localization in cell	41	305	1764	17583	1.3	0.42	2.1E-02	9.3E-02
GO:0006914	autophagy	10	305	314	17583	1.8	0.88	2.2E-02	9.4E-02
GO:0061919	process utilizing autophagic mechanism	10	305	314	17583	1.8	0.88	2.2E-02	9.4E-02
GO:0031327	negative regulation of cellular biosynthetic process	37	305	1566	17583	1.4	0.45	2.2E-02	9.4E-02

GO:0031329	regulation of cellular catabolic process	21	305	797	17583	1.5	0.60	2.2E-02	9.4E-02
GO:0045667	regulation of osteoblast differentiation	5	305	125	17583	2.3	1.21	2.2E-02	9.5E-02
GO:0032774	RNA biosynthetic process	17	305	617	17583	1.6	0.67	2.2E-02	9.7E-02
GO:0009101	glycoprotein biosynthetic process	9	305	276	17583	1.9	0.91	2.3E-02	9.8E-02
GO:0030097	hemopoiesis	18	305	663	17583	1.6	0.65	2.3E-02	9.8E-02
GO:0070085	glycosylation	8	305	238	17583	1.9	0.95	2.3E-02	9.8E-02
GO:0016310	phosphorylation	23	305	897	17583	1.5	0.56	2.4E-02	9.8E-02
GO:0061025	membrane fusion	6	305	163	17583	2.1	1.09	2.4E-02	9.8E-02
GO:0051028	mRNA transport	5	305	128	17583	2.3	1.17	2.4E-02	9.8E-02
GO:0010467	gene expression	49	305	2186	17583	1.3	0.37	2.4E-02	9.8E-02
GO:0071559	response to transforming growth factor beta	6	305	165	17583	2.1	1.07	2.5E-02	9.8E-02
GO:0007034	vacuolar transport	6	305	165	17583	2.1	1.07	2.5E-02	9.8E-02
GO:0008380	RNA splicing	11	305	366	17583	1.7	0.79	2.7E-02	9.8E-02
GO:0007041	lysosomal transport	5	305	131	17583	2.2	1.14	2.7E-02	9.8E-02
GO:2001022	positive regulation of response to DNA damage stimulus	6	305	168	17583	2.1	1.04	2.7E-02	9.8E-02
GO:0051172	negative regulation of nitrogen compound metabolic process	52	305	2357	17583	1.3	0.35	2.7E-02	9.8E-02
GO:0051168	nuclear export	5	305	132	17583	2.2	1.13	2.8E-02	9.8E-02
GO:0033043	regulation of organelle organization	29	305	1199	17583	1.4	0.48	2.8E-02	9.8E-02
GO:1901564	organonitrogen compound metabolic process	101	305	4982	17583	1.2	0.22	2.8E-02	9.8E-02
GO:0009890	negative regulation of biosynthetic process	37	305	1596	17583	1.3	0.42	2.8E-02	9.8E-02

GO:0044262	cellular carbohydrate metabolic process	6	305	169	17583	2.0	1.03	2.8E-02	9.8E-02
GO:0080134	regulation of response to stress	34	305	1447	17583	1.4	0.44	2.8E-02	9.8E-02
GO:1901360	organic cyclic compound metabolic process	69	305	3255	17583	1.2	0.29	2.9E-02	9.8E-02
GO:0065004	protein-DNA complex assembly	7	305	210	17583	1.9	0.94	3.0E-02	9.8E-02
GO:0046700	heterocycle catabolic process	10	305	332	17583	1.7	0.80	3.1E-02	9.8E-02
GO:1902903	regulation of supramolecular fiber	11	305	376	17583	1.7	0.75	3.2E-02	9.8E-02
GO:0006396	RNA processing	22	305	876	17583	1.4	0.53	3.2E-02	9.8E-02
GO:0044270	cellular nitrogen compound catabolic process	10	305	334	17583	1.7	0.79	3.2E-02	9.8E-02
GO:0045184	establishment of protein localization	30	305	1264	17583	1.4	0.45	3.2E-02	9.8E-02
GO:0034641	cellular nitrogen compound metabolic process	70	305	3333	17583	1.2	0.28	3.3E-02	9.8E-02
GO:0120031	plasma membrane bounded cell projection assembly	12	305	424	17583	1.6	0.71	3.4E-02	9.8E-02
GO:0015031	protein transport	28	305	1176	17583	1.4	0.46	3.5E-02	1.0E-01
GO:0006351	DNA-templated transcription	16	305	606	17583	1.5	0.61	3.6E-02	1.0E-01
GO:0032868	response to insulin	7	305	217	17583	1.9	0.90	3.6E-02	1.0E-01
GO:0009059	macromolecule biosynthetic process	34	305	1476	17583	1.3	0.41	3.6E-02	1.0E-01
GO:0097659	nucleic acid-templated transcription	16	305	607	17583	1.5	0.60	3.6E-02	1.0E-01
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	5	305	141	17583	2.0	1.03	3.6E-02	1.0E-01

GO:0071705	nitrogen compound transport	36	305	1581	17583	1.3	0.39	3.8E-02	1.1E-01
GO:0043413	macromolecule glycosylation	7	305	219	17583	1.8	0.88	3.8E-02	1.1E-01
GO:0006486	protein glycosylation	7	305	219	17583	1.8	0.88	3.8E-02	1.1E-01
GO:0006457	protein folding	7	305	220	17583	1.8	0.88	3.8E-02	1.1E-01
GO:2000146	negative regulation of cell motility	9	305	303	17583	1.7	0.78	3.9E-02	1.1E-01
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	5	305	144	17583	2.0	1.00	4.0E-02	1.1E-01
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	5	305	144	17583	2.0	1.00	4.0E-02	1.1E-01
GO:0016192	vesicle-mediated transport	32	305	1387	17583	1.3	0.41	4.0E-02	1.1E-01
GO:0007033	vacuole organization	6	305	183	17583	1.9	0.92	4.1E-02	1.1E-01
GO:0019439	aromatic compound catabolic process	10	305	348	17583	1.7	0.73	4.1E-02	1.1E-01
GO:0043543	protein acylation	6	305	184	17583	1.9	0.91	4.2E-02	1.2E-01
GO:0030031	cell projection assembly	12	305	437	17583	1.6	0.66	4.2E-02	1.2E-01
GO:0006468	protein phosphorylation	18	305	712	17583	1.5	0.54	4.2E-02	1.2E-01
GO:0010564	regulation of cell cycle process	18	305	714	17583	1.5	0.54	4.3E-02	1.2E-01
GO:0051493	regulation of cytoskeleton organization	14	305	529	17583	1.5	0.61	4.3E-02	1.2E-01
GO:0018105	peptidyl-serine phosphorylation	6	305	186	17583	1.9	0.90	4.4E-02	1.2E-01
GO:0015748	organophosphate ester transport	5	305	148	17583	1.9	0.96	4.4E-02	1.2E-01
GO:0000278	mitotic cell cycle	16	305	624	17583	1.5	0.56	4.5E-02	1.2E-01

GO:0051052	regulation of DNA metabolic process	14	305	533	17583	1.5	0.60	4.6E-02	1.2E-01
GO:0048519	negative regulation of biological process	104	305	5250	17583	1.1	0.19	4.6E-02	1.2E-01
GO:1901698	response to nitrogen compound	25	305	1058	17583	1.4	0.45	4.7E-02	1.2E-01
GO:0032956	regulation of actin cytoskeleton organization	10	305	359	17583	1.6	0.68	4.9E-02	1.2E-01
GO:0032869	cellular response to insulin stimulus	5	305	152	17583	1.9	0.92	4.9E-02	1.2E-01
GO:0010243	response to organonitrogen compound	23	305	967	17583	1.4	0.46	5.0E-02	1.2E-01
GO:0035556	intracellular signal transduction	34	305	1517	17583	1.3	0.37	5.0E-02	1.2E-01
GO:1901652	response to peptide	12	305	453	17583	1.5	0.61	5.3E-02	1.2E-01
GO:0009411	response to UV	5	305	155	17583	1.9	0.90	5.3E-02	1.2E-01
GO:0051098	regulation of binding	10	305	368	17583	1.6	0.65	5.7E-02	1.3E-01
GO:0050657	nucleic acid transport	5	305	158	17583	1.8	0.87	5.8E-02	1.3E-01
GO:0050658	RNA transport	5	305	158	17583	1.8	0.87	5.8E-02	1.3E-01
GO:0006887	exocytosis	7	305	241	17583	1.7	0.74	6.0E-02	1.4E-01
GO:0051236	establishment of RNA localization	5	305	160	17583	1.8	0.85	6.0E-02	1.4E-01
GO:0051641	cellular localization	55	305	2639	17583	1.2	0.26	6.1E-02	1.4E-01
GO:0010638	positive regulation of organelle organization	13	305	509	17583	1.5	0.56	6.1E-02	1.4E-01
GO:0016236	macroautophagy	6	305	201	17583	1.7	0.78	6.1E-02	1.4E-01
GO:0090501	RNA phosphodiester bond hydrolysis	5	305	162	17583	1.8	0.83	6.3E-02	1.4E-01
GO:0030336	negative regulation of cell migration	8	305	288	17583	1.6	0.68	6.5E-02	1.4E-01
GO:0009895	negative regulation of catabolic process	9	305	332	17583	1.6	0.64	6.5E-02	1.4E-01

GO:0010033	response to organic substance	51	305	2439	17583	1.2	0.27	6.5E-02	1.4E-01
GO:0006302	double-strand break repair	6	305	204	17583	1.7	0.76	6.5E-02	1.4E-01
GO:0018209	peptidyl-serine modification	6	305	204	17583	1.7	0.76	6.5E-02	1.4E-01
GO:0008654	phospholipid biosynthetic process	7	305	246	17583	1.6	0.71	6.6E-02	1.4E-01
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	6	305	205	17583	1.7	0.75	6.7E-02	1.4E-01
GO:0046474	glycerophospholipid biosynthetic process	6	305	205	17583	1.7	0.75	6.7E-02	1.4E-01
GO:0051640	organelle localization	13	305	517	17583	1.4	0.54	6.8E-02	1.4E-01
GO:0003205	cardiac chamber development	5	305	165	17583	1.7	0.80	6.8E-02	1.4E-01
GO:0045892	negative regulation of DNA-templated transcription	29	305	1303	17583	1.3	0.36	6.8E-02	1.4E-01
GO:1901361	organic cyclic compound catabolic process	10	305	381	17583	1.5	0.60	6.9E-02	1.4E-01
GO:1903507	negative regulation of nucleic acid-templated transcription	29	305	1305	17583	1.3	0.36	6.9E-02	1.4E-01
GO:0009056	catabolic process	42	305	1977	17583	1.2	0.29	7.0E-02	1.4E-01
GO:1902679	negative regulation of RNA biosynthetic process	29	305	1307	17583	1.3	0.36	7.1E-02	1.4E-01
GO:0051656	establishment of organelle localization	10	305	383	17583	1.5	0.59	7.1E-02	1.4E-01
GO:1903320	regulation of protein modification by small protein conjugation or removal	7	305	251	17583	1.6	0.69	7.2E-02	1.4E-01

GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	7	305	251	17583	1.6	0.69	7.2E-02	1.4E-01
GO:0031396	regulation of protein ubiquitination	6	305	209	17583	1.7	0.73	7.2E-02	1.4E-01
GO:0040013	negative regulation of locomotion	9	305	340	17583	1.5	0.61	7.3E-02	1.5E-01
GO:0044772	mitotic cell cycle phase transition	5	305	169	17583	1.7	0.77	7.4E-02	1.5E-01
GO:0051254	positive regulation of RNA metabolic process	39	305	1833	17583	1.2	0.29	7.6E-02	1.5E-01
GO:1901565	organonitrogen compound catabolic process	25	305	1117	17583	1.3	0.37	7.8E-02	1.5E-01
GO:0006282	regulation of DNA repair	6	305	213	17583	1.6	0.70	7.8E-02	1.5E-01
GO:0009792	embryo development ending in birth or egg	16	305	673	17583	1.4	0.45	7.9E-02	1.5E-01
GO:0071840	cellular component organization or biogenesis	110	305	5719	17583	1.1	0.15	8.3E-02	1.5E-01
GO:0016570	histone modification	10	305	394	17583	1.5	0.55	8.3E-02	1.5E-01
GO:0044403	biological process involved in symbiotic interaction	7	305	260	17583	1.6	0.63	8.4E-02	1.5E-01
GO:0007601	visual perception	6	305	218	17583	1.6	0.67	8.6E-02	1.6E-01
GO:0140014	mitotic nuclear division	5	305	176	17583	1.6	0.71	8.7E-02	1.6E-01
GO:0000165	MAPK cascade	6	305	219	17583	1.6	0.66	8.8E-02	1.6E-01
GO:0032970	regulation of actin filament-based process	10	305	399	17583	1.4	0.53	8.9E-02	1.6E-01
GO:0006338	chromatin remodeling	9	305	354	17583	1.5	0.55	9.0E-02	1.6E-01
GO:1901653	cellular response to peptide	8	305	309	17583	1.5	0.58	9.0E-02	1.6E-01
GO:0006886	intracellular protein	16	305	688	17583	1.3	0.42	9.2E-02	1.7E-01
GO:0044770	cell cycle phase transition	5	305	179	17583	1.6	0.69	9.2E-02	1.7E-01
GO:0050953	sensory perception of light stimulus	6	305	222	17583	1.6	0.64	9.3E-02	1.7E-01

	positive regulation of macromolecule biosynthetic								
GO:0010557	process	40	305	1920	17583	1.2	0.26	9.4E-02	1.7E-01
GO:0006403	RNA localization	5	305	181	17583	1.6	0.67	9.6E-02	1.7E-01
	glycerolipid biosynthetic								
GO:0045017	process	6	305	225	17583	1.5	0.62	9.8E-02	1.7E-01
	positive regulation of nucleobase-containing compound metabolic								
GO:0045935	process	42	305	2034	17583	1.2	0.25	9.9E-02	1.7E-01
	regulation of catabolic								
GO:0009894	process	22	305	995	17583	1.3	0.35	9.9E-02	1.7E-01
	positive regulation of nitrogen compound								
GO:0051173	metabolic process	62	305	3112	17583	1.1	0.20	1.0E-01	1.7E-01
	negative regulation of								
GO:2001234	apoptotic signaling pathway	6	305	227	17583	1.5	0.61	1.0E-01	1.7E-01
	regulation of apoptotic								
GO:2001233	signaling pathway	9	305	363	17583	1.4	0.52	1.0E-01	1.7E-01
GO:0022402	cell cycle process	20	305	899	17583	1.3	0.36	1.0E-01	1.7E-01
	chordate embryonic								
GO:0043009	development	15	305	651	17583	1.3	0.41	1.0E-01	1.7E-01
	positive regulation of								
GO:0050769	neurogenesis	6	305	229	17583	1.5	0.59	1.0E-01	1.8E-01
	regulation of								
	transmembrane receptor								
	protein serine/threonine								
GO:0090092	kinase signaling pathway	7	305	274	17583	1.5	0.56	1.1E-01	1.8E-01
	positive regulation of								
GO:0031331	cellular catabolic process	10	305	413	17583	1.4	0.48	1.1E-01	1.8E-01
	organic substance catabolic								
GO:1901575	process	35	305	1679	17583	1.2	0.27	1.1E-01	1.8E-01

GO:0009416	response to light stimulus cellular component	8	305	321	17583	1.4	0.52	1.1E-01	1.8E-01
GO:0016043	organization	105	305	5509	17583	1.1	0.14	1.1E-01	1.8E-01
GO:0006325	chromatin organization regulation of Ras protein	14	305	608	17583	1.3	0.41	1.1E-01	1.8E-01
GO:0046578	signal transduction	5	305	188	17583	1.5	0.62	1.1E-01	1.8E-01
GO:0046777	protein autophosphorylation response to peptide	5	305	188	17583	1.5	0.62	1.1E-01	1.8E-01
GO:0043434	hormone positive regulation of	9	305	369	17583	1.4	0.49	1.1E-01	1.8E-01
GO:0009896	catabolic process heterocycle biosynthetic	12	305	512	17583	1.4	0.43	1.1E-01	1.8E-01
GO:0018130	process	23	305	1063	17583	1.2	0.32	1.1E-01	1.8E-01
GO:0071702	organic substance transport regulation of cellular	40	305	1956	17583	1.2	0.24	1.2E-01	1.8E-01
GO:0051128	component organization protein localization to	48	305	2384	17583	1.2	0.22	1.2E-01	1.8E-01
GO:0034504	nucleus negative regulation of	5	305	192	17583	1.5	0.59	1.2E-01	1.9E-01
GO:0023057	signaling	28	305	1328	17583	1.2	0.28	1.2E-01	1.9E-01
GO:0006399	tRNA metabolic process aromatic compound	5	305	193	17583	1.5	0.58	1.2E-01	1.9E-01
GO:0019438	biosynthetic process negative regulation of	23	305	1072	17583	1.2	0.31	1.2E-01	1.9E-01
GO:1903828	protein localization regulation of establishment	5	305	194	17583	1.5	0.57	1.2E-01	1.9E-01
GO:0070201	of protein localization negative regulation of signal	12	305	524	17583	1.3	0.40	1.3E-01	2.0E-01
GO:0009968	transduction negative regulation of	26	305	1236	17583	1.2	0.28	1.3E-01	2.0E-01
GO:0051051	transport	10	305	429	17583	1.3	0.43	1.3E-01	2.0E-01

	cellular response to peptide								
GO:0071375	hormone stimulus	6	305	244	17583	1.4	0.50	1.3E-01	2.0E-01
GO:1903047	mitotic cell cycle process	12	305	531	17583	1.3	0.38	1.3E-01	2.1E-01
GO:0043393	regulation of protein binding	5	305	200	17583	1.4	0.53	1.4E-01	2.1E-01
	glycerophospholipid								
GO:0006650	metabolic process	7	305	292	17583	1.4	0.47	1.4E-01	2.1E-01
GO:0051169	nuclear transport	6	305	246	17583	1.4	0.49	1.4E-01	2.1E-01
GO:0006913	nucleocytoplasmic transport	6	305	246	17583	1.4	0.49	1.4E-01	2.1E-01
GO:0018205	peptidyl-lysine modification	7	305	293	17583	1.4	0.46	1.4E-01	2.1E-01
	nucleobase-containing								
	compound biosynthetic								
GO:0034654	process	21	305	991	17583	1.2	0.29	1.4E-01	2.1E-01
	cellular response to organic								
GO:0071310	substance	35	305	1728	17583	1.2	0.22	1.4E-01	2.2E-01
GO:0051321	meiotic cell cycle	6	305	249	17583	1.4	0.47	1.4E-01	2.2E-01
GO:1901654	response to ketone	5	305	204	17583	1.4	0.50	1.4E-01	2.2E-01
GO:0008104	protein localization	38	305	1892	17583	1.2	0.21	1.5E-01	2.2E-01
GO:0006909	phagocytosis	6	305	250	17583	1.4	0.47	1.5E-01	2.2E-01
	positive regulation of								
GO:0009891	biosynthetic process	41	305	2055	17583	1.2	0.20	1.5E-01	2.2E-01
GO:0016072	rRNA metabolic process	6	305	251	17583	1.4	0.46	1.5E-01	2.2E-01
	positive regulation of								
GO:0050679	epithelial cell proliferation	5	305	206	17583	1.4	0.48	1.5E-01	2.2E-01
	positive regulation of cell								
GO:0090068	cycle process	6	305	252	17583	1.4	0.46	1.5E-01	2.2E-01
	cellular macromolecule								
GO:0070727	localization	38	305	1898	17583	1.2	0.21	1.5E-01	2.2E-01
	regulation of								
GO:0001505	neurotransmitter levels	5	305	207	17583	1.4	0.48	1.5E-01	2.2E-01
GO:0048285	organelle fission	8	305	350	17583	1.3	0.40	1.6E-01	2.3E-01
	positive regulation of								
GO:0031328	cellular biosynthetic process	40	305	2016	17583	1.1	0.19	1.6E-01	2.3E-01

GO:0007517	muscle organ development	7	305	304	17583	1.3	0.41	1.6E-01	2.3E-01
GO:0045786	negative regulation of cell cycle	8	305	352	17583	1.3	0.39	1.6E-01	2.3E-01
GO:0006366	transcription by RNA polymerase II	8	305	352	17583	1.3	0.39	1.6E-01	2.3E-01
GO:0051223	regulation of protein transport	11	305	499	17583	1.3	0.35	1.6E-01	2.3E-01
GO:0009615	response to virus	8	305	354	17583	1.3	0.38	1.6E-01	2.4E-01
GO:0010648	negative regulation of cell communication	27	305	1328	17583	1.2	0.23	1.6E-01	2.4E-01
GO:0048589	developmental growth	9	305	404	17583	1.3	0.36	1.7E-01	2.4E-01
GO:0040007	growth establishment or	9	305	404	17583	1.3	0.36	1.7E-01	2.4E-01
GO:0007163	maintenance of cell polarity	5	305	213	17583	1.4	0.44	1.7E-01	2.4E-01
GO:0044782	cilium organization	8	305	356	17583	1.3	0.37	1.7E-01	2.4E-01
GO:0015980	energy derivation by oxidation of organic compounds	6	305	262	17583	1.3	0.40	1.7E-01	2.4E-01
GO:0042176	regulation of protein catabolic process	8	305	359	17583	1.3	0.36	1.7E-01	2.4E-01
GO:0034645	cellular macromolecule biosynthetic process	16	305	765	17583	1.2	0.27	1.8E-01	2.5E-01
GO:0043414	macromolecule methylation	6	305	267	17583	1.3	0.37	1.8E-01	2.6E-01
GO:0006644	phospholipid metabolic process	8	305	365	17583	1.3	0.34	1.9E-01	2.6E-01
GO:0044087	regulation of cellular component biogenesis	20	305	981	17583	1.2	0.23	1.9E-01	2.6E-01
GO:0045944	positive regulation of transcription by RNA polymerase II	25	305	1246	17583	1.2	0.21	1.9E-01	2.6E-01
GO:0071496	cellular response to external stimulus	7	305	318	17583	1.3	0.34	1.9E-01	2.6E-01

GO:0010604	positive regulation of macromolecule metabolic process	66	305	3487	17583	1.1	0.13	1.9E-01	2.6E-01
GO:0051246	regulation of protein metabolic process	48	305	2494	17583	1.1	0.15	1.9E-01	2.6E-01
GO:0045595	regulation of cell differentiation	31	305	1570	17583	1.1	0.19	1.9E-01	2.6E-01
GO:0018193	peptidyl-amino acid modification	17	305	828	17583	1.2	0.24	1.9E-01	2.6E-01
GO:1901362	organic cyclic compound biosynthetic process	24	305	1199	17583	1.2	0.21	2.0E-01	2.7E-01
GO:0022411	cellular component disassembly	7	305	321	17583	1.3	0.33	2.0E-01	2.7E-01
GO:1904951	positive regulation of establishment of protein localization	7	305	321	17583	1.3	0.33	2.0E-01	2.7E-01
GO:0060271	cilium assembly	7	305	323	17583	1.2	0.32	2.0E-01	2.7E-01
GO:0009790	embryo development	21	305	1044	17583	1.2	0.21	2.0E-01	2.7E-01
GO:0043066	negative regulation of apoptotic process	18	305	886	17583	1.2	0.23	2.0E-01	2.7E-01
GO:0048511	rhythmic process	6	305	275	17583	1.3	0.33	2.0E-01	2.7E-01
GO:0104004	cellular response to environmental stimulus	7	305	324	17583	1.2	0.32	2.0E-01	2.7E-01
GO:0071214	cellular response to abiotic stimulus	7	305	324	17583	1.2	0.32	2.0E-01	2.7E-01
GO:0071417	cellular response to organonitrogen compound	12	305	576	17583	1.2	0.26	2.0E-01	2.7E-01
GO:0051248	negative regulation of protein metabolic process	20	305	994	17583	1.2	0.21	2.0E-01	2.7E-01
GO:0000280	nuclear division	7	305	325	17583	1.2	0.31	2.0E-01	2.7E-01

	positive regulation of nervous system								
GO:0051962	development	6	305	277	17583	1.2	0.32	2.1E-01	2.8E-01
GO:0032880	regulation of protein localization	17	305	839	17583	1.2	0.22	2.1E-01	2.8E-01
GO:0060341	regulation of cellular localization	19	305	946	17583	1.2	0.21	2.1E-01	2.8E-01
GO:0048871	multicellular organismal homeostasis	12	305	581	17583	1.2	0.25	2.1E-01	2.8E-01
GO:1902531	regulation of intracellular signal transduction	33	305	1699	17583	1.1	0.16	2.1E-01	2.8E-01
GO:1901699	cellular response to nitrogen compound	13	305	635	17583	1.2	0.24	2.2E-01	2.9E-01
GO:0048585	negative regulation of response to stimulus	31	305	1593	17583	1.1	0.17	2.2E-01	2.9E-01
GO:0007167	enzyme-linked receptor protein signaling pathway	13	305	637	17583	1.2	0.23	2.2E-01	2.9E-01
GO:0120036	plasma membrane bounded cell projection organization	22	305	1112	17583	1.1	0.19	2.2E-01	2.9E-01
GO:0071495	cellular response to endogenous stimulus	23	305	1166	17583	1.1	0.19	2.2E-01	2.9E-01
GO:0051276	chromosome organization	9	305	433	17583	1.2	0.26	2.2E-01	2.9E-01
GO:0051668	localization within membrane	11	305	540	17583	1.2	0.23	2.3E-01	3.0E-01
GO:0043069	negative regulation of programmed cell death	18	305	908	17583	1.1	0.19	2.3E-01	3.0E-01
GO:1901137	carbohydrate derivative biosynthetic process	12	305	593	17583	1.2	0.22	2.3E-01	3.0E-01
GO:1990778	protein localization to cell periphery	5	305	240	17583	1.2	0.26	2.4E-01	3.1E-01
GO:0030334	regulation of cell migration	18	305	916	17583	1.1	0.18	2.4E-01	3.1E-01
GO:0060485	mesenchyme development	5	305	242	17583	1.2	0.25	2.4E-01	3.1E-01

GO:0031325	positive regulation of cellular metabolic process	57	305	3060	17583	1.1	0.10	2.5E-01	3.1E-01
GO:2000145	regulation of cell motility	19	305	974	17583	1.1	0.17	2.5E-01	3.2E-01
GO:0045787	positive regulation of cell cycle	7	305	344	17583	1.2	0.23	2.5E-01	3.2E-01
GO:0016032	viral process	5	305	244	17583	1.2	0.24	2.5E-01	3.2E-01
GO:0009314	response to radiation	9	305	449	17583	1.2	0.21	2.5E-01	3.2E-01
GO:0022613	ribonucleoprotein complex biogenesis	9	305	449	17583	1.2	0.21	2.5E-01	3.2E-01
GO:0031346	positive regulation of cell projection organization	7	305	347	17583	1.2	0.22	2.6E-01	3.2E-01
GO:1901576	organic substance biosynthetic process	47	305	2515	17583	1.1	0.11	2.6E-01	3.2E-01
GO:0045597	positive regulation of cell differentiation	17	305	873	17583	1.1	0.17	2.6E-01	3.2E-01
GO:0044089	positive regulation of cellular component	10	305	503	17583	1.1	0.20	2.6E-01	3.2E-01
GO:0072657	protein localization to membrane	9	305	451	17583	1.2	0.20	2.6E-01	3.2E-01
GO:0097305	response to alcohol	5	305	247	17583	1.2	0.22	2.6E-01	3.3E-01
GO:0048869	cellular developmental process	66	305	3579	17583	1.1	0.09	2.6E-01	3.3E-01
GO:0006605	protein targeting	5	305	248	17583	1.2	0.22	2.6E-01	3.3E-01
GO:0008284	positive regulation of cell population proliferation	18	305	931	17583	1.1	0.16	2.6E-01	3.3E-01
GO:0051607	defense response to virus	5	305	251	17583	1.1	0.20	2.7E-01	3.4E-01
GO:0043067	regulation of programmed cell death	28	305	1479	17583	1.1	0.13	2.7E-01	3.4E-01
GO:1903508	positive regulation of nucleic acid-templated transcription	32	305	1700	17583	1.1	0.12	2.7E-01	3.4E-01
GO:0045893	positive regulation of DNA-templated transcription	32	305	1700	17583	1.1	0.12	2.7E-01	3.4E-01

	defense response to								
GO:0140546	symbiont	5	305	252	17583	1.1	0.19	2.7E-01	3.4E-01
GO:0042254	ribosome biogenesis	6	305	303	17583	1.1	0.19	2.7E-01	3.4E-01
GO:0044249	cellular biosynthetic process	45	305	2421	17583	1.1	0.10	2.7E-01	3.4E-01
	response to endogenous								
GO:0009719	stimulus	27	305	1431	17583	1.1	0.12	2.8E-01	3.5E-01
	positive regulation of RNA								
GO:1902680	biosynthetic process	32	305	1706	17583	1.1	0.11	2.8E-01	3.5E-01
	positive regulation of protein								
GO:0051222	transport	6	305	305	17583	1.1	0.18	2.8E-01	3.5E-01
GO:0030030	cell projection organization	22	305	1158	17583	1.1	0.13	2.8E-01	3.5E-01
	glycerolipid metabolic								
GO:0046486	process	7	305	358	17583	1.1	0.17	2.8E-01	3.5E-01
GO:0033036	macromolecule localization	43	305	2323	17583	1.1	0.09	2.9E-01	3.5E-01
GO:0032940	secretion by cell	8	305	412	17583	1.1	0.16	2.9E-01	3.5E-01
GO:0030154	cell differentiation	65	305	3556	17583	1.1	0.08	2.9E-01	3.5E-01
GO:0048468	cell development	40	305	2160	17583	1.1	0.09	2.9E-01	3.6E-01
	positive regulation of								
GO:0051130	cellular component	20	305	1058	17583	1.1	0.12	2.9E-01	3.6E-01
	regulation of cellular								
	response to growth factor								
GO:0090287	stimulus	6	305	310	17583	1.1	0.16	2.9E-01	3.6E-01
	positive regulation of cell								
GO:0010720	development	9	305	467	17583	1.1	0.15	2.9E-01	3.6E-01
	regulation of apoptotic								
GO:0042981	process	27	305	1446	17583	1.1	0.11	3.0E-01	3.6E-01
	negative regulation of cell								
GO:0060548	death	19	305	1009	17583	1.1	0.12	3.0E-01	3.6E-01
	positive regulation of								
GO:0009893	metabolic process	69	305	3796	17583	1.0	0.07	3.0E-01	3.7E-01
	positive regulation of protein								
GO:0051247	metabolic process	27	305	1449	17583	1.1	0.10	3.0E-01	3.7E-01

	blood vessel								
GO:0048514	morphogenesis	8	305	419	17583	1.1	0.14	3.0E-01	3.7E-01
GO:0140352	export from cell	9	305	472	17583	1.1	0.14	3.0E-01	3.7E-01
	negative regulation of transcription by RNA polymerase II								
GO:0000122	regulation of innate immune response	18	305	959	17583	1.1	0.11	3.1E-01	3.7E-01
GO:0045088	carbohydrate metabolic process	7	305	368	17583	1.1	0.13	3.1E-01	3.7E-01
GO:0005975	methylation	9	305	474	17583	1.1	0.13	3.1E-01	3.7E-01
GO:0032259	response to cytokine	6	305	317	17583	1.1	0.13	3.1E-01	3.8E-01
GO:0034097	regulation of locomotion	15	305	800	17583	1.1	0.11	3.1E-01	3.8E-01
GO:0040012	regulation of cell development	19	305	1019	17583	1.1	0.10	3.2E-01	3.8E-01
GO:0060284	regulation of cell cycle phase transition	16	305	856	17583	1.1	0.11	3.2E-01	3.8E-01
GO:1901987	negative regulation of cell cycle process	8	305	425	17583	1.1	0.12	3.2E-01	3.8E-01
GO:0010948	positive regulation of leukocyte cell-cell adhesion	5	305	268	17583	1.1	0.11	3.2E-01	3.8E-01
GO:1903039	biosynthetic process	5	305	268	17583	1.1	0.11	3.2E-01	3.8E-01
GO:0009058	regulation of cell death	47	305	2584	17583	1.0	0.07	3.3E-01	3.9E-01
GO:0010941	developmental maturation	30	305	1634	17583	1.1	0.08	3.3E-01	3.9E-01
GO:0021700	cellular component	5	305	272	17583	1.1	0.08	3.3E-01	4.0E-01
GO:0044085	biogenesis	48	305	2651	17583	1.0	0.06	3.4E-01	4.0E-01
	regulation of mitotic cell cycle phase transition								
GO:1901990	muscle tissue development	6	305	327	17583	1.1	0.08	3.4E-01	4.0E-01
GO:0060537	organophosphate	6	305	327	17583	1.1	0.08	3.4E-01	4.0E-01
GO:0090407	biosynthetic process	10	305	542	17583	1.1	0.09	3.4E-01	4.0E-01
GO:0001525	angiogenesis	6	305	328	17583	1.1	0.08	3.4E-01	4.0E-01

GO:0032870	cellular response to hormone stimulus	9	305	489	17583	1.1	0.09	3.4E-01	4.0E-01
GO:0055082	cellular chemical homeostasis	10	305	547	17583	1.1	0.08	3.5E-01	4.1E-01
GO:0030162	regulation of proteolysis	13	305	711	17583	1.1	0.08	3.5E-01	4.1E-01
GO:0006796	phosphate-containing compound metabolic process	33	305	1826	17583	1.0	0.06	3.6E-01	4.2E-01
GO:0000904	cell morphogenesis involved in differentiation	10	305	551	17583	1.0	0.07	3.6E-01	4.2E-01
GO:0008219	cell death	20	305	1103	17583	1.0	0.06	3.6E-01	4.2E-01
GO:0036293	response to decreased oxygen levels	5	305	281	17583	1.0	0.04	3.6E-01	4.2E-01
GO:0001503	ossification	5	305	281	17583	1.0	0.04	3.6E-01	4.2E-01
GO:0090066	regulation of anatomical structure size	9	305	497	17583	1.0	0.06	3.6E-01	4.2E-01
GO:0061061	muscle structure development	9	305	498	17583	1.0	0.06	3.6E-01	4.2E-01
GO:0009725	response to hormone	14	305	773	17583	1.0	0.06	3.7E-01	4.2E-01
GO:0042060	wound healing	6	305	336	17583	1.0	0.04	3.7E-01	4.2E-01
GO:0010639	negative regulation of organelle organization	6	305	337	17583	1.0	0.04	3.7E-01	4.3E-01
GO:0070887	cellular response to chemical stimulus	42	305	2350	17583	1.0	0.04	3.8E-01	4.4E-01
GO:0001568	blood vessel development	9	305	504	17583	1.0	0.04	3.8E-01	4.4E-01
GO:1903706	regulation of hemopoiesis	7	305	395	17583	1.0	0.03	3.8E-01	4.4E-01
GO:0000226	microtubule cytoskeleton organization	10	305	561	17583	1.0	0.04	3.8E-01	4.4E-01
GO:0045596	negative regulation of cell differentiation	12	305	673	17583	1.0	0.04	3.9E-01	4.5E-01
GO:0006793	phosphorus metabolic process	33	305	1852	17583	1.0	0.04	3.9E-01	4.5E-01

GO:0061024	membrane organization	15	305	844	17583	1.0	0.04	3.9E-01	4.5E-01
GO:0010506	regulation of autophagy	6	305	347	17583	1.0	0.00	4.0E-01	4.5E-01
GO:0010628	positive regulation of gene expression	20	305	1127	17583	1.0	0.03	4.0E-01	4.6E-01
GO:0007059	chromosome segregation	5	305	294	17583	1.0	-0.03	4.0E-01	4.6E-01
GO:0002683	negative regulation of immune system process	8	305	461	17583	1.0	0.00	4.1E-01	4.6E-01
GO:0002521	leukocyte differentiation	7	305	406	17583	1.0	-0.01	4.1E-01	4.6E-01
GO:0051129	negative regulation of cellular component organization	12	305	686	17583	1.0	0.01	4.1E-01	4.7E-01
GO:0006915	apoptotic process	18	305	1028	17583	1.0	0.01	4.2E-01	4.8E-01
GO:0043254	regulation of protein-containing complex assembly	7	305	413	17583	1.0	-0.03	4.3E-01	4.8E-01
GO:0051054	positive regulation of DNA metabolic process	5	305	302	17583	1.0	-0.07	4.3E-01	4.8E-01
GO:0001944	vasculature development	9	305	525	17583	1.0	-0.02	4.3E-01	4.8E-01
GO:0032535	regulation of cellular component size	6	305	359	17583	1.0	-0.05	4.3E-01	4.9E-01
GO:0045862	positive regulation of proteolysis	6	305	359	17583	1.0	-0.05	4.3E-01	4.9E-01
GO:0051094	positive regulation of developmental process	23	305	1317	17583	1.0	0.01	4.3E-01	4.9E-01
GO:0060627	regulation of vesicle-mediated transport	9	305	528	17583	1.0	-0.03	4.3E-01	4.9E-01
GO:1903037	regulation of leukocyte cell-cell adhesion	6	305	361	17583	1.0	-0.06	4.4E-01	4.9E-01
GO:0033365	protein localization to organelle	12	305	699	17583	1.0	-0.01	4.4E-01	4.9E-01
GO:0030003	cellular cation homeostasis	7	305	418	17583	1.0	-0.05	4.4E-01	4.9E-01
GO:0034660	ncRNA metabolic process	9	305	531	17583	1.0	-0.03	4.4E-01	4.9E-01

	cellular response to growth								
GO:0071363	factor stimulus	8	305	475	17583	1.0	-0.04	4.4E-01	4.9E-01
GO:0048732	gland development	7	305	419	17583	1.0	-0.05	4.4E-01	5.0E-01
GO:0070482	response to oxygen levels	5	305	308	17583	0.9	-0.10	4.4E-01	5.0E-01
GO:0000902	cell morphogenesis	12	305	703	17583	1.0	-0.02	4.5E-01	5.0E-01
	cellular component								
GO:0022607	assembly	42	305	2411	17583	1.0	0.01	4.5E-01	5.0E-01
GO:0006950	response to stress	60	305	3442	17583	1.0	0.01	4.5E-01	5.0E-01
	cellular response to								
GO:0071345	cytokine stimulus	12	305	705	17583	1.0	-0.03	4.5E-01	5.0E-01
GO:0008283	cell population proliferation	12	305	707	17583	1.0	-0.03	4.6E-01	5.1E-01
GO:0097190	apoptotic signaling pathway	5	305	312	17583	0.9	-0.11	4.6E-01	5.1E-01
GO:0007281	germ cell development	5	305	312	17583	0.9	-0.11	4.6E-01	5.1E-01
	regulation of leukocyte								
GO:1902105	differentiation	5	305	313	17583	0.9	-0.12	4.6E-01	5.1E-01
	cellular process involved in								
	reproduction in multicellular								
GO:0022412	organism	7	305	426	17583	0.9	-0.08	4.6E-01	5.1E-01
	carbohydrate derivative								
GO:1901135	metabolic process	17	305	996	17583	1.0	-0.02	4.6E-01	5.1E-01
	cellular nitrogen compound								
GO:0044271	biosynthetic process	27	305	1567	17583	1.0	-0.01	4.6E-01	5.1E-01
GO:0008610	lipid biosynthetic process	10	305	599	17583	1.0	-0.06	4.7E-01	5.2E-01
GO:0070925	organelle assembly	14	305	827	17583	1.0	-0.04	4.7E-01	5.2E-01
	positive regulation of cell-								
GO:0022409	cell adhesion	5	305	316	17583	0.9	-0.13	4.7E-01	5.2E-01
GO:0050767	regulation of neurogenesis	6	305	374	17583	0.9	-0.11	4.7E-01	5.2E-01
	regulation of epithelial cell								
GO:0050678	proliferation	6	305	374	17583	0.9	-0.11	4.7E-01	5.2E-01
	positive regulation of								
GO:0048522	cellular process	97	305	5593	17583	1.0	0.00	4.7E-01	5.2E-01

GO:0044092	negative regulation of molecular function	17	305	1004	17583	1.0	-0.03	4.8E-01	5.3E-01
GO:0007346	regulation of mitotic cell cycle	8	305	491	17583	0.9	-0.09	4.8E-01	5.3E-01
GO:0030155	regulation of cell adhesion	13	305	778	17583	1.0	-0.05	4.8E-01	5.3E-01
GO:0048518	positive regulation of biological process	108	305	6241	17583	1.0	0.00	4.9E-01	5.3E-01
GO:0006873	cellular ion homeostasis	7	305	438	17583	0.9	-0.12	4.9E-01	5.4E-01
GO:0012501	programmed cell death	18	305	1070	17583	1.0	-0.04	4.9E-01	5.4E-01
GO:0031349	positive regulation of defense response	6	305	381	17583	0.9	-0.14	4.9E-01	5.4E-01
GO:1903131	mononuclear cell differentiation	5	305	325	17583	0.9	-0.17	5.0E-01	5.4E-01
GO:0016477	cell migration	15	305	900	17583	1.0	-0.06	5.0E-01	5.4E-01
GO:0050793	regulation of developmental process	42	305	2459	17583	1.0	-0.02	5.0E-01	5.5E-01
GO:1901700	response to oxygen- containing compound	26	305	1538	17583	1.0	-0.04	5.0E-01	5.5E-01
GO:0065003	protein-containing complex assembly	21	305	1254	17583	1.0	-0.05	5.1E-01	5.6E-01
GO:0031401	positive regulation of protein modification process	16	305	967	17583	1.0	-0.07	5.1E-01	5.6E-01
GO:0070848	response to growth factor	8	305	506	17583	0.9	-0.13	5.2E-01	5.6E-01
GO:0048729	tissue morphogenesis	9	305	565	17583	0.9	-0.12	5.2E-01	5.7E-01
GO:1902532	negative regulation of intracellular signal transduction	8	305	509	17583	0.9	-0.14	5.2E-01	5.7E-01
GO:0031399	regulation of protein modification process	25	305	1495	17583	1.0	-0.05	5.2E-01	5.7E-01
GO:0003002	regionalization	5	305	335	17583	0.9	-0.22	5.3E-01	5.7E-01
GO:0006875	cellular metal ion homeostasis	5	305	336	17583	0.9	-0.22	5.3E-01	5.7E-01

GO:0002831	regulation of response to biotic stimulus	7	305	455	17583	0.9	-0.17	5.3E-01	5.8E-01
GO:0007389	pattern specification process	7	305	455	17583	0.9	-0.17	5.3E-01	5.8E-01
GO:0030900	forebrain development	6	305	397	17583	0.9	-0.20	5.4E-01	5.8E-01
GO:0046649	lymphocyte activation	7	305	460	17583	0.9	-0.19	5.5E-01	5.9E-01
GO:1903829	positive regulation of protein localization	7	305	460	17583	0.9	-0.19	5.5E-01	5.9E-01
GO:0007276	gamete generation	12	305	755	17583	0.9	-0.13	5.5E-01	5.9E-01
GO:0008015	blood circulation	6	305	403	17583	0.9	-0.22	5.5E-01	5.9E-01
GO:0030335	positive regulation of cell migration	8	305	523	17583	0.9	-0.18	5.6E-01	6.0E-01
GO:0034762	regulation of transmembrane transport	9	305	582	17583	0.9	-0.17	5.6E-01	6.0E-01
GO:0046903	secretion	8	305	524	17583	0.9	-0.18	5.6E-01	6.0E-01
GO:0006091	generation of precursor metabolites and energy	6	305	408	17583	0.8	-0.24	5.6E-01	6.1E-01
GO:0051251	positive regulation of lymphocyte activation	6	305	408	17583	0.8	-0.24	5.6E-01	6.1E-01
GO:0007017	microtubule-based process	13	305	821	17583	0.9	-0.13	5.7E-01	6.1E-01
GO:0048646	anatomical structure formation involved in morphogenesis	15	305	945	17583	0.9	-0.13	5.8E-01	6.2E-01
GO:0007283	spermatogenesis	9	305	592	17583	0.9	-0.19	5.8E-01	6.2E-01
GO:0042592	homeostatic process	23	305	1417	17583	0.9	-0.10	5.8E-01	6.2E-01
GO:0019725	cellular homeostasis	10	305	653	17583	0.9	-0.18	5.8E-01	6.2E-01
GO:0048812	neuron projection morphogenesis	7	305	475	17583	0.8	-0.24	5.8E-01	6.2E-01
GO:0120035	regulation of plasma membrane bounded cell projection organization	10	305	658	17583	0.9	-0.19	5.9E-01	6.3E-01

	plasma membrane bounded								
	cell projection								
GO:0120039	morphogenesis	7	305	480	17583	0.8	-0.25	6.0E-01	6.3E-01
GO:0042221	response to chemical	64	305	3828	17583	1.0	-0.05	6.0E-01	6.4E-01
GO:0007409	axonogenesis	5	305	362	17583	0.8	-0.33	6.0E-01	6.4E-01
	regulation of multicellular								
GO:2000026	organismal development	22	305	1374	17583	0.9	-0.12	6.0E-01	6.4E-01
GO:0051716	cellular response to	109	305	6442	17583	1.0	-0.04	6.0E-01	6.4E-01
	organonitrogen compound								
GO:1901566	biosynthetic process	21	305	1317	17583	0.9	-0.12	6.1E-01	6.4E-01
	regulation of response to								
GO:0048583	stimulus	67	305	4008	17583	1.0	-0.05	6.1E-01	6.4E-01
	transmembrane receptor								
	protein tyrosine kinase								
GO:0007169	signaling pathway	6	305	424	17583	0.8	-0.29	6.1E-01	6.4E-01
	cell projection								
GO:0048858	morphogenesis	7	305	485	17583	0.8	-0.27	6.1E-01	6.4E-01
	positive regulation of cell								
GO:2000147	motility	8	305	546	17583	0.8	-0.24	6.1E-01	6.5E-01
	regulation of defense								
GO:0031347	response	11	305	726	17583	0.9	-0.20	6.1E-01	6.5E-01
GO:0035239	tube morphogenesis	10	305	667	17583	0.9	-0.21	6.1E-01	6.5E-01
GO:0050863	regulation of T cell	5	305	368	17583	0.8	-0.35	6.2E-01	6.5E-01
GO:0048232	male gamete generation	9	305	611	17583	0.8	-0.24	6.2E-01	6.6E-01
	regulation of cell projection								
GO:0031344	organization	10	305	672	17583	0.9	-0.22	6.2E-01	6.6E-01
	regulation of cation								
GO:1904062	transmembrane transport	5	305	371	17583	0.8	-0.36	6.3E-01	6.6E-01
	cell morphogenesis involved								
GO:0048667	in neuron differentiation	6	305	433	17583	0.8	-0.32	6.3E-01	6.6E-01
GO:0003013	circulatory system process	7	305	494	17583	0.8	-0.29	6.3E-01	6.6E-01
GO:0006810	transport	63	305	3800	17583	1.0	-0.07	6.3E-01	6.6E-01

GO:0030855	epithelial cell differentiation	9	305	617	17583	0.8	-0.25	6.3E-01	6.7E-01
GO:0009991	response to extracellular stimulus	7	305	497	17583	0.8	-0.30	6.3E-01	6.7E-01
GO:1902533	positive regulation of intracellular signal transduction	15	305	980	17583	0.9	-0.18	6.4E-01	6.7E-01
GO:0050727	regulation of inflammatory response	5	305	376	17583	0.8	-0.38	6.4E-01	6.7E-01
GO:0050878	regulation of body fluid levels	5	305	376	17583	0.8	-0.38	6.4E-01	6.7E-01
GO:0034765	regulation of ion transmembrane transport	7	305	499	17583	0.8	-0.31	6.4E-01	6.7E-01
GO:0040017	positive regulation of locomotion	8	305	561	17583	0.8	-0.28	6.4E-01	6.8E-01
GO:0043933	protein-containing complex organization	22	305	1404	17583	0.9	-0.15	6.4E-01	6.8E-01
GO:0009628	response to abiotic stimulus	17	305	1106	17583	0.9	-0.17	6.5E-01	6.8E-01
GO:0010975	regulation of neuron projection development	6	305	442	17583	0.8	-0.35	6.5E-01	6.8E-01
GO:1901701	cellular response to oxygen-containing compound	16	305	1050	17583	0.9	-0.19	6.5E-01	6.9E-01
GO:0032990	cell part morphogenesis	7	305	505	17583	0.8	-0.32	6.5E-01	6.9E-01
GO:0009611	response to wounding	6	305	446	17583	0.8	-0.37	6.6E-01	6.9E-01
GO:0035295	tube development	13	305	876	17583	0.9	-0.23	6.6E-01	7.0E-01
GO:0051234	establishment of localization skeletal system	65	305	3956	17583	0.9	-0.08	6.6E-01	7.0E-01
GO:0001501	development	7	305	514	17583	0.8	-0.35	6.7E-01	7.0E-01
GO:0055080	cation homeostasis	7	305	515	17583	0.8	-0.35	6.7E-01	7.1E-01
GO:0007010	cytoskeleton organization	19	305	1247	17583	0.9	-0.19	6.8E-01	7.1E-01
GO:0051960	regulation of nervous system development	6	305	454	17583	0.8	-0.39	6.8E-01	7.1E-01
GO:0001775	cell activation	10	305	702	17583	0.8	-0.28	6.8E-01	7.1E-01

	positive regulation of								
GO:0002696	leukocyte activation	6	305	455	17583	0.8	-0.40	6.8E-01	7.1E-01
GO:0045321	leukocyte activation	8	305	580	17583	0.8	-0.33	6.8E-01	7.1E-01
GO:0048598	embryonic morphogenesis	8	305	583	17583	0.8	-0.34	6.9E-01	7.2E-01
	regulation of immune								
GO:0002682	system process	23	305	1496	17583	0.9	-0.17	6.9E-01	7.2E-01
	regulation of metal ion								
GO:0010959	transport	5	305	396	17583	0.7	-0.46	6.9E-01	7.2E-01
GO:0051049	regulation of transport	27	305	1739	17583	0.9	-0.16	6.9E-01	7.2E-01
	modulation of chemical								
GO:0050804	synaptic transmission	6	305	462	17583	0.7	-0.42	6.9E-01	7.2E-01
	regulation of trans-synaptic								
GO:0099177	signaling	6	305	463	17583	0.7	-0.42	7.0E-01	7.3E-01
GO:0061564	axon development	5	305	401	17583	0.7	-0.48	7.0E-01	7.3E-01
GO:0098771	inorganic ion homeostasis	7	305	530	17583	0.8	-0.39	7.0E-01	7.3E-01
GO:0031667	response to nutrient levels	6	305	467	17583	0.7	-0.43	7.0E-01	7.3E-01
	positive regulation of cell								
GO:0050867	activation	6	305	471	17583	0.7	-0.45	7.1E-01	7.4E-01
GO:0048878	chemical homeostasis	13	305	908	17583	0.8	-0.28	7.1E-01	7.4E-01
	negative regulation of								
GO:0051093	developmental process	13	305	911	17583	0.8	-0.28	7.2E-01	7.5E-01
	positive regulation of cell								
GO:0045785	adhesion	6	305	474	17583	0.7	-0.45	7.2E-01	7.5E-01
	neuron projection								
GO:0031175	development	9	305	666	17583	0.8	-0.36	7.2E-01	7.5E-01
	regulation of cell-cell								
GO:0022407	adhesion	6	305	477	17583	0.7	-0.46	7.2E-01	7.5E-01
	cellular lipid metabolic								
GO:0044255	process	13	305	916	17583	0.8	-0.29	7.2E-01	7.5E-01
	regulation of signal								
GO:0009966	transduction	47	305	2966	17583	0.9	-0.13	7.3E-01	7.5E-01
GO:0050801	ion homeostasis	7	305	542	17583	0.7	-0.43	7.3E-01	7.5E-01

GO:0001817	regulation of cytokine production	10	305	731	17583	0.8	-0.34	7.3E-01	7.5E-01
GO:0032879	regulation of localization biological process involved in interspecies interaction	32	305	2073	17583	0.9	-0.17	7.3E-01	7.6E-01
GO:0044419	between organisms	24	305	1591	17583	0.9	-0.20	7.3E-01	7.6E-01
GO:0098609	cell-cell adhesion cellular component	7	305	543	17583	0.7	-0.43	7.3E-01	7.6E-01
GO:0032989	morphogenesis	8	305	607	17583	0.8	-0.40	7.3E-01	7.6E-01
GO:0031400	negative regulation of protein modification process	6	305	480	17583	0.7	-0.47	7.3E-01	7.6E-01
GO:0050776	regulation of immune response	13	305	920	17583	0.8	-0.30	7.3E-01	7.6E-01
GO:0042127	regulation of cell population proliferation	25	305	1654	17583	0.9	-0.20	7.3E-01	7.6E-01
GO:0019637	organophosphate metabolic process	13	305	926	17583	0.8	-0.31	7.4E-01	7.7E-01
GO:0043065	positive regulation of apoptotic process	6	305	488	17583	0.7	-0.50	7.5E-01	7.7E-01
GO:0048609	multicellular organismal reproductive process	12	305	869	17583	0.8	-0.33	7.5E-01	7.7E-01
GO:0009410	response to xenobiotic stimulus	5	305	424	17583	0.7	-0.56	7.5E-01	7.7E-01
GO:0048870	cell motility	15	305	1057	17583	0.8	-0.29	7.5E-01	7.8E-01
GO:0055065	metal ion homeostasis	5	305	425	17583	0.7	-0.56	7.5E-01	7.8E-01
GO:0023051	regulation of signaling	53	305	3352	17583	0.9	-0.13	7.5E-01	7.8E-01
GO:0007507	heart development	7	305	555	17583	0.7	-0.46	7.5E-01	7.8E-01
GO:1903530	regulation of secretion by cell	7	305	558	17583	0.7	-0.47	7.6E-01	7.8E-01
GO:0034470	ncRNA processing	5	305	430	17583	0.7	-0.58	7.6E-01	7.9E-01
GO:0019953	sexual reproduction	12	305	885	17583	0.8	-0.36	7.7E-01	7.9E-01

GO:0043068	positive regulation of programmed cell death	6	305	503	17583	0.7	-0.54	7.7E-01	8.0E-01
GO:0010942	positive regulation of cell death	7	305	569	17583	0.7	-0.50	7.7E-01	8.0E-01
GO:0051249	regulation of lymphocyte activation	7	305	577	17583	0.7	-0.52	7.9E-01	8.1E-01
GO:0007155	cell adhesion	13	305	963	17583	0.8	-0.36	7.9E-01	8.1E-01
GO:0051050	positive regulation of transport	12	305	902	17583	0.8	-0.38	7.9E-01	8.1E-01
GO:0022008	neurogenesis	18	305	1281	17583	0.8	-0.30	7.9E-01	8.2E-01
GO:0006897	endocytosis	6	305	515	17583	0.7	-0.57	7.9E-01	8.2E-01
GO:0006629	lipid metabolic process	17	305	1221	17583	0.8	-0.32	8.0E-01	8.2E-01
GO:0043604	amide biosynthetic process	6	305	517	17583	0.7	-0.58	8.0E-01	8.2E-01
GO:0072359	circulatory system development	12	305	907	17583	0.8	-0.39	8.0E-01	8.2E-01
GO:0032103	positive regulation of response to external stimulus	6	305	518	17583	0.7	-0.58	8.0E-01	8.2E-01
GO:0002009	morphogenesis of an epithelium	5	305	453	17583	0.6	-0.65	8.0E-01	8.2E-01
GO:0032504	multicellular organism reproduction	12	305	910	17583	0.8	-0.40	8.0E-01	8.2E-01
GO:0010646	regulation of cell communication	52	305	3362	17583	0.9	-0.17	8.0E-01	8.2E-01
GO:0051179	localization	71	305	4502	17583	0.9	-0.14	8.1E-01	8.3E-01
GO:0050865	regulation of cell activation	9	305	723	17583	0.7	-0.48	8.1E-01	8.3E-01
GO:0043603	amide metabolic process	10	305	798	17583	0.7	-0.47	8.2E-01	8.4E-01
GO:0002694	regulation of leukocyte activation	8	305	668	17583	0.7	-0.53	8.2E-01	8.4E-01
GO:0051239	regulation of multicellular organismal process	41	305	2734	17583	0.9	-0.21	8.3E-01	8.5E-01

GO:0001819	positive regulation of cytokine production	5	305	473	17583	0.6	-0.71	8.3E-01	8.5E-01
GO:0001932	regulation of protein phosphorylation	14	305	1068	17583	0.8	-0.40	8.3E-01	8.5E-01
GO:0003006	developmental process involved in reproduction	12	305	944	17583	0.7	-0.45	8.4E-01	8.6E-01
GO:0051046	regulation of secretion multicellular organism	7	305	615	17583	0.7	-0.61	8.4E-01	8.6E-01
GO:0007275	development	60	305	3903	17583	0.9	-0.17	8.4E-01	8.6E-01
GO:0032502	developmental process	90	305	5685	17583	0.9	-0.13	8.4E-01	8.6E-01
GO:0002684	positive regulation of immune system process	13	305	1014	17583	0.7	-0.44	8.5E-01	8.6E-01
GO:0030001	metal ion transport	7	305	624	17583	0.6	-0.63	8.5E-01	8.7E-01
GO:0045087	innate immune response	10	305	830	17583	0.7	-0.53	8.6E-01	8.7E-01
GO:0002376	immune system process	32	305	2229	17583	0.8	-0.27	8.6E-01	8.7E-01
GO:0048666	neuron development	10	305	832	17583	0.7	-0.53	8.6E-01	8.8E-01
GO:0065008	regulation of biological quality	41	305	2788	17583	0.8	-0.24	8.6E-01	8.8E-01
GO:0097435	supramolecular fiber organization	6	305	564	17583	0.6	-0.71	8.6E-01	8.8E-01
GO:0032101	regulation of response to external stimulus	13	305	1032	17583	0.7	-0.46	8.6E-01	8.8E-01
GO:0051345	positive regulation of hydrolase activity	6	305	565	17583	0.6	-0.71	8.6E-01	8.8E-01
GO:0043269	regulation of ion transport	8	305	704	17583	0.7	-0.61	8.7E-01	8.8E-01
GO:0022414	reproductive process	19	305	1425	17583	0.8	-0.38	8.7E-01	8.8E-01
GO:0051240	positive regulation of multicellular organismal process	20	305	1492	17583	0.8	-0.37	8.7E-01	8.8E-01
GO:0043086	negative regulation of catalytic activity	7	305	640	17583	0.6	-0.67	8.7E-01	8.8E-01

	cellular response to organic								
GO:0071407	cyclic compound	5	305	502	17583	0.6	-0.80	8.7E-01	8.9E-01
GO:0007420	brain development	9	305	778	17583	0.7	-0.58	8.7E-01	8.9E-01
	positive regulation of protein								
GO:0001934	phosphorylation	8	305	711	17583	0.6	-0.62	8.7E-01	8.9E-01
GO:0000003	reproduction	19	305	1435	17583	0.8	-0.39	8.7E-01	8.9E-01
	positive regulation of signal								
GO:0009967	transduction	20	305	1511	17583	0.8	-0.39	8.8E-01	9.0E-01
	defense response to other								
GO:0098542	organism	13	305	1058	17583	0.7	-0.50	8.8E-01	9.0E-01
	cell surface receptor								
GO:0007166	signaling pathway	30	305	2149	17583	0.8	-0.31	8.9E-01	9.0E-01
	regulation of molecular								
GO:0065009	function	37	305	2588	17583	0.8	-0.28	8.9E-01	9.0E-01
GO:0060429	epithelium development	13	305	1063	17583	0.7	-0.50	8.9E-01	9.0E-01
	response to organic cyclic								
GO:0014070	compound	10	305	864	17583	0.7	-0.58	8.9E-01	9.0E-01
GO:0050896	response to stimulus	130	305	8137	17583	0.9	-0.12	8.9E-01	9.0E-01
	anatomical structure								
GO:0048856	development	79	305	5143	17583	0.9	-0.18	8.9E-01	9.0E-01
GO:0009888	tissue development	23	305	1720	17583	0.8	-0.38	8.9E-01	9.1E-01
	regulation of								
GO:0042325	phosphorylation	15	305	1207	17583	0.7	-0.48	9.0E-01	9.1E-01
GO:0040011	locomotion	5	305	528	17583	0.5	-0.87	9.0E-01	9.1E-01
	actin filament-based								
GO:0030029	process	6	305	600	17583	0.6	-0.79	9.0E-01	9.1E-01
GO:0006518	peptide metabolic process	5	305	532	17583	0.5	-0.88	9.0E-01	9.1E-01
	response to inorganic								
GO:0010035	substance	5	305	537	17583	0.5	-0.90	9.1E-01	9.2E-01
GO:0051707	response to other organism	18	305	1422	17583	0.7	-0.45	9.1E-01	9.2E-01
	actin cytoskeleton								
GO:0030036	organization	5	305	539	17583	0.5	-0.90	9.1E-01	9.2E-01

GO:0023056	positive regulation of signaling	22	305	1684	17583	0.8	-0.41	9.1E-01	9.2E-01
GO:0043207	response to external biotic stimulus	18	305	1425	17583	0.7	-0.46	9.1E-01	9.2E-01
GO:0010647	positive regulation of cell communication	22	305	1685	17583	0.8	-0.41	9.1E-01	9.2E-01
GO:0060322	head development	9	305	826	17583	0.6	-0.67	9.1E-01	9.2E-01
GO:0009605	response to external stimulus	34	305	2452	17583	0.8	-0.32	9.1E-01	9.2E-01
GO:0045859	regulation of protein kinase activity	6	305	618	17583	0.6	-0.84	9.1E-01	9.2E-01
GO:0007417	central nervous system development	12	305	1041	17583	0.7	-0.59	9.2E-01	9.3E-01
GO:0008285	negative regulation of cell population proliferation	7	305	698	17583	0.6	-0.79	9.2E-01	9.3E-01
GO:0048584	positive regulation of response to stimulus	30	305	2223	17583	0.8	-0.36	9.2E-01	9.3E-01
GO:0030182	neuron differentiation	12	305	1052	17583	0.7	-0.60	9.3E-01	9.3E-01
GO:0048699	generation of neurons	13	305	1121	17583	0.7	-0.58	9.3E-01	9.3E-01
GO:0009607	response to biotic stimulus	18	305	1471	17583	0.7	-0.50	9.3E-01	9.4E-01
GO:0042327	positive regulation of phosphorylation	8	305	789	17583	0.6	-0.77	9.3E-01	9.4E-01
GO:0045937	positive regulation of phosphate metabolic process	9	305	867	17583	0.6	-0.74	9.4E-01	9.5E-01
GO:0010562	positive regulation of phosphorus metabolic process	9	305	867	17583	0.6	-0.74	9.4E-01	9.5E-01
GO:0019220	regulation of phosphate metabolic process	16	305	1355	17583	0.7	-0.55	9.4E-01	9.5E-01
GO:0051174	regulation of phosphorus metabolic process	16	305	1356	17583	0.7	-0.56	9.4E-01	9.5E-01

GO:0043408	regulation of MAPK cascade	6	305	668	17583	0.5	-0.95	9.5E-01	9.5E-01
GO:0055086	nucleobase-containing small molecule metabolic anatomical structure	5	305	596	17583	0.5	-1.05	9.5E-01	9.6E-01
GO:0009653	morphogenesis	29	305	2232	17583	0.7	-0.42	9.5E-01	9.6E-01
GO:0048731	system development nervous system	49	305	3507	17583	0.8	-0.31	9.5E-01	9.6E-01
GO:0007399	development	28	305	2189	17583	0.7	-0.44	9.6E-01	9.6E-01
GO:0040008	regulation of growth	5	305	609	17583	0.5	-1.08	9.6E-01	9.6E-01
GO:0033993	response to lipid	8	305	834	17583	0.6	-0.85	9.6E-01	9.6E-01
GO:0022603	regulation of anatomical structure morphogenesis	9	305	915	17583	0.6	-0.82	9.6E-01	9.6E-01
GO:0051338	regulation of transferase activity	8	305	858	17583	0.5	-0.90	9.6E-01	9.7E-01
GO:0007165	signal transduction	69	305	4807	17583	0.8	-0.27	9.7E-01	9.7E-01
GO:0043549	regulation of kinase activity	6	305	723	17583	0.5	-1.06	9.7E-01	9.7E-01
GO:0051241	negative regulation of multicellular organismal process	10	305	1028	17583	0.6	-0.83	9.7E-01	9.8E-01
GO:0051336	regulation of hydrolase activity	9	305	968	17583	0.5	-0.90	9.8E-01	9.8E-01
GO:0050778	positive regulation of immune response	5	305	671	17583	0.4	-1.22	9.8E-01	9.8E-01
GO:0006812	cation transport	7	305	849	17583	0.5	-1.07	9.8E-01	9.8E-01
GO:0006955	immune response	17	305	1599	17583	0.6	-0.71	9.8E-01	9.9E-01
GO:0055085	transmembrane transport	11	305	1209	17583	0.5	-0.93	9.9E-01	9.9E-01
GO:0023052	signaling	70	305	5106	17583	0.8	-0.34	9.9E-01	9.9E-01
GO:0009617	response to bacterium	5	305	751	17583	0.4	-1.38	9.9E-01	9.9E-01
GO:0006952	defense response	14	305	1466	17583	0.6	-0.86	9.9E-01	9.9E-01
GO:0050790	regulation of catalytic	19	305	1838	17583	0.6	-0.75	9.9E-01	1.0E+00
GO:0006811	ion transport	10	305	1194	17583	0.5	-1.05	9.9E-01	1.0E+00

GO:0007154	cell communication multicellular organismal	71	305	5269	17583	0.8	-0.36	9.9E-01	1.0E+00
GO:0032501	process	88	305	6337	17583	0.8	-0.32	1.0E+00	1.0E+00
GO:0007600	sensory perception carboxylic acid metabolic	7	305	981	17583	0.4	-1.28	1.0E+00	1.0E+00
GO:0019752	process animal organ	5	305	818	17583	0.4	-1.50	1.0E+00	1.0E+00
GO:0009887	morphogenesis	7	305	992	17583	0.4	-1.30	1.0E+00	1.0E+00
GO:0007267	cell-cell signaling	8	305	1077	17583	0.4	-1.22	1.0E+00	1.0E+00
GO:0048513	animal organ development	33	305	2895	17583	0.7	-0.61	1.0E+00	1.0E+00
GO:0043436	oxoacid metabolic process organic acid metabolic	5	305	840	17583	0.3	-1.54	1.0E+00	1.0E+00
GO:0006082	process positive regulation of	5	305	850	17583	0.3	-1.56	1.0E+00	1.0E+00
GO:0043085	catalytic activity ion transmembrane	8	305	1112	17583	0.4	-1.27	1.0E+00	1.0E+00
GO:0034220	transport positive regulation of	5	305	885	17583	0.3	-1.62	1.0E+00	1.0E+00
GO:0044093	molecular function small molecule metabolic	12	305	1513	17583	0.5	-1.13	1.0E+00	1.0E+00
GO:0044281	process	13	305	1649	17583	0.5	-1.14	1.0E+00	1.0E+00
GO:0003008	system process	18	305	2054	17583	0.5	-0.99	1.0E+00	1.0E+00
GO:0050877	nervous system process G protein-coupled receptor	9	305	1447	17583	0.4	-1.48	1.0E+00	1.0E+00
GO:0007186	signaling pathway	5	305	1216	17583	0.2	-2.08	1.0E+00	1.0E+00