

Supplementary Table 7. *Gene set enrichment analyses in Gene Ontology's biological processes for genes in the "A" cluster.* Columns are the same with Table S6.

path	desc	p	m	P	M	nrich	log2FC	pval	fdr
GO:0019222	regulation of metabolic process	160	309	6669	17583	1.37	0.45	2.3E-07	1.0E-04
GO:0009725	response to hormone	33	309	773	17583	2.43	1.28	8.6E-07	3.6E-04
	cellular response to hormone								
GO:0032870	stimulus	24	309	489	17583	2.79	1.48	1.9E-06	8.0E-04
	cellular response to organic								
GO:0071310	substance	56	309	1728	17583	1.84	0.88	2.2E-06	8.7E-04
GO:0009894	regulation of catabolic process	38	309	995	17583	2.17	1.12	2.2E-06	8.7E-04
GO:0010506	regulation of autophagy	19	309	347	17583	3.12	1.64	3.6E-06	1.3E-03
	regulation of cellular catabolic								
GO:0031329	process	32	309	797	17583	2.28	1.19	4.6E-06	1.6E-03
	regulation of cellular metabolic								
GO:0031323	process	134	309	5561	17583	1.37	0.46	4.8E-06	1.6E-03
	cellular response to chemical								
GO:0070887	stimulus	69	309	2350	17583	1.67	0.74	4.8E-06	1.6E-03
	steroid hormone mediated								
GO:0043401	signaling pathway	8	309	75	17583	6.07	2.60	6.5E-06	2.0E-03
	regulation of macromolecule								
GO:0060255	metabolic process	144	309	6147	17583	1.33	0.41	8.2E-06	2.5E-03
	positive regulation of metabolic								
GO:0009893	process	98	309	3796	17583	1.47	0.55	1.1E-05	3.3E-03
	hormone-mediated signaling								
GO:0009755	pathway	10	309	128	17583	4.45	2.15	1.6E-05	4.8E-03
	regulation of cellular								
GO:0031326	biosynthetic process	102	309	4057	17583	1.43	0.52	2.2E-05	5.6E-03
	negative regulation of metabolic								
GO:0009892	process	79	309	2934	17583	1.53	0.62	2.4E-05	5.9E-03
GO:0010507	negative regulation of	8	309	88	17583	5.17	2.37	2.4E-05	6.0E-03
	regulation of nitrogen compound								
GO:0051171	metabolic process	132	309	5628	17583	1.33	0.42	2.7E-05	6.4E-03

GO:0051090	regulation of DNA-binding transcription factor activity	20	309	434	17583	2.62	1.39	3.0E-05	7.0E-03
GO:0030522	intracellular receptor signaling pathway	11	309	162	17583	3.86	1.95	3.0E-05	7.0E-03
GO:0032868	response to insulin	13	309	217	17583	3.41	1.77	3.1E-05	7.2E-03
GO:0010033	response to organic substance	68	309	2439	17583	1.59	0.67	3.2E-05	7.3E-03
GO:0019068	virion assembly	5	309	36	17583	7.90	2.98	3.5E-05	7.8E-03
GO:0051246	regulation of protein metabolic process	69	309	2494	17583	1.57	0.65	3.6E-05	7.8E-03
GO:0065009	regulation of molecular function establishment of vesicle	71	309	2588	17583	1.56	0.64	3.6E-05	7.8E-03
GO:0051650	localization	11	309	167	17583	3.75	1.91	4.1E-05	8.7E-03
GO:1901701	cellular response to oxygen-containing compound	36	309	1050	17583	1.95	0.96	4.3E-05	8.8E-03
GO:0009889	regulation of biosynthetic process	102	309	4122	17583	1.41	0.49	4.3E-05	8.8E-03
GO:0030518	intracellular steroid hormone receptor signaling pathway	6	309	55	17583	6.21	2.63	4.8E-05	9.5E-03
GO:0031325	positive regulation of cellular metabolic process	80	309	3060	17583	1.49	0.57	6.0E-05	1.1E-02
GO:0051240	positive regulation of multicellular organismal process	46	309	1492	17583	1.75	0.81	6.3E-05	1.2E-02
GO:0031324	negative regulation of cellular metabolic process	62	309	2218	17583	1.59	0.67	6.9E-05	1.3E-02
GO:0071383	cellular response to steroid hormone stimulus	10	309	150	17583	3.79	1.92	7.1E-05	1.3E-02
GO:1903506	regulation of nucleic acid-templated transcription	87	309	3422	17583	1.45	0.53	7.4E-05	1.3E-02
GO:0051252	regulation of RNA metabolic process	93	309	3724	17583	1.42	0.51	7.7E-05	1.3E-02
GO:2001141	regulation of RNA biosynthetic process	87	309	3431	17583	1.44	0.53	8.1E-05	1.4E-02

GO:0051648	vesicle localization	11	309	180	17583	3.48	1.80	8.4E-05	1.4E-02
GO:0009895	negative regulation of catabolic process	16	309	332	17583	2.74	1.46	8.6E-05	1.4E-02
GO:0010468	regulation of gene expression regulation of dendritic spine	114	309	4813	17583	1.35	0.43	9.1E-05	1.5E-02
GO:0061001	morphogenesis	5	309	43	17583	6.62	2.73	9.9E-05	1.6E-02
GO:0043434	response to peptide hormone	17	309	369	17583	2.62	1.39	1.0E-04	1.6E-02
GO:0071396	cellular response to lipid regulation of primary metabolic process	21	309	508	17583	2.35	1.23	1.0E-04	1.6E-02
GO:0080090	regulation of DNA-templated transcription	132	309	5782	17583	1.30	0.38	1.1E-04	1.6E-02
GO:0006355	regulation of nucleobase-containing compound metabolic process	86	309	3420	17583	1.43	0.52	1.2E-04	1.8E-02
GO:0019219	positive regulation of biological process	98	309	4030	17583	1.38	0.47	1.3E-04	1.9E-02
GO:0048518	positive regulation of cellular process	140	309	6241	17583	1.28	0.35	1.4E-04	1.9E-02
GO:0031331	catabolic process	18	309	413	17583	2.48	1.31	1.4E-04	1.9E-02
GO:0048545	response to steroid hormone	14	309	284	17583	2.81	1.49	1.6E-04	2.2E-02
GO:0033993	response to lipid positive regulation of molecular function	29	309	834	17583	1.98	0.98	1.7E-04	2.2E-02
GO:0044093	regulation of macromolecule biosynthetic process	45	309	1513	17583	1.69	0.76	1.7E-04	2.3E-02
GO:0010556	regulation of multicellular organismal process	95	309	3907	17583	1.38	0.47	1.8E-04	2.3E-02
GO:0051239	regulation of gluconeogenesis	71	309	2734	17583	1.48	0.56	2.1E-04	2.5E-02
GO:0006111	negative regulation of nitrogen compound metabolic process	5	309	49	17583	5.81	2.54	2.1E-04	2.5E-02
GO:0051172		63	309	2357	17583	1.52	0.60	2.2E-04	2.5E-02

GO:0010604	positive regulation of macromolecule metabolic process	86	309	3487	17583	1.40	0.49	2.4E-04	2.5E-02
GO:0051247	positive regulation of protein metabolic process	43	309	1449	17583	1.69	0.76	2.5E-04	2.5E-02
GO:1901700	response to oxygen-containing compound	45	309	1538	17583	1.66	0.74	2.5E-04	2.5E-02
GO:0051091	positive regulation of DNA- binding transcription factor activity	13	309	264	17583	2.80	1.49	2.5E-04	2.5E-02
GO:0044087	regulation of cellular component biogenesis	32	309	981	17583	1.86	0.89	2.7E-04	2.5E-02
GO:0120161	regulation of cold-induced thermogenesis	9	309	147	17583	3.48	1.80	2.8E-04	2.5E-02
GO:0120009	intermembrane lipid transfer	5	309	52	17583	5.47	2.45	2.9E-04	2.5E-02
GO:0009896	positive regulation of catabolic process	20	309	512	17583	2.22	1.15	3.0E-04	2.5E-02
GO:0019058	viral life cycle	10	309	177	17583	3.21	1.68	3.0E-04	2.5E-02
GO:0051173	positive regulation of nitrogen compound metabolic process	78	309	3112	17583	1.43	0.51	3.0E-04	2.5E-02
GO:0032330	regulation of chondrocyte differentiation	5	309	53	17583	5.37	2.42	3.2E-04	2.5E-02
GO:0048522	positive regulation of cellular process	126	309	5593	17583	1.28	0.36	3.2E-04	2.6E-02
GO:0120162	positive regulation of cold- induced thermogenesis	7	309	98	17583	4.06	2.02	3.3E-04	2.6E-02
GO:0042221	response to chemical	92	309	3828	17583	1.37	0.45	3.5E-04	2.7E-02
GO:0032869	cellular response to insulin stimulus	9	309	152	17583	3.37	1.75	3.6E-04	2.8E-02
GO:0009719	response to endogenous stimulus	42	309	1431	17583	1.67	0.74	3.7E-04	2.8E-02
GO:0016032	viral process	12	309	244	17583	2.80	1.48	4.0E-04	3.0E-02

GO:0042472	inner ear morphogenesis	7	309	102	17583	3.91	1.97	4.4E-04	3.3E-02
GO:1901652	response to peptide	18	309	453	17583	2.26	1.18	4.4E-04	3.3E-02
GO:0006914	autophagy	14	309	314	17583	2.54	1.34	4.7E-04	3.4E-02
	process utilizing autophagic								
GO:0061919	mechanism	14	309	314	17583	2.54	1.34	4.7E-04	3.4E-02
GO:0019318	hexose metabolic process	9	309	157	17583	3.26	1.71	4.7E-04	3.4E-02
	regulation of protein								
GO:0031399	modification process	43	309	1495	17583	1.64	0.71	4.9E-04	3.5E-02
GO:1901698	response to nitrogen compound	33	309	1058	17583	1.77	0.83	5.0E-04	3.6E-02
GO:0016241	regulation of macroautophagy	9	309	160	17583	3.20	1.68	5.4E-04	3.8E-02
	negative regulation of								
GO:0009890	biosynthetic process	45	309	1596	17583	1.60	0.68	5.7E-04	4.0E-02
GO:0030036	actin cytoskeleton organization	20	309	539	17583	2.11	1.08	5.9E-04	4.0E-02
	cellular response to organic								
GO:0071407	cyclic compound	19	309	502	17583	2.15	1.11	6.0E-04	4.1E-02
	regulation of transcription by								
GO:0006357	RNA polymerase II	66	309	2592	17583	1.45	0.53	6.1E-04	4.1E-02
GO:0006635	fatty acid beta-oxidation	5	309	60	17583	4.74	2.25	6.3E-04	4.1E-02
GO:0019395	fatty acid oxidation	6	309	83	17583	4.11	2.04	6.4E-04	4.2E-02
	negative regulation of cellular								
GO:0031327	biosynthetic process	44	309	1566	17583	1.60	0.68	7.0E-04	4.5E-02
	cellular response to								
GO:0071495	endogenous stimulus	35	309	1166	17583	1.71	0.77	7.1E-04	4.5E-02
GO:1902115	regulation of organelle	11	309	231	17583	2.71	1.44	8.3E-04	4.5E-02
	cellular response to nitrogen								
GO:1901699	compound	22	309	635	17583	1.97	0.98	8.8E-04	4.5E-02
GO:0051179	localization	103	309	4502	17583	1.30	0.38	8.9E-04	4.5E-02
	response to organonitrogen								
GO:0010243	compound	30	309	967	17583	1.77	0.82	9.2E-04	4.5E-02
GO:0034440	lipid oxidation	6	309	89	17583	3.84	1.94	9.7E-04	4.8E-02
GO:0030029	actin filament-based process	21	309	600	17583	1.99	0.99	9.7E-04	4.8E-02
GO:0007032	endosome organization	6	309	91	17583	3.75	1.91	1.1E-03	5.3E-02

GO:0043085	positive regulation of catalytic activity	33	309	1112	17583	1.69	0.76	1.2E-03	5.5E-02
GO:0050954	sensory perception of mechanical stimulus	9	309	177	17583	2.89	1.53	1.2E-03	5.5E-02
GO:0005996	monosaccharide metabolic process	9	309	177	17583	2.89	1.53	1.2E-03	5.5E-02
GO:0010876	lipid localization	15	309	382	17583	2.23	1.16	1.2E-03	5.8E-02
GO:0016192	vesicle-mediated transport	39	309	1387	17583	1.60	0.68	1.3E-03	6.2E-02
GO:0071375	cellular response to peptide hormone stimulus	11	309	244	17583	2.57	1.36	1.3E-03	6.2E-02
GO:0010605	negative regulation of macromolecule metabolic process	67	309	2717	17583	1.40	0.49	1.3E-03	6.2E-02
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	6	309	94	17583	3.63	1.86	1.3E-03	6.2E-02
GO:0014070	response to organic cyclic compound	27	309	864	17583	1.78	0.83	1.4E-03	6.3E-02
GO:0051248	negative regulation of protein metabolic process	30	309	994	17583	1.72	0.78	1.4E-03	6.5E-02
GO:0042471	ear morphogenesis	7	309	123	17583	3.24	1.70	1.5E-03	6.7E-02
GO:0031330	negative regulation of cellular catabolic process	11	309	248	17583	2.52	1.34	1.5E-03	6.7E-02
GO:0061035	regulation of cartilage development	5	309	71	17583	4.01	2.00	1.5E-03	6.7E-02
GO:0007605	sensory perception of sound	8	309	154	17583	2.96	1.56	1.6E-03	6.7E-02
GO:0006810	transport	88	309	3800	17583	1.32	0.40	1.6E-03	6.7E-02
GO:0051234	establishment of localization	91	309	3956	17583	1.31	0.39	1.7E-03	6.7E-02
GO:0022411	cellular component disassembly	13	309	321	17583	2.30	1.20	1.7E-03	6.7E-02
GO:0031401	positive regulation of protein modification process	29	309	967	17583	1.71	0.77	1.8E-03	6.8E-02

GO:0000045	autophagosome assembly negative regulation of macromolecule biosynthetic	5	309	74	17583	3.84	1.94	1.9E-03	7.0E-02
GO:0010558	process	41	309	1510	17583	1.55	0.63	2.0E-03	7.0E-02
GO:0050790	regulation of catalytic activity regulation of organelle	48	309	1838	17583	1.49	0.57	2.0E-03	7.0E-02
GO:0033043	organization regulation of pattern recognition	34	309	1199	17583	1.61	0.69	2.2E-03	7.0E-02
GO:0062207	receptor signaling pathway	6	309	103	17583	3.31	1.73	2.3E-03	7.0E-02
GO:0019751	polyol metabolic process negative regulation of gene	6	309	104	17583	3.28	1.71	2.4E-03	7.0E-02
GO:0010629	expression	27	309	900	17583	1.71	0.77	2.5E-03	7.0E-02
GO:0016050	vesicle organization regulation of protein-containing	13	309	338	17583	2.19	1.13	2.7E-03	7.0E-02
GO:0043254	complex assembly	15	309	413	17583	2.07	1.05	2.7E-03	7.0E-02
GO:0016236	macroautophagy	9	309	201	17583	2.55	1.35	3.0E-03	7.0E-02
GO:1905037	autophagosome organization cellular response to chemical	5	309	81	17583	3.51	1.81	3.0E-03	7.0E-02
GO:0062197	stress cellular response to	11	309	270	17583	2.32	1.21	3.1E-03	7.0E-02
GO:0071417	organonitrogen compound	19	309	576	17583	1.88	0.91	3.1E-03	7.0E-02
GO:0001558	regulation of cell growth positive regulation of protein	15	309	418	17583	2.04	1.03	3.1E-03	7.0E-02
GO:1903829	localization	16	309	460	17583	1.98	0.98	3.3E-03	7.0E-02
GO:1901653	cellular response to peptide positive regulation of lipid	12	309	309	17583	2.21	1.14	3.4E-03	7.0E-02
GO:0046889	biosynthetic process regulation of proteasomal ubiquitin-dependent protein	5	309	84	17583	3.39	1.76	3.6E-03	7.0E-02
GO:0032434	catabolic process	7	309	142	17583	2.81	1.49	3.7E-03	7.0E-02

	positive regulation of ubiquitin-dependent protein catabolic process								
GO:2000060	process	6	309	113	17583	3.02	1.60	3.8E-03	7.0E-02
GO:0009062	fatty acid catabolic process	5	309	85	17583	3.35	1.74	3.8E-03	7.0E-02
GO:0009267	cellular response to starvation	8	309	175	17583	2.60	1.38	3.9E-03	7.0E-02
	regulation of protein ubiquitination								
GO:0031396	ubiquitination	9	309	209	17583	2.45	1.29	4.0E-03	7.0E-02
GO:0010508	positive regulation of autophagy	7	309	144	17583	2.77	1.47	4.0E-03	7.0E-02
GO:0042632	cholesterol homeostasis	5	309	86	17583	3.31	1.73	4.1E-03	7.0E-02
	regulation of histone modification								
GO:0031056	modification	7	309	145	17583	2.75	1.46	4.1E-03	7.0E-02
GO:0030258	lipid modification	8	309	177	17583	2.57	1.36	4.2E-03	7.0E-02
GO:0055092	sterol homeostasis	5	309	87	17583	3.27	1.71	4.3E-03	7.0E-02
	cell morphogenesis involved in neuron differentiation								
GO:0048667	neuron differentiation	15	309	433	17583	1.97	0.98	4.3E-03	7.0E-02
	negative regulation of biological process								
GO:0048519	process	113	309	5250	17583	1.22	0.29	4.4E-03	7.0E-02
GO:0006066	alcohol metabolic process	12	309	320	17583	2.13	1.09	4.5E-03	7.0E-02
GO:0060191	regulation of lipase activity	5	309	88	17583	3.23	1.69	4.6E-03	7.0E-02
	positive regulation of proteasomal protein catabolic process								
GO:1901800	process	6	309	117	17583	2.92	1.55	4.6E-03	7.0E-02
	negative regulation of DNA-templated transcription								
GO:0045892	templated transcription	35	309	1303	17583	1.53	0.61	4.6E-03	7.0E-02
	positive regulation of lipid metabolic process								
GO:0045834	metabolic process	7	309	148	17583	2.69	1.43	4.7E-03	7.0E-02
GO:0006996	organelle organization	70	309	3011	17583	1.32	0.40	4.8E-03	7.0E-02
	negative regulation of nucleic acid-templated transcription								
GO:1903507	acid-templated transcription	35	309	1305	17583	1.53	0.61	4.8E-03	7.0E-02
	regulation of mitotic nuclear division								
GO:0007088	division	6	309	118	17583	2.89	1.53	4.8E-03	7.0E-02

GO:1902679	negative regulation of RNA biosynthetic process	35	309	1307	17583	1.52	0.61	4.9E-03	7.0E-02
GO:1903320	regulation of protein modification by small protein conjugation or removal	10	309	251	17583	2.27	1.18	5.0E-03	7.0E-02
GO:0019221	cytokine-mediated signaling pathway	13	309	363	17583	2.04	1.03	5.1E-03	7.0E-02
GO:0031668	cellular response to extracellular stimulus	10	309	252	17583	2.26	1.18	5.1E-03	7.0E-02
GO:0007033	vacuole organization	8	309	183	17583	2.49	1.31	5.2E-03	7.0E-02
GO:0051345	positive regulation of hydrolase activity	18	309	565	17583	1.81	0.86	5.4E-03	7.0E-02
GO:0044282	small molecule catabolic process	13	309	366	17583	2.02	1.02	5.5E-03	7.0E-02
GO:0034599	cellular response to oxidative stress	9	309	220	17583	2.33	1.22	5.7E-03	7.0E-02
GO:0002698	negative regulation of immune effector process	6	309	122	17583	2.80	1.48	5.8E-03	7.0E-02
GO:0090630	activation of GTPase activity	6	309	122	17583	2.80	1.48	5.8E-03	7.0E-02
GO:0051128	regulation of cellular component organization	57	309	2384	17583	1.36	0.44	5.9E-03	7.0E-02
GO:0045995	regulation of embryonic development	5	309	93	17583	3.06	1.61	6.0E-03	7.0E-02
GO:0031669	cellular response to nutrient levels	9	309	222	17583	2.31	1.21	6.0E-03	7.0E-02
GO:0030308	negative regulation of cell growth	8	309	188	17583	2.42	1.28	6.1E-03	7.0E-02
GO:2000026	regulation of multicellular organismal development	36	309	1374	17583	1.49	0.58	6.2E-03	7.0E-02
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	5	309	94	17583	3.03	1.60	6.3E-03	7.0E-02

GO:0042327	positive regulation of phosphorylation	23	309	789	17583	1.66	0.73	6.6E-03	7.0E-02
GO:0006665	sphingolipid metabolic process	7	309	157	17583	2.54	1.34	6.7E-03	7.0E-02
GO:0071222	cellular response to lipopolysaccharide	8	309	191	17583	2.38	1.25	6.8E-03	7.0E-02
GO:0055088	lipid homeostasis	7	309	158	17583	2.52	1.33	6.9E-03	7.0E-02
GO:0035967	cellular response to topologically incorrect protein regulation of carbohydrate	5	309	96	17583	2.96	1.57	6.9E-03	7.0E-02
GO:0043255	biosynthetic process	5	309	96	17583	2.96	1.57	6.9E-03	7.0E-02
GO:0062014	negative regulation of small molecule metabolic process	5	309	96	17583	2.96	1.57	6.9E-03	7.0E-02
GO:0061136	regulation of proteasomal protein catabolic process	8	309	192	17583	2.37	1.25	7.0E-03	7.0E-02
GO:0048839	inner ear development	8	309	192	17583	2.37	1.25	7.0E-03	7.0E-02
GO:0007015	actin filament organization	10	309	263	17583	2.16	1.11	7.0E-03	7.0E-02
GO:0071216	cellular response to biotic stimulus	9	309	227	17583	2.26	1.17	7.0E-03	7.0E-02
GO:0009991	response to extracellular stimulus	16	309	497	17583	1.83	0.87	7.1E-03	7.0E-02
GO:1903050	regulation of proteolysis involved in protein catabolic process	9	309	229	17583	2.24	1.16	7.5E-03	7.0E-02
GO:0007204	positive regulation of cytosolic calcium ion concentration	8	309	194	17583	2.35	1.23	7.5E-03	7.0E-02
GO:0030030	cell projection organization	31	309	1158	17583	1.52	0.61	7.5E-03	7.0E-02
GO:0031328	positive regulation of cellular biosynthetic process	49	309	2016	17583	1.38	0.47	7.5E-03	7.0E-02
GO:0042325	regulation of phosphorylation	32	309	1207	17583	1.51	0.59	7.7E-03	7.0E-02
GO:0043068	positive regulation of programmed cell death	16	309	503	17583	1.81	0.86	7.9E-03	7.0E-02
GO:0044089	positive regulation of cellular component biogenesis	16	309	503	17583	1.81	0.86	7.9E-03	7.0E-02

GO:0032271	regulation of protein polymerization	8	309	196	17583	2.32	1.22	8.0E-03	7.0E-02
GO:0099175	regulation of postsynapse organization	5	309	99	17583	2.87	1.52	8.0E-03	7.0E-02
GO:0051656	establishment of organelle localization	13	309	383	17583	1.93	0.95	8.1E-03	7.0E-02
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	39	309	1541	17583	1.44	0.53	8.2E-03	7.0E-02
GO:0080134	regulation of response to stress	37	309	1447	17583	1.46	0.54	8.3E-03	7.0E-02
GO:0006869	lipid transport	12	309	345	17583	1.98	0.98	8.3E-03	7.0E-02
GO:0002682	regulation of immune system process	38	309	1496	17583	1.45	0.53	8.4E-03	7.0E-02
GO:0019220	regulation of phosphate metabolic process	35	309	1355	17583	1.47	0.56	8.5E-03	7.0E-02
GO:0051174	regulation of phosphorus metabolic process	35	309	1356	17583	1.47	0.55	8.6E-03	7.0E-02
GO:0031667	response to nutrient levels	15	309	467	17583	1.83	0.87	8.7E-03	7.0E-02
GO:0031334	positive regulation of protein-containing complex assembly	8	309	199	17583	2.29	1.19	8.8E-03	7.0E-02
GO:0010906	regulation of glucose metabolic process	5	309	101	17583	2.82	1.49	8.8E-03	7.0E-02
GO:0000904	cell morphogenesis involved in differentiation	17	309	551	17583	1.76	0.81	8.9E-03	7.0E-02
GO:0071219	cellular response to molecule of bacterial origin	8	309	200	17583	2.28	1.19	9.0E-03	7.0E-02
GO:0043549	regulation of kinase activity	21	309	723	17583	1.65	0.72	9.0E-03	7.0E-02
GO:0006629	lipid metabolic process	32	309	1221	17583	1.49	0.58	9.1E-03	7.0E-02
GO:0090090	negative regulation of canonical Wnt signaling pathway	6	309	133	17583	2.57	1.36	9.2E-03	7.0E-02
GO:0044281	small molecule metabolic process	41	309	1649	17583	1.41	0.50	9.2E-03	7.0E-02

GO:0015850	organic hydroxy compound transport	7	309	167	17583	2.39	1.25	9.5E-03	7.0E-02
GO:0048523	negative regulation of cellular process	100	309	4675	17583	1.22	0.28	9.6E-03	7.0E-02
GO:0032496	response to lipopolysaccharide	11	309	313	17583	2.00	1.00	9.7E-03	7.0E-02
GO:1903008	organelle disassembly	5	309	103	17583	2.76	1.47	9.7E-03	7.0E-02
GO:0051235	maintenance of location	7	309	168	17583	2.37	1.25	9.8E-03	7.0E-02
GO:0051253	negative regulation of RNA metabolic process	36	309	1416	17583	1.45	0.53	9.8E-03	7.0E-02
GO:0016051	carbohydrate biosynthetic process	6	309	135	17583	2.53	1.34	9.9E-03	7.0E-02
GO:0005975	carbohydrate metabolic process	15	309	474	17583	1.80	0.85	1.0E-02	7.0E-02
GO:0051129	negative regulation of cellular component organization	20	309	686	17583	1.66	0.73	1.0E-02	7.0E-02
GO:0062012	regulation of small molecule metabolic process	11	309	316	17583	1.98	0.99	1.0E-02	7.0E-02
GO:0046890	regulation of lipid biosynthetic process	7	309	170	17583	2.34	1.23	1.1E-02	7.0E-02
GO:0006643	membrane lipid metabolic process	8	309	205	17583	2.22	1.15	1.1E-02	7.0E-02
GO:0030148	sphingolipid biosynthetic process	5	309	105	17583	2.71	1.44	1.1E-02	7.0E-02
GO:0051047	positive regulation of secretion	11	309	317	17583	1.97	0.98	1.1E-02	7.0E-02
GO:0045937	positive regulation of phosphate metabolic process	24	309	867	17583	1.58	0.66	1.1E-02	7.0E-02
GO:0010562	positive regulation of phosphorus metabolic process	24	309	867	17583	1.58	0.66	1.1E-02	7.0E-02
GO:0009891	positive regulation of biosynthetic process	49	309	2055	17583	1.36	0.44	1.1E-02	7.0E-02
GO:0042770	signal transduction in response to DNA damage	6	309	137	17583	2.49	1.32	1.1E-02	7.0E-02

GO:0000122	negative regulation of transcription by RNA polymerase II	26	309	959	17583	1.54	0.63	1.1E-02	7.0E-02
GO:0071496	cellular response to external stimulus	11	309	318	17583	1.97	0.98	1.1E-02	7.0E-02
GO:0043433	negative regulation of DNA-binding transcription factor activity	7	309	171	17583	2.33	1.22	1.1E-02	7.0E-02
GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	5	309	106	17583	2.68	1.42	1.1E-02	7.0E-02
GO:1903052	positive regulation of proteolysis involved in protein catabolic process	6	309	138	17583	2.47	1.31	1.1E-02	7.0E-02
GO:0044000	movement in host	6	309	138	17583	2.47	1.31	1.1E-02	7.0E-02
GO:0045861	negative regulation of proteolysis	11	309	319	17583	1.96	0.97	1.1E-02	7.0E-02
GO:0033674	positive regulation of kinase activity	14	309	439	17583	1.81	0.86	1.1E-02	7.0E-02
GO:0016043	cellular component organization	115	309	5509	17583	1.19	0.25	1.1E-02	7.0E-02
GO:0042176	regulation of protein catabolic process	12	309	359	17583	1.90	0.93	1.1E-02	7.0E-02
GO:0032006	regulation of TOR signaling	5	309	107	17583	2.66	1.41	1.2E-02	7.0E-02
GO:0030217	T cell differentiation	7	309	173	17583	2.30	1.20	1.2E-02	7.0E-02
GO:0033554	cellular response to stress	39	309	1576	17583	1.41	0.49	1.2E-02	7.0E-02
GO:0045732	positive regulation of protein catabolic process	8	309	209	17583	2.18	1.12	1.2E-02	7.0E-02
GO:0062013	positive regulation of small molecule metabolic process	6	309	140	17583	2.44	1.29	1.2E-02	7.0E-02
GO:0046718	viral entry into host cell	5	309	108	17583	2.63	1.40	1.2E-02	7.0E-02
GO:0048666	neuron development	23	309	832	17583	1.57	0.65	1.2E-02	7.0E-02
GO:0010942	positive regulation of cell death	17	309	569	17583	1.70	0.77	1.2E-02	7.0E-02

	regulation of ubiquitin- dependent protein catabolic								
GO:2000058	process	7	309	175	17583	2.28	1.19	1.2E-02	7.0E-02
GO:0033036	macromolecule localization	54	309	2323	17583	1.32	0.40	1.2E-02	7.0E-02
GO:0009056	catabolic process	47	309	1977	17583	1.35	0.44	1.3E-02	7.0E-02
	positive regulation of apoptotic								
GO:0043065	process	15	309	488	17583	1.75	0.81	1.3E-02	7.0E-02
GO:0030100	regulation of endocytosis	8	309	212	17583	2.15	1.10	1.3E-02	7.0E-02
GO:0042594	response to starvation	8	309	212	17583	2.15	1.10	1.3E-02	7.0E-02
	negative regulation of protein								
GO:0042177	catabolic process	5	309	110	17583	2.59	1.37	1.3E-02	7.0E-02
GO:0044409	entry into host	5	309	110	17583	2.59	1.37	1.3E-02	7.0E-02
	positive regulation of RNA								
GO:0051254	metabolic process	44	309	1833	17583	1.37	0.45	1.3E-02	7.0E-02
	regulation of protein kinase								
GO:0045859	activity	18	309	618	17583	1.66	0.73	1.3E-02	7.0E-02
	regulation of protein								
GO:0001932	phosphorylation	28	309	1068	17583	1.49	0.58	1.3E-02	7.0E-02
	positive regulation of secretion								
GO:1903532	by cell	10	309	289	17583	1.97	0.98	1.4E-02	7.0E-02
	membrane lipid biosynthetic								
GO:0046467	process	6	309	144	17583	2.37	1.25	1.4E-02	7.0E-02
GO:0016052	carbohydrate catabolic process	5	309	112	17583	2.54	1.35	1.4E-02	7.0E-02
	monocarboxylic acid catabolic								
GO:0072329	process	5	309	112	17583	2.54	1.35	1.4E-02	7.0E-02
GO:0031175	neuron projection development	19	309	666	17583	1.62	0.70	1.4E-02	7.0E-02
GO:0030162	regulation of proteolysis	20	309	711	17583	1.60	0.68	1.4E-02	7.0E-02
	response to molecule of								
GO:0002237	bacterial origin	11	309	331	17583	1.89	0.92	1.5E-02	7.0E-02
GO:0007584	response to nutrient	6	309	146	17583	2.34	1.23	1.5E-02	7.0E-02
GO:0051783	regulation of nuclear division	6	309	146	17583	2.34	1.23	1.5E-02	7.0E-02

GO:0019216	regulation of lipid metabolic process	11	309	332	17583	1.89	0.91	1.5E-02	7.0E-02
GO:0048562	embryonic organ morphogenesis	10	309	293	17583	1.94	0.96	1.5E-02	7.0E-02
GO:0002697	regulation of immune effector process	12	309	373	17583	1.83	0.87	1.5E-02	7.0E-02
GO:0010675	regulation of cellular carbohydrate metabolic process	6	309	147	17583	2.32	1.22	1.5E-02	7.0E-02
GO:0008202	steroid metabolic process	9	309	257	17583	1.99	0.99	1.6E-02	7.0E-02
GO:0032652	regulation of interleukin-1 production	5	309	115	17583	2.47	1.31	1.6E-02	7.0E-02
GO:0120032	regulation of plasma membrane bounded cell projection assembly	8	309	220	17583	2.07	1.05	1.6E-02	7.0E-02
GO:0043583	ear development	8	309	220	17583	2.07	1.05	1.6E-02	7.0E-02
GO:0050793	regulation of developmental process	56	309	2459	17583	1.30	0.37	1.6E-02	7.0E-02
GO:0006006	glucose metabolic process	5	309	116	17583	2.45	1.29	1.7E-02	7.0E-02
GO:0030278	regulation of ossification	5	309	116	17583	2.45	1.29	1.7E-02	7.0E-02
GO:0034614	cellular response to reactive oxygen species	5	309	116	17583	2.45	1.29	1.7E-02	7.0E-02
GO:0050777	negative regulation of immune response	7	309	185	17583	2.15	1.11	1.7E-02	7.0E-02
GO:0006950	response to stress	75	309	3442	17583	1.24	0.31	1.7E-02	7.0E-02
GO:0060491	regulation of cell projection assembly	8	309	222	17583	2.05	1.04	1.7E-02	7.0E-02
GO:0034032	purine nucleoside bisphosphate metabolic process	5	309	117	17583	2.43	1.28	1.7E-02	7.0E-02
GO:0033875	ribonucleoside bisphosphate metabolic process	5	309	117	17583	2.43	1.28	1.7E-02	7.0E-02
GO:0033865	nucleoside bisphosphate metabolic process	5	309	117	17583	2.43	1.28	1.7E-02	7.0E-02

	regulation of cytokine								
GO:0002718	production involved in immune	5	309	118	17583	2.41	1.27	1.8E-02	7.1E-02
GO:0008203	cholesterol metabolic process	5	309	118	17583	2.41	1.27	1.8E-02	7.1E-02
	transmembrane receptor protein								
	tyrosine kinase signaling								
GO:0007169	pathway	13	309	424	17583	1.74	0.80	1.8E-02	7.1E-02
	negative regulation of amide								
GO:0034249	metabolic process	7	309	188	17583	2.12	1.08	1.8E-02	7.1E-02
	regulation of production of								
	molecular mediator of immune								
GO:0002700	response	7	309	188	17583	2.12	1.08	1.8E-02	7.1E-02
GO:0046777	protein autophosphorylation	7	309	188	17583	2.12	1.08	1.8E-02	7.1E-02
GO:0001817	regulation of cytokine	20	309	731	17583	1.56	0.64	1.9E-02	7.4E-02
	positive regulation of NF-								
	kappaB transcription factor								
GO:0051092	activity	6	309	154	17583	2.22	1.15	1.9E-02	7.5E-02
GO:0044248	cellular catabolic process	39	309	1630	17583	1.36	0.45	1.9E-02	7.5E-02
GO:0008610	lipid biosynthetic process	17	309	599	17583	1.61	0.69	1.9E-02	7.6E-02
	positive regulation of protein								
GO:0051222	transport	10	309	305	17583	1.87	0.90	1.9E-02	7.6E-02
	cellular component organization								
GO:0071840	or biogenesis	117	309	5719	17583	1.16	0.22	2.0E-02	7.6E-02
GO:0044255	cellular lipid metabolic process	24	309	916	17583	1.49	0.58	2.0E-02	7.7E-02
GO:0097485	neuron projection guidance	8	309	228	17583	2.00	1.00	2.0E-02	7.7E-02
GO:0007411	axon guidance	8	309	228	17583	2.00	1.00	2.0E-02	7.7E-02
GO:0044242	cellular lipid catabolic process	7	309	191	17583	2.09	1.06	2.0E-02	7.7E-02
GO:0032355	response to estradiol	5	309	121	17583	2.35	1.23	2.0E-02	7.8E-02
GO:0000075	cell cycle checkpoint signaling	6	309	156	17583	2.19	1.13	2.0E-02	8.0E-02
	positive regulation of								
	nucleobase-containing								
GO:0045935	compound metabolic process	47	309	2034	17583	1.31	0.39	2.0E-02	8.0E-02

GO:0001819	positive regulation of cytokine production	14	309	473	17583	1.68	0.75	2.1E-02	8.0E-02
GO:1901615	organic hydroxy compound metabolic process	14	309	474	17583	1.68	0.75	2.1E-02	8.1E-02
GO:0051640	organelle localization	15	309	517	17583	1.65	0.72	2.1E-02	8.1E-02
GO:0051336	regulation of hydrolase activity	25	309	968	17583	1.47	0.56	2.1E-02	8.1E-02
GO:0051701	biological process involved in interaction with host	6	309	157	17583	2.17	1.12	2.1E-02	8.1E-02
GO:0042593	glucose homeostasis	7	309	194	17583	2.05	1.04	2.2E-02	8.2E-02
GO:0006325	chromatin organization	17	309	608	17583	1.59	0.67	2.2E-02	8.4E-02
GO:0019637	organophosphate metabolic process	24	309	926	17583	1.47	0.56	2.2E-02	8.5E-02
GO:0033500	carbohydrate homeostasis	7	309	195	17583	2.04	1.03	2.2E-02	8.5E-02
GO:0007093	mitotic cell cycle checkpoint signaling	5	309	124	17583	2.29	1.20	2.2E-02	8.5E-02
GO:0040008	regulation of growth	17	309	609	17583	1.59	0.67	2.2E-02	8.5E-02
GO:0097193	intrinsic apoptotic signaling pathway	6	309	159	17583	2.15	1.10	2.2E-02	8.6E-02
GO:0097190	apoptotic signaling pathway	10	309	312	17583	1.82	0.87	2.3E-02	8.6E-02
GO:1903508	positive regulation of nucleic acid-templated transcription	40	309	1700	17583	1.34	0.42	2.3E-02	8.8E-02
GO:0045893	positive regulation of DNA-templated transcription	40	309	1700	17583	1.34	0.42	2.3E-02	8.8E-02
GO:1903313	positive regulation of mRNA metabolic process	5	309	125	17583	2.28	1.19	2.3E-02	8.8E-02
GO:0006338	chromatin remodeling	11	309	354	17583	1.77	0.82	2.3E-02	8.8E-02
GO:0006793	phosphorus metabolic process	43	309	1852	17583	1.32	0.40	2.4E-02	8.9E-02
GO:1901991	negative regulation of mitotic cell cycle phase transition	6	309	161	17583	2.12	1.08	2.4E-02	8.9E-02
GO:0018108	peptidyl-tyrosine phosphorylation	6	309	161	17583	2.12	1.08	2.4E-02	8.9E-02
GO:0000902	cell morphogenesis	19	309	703	17583	1.54	0.62	2.4E-02	8.9E-02

GO:1902680	positive regulation of RNA biosynthetic process	40	309	1706	17583	1.33	0.42	2.4E-02	8.9E-02
GO:0072659	protein localization to plasma membrane	7	309	199	17583	2.00	1.00	2.5E-02	8.9E-02
GO:0048858	cell projection morphogenesis	14	309	485	17583	1.64	0.72	2.5E-02	8.9E-02
GO:0046661	male sex differentiation	6	309	163	17583	2.09	1.07	2.5E-02	8.9E-02
GO:0018212	peptidyl-tyrosine modification	6	309	163	17583	2.09	1.07	2.5E-02	8.9E-02
GO:0034250	positive regulation of amide metabolic process	6	309	163	17583	2.09	1.07	2.5E-02	8.9E-02
GO:0043393	regulation of protein binding	7	309	200	17583	1.99	0.99	2.5E-02	8.9E-02
GO:0032956	regulation of actin cytoskeleton organization	11	309	359	17583	1.74	0.80	2.5E-02	8.9E-02
GO:0045862	positive regulation of proteolysis	11	309	359	17583	1.74	0.80	2.5E-02	8.9E-02
GO:0061564	axon development	12	309	401	17583	1.70	0.77	2.6E-02	8.9E-02
GO:0009259	ribonucleotide metabolic process	12	309	401	17583	1.70	0.77	2.6E-02	8.9E-02
GO:1902652	secondary alcohol metabolic process	5	309	128	17583	2.22	1.15	2.6E-02	8.9E-02
GO:0043547	positive regulation of GTPase activity	9	309	279	17583	1.84	0.88	2.6E-02	8.9E-02
GO:0001934	positive regulation of protein phosphorylation	19	309	711	17583	1.52	0.60	2.7E-02	8.9E-02
GO:0007034	vacuolar transport	6	309	165	17583	2.07	1.05	2.7E-02	8.9E-02
GO:0007409	axonogenesis	11	309	362	17583	1.73	0.79	2.7E-02	8.9E-02
GO:1904951	positive regulation of establishment of protein localization	10	309	321	17583	1.77	0.83	2.7E-02	8.9E-02
GO:0010557	positive regulation of macromolecule biosynthetic process	44	309	1920	17583	1.30	0.38	2.7E-02	8.9E-02
GO:0065008	regulation of biological quality	61	309	2788	17583	1.25	0.32	2.7E-02	8.9E-02

GO:0040029	epigenetic regulation of gene expression	5	309	130	17583	2.19	1.13	2.7E-02	8.9E-02
GO:1903305	regulation of regulated secretory pathway	5	309	130	17583	2.19	1.13	2.7E-02	8.9E-02
GO:0006979	response to oxidative stress	11	309	363	17583	1.72	0.79	2.7E-02	8.9E-02
GO:0031647	regulation of protein stability	10	309	322	17583	1.77	0.82	2.8E-02	8.9E-02
GO:0017148	negative regulation of	6	309	166	17583	2.06	1.04	2.8E-02	8.9E-02
GO:0010817	regulation of hormone levels response to inorganic substance	15	309	536	17583	1.59	0.67	2.8E-02	8.9E-02
GO:0010035	phosphate-containing compound metabolic process	15	309	537	17583	1.59	0.67	2.8E-02	8.9E-02
GO:0006796	regulation of programmed cell death	42	309	1826	17583	1.31	0.39	2.9E-02	8.9E-02
GO:0043067	hormone metabolic process	35	309	1479	17583	1.35	0.43	2.9E-02	8.9E-02
GO:0042445	negative regulation of Wnt signaling pathway	7	309	205	17583	1.94	0.96	2.9E-02	8.9E-02
GO:0030178	regulation of double-strand break repair	6	309	168	17583	2.03	1.02	2.9E-02	8.9E-02
GO:2000779	regulation of protein serine/threonine kinase activity	5	309	132	17583	2.16	1.11	2.9E-02	8.9E-02
GO:0071900	regulation of transferase activity	11	309	367	17583	1.71	0.77	2.9E-02	8.9E-02
GO:0051338	negative regulation of growth	22	309	858	17583	1.46	0.55	3.0E-02	8.9E-02
GO:0045926	leukocyte migration	8	309	245	17583	1.86	0.89	3.0E-02	8.9E-02
GO:0050900	ribose phosphate metabolic process	8	309	245	17583	1.86	0.89	3.0E-02	8.9E-02
GO:0019693	regulation of innate immune response	12	309	410	17583	1.67	0.74	3.0E-02	8.9E-02
GO:0045088	sterol metabolic process	11	309	368	17583	1.70	0.77	3.0E-02	8.9E-02
GO:0016125	positive regulation of production of molecular mediator of immune response	5	309	133	17583	2.14	1.10	3.0E-02	8.9E-02
GO:0002702		5	309	133	17583	2.14	1.10	3.0E-02	8.9E-02

GO:0001505	regulation of neurotransmitter levels	7	309	207	17583	1.92	0.94	3.0E-02	8.9E-02
GO:0010941	regulation of cell death	38	309	1634	17583	1.32	0.40	3.0E-02	8.9E-02
GO:0030833	regulation of actin filament polymerization	5	309	135	17583	2.11	1.08	3.2E-02	8.9E-02
GO:0009605	response to external stimulus	54	309	2452	17583	1.25	0.33	3.2E-02	8.9E-02
GO:0060828	regulation of canonical Wnt signaling pathway	8	309	249	17583	1.83	0.87	3.2E-02	8.9E-02
GO:0042981	regulation of apoptotic process	34	309	1446	17583	1.34	0.42	3.3E-02	8.9E-02
GO:0051130	positive regulation of cellular component organization	26	309	1058	17583	1.40	0.48	3.3E-02	8.9E-02
GO:0032990	cell part morphogenesis	14	309	505	17583	1.58	0.66	3.4E-02	8.9E-02
GO:0045727	positive regulation of translation	5	309	137	17583	2.08	1.05	3.4E-02	8.9E-02
GO:1902600	proton transmembrane transport	5	309	137	17583	2.08	1.05	3.4E-02	8.9E-02
GO:0050821	protein stabilization	7	309	212	17583	1.88	0.91	3.4E-02	8.9E-02
GO:0034248	regulation of amide metabolic process	13	309	462	17583	1.60	0.68	3.4E-02	8.9E-02
GO:0050878	regulation of body fluid levels	11	309	376	17583	1.66	0.74	3.5E-02	8.9E-02
GO:1902903	regulation of supramolecular fiber organization	11	309	376	17583	1.66	0.74	3.5E-02	8.9E-02
GO:0006282	regulation of DNA repair	7	309	213	17583	1.87	0.90	3.5E-02	8.9E-02
GO:0051716	cellular response to stimulus	128	309	6442	17583	1.13	0.18	3.5E-02	8.9E-02
GO:0010638	positive regulation of organelle organization	14	309	509	17583	1.57	0.65	3.6E-02	9.2E-02
GO:0002699	positive regulation of immune effector process	8	309	254	17583	1.79	0.84	3.6E-02	9.2E-02
GO:0050684	regulation of mRNA processing	5	309	139	17583	2.05	1.03	3.6E-02	9.2E-02
GO:0010639	negative regulation of organelle organization	10	309	337	17583	1.69	0.76	3.7E-02	9.3E-02
GO:0010256	endomembrane system organization	15	309	555	17583	1.54	0.62	3.7E-02	9.3E-02

GO ID	GO Term	Count	309	177	17583	1.93	0.95	3.7E-02	9.4E-02
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6	309	177	17583	1.93	0.95	3.7E-02	9.4E-02
GO:0015698	inorganic anion transport	6	309	177	17583	1.93	0.95	3.7E-02	9.4E-02
GO:0050896	response to stimulus	158	309	8137	17583	1.10	0.14	3.7E-02	9.4E-02
GO:0008584	male gonad development	5	309	140	17583	2.03	1.02	3.7E-02	9.4E-02
GO:0010977	negative regulation of neuron projection development	5	309	140	17583	2.03	1.02	3.7E-02	9.4E-02
GO:0007599	hemostasis	6	309	178	17583	1.92	0.94	3.8E-02	9.6E-02
GO:0006109	regulation of carbohydrate metabolic process	6	309	178	17583	1.92	0.94	3.8E-02	9.6E-02
GO:0099504	synaptic vesicle cycle	5	309	141	17583	2.02	1.01	3.8E-02	9.7E-02
GO:0046546	development of primary male sexual characteristics	5	309	141	17583	2.02	1.01	3.8E-02	9.7E-02
GO:0032984	protein-containing complex disassembly	5	309	141	17583	2.02	1.01	3.8E-02	9.7E-02
GO:0048583	regulation of response to stimulus	83	309	4008	17583	1.18	0.24	3.9E-02	9.8E-02
GO:1901564	organonitrogen compound metabolic process	101	309	4982	17583	1.15	0.21	3.9E-02	9.8E-02
GO:0031333	negative regulation of protein-containing complex assembly	5	309	142	17583	2.00	1.00	4.0E-02	9.9E-02
GO:0035556	intracellular signal transduction	35	309	1517	17583	1.31	0.39	4.0E-02	9.9E-02
GO:0051641	cellular localization	57	309	2639	17583	1.23	0.30	4.0E-02	1.0E-01
GO:0034976	response to endoplasmic reticulum stress	7	309	220	17583	1.81	0.86	4.1E-02	1.0E-01
GO:1901988	negative regulation of cell cycle phase transition	7	309	220	17583	1.81	0.86	4.1E-02	1.0E-01

GO:0048812	neuron projection morphogenesis	13	309	475	17583	1.56	0.64	4.2E-02	1.0E-01
GO:0050714	positive regulation of protein secretion	5	309	144	17583	1.98	0.98	4.2E-02	1.0E-01
GO:0006473	protein acetylation	5	309	144	17583	1.98	0.98	4.2E-02	1.0E-01
GO:0035966	response to topologically incorrect protein	5	309	144	17583	1.98	0.98	4.2E-02	1.0E-01
GO:0061024	membrane organization	21	309	844	17583	1.42	0.50	4.3E-02	1.1E-01
GO:0006790	sulfur compound metabolic process	10	309	346	17583	1.64	0.72	4.3E-02	1.1E-01
GO:0007517	muscle organ development	9	309	304	17583	1.68	0.75	4.3E-02	1.1E-01
GO:1902806	regulation of cell cycle G1/S phase transition	6	309	184	17583	1.86	0.89	4.4E-02	1.1E-01
GO:1903311	regulation of mRNA metabolic process	9	309	306	17583	1.67	0.74	4.5E-02	1.1E-01
GO:0120039	plasma membrane bounded cell projection morphogenesis	13	309	480	17583	1.54	0.62	4.5E-02	1.1E-01
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	6	309	185	17583	1.85	0.88	4.5E-02	1.1E-01
GO:0060538	skeletal muscle organ development	5	309	147	17583	1.94	0.95	4.6E-02	1.1E-01
GO:0016570	histone modification	11	309	394	17583	1.59	0.67	4.6E-02	1.1E-01
GO:1901135	carbohydrate derivative metabolic process	24	309	996	17583	1.37	0.46	4.7E-02	1.1E-01
GO:0051493	regulation of cytoskeleton organization	14	309	529	17583	1.51	0.59	4.8E-02	1.1E-01
GO:1903039	positive regulation of leukocyte cell-cell adhesion	8	309	268	17583	1.70	0.76	4.8E-02	1.1E-01
GO:0001959	regulation of cytokine-mediated signaling pathway	5	309	149	17583	1.91	0.93	4.8E-02	1.1E-01

GO:0031345	negative regulation of cell projection organization	6	309	188	17583	1.82	0.86	4.9E-02	1.1E-01
GO:0045944	positive regulation of transcription by RNA polymerase II	29	309	1246	17583	1.32	0.41	4.9E-02	1.1E-01
GO:0099003	vesicle-mediated transport in synapse	5	309	150	17583	1.90	0.92	4.9E-02	1.1E-01
GO:0051347	positive regulation of transferase activity	14	309	532	17583	1.50	0.58	5.0E-02	1.1E-01
GO:0007010	cytoskeleton organization	29	309	1247	17583	1.32	0.40	5.0E-02	1.1E-01
GO:0090596	sensory organ morphogenesis	8	309	270	17583	1.69	0.75	5.0E-02	1.1E-01
GO:0071466	cellular response to xenobiotic stimulus	6	309	189	17583	1.81	0.85	5.0E-02	1.1E-01
GO:0032970	regulation of actin filament-based process	11	309	399	17583	1.57	0.65	5.0E-02	1.1E-01
GO:0048878	chemical homeostasis	22	309	908	17583	1.38	0.46	5.1E-02	1.1E-01
GO:0031344	regulation of cell projection organization	17	309	672	17583	1.44	0.53	5.1E-02	1.1E-01
GO:0050728	negative regulation of inflammatory response	5	309	152	17583	1.87	0.90	5.2E-02	1.1E-01
GO:0007005	mitochondrion organization	12	309	446	17583	1.53	0.61	5.2E-02	1.1E-01
GO:0022409	positive regulation of cell-cell adhesion	9	309	316	17583	1.62	0.70	5.3E-02	1.1E-01
GO:0002819	regulation of adaptive immune response	6	309	192	17583	1.78	0.83	5.3E-02	1.1E-01
GO:0051495	positive regulation of cytoskeleton organization	6	309	193	17583	1.77	0.82	5.5E-02	1.1E-01
GO:0008064	regulation of actin polymerization or depolymerization	5	309	154	17583	1.85	0.89	5.5E-02	1.1E-01
GO:0090316	positive regulation of intracellular protein transport	5	309	154	17583	1.85	0.89	5.5E-02	1.1E-01

GO:0046907	intracellular transport	31	309	1358	17583	1.30	0.38	5.5E-02	1.1E-01
GO:0031347	regulation of defense response	18	309	726	17583	1.41	0.50	5.5E-02	1.1E-01
GO:0016197	endosomal transport	7	309	234	17583	1.70	0.77	5.5E-02	1.1E-01
	plasma membrane bounded cell								
GO:0120036	projection organization	26	309	1112	17583	1.33	0.41	5.5E-02	1.1E-01
GO:0009411	response to UV	5	309	155	17583	1.84	0.88	5.6E-02	1.2E-01
GO:0050776	regulation of immune response	22	309	920	17583	1.36	0.44	5.7E-02	1.2E-01
	positive regulation of								
GO:0032388	intracellular transport	6	309	195	17583	1.75	0.81	5.7E-02	1.2E-01
GO:0031589	cell-substrate adhesion	6	309	195	17583	1.75	0.81	5.7E-02	1.2E-01
	positive regulation of cell								
GO:0045597	differentiation	21	309	873	17583	1.37	0.45	5.8E-02	1.2E-01
	positive regulation of protein								
GO:0045860	kinase activity	10	309	364	17583	1.56	0.64	5.8E-02	1.2E-01
GO:0030098	lymphocyte differentiation	8	309	279	17583	1.63	0.71	5.9E-02	1.2E-01
GO:0009888	tissue development	38	309	1720	17583	1.26	0.33	5.9E-02	1.2E-01
	positive regulation of								
GO:0051094	developmental process	30	309	1317	17583	1.30	0.37	5.9E-02	1.2E-01
	regulation of actin filament								
GO:0030832	length	5	309	157	17583	1.81	0.86	5.9E-02	1.2E-01
GO:0050770	regulation of axonogenesis	5	309	157	17583	1.81	0.86	5.9E-02	1.2E-01
	regulation of response to biotic								
GO:0002831	stimulus	12	309	455	17583	1.50	0.59	5.9E-02	1.2E-01
	regulation of leukocyte								
GO:0002703	mediated immunity	7	309	238	17583	1.67	0.74	6.0E-02	1.2E-01
GO:0017157	regulation of exocytosis	6	309	198	17583	1.72	0.79	6.1E-02	1.2E-01
GO:0043087	regulation of GTPase activity	10	309	368	17583	1.55	0.63	6.1E-02	1.3E-01
GO:0051098	regulation of binding	10	309	368	17583	1.55	0.63	6.1E-02	1.3E-01
	regulation of response to								
GO:1903034	wounding	5	309	159	17583	1.79	0.84	6.2E-02	1.3E-01
	protein localization to cell								
GO:1990778	periphery	7	309	240	17583	1.66	0.73	6.2E-02	1.3E-01

GO:0006631	fatty acid metabolic process	9	309	326	17583	1.57	0.65	6.3E-02	1.3E-01
	regulation of response to								
GO:0060759	cytokine stimulus	5	309	160	17583	1.78	0.83	6.4E-02	1.3E-01
	regulation of mitotic cell cycle								
GO:1901990	phase transition	9	309	327	17583	1.57	0.65	6.4E-02	1.3E-01
	negative regulation of immune								
GO:0002683	system process	12	309	461	17583	1.48	0.57	6.4E-02	1.3E-01
GO:0006935	chemotaxis	13	309	507	17583	1.46	0.55	6.5E-02	1.3E-01
	regulation of endopeptidase								
GO:0052548	activity	9	309	328	17583	1.56	0.64	6.5E-02	1.3E-01
GO:0042330	taxis	13	309	509	17583	1.45	0.54	6.6E-02	1.3E-01
	regulation of inflammatory								
GO:0050727	response	10	309	376	17583	1.51	0.60	6.9E-02	1.3E-01
	phospholipid biosynthetic								
GO:0008654	process	7	309	246	17583	1.62	0.70	7.0E-02	1.3E-01
GO:1905952	regulation of lipid localization	5	309	164	17583	1.73	0.79	7.0E-02	1.3E-01
	regulation of tumor necrosis								
GO:0032680	factor production	5	309	164	17583	1.73	0.79	7.0E-02	1.3E-01
	negative regulation of response								
GO:0048585	to stimulus	35	309	1593	17583	1.25	0.32	7.0E-02	1.3E-01
	cellular component								
GO:0032989	morphogenesis	15	309	607	17583	1.41	0.49	7.1E-02	1.3E-01
GO:0016042	lipid catabolic process	8	309	290	17583	1.57	0.65	7.1E-02	1.3E-01
GO:0006897	endocytosis	13	309	515	17583	1.44	0.52	7.2E-02	1.3E-01
GO:0009410	response to xenobiotic stimulus	11	309	424	17583	1.48	0.56	7.2E-02	1.3E-01
GO:0071702	organic substance transport	42	309	1956	17583	1.22	0.29	7.2E-02	1.3E-01
	reproductive structure								
GO:0048608	development	8	309	291	17583	1.56	0.65	7.2E-02	1.3E-01
GO:0034097	response to cytokine	19	309	800	17583	1.35	0.43	7.2E-02	1.3E-01
	response to reactive oxygen								
GO:0000302	species	5	309	166	17583	1.71	0.78	7.3E-02	1.3E-01

GO:0071345	cellular response to cytokine stimulus	17	309	705	17583	1.37	0.46	7.3E-02	1.3E-01
GO:1901987	regulation of cell cycle phase transition	11	309	425	17583	1.47	0.56	7.3E-02	1.3E-01
GO:0009117	nucleotide metabolic process	13	309	517	17583	1.43	0.52	7.3E-02	1.3E-01
GO:0006469	negative regulation of protein kinase activity	6	309	207	17583	1.65	0.72	7.3E-02	1.3E-01
GO:0045927	positive regulation of growth	7	309	249	17583	1.60	0.68	7.4E-02	1.3E-01
GO:0120035	regulation of plasma membrane bounded cell projection organization	16	309	658	17583	1.38	0.47	7.4E-02	1.3E-01
GO:0097435	supramolecular fiber organization	14	309	564	17583	1.41	0.50	7.4E-02	1.3E-01
GO:0098656	anion transmembrane transport	7	309	250	17583	1.59	0.67	7.5E-02	1.4E-01
GO:0072594	establishment of protein localization to organelle	9	309	337	17583	1.52	0.60	7.5E-02	1.4E-01
GO:0045930	negative regulation of mitotic cell cycle	6	309	208	17583	1.64	0.71	7.5E-02	1.4E-01
GO:0009150	purine ribonucleotide metabolic process	10	309	382	17583	1.49	0.57	7.5E-02	1.4E-01
GO:0010950	positive regulation of endopeptidase activity	5	309	168	17583	1.69	0.76	7.6E-02	1.4E-01
GO:2001022	positive regulation of response to DNA damage stimulus	5	309	168	17583	1.69	0.76	7.6E-02	1.4E-01
GO:0051051	negative regulation of transport reproductive system	11	309	429	17583	1.46	0.55	7.7E-02	1.4E-01
GO:0061458	development	8	309	295	17583	1.54	0.63	7.7E-02	1.4E-01
GO:0009966	regulation of signal transduction	61	309	2966	17583	1.17	0.23	7.8E-02	1.4E-01
GO:0044262	cellular carbohydrate metabolic process	5	309	169	17583	1.68	0.75	7.8E-02	1.4E-01
GO:0032879	regulation of localization	44	309	2073	17583	1.21	0.27	7.8E-02	1.4E-01

GO:0051649	establishment of localization in cell	38	309	1764	17583	1.23	0.29	7.9E-02	1.4E-01
GO:0022407	regulation of cell-cell adhesion	12	309	477	17583	1.43	0.52	7.9E-02	1.4E-01
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	5	309	170	17583	1.67	0.74	8.0E-02	1.4E-01
GO:0006753	nucleoside phosphate metabolic process	13	309	525	17583	1.41	0.49	8.1E-02	1.4E-01
GO:0055085	transmembrane transport	27	309	1209	17583	1.27	0.35	8.2E-02	1.4E-01
GO:0051093	negative regulation of developmental process	21	309	911	17583	1.31	0.39	8.2E-02	1.4E-01
GO:0023051	regulation of signaling	68	309	3352	17583	1.15	0.21	8.2E-02	1.4E-01
GO:0040011	locomotion	13	309	528	17583	1.40	0.49	8.4E-02	1.4E-01
GO:0060627	regulation of vesicle-mediated transport	13	309	528	17583	1.40	0.49	8.4E-02	1.4E-01
GO:0007399	nervous system development	46	309	2189	17583	1.20	0.26	8.4E-02	1.4E-01
GO:0051726	regulation of cell cycle	25	309	1113	17583	1.28	0.35	8.5E-02	1.4E-01
GO:0007596	blood coagulation	5	309	173	17583	1.64	0.72	8.5E-02	1.4E-01
GO:0045595	regulation of cell differentiation	34	309	1570	17583	1.23	0.30	8.5E-02	1.4E-01
GO:0030334	regulation of cell migration	21	309	916	17583	1.30	0.38	8.6E-02	1.4E-01
GO:0045596	negative regulation of cell differentiation	16	309	673	17583	1.35	0.44	8.6E-02	1.4E-01
GO:0042110	T cell activation	8	309	302	17583	1.51	0.59	8.6E-02	1.4E-01
GO:0010646	regulation of cell communication	68	309	3362	17583	1.15	0.20	8.6E-02	1.4E-01
GO:0007154	cell communication	103	309	5269	17583	1.11	0.15	8.7E-02	1.4E-01
GO:0044237	cellular metabolic process	125	309	6489	17583	1.10	0.13	8.7E-02	1.4E-01
GO:1902905	positive regulation of supramolecular fiber organization	5	309	174	17583	1.64	0.71	8.7E-02	1.4E-01
GO:0050866	negative regulation of cell activation	6	309	216	17583	1.58	0.66	8.7E-02	1.5E-01

GO:0002706	regulation of lymphocyte mediated immunity	5	309	175	17583	1.63	0.70	8.9E-02	1.5E-01
GO:0009266	response to temperature stimulus	5	309	175	17583	1.63	0.70	8.9E-02	1.5E-01
GO:0050817	coagulation	5	309	175	17583	1.63	0.70	8.9E-02	1.5E-01
GO:1901575	organic substance catabolic process	36	309	1679	17583	1.22	0.29	8.9E-02	1.5E-01
GO:0044403	biological process involved in symbiotic interaction	7	309	260	17583	1.53	0.62	8.9E-02	1.5E-01
GO:0051099	positive regulation of binding	5	309	176	17583	1.62	0.69	9.1E-02	1.5E-01
GO:0140014	mitotic nuclear division	5	309	176	17583	1.62	0.69	9.1E-02	1.5E-01
GO:0043413	macromolecule glycosylation	6	309	219	17583	1.56	0.64	9.2E-02	1.5E-01
GO:0006486	protein glycosylation	6	309	219	17583	1.56	0.64	9.2E-02	1.5E-01
GO:0072521	purine-containing compound metabolic process	12	309	490	17583	1.39	0.48	9.3E-02	1.5E-01
GO:0070925	organelle assembly	19	309	827	17583	1.31	0.39	9.3E-02	1.5E-01
GO:0007346	regulation of mitotic cell cycle	12	309	491	17583	1.39	0.48	9.4E-02	1.6E-01
GO:0010952	positive regulation of peptidase activity	5	309	178	17583	1.60	0.68	9.5E-02	1.6E-01
GO:0010628	positive regulation of gene expression	25	309	1127	17583	1.26	0.34	9.5E-02	1.6E-01
GO:0051241	negative regulation of multicellular organismal process	23	309	1028	17583	1.27	0.35	9.5E-02	1.6E-01
GO:0008406	gonad development	6	309	221	17583	1.54	0.63	9.6E-02	1.6E-01
GO:0051668	localization within membrane	13	309	540	17583	1.37	0.45	9.6E-02	1.6E-01
GO:0044770	cell cycle phase transition	5	309	179	17583	1.59	0.67	9.6E-02	1.6E-01
GO:0032101	regulation of response to external stimulus	23	309	1032	17583	1.27	0.34	9.9E-02	1.6E-01
GO:2001020	regulation of response to DNA damage stimulus	8	309	311	17583	1.46	0.55	9.9E-02	1.6E-01
GO:0061448	connective tissue development	6	309	223	17583	1.53	0.61	9.9E-02	1.6E-01
GO:0002685	regulation of leukocyte	6	309	223	17583	1.53	0.61	9.9E-02	1.6E-01

GO:0044283	small molecule biosynthetic process	11	309	449	17583	1.39	0.48	9.9E-02	1.6E-01
GO:0006417	regulation of translation	10	309	403	17583	1.41	0.50	1.0E-01	1.6E-01
GO:2001257	regulation of cation channel activity	5	309	181	17583	1.57	0.65	1.0E-01	1.6E-01
GO:0036211	protein modification process	54	309	2645	17583	1.16	0.22	1.0E-01	1.6E-01
GO:0010948	negative regulation of cell cycle process	7	309	268	17583	1.49	0.57	1.0E-01	1.6E-01
GO:0048856	anatomical structure development	100	309	5143	17583	1.11	0.15	1.0E-01	1.6E-01
GO:0072657	protein localization to membrane	11	309	451	17583	1.39	0.47	1.0E-01	1.6E-01
GO:0023061	signal release	5	309	183	17583	1.55	0.64	1.0E-01	1.6E-01
GO:0048568	embryonic organ development	11	309	453	17583	1.38	0.47	1.0E-01	1.6E-01
GO:0046395	carboxylic acid catabolic process	6	309	226	17583	1.51	0.60	1.0E-01	1.6E-01
GO:0045137	development of primary sexual characteristics	6	309	226	17583	1.51	0.60	1.0E-01	1.6E-01
GO:0043436	oxoacid metabolic process	19	309	840	17583	1.29	0.36	1.0E-01	1.6E-01
GO:0110053	regulation of actin filament organization	7	309	270	17583	1.48	0.56	1.0E-01	1.6E-01
GO:0051348	negative regulation of transferase activity	7	309	270	17583	1.48	0.56	1.0E-01	1.6E-01
GO:1903037	regulation of leukocyte cell-cell adhesion	9	309	361	17583	1.42	0.50	1.1E-01	1.6E-01
GO:0009205	purine ribonucleoside triphosphate metabolic process	5	309	184	17583	1.55	0.63	1.1E-01	1.6E-01
GO:0043543	protein acylation	5	309	184	17583	1.55	0.63	1.1E-01	1.6E-01
GO:0071241	cellular response to inorganic substance	6	309	229	17583	1.49	0.58	1.1E-01	1.7E-01
GO:0032787	monocarboxylic acid metabolic process	12	309	505	17583	1.35	0.44	1.1E-01	1.7E-01

GO:0033365	protein localization to organelle	16	309	699	17583	1.30	0.38	1.1E-01	1.7E-01
GO:0006644	phospholipid metabolic process	9	309	365	17583	1.40	0.49	1.1E-01	1.7E-01
GO:0016054	organic acid catabolic process	6	309	230	17583	1.48	0.57	1.1E-01	1.7E-01
GO:0052547	regulation of peptidase activity	10	309	412	17583	1.38	0.47	1.1E-01	1.7E-01
	regulation of MAP kinase								
GO:0043405	activity	5	309	187	17583	1.52	0.61	1.1E-01	1.7E-01
GO:1901214	regulation of neuron death	8	309	320	17583	1.42	0.51	1.1E-01	1.7E-01
	purine nucleotide metabolic								
GO:0006163	process	11	309	460	17583	1.36	0.44	1.1E-01	1.7E-01
	negative regulation of kinase								
GO:0033673	activity	6	309	231	17583	1.48	0.56	1.1E-01	1.7E-01
	protein-DNA complex subunit								
GO:0071824	organization	6	309	231	17583	1.48	0.56	1.1E-01	1.7E-01
GO:0006082	organic acid metabolic process	19	309	850	17583	1.27	0.35	1.1E-01	1.7E-01
GO:0010038	response to metal ion	9	309	367	17583	1.40	0.48	1.1E-01	1.7E-01
	regulation of Ras protein signal								
GO:0046578	transduction	5	309	188	17583	1.51	0.60	1.1E-01	1.7E-01
	regulation of mRNA catabolic								
GO:0061013	process	5	309	188	17583	1.51	0.60	1.1E-01	1.7E-01
GO:0007548	sex differentiation	7	309	276	17583	1.44	0.53	1.1E-01	1.7E-01
GO:0030182	neuron differentiation	23	309	1052	17583	1.24	0.32	1.1E-01	1.7E-01
GO:0000209	protein polyubiquitination	6	309	232	17583	1.47	0.56	1.2E-01	1.7E-01
GO:0051050	positive regulation of transport	20	309	902	17583	1.26	0.34	1.2E-01	1.7E-01
	purine nucleoside triphosphate								
GO:0009144	metabolic process	5	309	189	17583	1.51	0.59	1.2E-01	1.7E-01
	negative regulation of molecular								
GO:0044092	function	22	309	1004	17583	1.25	0.32	1.2E-01	1.7E-01
GO:0022607	cellular component assembly	49	309	2411	17583	1.16	0.21	1.2E-01	1.7E-01
GO:0048167	regulation of synaptic plasticity	5	309	190	17583	1.50	0.58	1.2E-01	1.7E-01
	regulation of cellular response								
GO:0080135	to stress	16	309	707	17583	1.29	0.36	1.2E-01	1.8E-01

	regulation of cysteine-type								
GO:2000116	endopeptidase activity	6	309	234	17583	1.46	0.55	1.2E-01	1.8E-01
GO:0048513	animal organ development	58	309	2895	17583	1.14	0.19	1.2E-01	1.8E-01
GO:1903131	mononuclear cell differentiation	8	309	325	17583	1.40	0.49	1.2E-01	1.8E-01
	negative regulation of cell-cell								
GO:0022408	adhesion	5	309	191	17583	1.49	0.57	1.2E-01	1.8E-01
	ribonucleoside triphosphate								
GO:0009199	metabolic process	5	309	191	17583	1.49	0.57	1.2E-01	1.8E-01
	negative regulation of								
GO:0045936	phosphate metabolic process	10	309	419	17583	1.36	0.44	1.2E-01	1.8E-01
	negative regulation of								
GO:0010563	phosphorus metabolic process	10	309	420	17583	1.35	0.44	1.2E-01	1.8E-01
GO:0098657	import into cell	5	309	192	17583	1.48	0.57	1.2E-01	1.8E-01
GO:0034504	protein localization to nucleus	5	309	192	17583	1.48	0.57	1.2E-01	1.8E-01
GO:0045765	regulation of angiogenesis	7	309	281	17583	1.42	0.50	1.2E-01	1.8E-01
	regulation of Wnt signaling								
GO:0030111	pathway	8	309	327	17583	1.39	0.48	1.2E-01	1.8E-01
GO:0008104	protein localization	39	309	1892	17583	1.17	0.23	1.2E-01	1.8E-01
GO:0051046	regulation of secretion	14	309	615	17583	1.30	0.37	1.3E-01	1.8E-01
GO:0010564	regulation of cell cycle process	16	309	714	17583	1.28	0.35	1.3E-01	1.9E-01
GO:0070085	glycosylation	6	309	238	17583	1.43	0.52	1.3E-01	1.9E-01
	negative regulation of leukocyte								
GO:0002695	activation	5	309	194	17583	1.47	0.55	1.3E-01	1.9E-01
GO:0007423	sensory organ development	13	309	568	17583	1.30	0.38	1.3E-01	1.9E-01
	cellular macromolecule								
GO:0070727	localization	39	309	1898	17583	1.17	0.23	1.3E-01	1.9E-01
	regulation of vasculature								
GO:1901342	development	7	309	285	17583	1.40	0.48	1.3E-01	1.9E-01
GO:0012501	programmed cell death	23	309	1070	17583	1.22	0.29	1.3E-01	1.9E-01
	negative regulation of cell								
GO:0010648	communication	28	309	1328	17583	1.20	0.26	1.3E-01	1.9E-01

GO:0045785	positive regulation of cell adhesion	11	309	474	17583	1.32	0.40	1.3E-01	1.9E-01
GO:0030335	positive regulation of cell migration	12	309	523	17583	1.31	0.38	1.3E-01	1.9E-01
GO:0009913	epidermal cell differentiation	5	309	197	17583	1.44	0.53	1.3E-01	1.9E-01
GO:0044419	biological process involved in interspecies interaction between organisms	33	309	1591	17583	1.18	0.24	1.3E-01	1.9E-01
GO:2000145	regulation of cell motility	21	309	974	17583	1.23	0.29	1.4E-01	1.9E-01
GO:0000278	mitotic cell cycle	14	309	624	17583	1.28	0.35	1.4E-01	1.9E-01
GO:0007049	cell cycle	27	309	1283	17583	1.20	0.26	1.4E-01	1.9E-01
GO:0071902	positive regulation of protein serine/threonine kinase activity	5	309	199	17583	1.43	0.52	1.4E-01	2.0E-01
GO:0071248	cellular response to metal ion	5	309	199	17583	1.43	0.52	1.4E-01	2.0E-01
GO:0006915	apoptotic process	22	309	1028	17583	1.22	0.28	1.4E-01	2.0E-01
GO:0031400	negative regulation of protein modification process	11	309	480	17583	1.30	0.38	1.4E-01	2.0E-01
GO:0030705	cytoskeleton-dependent intracellular transport	5	309	200	17583	1.42	0.51	1.4E-01	2.0E-01
GO:0048193	Golgi vesicle transport	7	309	291	17583	1.37	0.45	1.4E-01	2.0E-01
GO:0030155	regulation of cell adhesion	17	309	778	17583	1.24	0.31	1.4E-01	2.0E-01
GO:1903047	mitotic cell cycle process	12	309	531	17583	1.29	0.36	1.4E-01	2.0E-01
GO:0018205	peptidyl-lysine modification	7	309	293	17583	1.36	0.44	1.5E-01	2.0E-01
GO:0006954	inflammatory response	12	309	532	17583	1.28	0.36	1.5E-01	2.0E-01
GO:0031348	negative regulation of defense response	6	309	247	17583	1.38	0.47	1.5E-01	2.0E-01
GO:0032886	regulation of microtubule-based process	6	309	248	17583	1.38	0.46	1.5E-01	2.0E-01
GO:0045089	positive regulation of innate immune response	6	309	249	17583	1.37	0.46	1.5E-01	2.0E-01
GO:0006302	double-strand break repair	5	309	204	17583	1.39	0.48	1.5E-01	2.0E-01

GO ID	GO Term	Count	Ratio	Count	Ratio	Count	Ratio	Count	Ratio
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	5	309	204	17583	1.39	0.48	1.5E-01	2.0E-01
GO:0033044	regulation of chromosome organization	6	309	252	17583	1.35	0.44	1.6E-01	2.1E-01
GO:0009100	glycoprotein metabolic process	8	309	346	17583	1.32	0.40	1.6E-01	2.1E-01
GO:0010608	post-transcriptional regulation of gene expression	11	309	491	17583	1.27	0.35	1.6E-01	2.1E-01
GO:0090407	organophosphate biosynthetic process	12	309	542	17583	1.26	0.33	1.6E-01	2.2E-01
GO:0009260	ribonucleotide biosynthetic process	5	309	208	17583	1.37	0.45	1.6E-01	2.2E-01
GO:0009141	nucleoside triphosphate metabolic process	5	309	208	17583	1.37	0.45	1.6E-01	2.2E-01
GO:0060326	cell chemotaxis	5	309	209	17583	1.36	0.45	1.6E-01	2.2E-01
GO:0008152	metabolic process	148	309	7967	17583	1.06	0.08	1.6E-01	2.2E-01
GO:0016310	phosphorylation	19	309	897	17583	1.21	0.27	1.6E-01	2.2E-01
GO:0008219	cell death	23	309	1103	17583	1.19	0.25	1.6E-01	2.2E-01
GO:0032102	negative regulation of response to external stimulus	9	309	398	17583	1.29	0.36	1.6E-01	2.2E-01
GO:0051056	regulation of small GTPase mediated signal transduction	7	309	303	17583	1.31	0.39	1.7E-01	2.2E-01
GO:2000147	positive regulation of cell motility	12	309	546	17583	1.25	0.32	1.7E-01	2.2E-01
GO:0055086	nucleobase-containing small molecule metabolic process	13	309	596	17583	1.24	0.31	1.7E-01	2.2E-01
GO:0006820	anion transport	10	309	448	17583	1.27	0.35	1.7E-01	2.2E-01
GO:0009628	response to abiotic stimulus	23	309	1106	17583	1.18	0.24	1.7E-01	2.2E-01
GO:0045786	negative regulation of cell cycle	8	309	352	17583	1.29	0.37	1.7E-01	2.2E-01
GO:0061061	muscle structure development	11	309	498	17583	1.26	0.33	1.7E-01	2.2E-01
GO:0009314	response to radiation	10	309	449	17583	1.27	0.34	1.7E-01	2.2E-01
GO:0045184	establishment of protein localization	26	309	1264	17583	1.17	0.23	1.7E-01	2.2E-01

	multicellular organism								
GO:0007275	development	75	309	3903	17583	1.09	0.13	1.7E-01	2.2E-01
GO:0051049	regulation of transport	35	309	1739	17583	1.15	0.20	1.7E-01	2.3E-01
	inorganic ion transmembrane								
GO:0098660	transport	15	309	699	17583	1.22	0.29	1.7E-01	2.3E-01
	establishment of protein								
GO:0090150	localization to membrane	5	309	212	17583	1.34	0.42	1.7E-01	2.3E-01
GO:0009617	response to bacterium	16	309	751	17583	1.21	0.28	1.7E-01	2.3E-01
	positive regulation of response								
GO:0048584	to stimulus	44	309	2223	17583	1.13	0.17	1.7E-01	2.3E-01
	regulation of ion								
GO:0032412	transmembrane transporter	6	309	260	17583	1.31	0.39	1.7E-01	2.3E-01
GO:0070482	response to oxygen levels	7	309	308	17583	1.29	0.37	1.8E-01	2.3E-01
	ribose phosphate biosynthetic								
GO:0046390	process	5	309	215	17583	1.32	0.40	1.8E-01	2.3E-01
	negative regulation of neuron								
GO:1901215	death	5	309	215	17583	1.32	0.40	1.8E-01	2.3E-01
	positive regulation of immune								
GO:0002684	system process	21	309	1014	17583	1.18	0.24	1.8E-01	2.3E-01
GO:0046486	glycerolipid metabolic process	8	309	358	17583	1.27	0.35	1.8E-01	2.3E-01
GO:0023057	negative regulation of signaling	27	309	1328	17583	1.16	0.21	1.8E-01	2.3E-01
	regulation of cellular component								
GO:0032535	size	8	309	359	17583	1.27	0.34	1.8E-01	2.3E-01
GO:0048699	generation of neurons	23	309	1121	17583	1.17	0.22	1.8E-01	2.4E-01
	vascular process in circulatory								
GO:0003018	system	6	309	264	17583	1.29	0.37	1.8E-01	2.4E-01
GO:0030163	protein catabolic process	16	309	760	17583	1.20	0.26	1.8E-01	2.4E-01
GO:0051301	cell division	11	309	508	17583	1.23	0.30	1.9E-01	2.4E-01
GO:1903530	regulation of secretion by cell	12	309	558	17583	1.22	0.29	1.9E-01	2.4E-01
	regulation of anatomical								
GO:0022603	structure morphogenesis	19	309	915	17583	1.18	0.24	1.9E-01	2.4E-01
GO:0040012	regulation of locomotion	21	309	1019	17583	1.17	0.23	1.9E-01	2.4E-01

GO:0022008	neurogenesis	26	309	1281	17583	1.15	0.21	1.9E-01	2.4E-01
GO:0008544	epidermis development	7	309	314	17583	1.27	0.34	1.9E-01	2.4E-01
GO:0040017	positive regulation of locomotion	12	309	561	17583	1.22	0.28	1.9E-01	2.4E-01
GO:0032940	secretion by cell	9	309	412	17583	1.24	0.31	1.9E-01	2.4E-01
GO:0006457	protein folding	5	309	220	17583	1.29	0.37	1.9E-01	2.4E-01
GO:0050804	modulation of chemical synaptic transmission	10	309	462	17583	1.23	0.30	1.9E-01	2.4E-01
GO:0099177	regulation of trans-synaptic signaling	10	309	463	17583	1.23	0.30	1.9E-01	2.4E-01
GO:0001666	response to hypoxia	6	309	268	17583	1.27	0.35	1.9E-01	2.4E-01
GO:0019752	carboxylic acid metabolic process	17	309	818	17583	1.18	0.24	1.9E-01	2.4E-01
GO:0009968	negative regulation of signal transduction	25	309	1236	17583	1.15	0.20	2.0E-01	2.5E-01
GO:0006807	nitrogen compound metabolic process	124	309	6674	17583	1.06	0.08	2.0E-01	2.5E-01
GO:0019538	protein metabolic process	74	309	3891	17583	1.08	0.11	2.0E-01	2.5E-01
GO:0022898	regulation of transmembrane transporter activity	6	309	270	17583	1.26	0.34	2.0E-01	2.5E-01
GO:0033157	regulation of intracellular protein transport	5	309	223	17583	1.28	0.35	2.0E-01	2.5E-01
GO:0044238	primary metabolic process	133	309	7194	17583	1.05	0.07	2.0E-01	2.6E-01
GO:0009416	response to light stimulus	7	309	321	17583	1.24	0.31	2.1E-01	2.6E-01
GO:0045017	glycerolipid biosynthetic process	5	309	225	17583	1.26	0.34	2.1E-01	2.6E-01
GO:0140352	export from cell	10	309	472	17583	1.21	0.27	2.1E-01	2.6E-01
GO:0002833	positive regulation of response to biotic stimulus	6	309	275	17583	1.24	0.31	2.1E-01	2.6E-01
GO:0044085	cellular component biogenesis	51	309	2651	17583	1.09	0.13	2.1E-01	2.6E-01
GO:0010466	negative regulation of peptidase activity	5	309	228	17583	1.25	0.32	2.1E-01	2.6E-01

	glycoprotein biosynthetic								
GO:0009101	process	6	309	276	17583	1.24	0.31	2.1E-01	2.6E-01
GO:0034220	ion transmembrane transport	18	309	885	17583	1.16	0.21	2.1E-01	2.7E-01
GO:0007165	signal transduction	90	309	4807	17583	1.07	0.09	2.2E-01	2.7E-01
GO:0030198	extracellular matrix organization	6	309	278	17583	1.23	0.30	2.2E-01	2.7E-01
GO:0016567	protein ubiquitination	14	309	681	17583	1.17	0.23	2.2E-01	2.7E-01
GO:0042592	homeostatic process	28	309	1417	17583	1.12	0.17	2.2E-01	2.7E-01
	extracellular structure								
GO:0043062	organization	6	309	279	17583	1.22	0.29	2.2E-01	2.7E-01
	immune response-regulating								
	cell surface receptor signaling								
GO:0002768	pathway	7	309	328	17583	1.21	0.28	2.2E-01	2.7E-01
	regulation of muscle system								
GO:0090257	process	5	309	231	17583	1.23	0.30	2.2E-01	2.7E-01
	regulation of intracellular								
GO:0032386	transport	7	309	329	17583	1.21	0.28	2.2E-01	2.7E-01
GO:0032880	regulation of protein localization	17	309	839	17583	1.15	0.21	2.2E-01	2.7E-01
	external encapsulating structure								
GO:0045229	organization	6	309	281	17583	1.22	0.28	2.3E-01	2.8E-01
	response to decreased oxygen								
GO:0036293	levels	6	309	281	17583	1.22	0.28	2.3E-01	2.8E-01
GO:0048598	embryonic morphogenesis	12	309	583	17583	1.17	0.23	2.3E-01	2.8E-01
	organonitrogen compound								
GO:1901566	biosynthetic process	26	309	1317	17583	1.12	0.17	2.3E-01	2.8E-01
GO:0006520	amino acid metabolic process	6	309	282	17583	1.21	0.28	2.3E-01	2.8E-01
	positive regulation of defense								
GO:0031349	response	8	309	381	17583	1.19	0.26	2.3E-01	2.8E-01
	response to external biotic								
GO:0043207	stimulus	28	309	1425	17583	1.12	0.16	2.3E-01	2.8E-01
	negative regulation of cytokine								
GO:0001818	production	6	309	283	17583	1.21	0.27	2.3E-01	2.8E-01
GO:0023052	signaling	95	309	5106	17583	1.06	0.08	2.3E-01	2.8E-01

	enzyme-linked receptor protein								
GO:0007167	signaling pathway	13	309	637	17583	1.16	0.22	2.3E-01	2.8E-01
GO:0051276	chromosome organization	9	309	433	17583	1.18	0.24	2.3E-01	2.8E-01
	regulation of cellular								
	macromolecule biosynthetic								
GO:2000112	process	10	309	485	17583	1.17	0.23	2.4E-01	2.8E-01
	cellular response to DNA								
GO:0006974	damage stimulus	15	309	743	17583	1.15	0.20	2.4E-01	2.8E-01
	regulation of synapse								
GO:0050807	organization	5	309	236	17583	1.21	0.27	2.4E-01	2.8E-01
GO:0016477	cell migration	18	309	900	17583	1.14	0.19	2.4E-01	2.8E-01
	negative regulation of catalytic								
GO:0043086	activity	13	309	640	17583	1.16	0.21	2.4E-01	2.9E-01
	organic substance biosynthetic								
GO:1901576	process	48	309	2515	17583	1.09	0.12	2.4E-01	2.9E-01
GO:0048731	system development	66	309	3507	17583	1.07	0.10	2.4E-01	2.9E-01
GO:0042060	wound healing	7	309	336	17583	1.19	0.25	2.4E-01	2.9E-01
GO:0032409	regulation of transporter activity	6	309	287	17583	1.19	0.25	2.4E-01	2.9E-01
	organonitrogen compound								
GO:1901565	catabolic process	22	309	1117	17583	1.12	0.16	2.4E-01	2.9E-01
	negative regulation of cell								
GO:0010721	development	6	309	288	17583	1.19	0.25	2.4E-01	2.9E-01
	proteolysis involved in protein								
GO:0051603	catabolic process	13	309	645	17583	1.15	0.20	2.5E-01	2.9E-01
	protein modification by small								
GO:0032446	protein conjugation	15	309	751	17583	1.14	0.18	2.5E-01	3.0E-01
GO:0009058	biosynthetic process	49	309	2584	17583	1.08	0.11	2.5E-01	3.0E-01
GO:0006887	exocytosis	5	309	241	17583	1.18	0.24	2.5E-01	3.0E-01
GO:0044249	cellular biosynthetic process	46	309	2421	17583	1.08	0.11	2.5E-01	3.0E-01
GO:0015031	protein transport	23	309	1176	17583	1.11	0.15	2.5E-01	3.0E-01
GO:0060485	mesenchyme development	5	309	242	17583	1.18	0.23	2.5E-01	3.0E-01
GO:0016311	dephosphorylation	5	309	242	17583	1.18	0.23	2.5E-01	3.0E-01

GO:0050803	regulation of synapse structure or activity	5	309	242	17583	1.18	0.23	2.5E-01	3.0E-01
GO:0006650	glycerophospholipid metabolic process	6	309	292	17583	1.17	0.23	2.6E-01	3.0E-01
GO:0043412	macromolecule modification	54	309	2865	17583	1.07	0.10	2.6E-01	3.0E-01
GO:0006816	calcium ion transport	5	309	243	17583	1.17	0.23	2.6E-01	3.0E-01
GO:0090066	regulation of anatomical structure size	10	309	497	17583	1.14	0.20	2.6E-01	3.1E-01
GO:0009611	response to wounding	9	309	446	17583	1.15	0.20	2.6E-01	3.1E-01
GO:1903706	regulation of hemopoiesis	8	309	395	17583	1.15	0.20	2.6E-01	3.1E-01
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	7	309	345	17583	1.15	0.21	2.6E-01	3.1E-01
GO:0098662	inorganic cation transmembrane transport	12	309	602	17583	1.13	0.18	2.6E-01	3.1E-01
GO:0050870	positive regulation of T cell activation	5	309	245	17583	1.16	0.22	2.6E-01	3.1E-01
GO:0051223	regulation of protein transport	10	309	499	17583	1.14	0.19	2.6E-01	3.1E-01
GO:0043933	protein-containing complex organization	27	309	1404	17583	1.09	0.13	2.7E-01	3.2E-01
GO:0044271	cellular nitrogen compound biosynthetic process	30	309	1567	17583	1.09	0.12	2.7E-01	3.2E-01
GO:0006811	ion transport	23	309	1194	17583	1.10	0.13	2.8E-01	3.2E-01
GO:0071704	organic substance metabolic process	137	309	7534	17583	1.03	0.05	2.8E-01	3.2E-01
GO:0002429	immune response-activating cell surface receptor signaling pathway	6	309	300	17583	1.14	0.19	2.8E-01	3.2E-01
GO:0006909	phagocytosis	5	309	250	17583	1.14	0.19	2.8E-01	3.2E-01
GO:0006952	defense response	28	309	1466	17583	1.09	0.12	2.8E-01	3.2E-01
GO:0046883	regulation of hormone secretion	5	309	251	17583	1.13	0.18	2.8E-01	3.3E-01

GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	5	309	251	17583	1.13	0.18	2.8E-01	3.3E-01
GO:0009653	anatomical structure morphogenesis	42	309	2232	17583	1.07	0.10	2.8E-01	3.3E-01
GO:0051054	positive regulation of DNA metabolic process	6	309	302	17583	1.13	0.18	2.8E-01	3.3E-01
GO:1902532	negative regulation of intracellular signal transduction	10	309	509	17583	1.12	0.16	2.8E-01	3.3E-01
GO:0009607	response to biotic stimulus	28	309	1471	17583	1.08	0.12	2.8E-01	3.3E-01
GO:0032502	developmental process	104	309	5685	17583	1.04	0.06	2.8E-01	3.3E-01
GO:0002521	leukocyte differentiation	8	309	406	17583	1.12	0.17	2.9E-01	3.3E-01
GO:0002694	regulation of leukocyte	13	309	668	17583	1.11	0.15	2.9E-01	3.3E-01
GO:0018193	peptidyl-amino acid modification	16	309	828	17583	1.10	0.14	2.9E-01	3.3E-01
GO:0044782	cilium organization	7	309	356	17583	1.12	0.16	2.9E-01	3.3E-01
GO:0006091	generation of precursor metabolites and energy	8	309	408	17583	1.12	0.16	2.9E-01	3.3E-01
GO:0051251	positive regulation of lymphocyte activation	8	309	408	17583	1.12	0.16	2.9E-01	3.3E-01
GO:0046649	lymphocyte activation	9	309	460	17583	1.11	0.15	2.9E-01	3.4E-01
GO:0050865	regulation of cell activation	14	309	723	17583	1.10	0.14	2.9E-01	3.4E-01
GO:0051707	response to other organism	27	309	1422	17583	1.08	0.11	2.9E-01	3.4E-01
GO:0050778	positive regulation of immune response	13	309	671	17583	1.10	0.14	2.9E-01	3.4E-01
GO:0009887	animal organ morphogenesis	19	309	992	17583	1.09	0.12	2.9E-01	3.4E-01
GO:0009057	macromolecule catabolic process	19	309	992	17583	1.09	0.12	2.9E-01	3.4E-01
GO:0001501	skeletal system development	10	309	514	17583	1.11	0.15	3.0E-01	3.4E-01
GO:0048872	homeostasis of number of cells	5	309	256	17583	1.11	0.15	3.0E-01	3.4E-01
GO:0051924	regulation of calcium ion transport	5	309	256	17583	1.11	0.15	3.0E-01	3.4E-01

	regulation of intracellular signal								
GO:1902531	transduction	32	309	1699	17583	1.07	0.10	3.0E-01	3.4E-01
GO:0022604	regulation of cell	6	309	309	17583	1.10	0.14	3.0E-01	3.4E-01
GO:0043604	amide biosynthetic process	10	309	517	17583	1.10	0.14	3.0E-01	3.4E-01
GO:0098655	cation transmembrane transport	13	309	677	17583	1.09	0.13	3.0E-01	3.5E-01
GO:0060341	regulation of cellular localization	18	309	946	17583	1.08	0.11	3.1E-01	3.5E-01
	positive regulation of cell								
GO:0010720	development	9	309	467	17583	1.10	0.13	3.1E-01	3.5E-01
GO:0050708	regulation of protein secretion	5	309	260	17583	1.09	0.13	3.1E-01	3.5E-01
	negative regulation of								
GO:0042326	phosphorylation	7	309	363	17583	1.10	0.13	3.1E-01	3.5E-01
	regulation of apoptotic signaling								
GO:2001233	pathway	7	309	363	17583	1.10	0.13	3.1E-01	3.5E-01
	cell surface receptor signaling								
GO:0007166	pathway	40	309	2149	17583	1.06	0.08	3.1E-01	3.5E-01
	ubiquitin-dependent protein								
GO:0006511	catabolic process	11	309	574	17583	1.09	0.12	3.1E-01	3.5E-01
	regulation of leukocyte								
GO:1902105	differentiation	6	309	313	17583	1.09	0.13	3.1E-01	3.5E-01
GO:0009165	nucleotide biosynthetic process	5	309	262	17583	1.09	0.12	3.1E-01	3.6E-01
	regulation of developmental								
GO:0048638	growth	6	309	314	17583	1.09	0.12	3.2E-01	3.6E-01
	regulation of establishment of								
GO:0070201	protein localization	10	309	524	17583	1.09	0.12	3.2E-01	3.6E-01
GO:0046903	secretion	10	309	524	17583	1.09	0.12	3.2E-01	3.6E-01
	nucleoside phosphate								
GO:1901293	biosynthetic process	5	309	264	17583	1.08	0.11	3.2E-01	3.6E-01
	heterocycle biosynthetic								
GO:0018130	process	20	309	1063	17583	1.07	0.10	3.2E-01	3.6E-01
GO:0050863	regulation of T cell activation	7	309	368	17583	1.08	0.11	3.2E-01	3.6E-01
GO:0060548	negative regulation of cell death	19	309	1009	17583	1.07	0.10	3.2E-01	3.6E-01
GO:0006812	cation transport	16	309	849	17583	1.07	0.10	3.2E-01	3.6E-01

GO:0034762	regulation of transmembrane transport	11	309	582	17583	1.08	0.10	3.3E-01	3.7E-01
GO:1904062	regulation of cation transmembrane transport	7	309	371	17583	1.07	0.10	3.3E-01	3.7E-01
GO:0001933	negative regulation of protein phosphorylation	6	309	319	17583	1.07	0.10	3.3E-01	3.7E-01
GO:0019941	modification-dependent protein catabolic process	11	309	584	17583	1.07	0.10	3.3E-01	3.7E-01
GO:0019438	aromatic compound biosynthetic process	20	309	1072	17583	1.06	0.09	3.3E-01	3.7E-01
GO:0051052	regulation of DNA metabolic process	10	309	533	17583	1.07	0.09	3.4E-01	3.8E-01
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	7	309	374	17583	1.07	0.09	3.4E-01	3.8E-01
GO:0060284	regulation of cell development	16	309	856	17583	1.06	0.09	3.4E-01	3.8E-01
GO:0010498	proteasomal protein catabolic process	7	309	376	17583	1.06	0.08	3.4E-01	3.8E-01
GO:0104004	cellular response to environmental stimulus	6	309	324	17583	1.05	0.08	3.4E-01	3.8E-01
GO:0071214	cellular response to abiotic stimulus	6	309	324	17583	1.05	0.08	3.4E-01	3.8E-01
GO:0008285	negative regulation of cell population proliferation	13	309	698	17583	1.06	0.08	3.4E-01	3.8E-01
GO:0023056	positive regulation of signaling	31	309	1684	17583	1.05	0.07	3.5E-01	3.9E-01
GO:0010647	positive regulation of cell communication	31	309	1685	17583	1.05	0.07	3.5E-01	3.9E-01
GO:1901137	carbohydrate derivative biosynthetic process	11	309	593	17583	1.06	0.08	3.5E-01	3.9E-01

	regulation of transmembrane receptor protein serine/threonine kinase								
GO:0090092	signaling pathway	5	309	274	17583	1.04	0.05	3.5E-01	3.9E-01
GO:0043269	regulation of ion transport	13	309	704	17583	1.05	0.07	3.6E-01	4.0E-01
GO:0050801	ion homeostasis	10	309	542	17583	1.05	0.07	3.6E-01	4.0E-01
	modification-dependent macromolecule catabolic								
GO:0043632	process	11	309	596	17583	1.05	0.07	3.6E-01	4.0E-01
GO:0071705	nitrogen compound transport	29	309	1581	17583	1.04	0.06	3.6E-01	4.0E-01
GO:0030031	cell projection assembly	8	309	437	17583	1.04	0.06	3.6E-01	4.0E-01
	organic cyclic compound								
GO:1901362	biosynthetic process	22	309	1199	17583	1.04	0.06	3.6E-01	4.0E-01
	negative regulation of hydrolase								
GO:0051346	activity	6	309	333	17583	1.03	0.04	3.7E-01	4.1E-01
GO:0198738	cell-cell signaling by wnt	5	309	280	17583	1.02	0.02	3.7E-01	4.1E-01
GO:0016055	Wnt signaling pathway	5	309	280	17583	1.02	0.02	3.7E-01	4.1E-01
GO:0006468	protein phosphorylation	13	309	712	17583	1.04	0.06	3.7E-01	4.1E-01
	cellular nitrogen compound								
GO:0044270	catabolic process	6	309	334	17583	1.02	0.03	3.7E-01	4.1E-01
	regulation of neuron projection								
GO:0010975	development	8	309	442	17583	1.03	0.04	3.7E-01	4.1E-01
GO:0003002	regionalization	6	309	335	17583	1.02	0.03	3.8E-01	4.1E-01
GO:0016071	mRNA metabolic process	11	309	606	17583	1.03	0.05	3.8E-01	4.2E-01
	nucleobase-containing								
GO:0034654	compound biosynthetic process	18	309	991	17583	1.03	0.05	3.8E-01	4.2E-01
	regulation of ion								
GO:0034765	transmembrane transport	9	309	499	17583	1.03	0.04	3.8E-01	4.2E-01
GO:0048468	cell development	39	309	2160	17583	1.03	0.04	3.9E-01	4.2E-01
	immune response-regulating								
GO:0002764	signaling pathway	7	309	394	17583	1.01	0.02	3.9E-01	4.3E-01

GO:0043066	negative regulation of apoptotic process	16	309	886	17583	1.03	0.04	3.9E-01	4.3E-01
GO:0043270	positive regulation of ion transport	5	309	287	17583	0.99	-0.01	3.9E-01	4.3E-01
GO:0006259	DNA metabolic process	14	309	778	17583	1.02	0.03	3.9E-01	4.3E-01
GO:0007162	negative regulation of cell adhesion	5	309	288	17583	0.99	-0.02	3.9E-01	4.3E-01
GO:0010959	regulation of metal ion transport	7	309	396	17583	1.01	0.01	4.0E-01	4.3E-01
GO:0045787	positive regulation of cell cycle	6	309	344	17583	0.99	-0.01	4.0E-01	4.4E-01
GO:0030855	epithelial cell differentiation	11	309	617	17583	1.01	0.02	4.0E-01	4.4E-01
GO:0070647	protein modification by small protein conjugation or removal	16	309	893	17583	1.02	0.03	4.0E-01	4.4E-01
GO:0002696	positive regulation of leukocyte activation	8	309	455	17583	1.00	0.00	4.1E-01	4.4E-01
GO:0044057	regulation of system process	10	309	566	17583	1.01	0.01	4.1E-01	4.4E-01
GO:0019439	aromatic compound catabolic process	6	309	348	17583	0.98	-0.03	4.1E-01	4.5E-01
GO:0009967	positive regulation of signal transduction	27	309	1511	17583	1.02	0.02	4.1E-01	4.5E-01
GO:0022402	cell cycle process	16	309	899	17583	1.01	0.02	4.1E-01	4.5E-01
GO:0002252	immune effector process	8	309	458	17583	0.99	-0.01	4.1E-01	4.5E-01
GO:0048589	developmental growth	7	309	404	17583	0.99	-0.02	4.2E-01	4.5E-01
GO:0040007	growth	7	309	404	17583	0.99	-0.02	4.2E-01	4.5E-01
GO:0006366	transcription by RNA polymerase II	6	309	352	17583	0.97	-0.04	4.2E-01	4.6E-01
GO:0032103	positive regulation of response to external stimulus	9	309	518	17583	0.99	-0.02	4.3E-01	4.6E-01
GO:0043069	negative regulation of programmed cell death	16	309	908	17583	1.00	0.00	4.3E-01	4.6E-01
GO:0043603	amide metabolic process	14	309	798	17583	1.00	0.00	4.3E-01	4.6E-01
GO:0006886	intracellular protein transport	12	309	688	17583	0.99	-0.01	4.3E-01	4.7E-01

GO:0051249	regulation of lymphocyte activation	10	309	577	17583	0.99	-0.02	4.3E-01	4.7E-01
GO:0034641	cellular nitrogen compound metabolic process	59	309	3333	17583	1.01	0.01	4.4E-01	4.7E-01
GO:0045321	leukocyte activation	10	309	580	17583	0.98	-0.03	4.4E-01	4.7E-01
GO:0042254	ribosome biogenesis	5	309	303	17583	0.94	-0.09	4.4E-01	4.7E-01
GO:0065003	protein-containing complex assembly	22	309	1254	17583	1.00	0.00	4.5E-01	4.8E-01
GO:0050867	positive regulation of cell activation	8	309	471	17583	0.97	-0.05	4.5E-01	4.8E-01
GO:0098771	inorganic ion homeostasis	9	309	530	17583	0.97	-0.05	4.5E-01	4.8E-01
GO:0042127	regulation of cell population proliferation	29	309	1654	17583	1.00	0.00	4.6E-01	4.9E-01
GO:0048732	gland development	7	309	419	17583	0.95	-0.07	4.6E-01	4.9E-01
GO:0002757	immune response-activating signaling pathway	6	309	365	17583	0.94	-0.10	4.6E-01	4.9E-01
GO:0090287	regulation of cellular response to growth factor stimulus	5	309	310	17583	0.92	-0.12	4.6E-01	4.9E-01
GO:0001775	cell activation	12	309	702	17583	0.97	-0.04	4.6E-01	4.9E-01
GO:0043410	positive regulation of MAPK cascade	8	309	479	17583	0.95	-0.07	4.7E-01	5.0E-01
GO:0009790	embryo development	18	309	1044	17583	0.98	-0.03	4.7E-01	5.0E-01
GO:0042391	regulation of membrane potential	7	309	427	17583	0.93	-0.10	4.8E-01	5.1E-01
GO:0060322	head development	14	309	826	17583	0.96	-0.05	4.9E-01	5.1E-01
GO:0045087	innate immune response	14	309	830	17583	0.96	-0.06	4.9E-01	5.2E-01
GO:0048870	cell motility	18	309	1057	17583	0.97	-0.05	4.9E-01	5.2E-01
GO:0006351	DNA-templated transcription	10	309	606	17583	0.94	-0.09	5.0E-01	5.3E-01
GO:0097659	nucleic acid-templated transcription	10	309	607	17583	0.94	-0.09	5.0E-01	5.3E-01
GO:0060271	cilium assembly	5	309	323	17583	0.88	-0.18	5.0E-01	5.3E-01
GO:0003013	circulatory system process	8	309	494	17583	0.92	-0.12	5.0E-01	5.3E-01

	organic cyclic compound								
GO:1901361	catabolic process	6	309	381	17583	0.90	-0.16	5.1E-01	5.3E-01
GO:0006873	cellular ion homeostasis	7	309	438	17583	0.91	-0.14	5.1E-01	5.3E-01
GO:0000280	nuclear division	5	309	325	17583	0.88	-0.19	5.1E-01	5.3E-01
	macromolecule metabolic								
GO:0043170	process	101	309	5792	17583	0.99	-0.01	5.1E-01	5.4E-01
GO:0060537	muscle tissue development	5	309	327	17583	0.87	-0.20	5.2E-01	5.4E-01
GO:0006281	DNA repair	8	309	499	17583	0.91	-0.13	5.2E-01	5.4E-01
GO:0048869	cellular developmental process	62	309	3579	17583	0.99	-0.02	5.2E-01	5.4E-01
	cellular macromolecule								
GO:0044265	catabolic process	13	309	786	17583	0.94	-0.09	5.2E-01	5.4E-01
	cellular macromolecule								
GO:0044260	metabolic process	43	309	2498	17583	0.98	-0.03	5.2E-01	5.4E-01
	cellular aromatic compound								
GO:0006725	metabolic process	52	309	3013	17583	0.98	-0.03	5.2E-01	5.5E-01
GO:0032774	RNA biosynthetic process	10	309	617	17583	0.92	-0.12	5.2E-01	5.5E-01
	macromolecule biosynthetic								
GO:0009059	process	25	309	1476	17583	0.96	-0.05	5.3E-01	5.5E-01
	microtubule cytoskeleton								
GO:0000226	organization	9	309	561	17583	0.91	-0.13	5.3E-01	5.5E-01
GO:0007155	cell adhesion	16	309	963	17583	0.95	-0.08	5.3E-01	5.5E-01
GO:0046700	heterocycle catabolic process	5	309	332	17583	0.86	-0.22	5.3E-01	5.5E-01
GO:0046483	heterocycle metabolic process	51	309	2966	17583	0.98	-0.03	5.3E-01	5.6E-01
GO:0006397	mRNA processing	7	309	448	17583	0.89	-0.17	5.3E-01	5.6E-01
	organic cyclic compound								
GO:1901360	metabolic process	56	309	3255	17583	0.98	-0.03	5.4E-01	5.6E-01
	non-membrane-bounded								
GO:0140694	organelle assembly	5	309	335	17583	0.85	-0.24	5.4E-01	5.6E-01
GO:0007389	pattern specification process	7	309	455	17583	0.88	-0.19	5.5E-01	5.7E-01
GO:0030154	cell differentiation	61	309	3556	17583	0.98	-0.03	5.5E-01	5.7E-01
GO:0055080	cation homeostasis	8	309	515	17583	0.88	-0.18	5.5E-01	5.8E-01
GO:0043043	peptide biosynthetic process	6	309	399	17583	0.86	-0.22	5.6E-01	5.8E-01

	positive regulation of cell								
GO:0031346	projection organization	5	309	347	17583	0.82	-0.29	5.7E-01	5.9E-01
GO:0048285	organelle fission	5	309	350	17583	0.81	-0.30	5.8E-01	6.0E-01
	cellular macromolecule								
GO:0034645	biosynthetic process	12	309	765	17583	0.89	-0.16	5.9E-01	6.1E-01
	defense response to other								
GO:0098542	organism	17	309	1058	17583	0.91	-0.13	5.9E-01	6.1E-01
GO:0009615	response to virus	5	309	354	17583	0.80	-0.32	5.9E-01	6.1E-01
	anatomical structure formation								
GO:0048646	involved in morphogenesis	15	309	945	17583	0.90	-0.15	6.0E-01	6.2E-01
GO:0019725	cellular homeostasis	10	309	653	17583	0.87	-0.20	6.0E-01	6.2E-01
GO:0002376	immune system process	37	309	2229	17583	0.94	-0.08	6.1E-01	6.3E-01
	plasma membrane bounded cell								
GO:0120031	projection assembly	6	309	424	17583	0.81	-0.31	6.2E-01	6.4E-01
GO:0030097	hemopoiesis	10	309	663	17583	0.86	-0.22	6.2E-01	6.4E-01
GO:0055065	metal ion homeostasis	6	309	425	17583	0.80	-0.32	6.2E-01	6.4E-01
GO:0055082	cellular chemical homeostasis	8	309	547	17583	0.83	-0.26	6.3E-01	6.5E-01
GO:0043408	regulation of MAPK cascade	10	309	668	17583	0.85	-0.23	6.3E-01	6.5E-01
GO:0006412	translation	5	309	370	17583	0.77	-0.38	6.4E-01	6.5E-01
GO:0002253	activation of immune response	6	309	434	17583	0.79	-0.35	6.4E-01	6.6E-01
GO:0050767	regulation of neurogenesis	5	309	374	17583	0.76	-0.39	6.5E-01	6.6E-01
	regulation of epithelial cell								
GO:0050678	proliferation	5	309	374	17583	0.76	-0.39	6.5E-01	6.6E-01
	nucleobase-containing								
GO:0006139	compound metabolic process	46	309	2793	17583	0.94	-0.09	6.5E-01	6.7E-01
	positive regulation of								
GO:1902533	intracellular signal transduction	15	309	980	17583	0.87	-0.20	6.6E-01	6.7E-01
GO:0030001	metal ion transport	9	309	624	17583	0.82	-0.29	6.6E-01	6.8E-01
GO:0048729	tissue morphogenesis	8	309	565	17583	0.81	-0.31	6.6E-01	6.8E-01
	positive regulation of cell								
GO:0008284	population proliferation	14	309	931	17583	0.86	-0.22	6.7E-01	6.9E-01

	ribonucleoprotein complex								
GO:0022613	biogenesis	6	309	449	17583	0.76	-0.40	6.8E-01	6.9E-01
	regulation of nervous system								
GO:0051960	development	6	309	454	17583	0.75	-0.41	6.9E-01	7.0E-01
GO:0007017	microtubule-based process	12	309	821	17583	0.83	-0.27	6.9E-01	7.0E-01
GO:0006955	immune response	25	309	1599	17583	0.89	-0.17	6.9E-01	7.1E-01
	developmental process involved								
GO:0003006	in reproduction	14	309	944	17583	0.84	-0.24	6.9E-01	7.1E-01
	multicellular organismal								
GO:0048871	homeostasis	8	309	581	17583	0.78	-0.35	7.0E-01	7.1E-01
GO:0030900	forebrain development	5	309	397	17583	0.72	-0.48	7.0E-01	7.2E-01
GO:0007267	cell-cell signaling	16	309	1077	17583	0.85	-0.24	7.1E-01	7.2E-01
GO:0007420	brain development	11	309	778	17583	0.80	-0.31	7.2E-01	7.3E-01
GO:0006518	peptide metabolic process	7	309	532	17583	0.75	-0.42	7.2E-01	7.3E-01
GO:0072359	circulatory system development	13	309	907	17583	0.82	-0.29	7.3E-01	7.4E-01
	central nervous system								
GO:0007417	development	15	309	1041	17583	0.82	-0.29	7.5E-01	7.6E-01
GO:0030003	cellular cation homeostasis	5	309	418	17583	0.68	-0.56	7.5E-01	7.6E-01
GO:0007507	heart development	7	309	555	17583	0.72	-0.48	7.6E-01	7.7E-01
GO:0034470	ncRNA processing	5	309	430	17583	0.66	-0.60	7.7E-01	7.8E-01
GO:0060429	epithelium development	15	309	1063	17583	0.80	-0.32	7.7E-01	7.8E-01
GO:0034330	cell junction organization	6	309	512	17583	0.67	-0.58	8.0E-01	8.1E-01
GO:0090304	nucleic acid metabolic process	34	309	2247	17583	0.86	-0.22	8.0E-01	8.1E-01
GO:0001944	vasculature development	6	309	525	17583	0.65	-0.62	8.2E-01	8.3E-01
GO:0007600	sensory perception	13	309	981	17583	0.75	-0.41	8.2E-01	8.3E-01
GO:0034660	ncRNA metabolic process	6	309	531	17583	0.64	-0.64	8.3E-01	8.4E-01
GO:0099536	synaptic signaling	5	309	464	17583	0.61	-0.71	8.3E-01	8.4E-01
GO:0007610	behavior	7	309	603	17583	0.66	-0.60	8.4E-01	8.4E-01
GO:0000003	reproduction	20	309	1435	17583	0.79	-0.33	8.4E-01	8.5E-01
GO:0098609	cell-cell adhesion	6	309	543	17583	0.63	-0.67	8.4E-01	8.5E-01
GO:0006508	proteolysis	17	309	1258	17583	0.77	-0.38	8.5E-01	8.5E-01
GO:0035295	tube development	11	309	876	17583	0.71	-0.48	8.5E-01	8.5E-01

GO:0006396	RNA processing	11	309	876	17583	0.71	-0.48	8.5E-01	8.5E-01
GO:0008283	cell population proliferation	8	309	707	17583	0.64	-0.64	8.8E-01	8.8E-01
GO:0022414	reproductive process	19	309	1425	17583	0.76	-0.40	8.8E-01	8.9E-01
GO:0001568	blood vessel development	5	309	504	17583	0.56	-0.82	8.8E-01	8.9E-01
GO:0070848	response to growth factor	5	309	506	17583	0.56	-0.83	8.8E-01	8.9E-01
GO:0016070	RNA metabolic process	22	309	1619	17583	0.77	-0.37	8.8E-01	8.9E-01
	chordate embryonic								
GO:0043009	development	7	309	651	17583	0.61	-0.71	8.9E-01	8.9E-01
	multicellular organismal								
GO:0048609	reproductive process	10	309	869	17583	0.65	-0.61	9.0E-01	9.1E-01
GO:0035239	tube morphogenesis	7	309	667	17583	0.60	-0.74	9.0E-01	9.1E-01
	embryo development ending in								
GO:0009792	birth or egg hatching	7	309	673	17583	0.59	-0.76	9.1E-01	9.1E-01
	G protein-coupled receptor								
GO:0007186	signaling pathway	15	309	1216	17583	0.70	-0.51	9.1E-01	9.2E-01
GO:0019953	sexual reproduction	10	309	885	17583	0.64	-0.64	9.1E-01	9.2E-01
	multicellular organism								
GO:0032504	reproduction	10	309	910	17583	0.63	-0.68	9.3E-01	9.3E-01
GO:0032501	multicellular organismal process	98	309	6337	17583	0.88	-0.18	9.4E-01	9.4E-01
GO:0010467	gene expression	29	309	2186	17583	0.75	-0.41	9.4E-01	9.5E-01
GO:0007283	spermatogenesis	5	309	592	17583	0.48	-1.06	9.5E-01	9.5E-01
GO:0007276	gamete generation	7	309	755	17583	0.53	-0.92	9.6E-01	9.6E-01
GO:0048232	male gamete generation	5	309	611	17583	0.47	-1.10	9.6E-01	9.6E-01
GO:0003008	system process	26	309	2054	17583	0.72	-0.47	9.6E-01	9.6E-01
GO:0002250	adaptive immune response	5	309	652	17583	0.44	-1.20	9.7E-01	9.8E-01
GO:0051606	detection of stimulus	5	309	676	17583	0.42	-1.25	9.8E-01	9.8E-01
GO:0050877	nervous system process	14	309	1447	17583	0.55	-0.86	9.9E-01	9.9E-01