Supplementary Figures

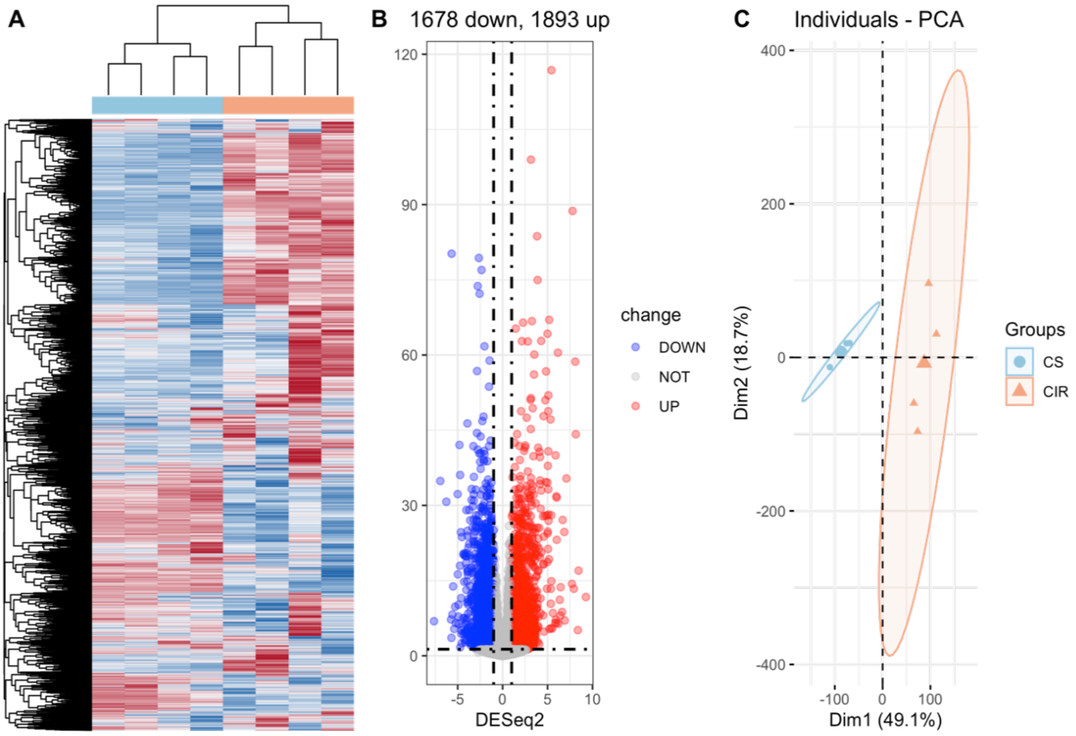


Figure S1 PCA plot(A), Heatmap (B) and Volcano plot(C)of 3571 mouse DEGs. In the volcano plots of DEGs, the horizontal axis represents the log2foldchange (CIR verse CS), the vertical axis represents the -log10(p-value) of DEGs. Colors represent different genes: Grey nodes represent genes without significantly different expression, red nodes represent up-regulated genes, and blue nodes represent down-regulated genes.

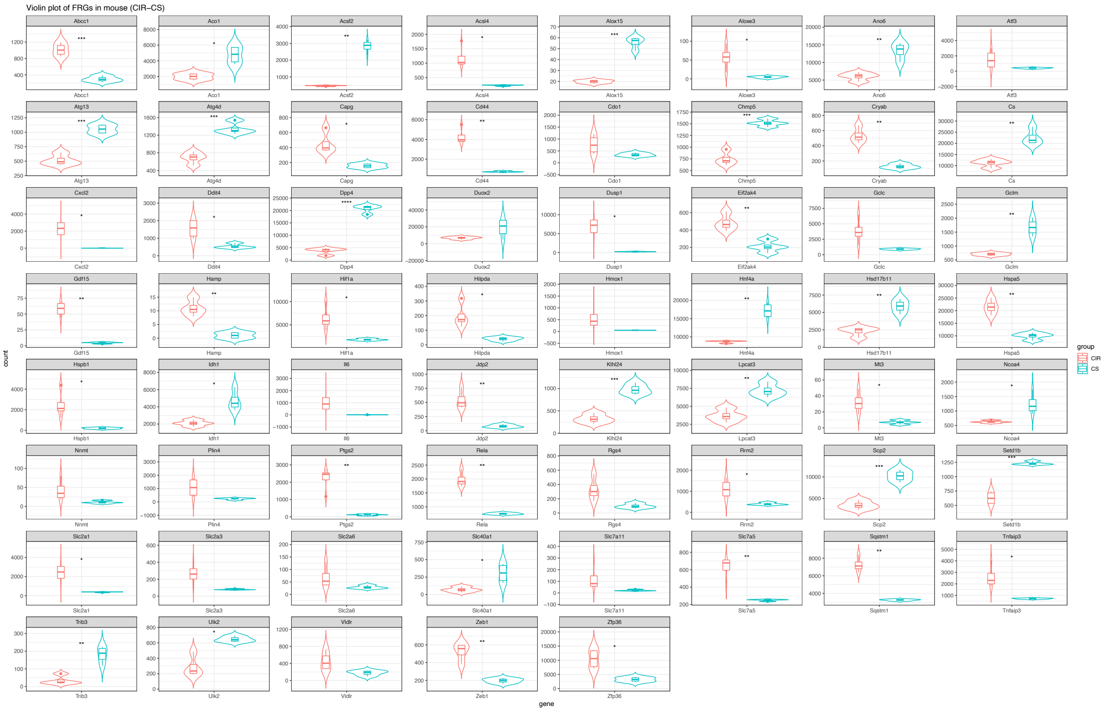


Figure S2 The violin plot of the FRGs between mouse intestinal I/R samples (CIR)and Sham samples (CS). Student's t-tests were utilized for the analysis between two groups (*p<0.05, **p<0.01, ***p<0.001, ***p<0.0001).

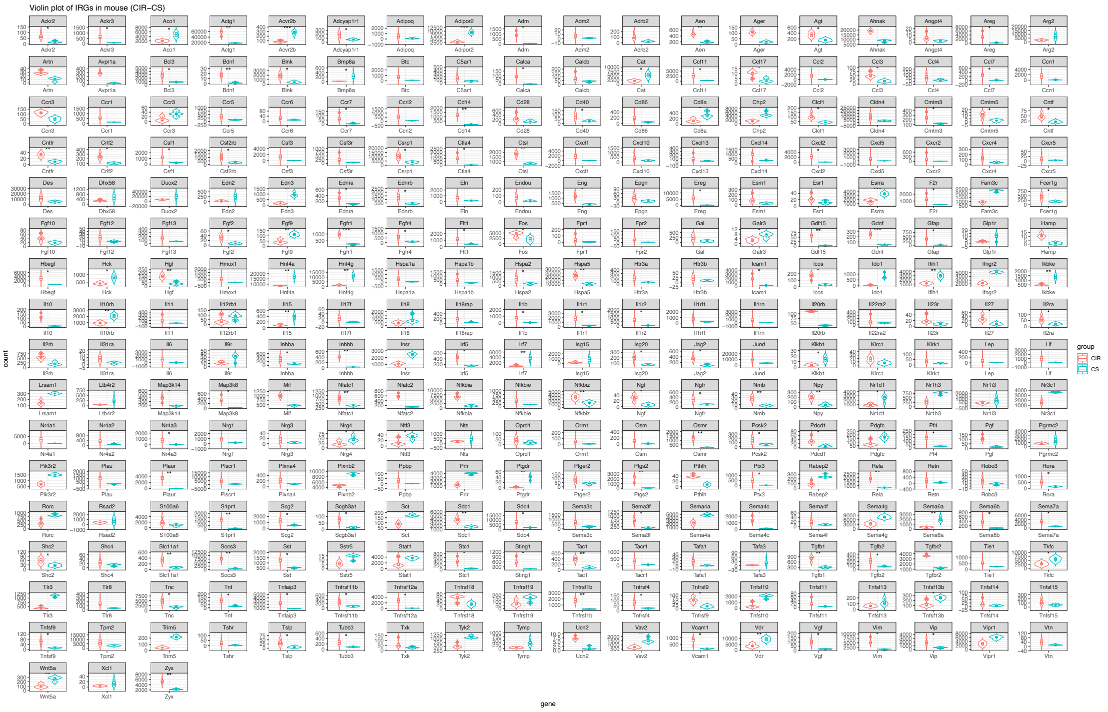
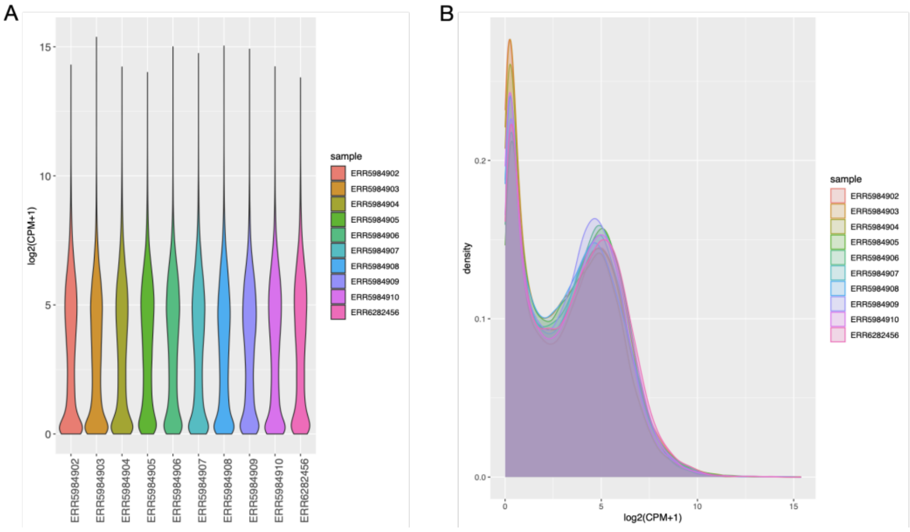


Figure S3 The violin plot of the IRGs between mouse intestinal I/R samples (CIR)and Sham samples (CS). Student's t-tests were utilized for the analysis between two groups (*$p<0.05$, **$p<0.01$, ***$p<0.001$, ***$p<0.0001$).



run_accession	Group
ERR5984902	A2
ERR6282456	A1
ERR5984903	A3
ERR5984904	A4
ERR5984905	A5
ERR5984906	C1
ERR5984907	C2
ERR5984908	C3
ERR5984909	C4
ERR5984910	C5

Figure S4 Violin plot(A) and density plot (B)of human samples datasets.

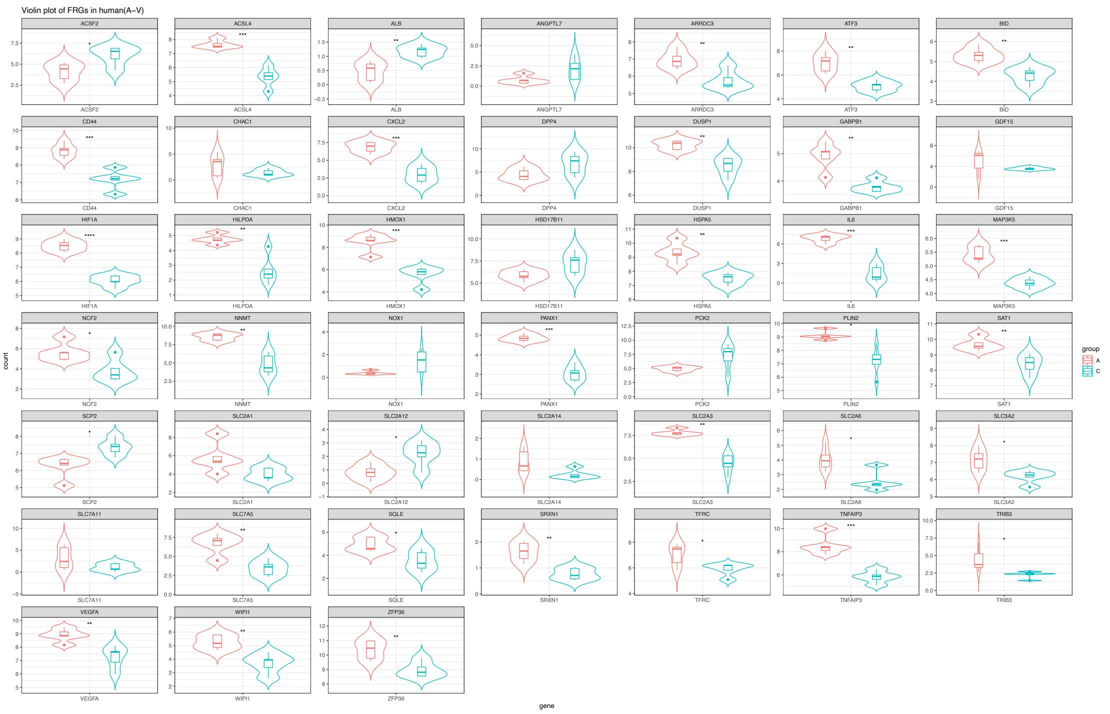


Figure S5 The violin plot of the FRGs between human intestinal I/R samples (A)and control samples(C). Student's t-tests were utilized for the analysis between two groups (*p<0.05, **p<0.01, ***p<0.001, ***p<0.0001).

Figure S6 The violin plot of the FRGs between human intestinal I/R samples (A)and control samples(C). Student's t-tests were utilized for the analysis between two groups (*p<0.05, **p<0.01, ***p<0.001, ***p<0.0001).

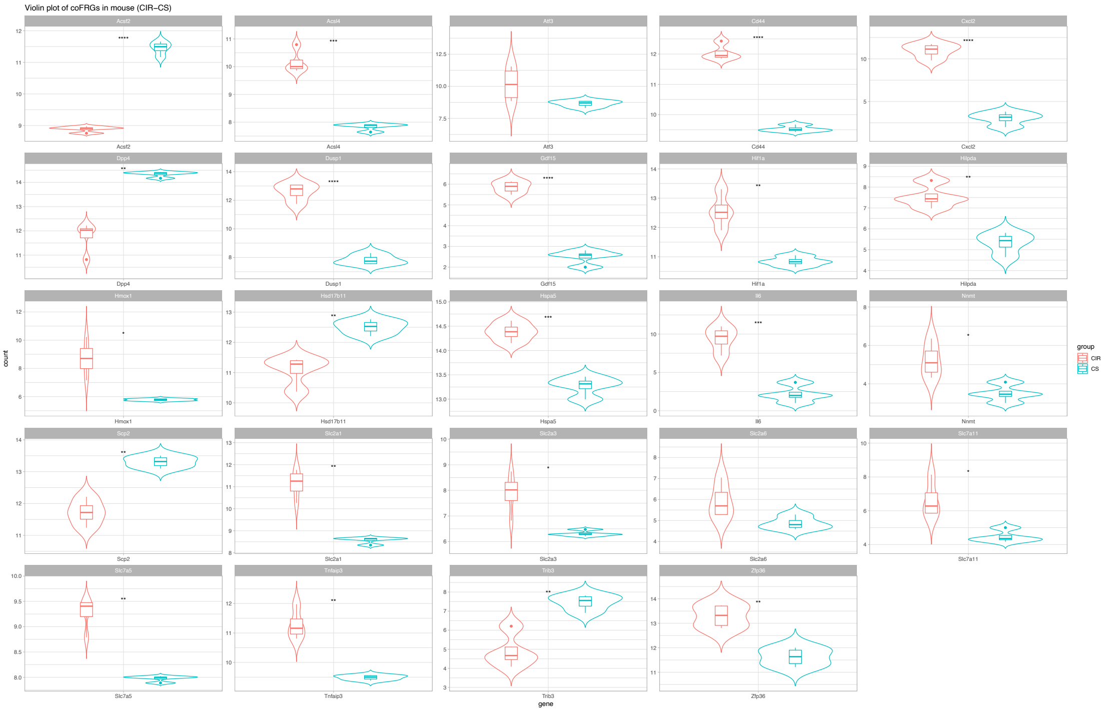


Figure S7 The violin plot of the coFRGs between mouse intestinal I/R samples (CIR)and Sham samples (CS). Student's t-tests were utilized for the analysis between two groups (*$p<0.05$, **$p<0.01$, ***$p<0.001$, ***$p<0.0001$).

Figure S8 The violin plot of the coIRGs between mouse intestinal I/R samples (CIR)and Sham samples (CS). Student's t-tests were utilized for the analysis between two groups (*p<0.05, **p<0.01, ***p<0.001, ***p<0.0001).

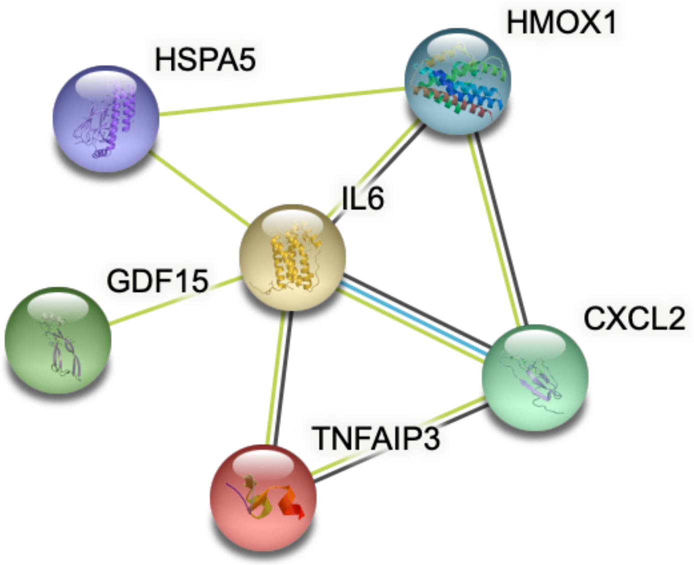


Figure S9 The Protein-protein interaction of the 6 hub genes (STRING).

Supplementary Tables

Table S1 3571 DEGs obtained from the 4 mice intestinal I/R injury samples and 4 sham samples

	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	change
Cd8a	227.5969	-1.4471	0.3390	-4.2683	0.0000	0.0001	DOWN
Ctsl	1290.2801	1.1249	0.1465	7.6769	0.0000	0.0000	UP
Fcer1g	295.2864	1.1507	0.2747	4.1890	0.0000	0.0001	UP
Hspa1a	249.8522	3.0017	0.5136	5.8444	0.0000	0.0000	UP
Hspa1b	315.4612	2.7424	0.5231	5.2427	0.0000	0.0000	UP
Hspa2	528.0201	1.8699	0.3681	5.0796	0.0000	0.0000	UP
Hspa5	15590.4584	1.0396	0.1319	7.8797	0.0000	0.0000	UP
Orm1	29.9014	3.0789	0.7494	4.1083	0.0000	0.0002	UP
Tnf	62.0875	1.8857	0.3764	5.0093	0.0000	0.0000	UP
Aen	334.2983	1.2905	0.1824	7.0758	0.0000	0.0000	UP

Isg20	127.7586	1.3356	0.2722	4.9059	0.0000	0.0000	UP
Bcl3	1794.9644	1.7614	0.2588	6.8057	0.0000	0.0000	UP
Duox2	12897.4764	-1.4778	0.4445	-3.3248	0.0009	0.0028	DOWN
Tlr3	799.7092	-1.4546	0.1214	-11.9811	0.0000	0.0000	DOWN
Ifih1	2092.9377	-1.4353	0.1990	-7.2124	0.0000	0.0000	DOWN
Trim5	134.8520	-2.2982	0.2166	-10.6115	0.0000	0.0000	DOWN
Ido1	427.1897	-4.2875	0.5384	-7.9631	0.0000	0.0000	DOWN
Gdf15	30.7772	3.5349	0.4410	8.0148	0.0000	0.0000	UP
Adipoq	316.6370	2.2755	0.8419	2.7027	0.0069	0.0169	UP
Stat1	2772.7339	-1.1007	0.4070	-2.7043	0.0068	0.0168	DOWN
Socs3	4125.9661	3.4227	0.2568	13.3304	0.0000	0.0000	UP
Tnfsf10	1226.0547	-2.3448	0.5273	-4.4469	0.0000	0.0000	DOWN
Il15	230.5672	-2.1466	0.2655	-8.0847	0.0000	0.0000	DOWN
Cd40	55.7655	1.3622	0.3393	4.0152	0.0001	0.0002	UP
Zyx	3782.3772	1.2005	0.1989	6.0354	0.0000	0.0000	UP
Ikbke	946.8417	-1.4938	0.1602	-9.3267	0.0000	0.0000	DOWN
Isg15	570.8959	-2.0794	0.5153	-4.0356	0.0001	0.0002	DOWN
Dhx58	429.2746	-1.0568	0.3209	-3.2928	0.0010	0.0031	DOWN
Tnfaip3	1622.8784	1.7687	0.2201	8.0374	0.0000	0.0000	UP
F2r	912.8571	1.3448	0.2131	6.3095	0.0000	0.0000	UP
Eln	408.9123	1.6781	0.4354	3.8541	0.0001	0.0004	UP
Il27	18.2204	2.4422	0.6700	3.6449	0.0003	0.0009	UP
Lep	44.0533	6.4205	1.1195	5.7350	0.0000	0.0000	UP
Klkb1	9.6089	-1.8424	0.5788	-3.1833	0.0015	0.0043	DOWN
Csrp1	6886.7479	1.5611	0.2602	5.9999	0.0000	0.0000	UP
Irf5	294.2020	1.4688	0.1865	7.8771	0.0000	0.0000	UP
Ccr6	19.3927	1.3442	0.6079	2.2113	0.0270	0.0551	UP
Tlr8	108.2786	1.8988	0.3562	5.3315	0.0000	0.0000	UP
Wnt5a	185.7663	-1.4883	0.2747	-5.4176	0.0000	0.0000	DOWN
Tyk2	825.3344	-1.0464	0.1512	-6.9223	0.0000	0.0000	DOWN
Tpm2	4704.9575	1.1781	0.3252	3.6222	0.0003	0.0010	UP
Ahnak	13851.4570	1.0742	0.1344	7.9921	0.0000	0.0000	UP
Fgf2	19.2054	2.1298	0.4987	4.2707	0.0000	0.0001	UP
Tkfc	4367.0719	-1.0821	0.3361	-3.2196	0.0013	0.0039	DOWN
Nfkbiz	2298.6601	1.0427	0.2926	3.5635	0.0004	0.0013	UP
Robo3	12.6593	1.2541	0.6031	2.0796	0.0376	0.0734	UP
Slc11a1	203.6359	2.0600	0.2638	7.8087	0.0000	0.0000	UP
Sting1	407.4664	1.7812	0.2500	7.1242	0.0000	0.0000	UP
Des	8465.1672	1.2615	0.3116	4.0485	0.0001	0.0002	UP
Ccl4	45.3456	1.8442	0.5730	3.2186	0.0013	0.0039	UP

Tnfsf11	12.5704	2.5994	0.7400	3.5126	0.0004	0.0015	UP
Klrk1	29.5223	1.4086	0.4632	3.0412	0.0024	0.0066	UP
Jund	6721.6621	1.4547	0.3706	3.9250	0.0001	0.0003	UP
Cldn4	6187.9170	1.7802	0.3692	4.8221	0.0000	0.0000	UP
Irf7	2415.3203	-2.0771	0.2606	-7.9691	0.0000	0.0000	DOWN
Il18	649.7685	-1.2620	0.5021	-2.5134	0.0120	0.0273	DOWN
Rela	1358.0706	1.3273	0.1449	9.1622	0.0000	0.0000	UP
Ptx3	250.2602	6.0073	0.5079	11.8274	0.0000	0.0000	UP
Ptgs2	1136.5882	4.1587	0.3127	13.2998	0.0000	0.0000	UP
Cd14	644.1302	3.2562	0.1876	17.3580	0.0000	0.0000	UP
Hmox1	305.1982	3.3243	0.5391	6.1665	0.0000	0.0000	UP
Hgf	93.0960	1.6682	0.3481	4.7919	0.0000	0.0000	UP
Plscr1	3054.1144	2.5734	0.4675	5.5051	0.0000	0.0000	UP
Rsad2	587.1257	-1.0783	0.5172	-2.0851	0.0371	0.0725	DOWN
Pdcd1	21.1244	2.4063	0.5568	4.3215	0.0000	0.0001	UP
Pcsk2	108.1203	1.5483	0.3273	4.7303	0.0000	0.0000	UP
Arg2	4990.1736	-1.8455	0.4158	-4.4381	0.0000	0.0000	DOWN
Vtn	27.4525	1.3735	0.4883	2.8128	0.0049	0.0125	UP
Vim	3442.4428	1.9946	0.1899	10.5063	0.0000	0.0000	UP
Vcam1	468.6553	2.1333	0.2912	7.3251	0.0000	0.0000	UP
Gfap	205.5190	4.9939	0.4028	12.3966	0.0000	0.0000	UP
Ager	65.0550	2.1622	0.2832	7.6359	0.0000	0.0000	UP
Actg1	37525.2261	1.5157	0.1884	8.0452	0.0000	0.0000	UP
Aco1	3419.0380	-1.3362	0.2270	-5.8872	0.0000	0.0000	DOWN
Ccl17	6.5598	1.5491	0.6772	2.2875	0.0222	0.0466	UP
Ccr3	21.4437	-1.8672	0.7368	-2.5341	0.0113	0.0259	DOWN
Ackr2	43.5586	1.9654	0.3828	5.1346	0.0000	0.0000	UP
Ccr7	40.6873	2.9575	0.4896	6.0404	0.0000	0.0000	UP
Ccr8	13.2033	3.2619	0.9892	3.2975	0.0010	0.0030	UP
Ccl2	727.9533	6.6747	0.6105	10.9336	0.0000	0.0000	UP
Ccl7	124.3371	5.3646	0.7103	7.5526	0.0000	0.0000	UP
Ccl3	34.1382	1.5163	0.3601	4.2111	0.0000	0.0001	UP
Ccl11	1471.8159	2.9882	0.3715	8.0430	0.0000	0.0000	UP
Ccr5	227.3287	1.3817	0.3723	3.7108	0.0002	0.0008	UP
Xcl1	10.0805	-1.8660	0.7105	-2.6261	0.0086	0.0206	DOWN
Ccr1	371.1873	2.1960	0.3301	6.6523	0.0000	0.0000	UP
Cxcl1	867.7628	8.1380	0.5787	14.0631	0.0000	0.0000	UP
Cxcl10	301.3703	1.5189	0.5191	2.9261	0.0034	0.0091	UP
Cxcr4	91.3036	1.5546	0.3380	4.6000	0.0000	0.0000	UP
Cxcl2	1109.5094	8.0792	0.4970	16.2544	0.0000	0.0000	UP

Tafa3	15.3327	-2.8670	0.7634	-3.7554	0.0002	0.0006	DOWN
Tafa1	10.6106	2.0544	0.6214	3.3060	0.0009	0.0029	UP
Il6	501.4205	7.7089	0.9835	7.8384	0.0000	0.0000	UP
Il1b	351.6263	4.0513	0.4190	9.6682	0.0000	0.0000	UP
Il13	3.5445	-3.0863	1.2798	-2.4116	0.0159	0.0348	DOWN
Il10	57.4555	4.5759	0.4480	10.2137	0.0000	0.0000	UP
Mif	724.1155	1.0941	0.1446	7.5673	0.0000	0.0000	UP
Ptgdr	21.4964	-4.6161	0.6616	-6.9771	0.0000	0.0000	DOWN
Cd86	130.0022	1.8288	0.3392	5.3921	0.0000	0.0000	UP
Hck	630.0341	-1.0380	0.2352	-4.4140	0.0000	0.0000	DOWN
Vdr	6650.4872	-1.4275	0.2697	-5.2933	0.0000	0.0000	DOWN
Txk	45.5208	1.0923	0.4407	2.4786	0.0132	0.0297	UP
Blnk	1192.6916	1.9232	0.3304	5.8203	0.0000	0.0000	UP
Vav2	1157.7942	-1.1699	0.1885	-6.2064	0.0000	0.0000	DOWN
Chp2	3212.4309	-2.1076	0.3611	-5.8369	0.0000	0.0000	DOWN
Nfatc1	593.3243	1.1259	0.1548	7.2743	0.0000	0.0000	UP
Nfatc2	367.2020	2.0003	0.1815	11.0196	0.0000	0.0000	UP
Cxcl13	65.4217	1.8257	0.5461	3.3433	0.0008	0.0026	UP
Cxcl14	591.8227	1.5033	0.4364	3.4449	0.0006	0.0019	UP
Cxcl3	38.2962	6.6168	1.1001	6.0146	0.0000	0.0000	UP
Cxcl5	373.1196	5.5953	0.9431	5.9328	0.0000	0.0000	UP
Ccn1	792.7650	3.7261	0.4527	8.2308	0.0000	0.0000	UP
Edn2	141.1783	-2.7715	0.5804	-4.7748	0.0000	0.0000	DOWN
Edn3	557.3270	-2.6418	0.3187	-8.2891	0.0000	0.0000	DOWN
Fgf10	28.3103	1.1197	0.4036	2.7738	0.0055	0.0139	UP
Pf4	81.0669	2.4464	0.3389	7.2183	0.0000	0.0000	UP
Plau	568.1669	1.9690	0.4330	4.5470	0.0000	0.0000	UP
Ppbp	16.6601	5.3876	1.1547	4.6658	0.0000	0.0000	UP
Sema3c	511.3114	1.6340	0.3519	4.6428	0.0000	0.0000	UP
Sema3f	435.3304	1.8007	0.2145	8.3964	0.0000	0.0000	UP
Sema4a	3613.2810	-1.1522	0.2104	-5.4760	0.0000	0.0000	DOWN
Sema4c	792.2646	3.1488	0.2700	11.6606	0.0000	0.0000	UP
Sema4f	14.3754	1.3822	0.5401	2.5594	0.0105	0.0243	UP
Sema4g	5591.5803	-1.3154	0.2156	-6.0995	0.0000	0.0000	DOWN
Sema6a	1200.4562	-2.4929	0.2545	-9.7958	0.0000	0.0000	DOWN
Sema6b	246.9383	2.0985	0.2855	7.3499	0.0000	0.0000	UP
Sema7a	2107.6893	2.0205	0.3569	5.6612	0.0000	0.0000	UP
Tnc	3189.5424	1.4892	0.2965	5.0225	0.0000	0.0000	UP
Tymp	221.5310	-2.8505	0.5345	-5.3329	0.0000	0.0000	DOWN
C5ar1	117.0653	1.7913	0.3793	4.7231	0.0000	0.0000	UP

Ccrl2	300.0464	2.8836	0.3854	7.4828	0.0000	0.0000	UP
Cxcr5	8.9734	1.9975	0.8843	2.2587	0.0239	0.0497	UP
Ackr3	375.5374	2.6985	0.2722	9.9135	0.0000	0.0000	UP
Ednra	215.2956	1.5370	0.2937	5.2335	0.0000	0.0000	UP
Ednrb	848.5889	1.6171	0.2192	7.3789	0.0000	0.0000	UP
Fpr1	27.5245	2.9024	0.8818	3.2916	0.0010	0.0031	UP
Fpr2	25.4664	3.9570	0.8139	4.8618	0.0000	0.0000	UP
Cxcr2	97.0042	5.2049	1.1353	4.5847	0.0000	0.0000	UP
Ltb4r2	146.4179	-3.0707	0.5180	-5.9284	0.0000	0.0000	DOWN
Plaur	1692.0029	5.4275	0.2355	23.0473	0.0000	0.0000	UP
Plxna4	149.7609	1.2003	0.3204	3.7465	0.0002	0.0007	UP
Plxnb2	6925.4316	-1.0110	0.0964	-10.4874	0.0000	0.0000	DOWN
Adm	465.1429	4.1666	0.3340	12.4732	0.0000	0.0000	UP
Adm2	3.8037	2.6914	1.3152	2.0464	0.0407	0.0785	UP
Agt	251.6757	1.0058	0.2340	4.2984	0.0000	0.0001	UP
Areg	1686.0722	4.9998	0.4828	10.3553	0.0000	0.0000	UP
Artn	19.6012	1.4555	0.4432	3.2839	0.0010	0.0032	UP
Bdnf	9.0312	3.7069	0.7983	4.6437	0.0000	0.0000	UP
Bmp8a	130.2823	-4.3890	0.4670	-9.3981	0.0000	0.0000	DOWN
Btc	431.6760	2.9398	0.4651	6.3201	0.0000	0.0000	UP
Calca	45.2108	6.4524	0.8438	7.6472	0.0000	0.0000	UP
Calcb	63.3434	1.1707	0.4333	2.7014	0.0069	0.0169	UP
Cat	3684.0298	-1.5429	0.2793	-5.5234	0.0000	0.0000	DOWN
Clcf1	73.3329	1.3816	0.2795	4.9430	0.0000	0.0000	UP
Cmtm3	187.3383	1.0314	0.1964	5.2517	0.0000	0.0000	UP
Cmtm5	6.2389	2.1545	0.7964	2.7052	0.0068	0.0168	UP
Cntf	34.3813	1.0826	0.3100	3.4917	0.0005	0.0016	UP
Csf1	730.6519	2.2143	0.3281	6.7492	0.0000	0.0000	UP
Csf3	613.9188	8.4430	0.9851	8.5709	0.0000	0.0000	UP
Epgn	17.0214	2.3521	0.7489	3.1408	0.0017	0.0049	UP
Ereg	3109.5859	5.0281	0.3869	12.9956	0.0000	0.0000	UP
Esm1	64.2112	1.9521	0.4934	3.9566	0.0001	0.0003	UP
Fam3c	1617.6622	-1.4279	0.1371	-10.4118	0.0000	0.0000	DOWN
Fgf12	11.8019	1.5921	0.6091	2.6137	0.0090	0.0212	UP
Fgf13	108.1787	1.3187	0.3435	3.8394	0.0001	0.0005	UP
Fgf9	80.1851	-1.4580	0.2733	-5.3337	0.0000	0.0000	DOWN
Gal	149.4138	1.8420	0.5054	3.6443	0.0003	0.0009	UP
Gdnf	148.0060	2.4183	0.2048	11.8063	0.0000	0.0000	UP
Hamp	5.9230	3.3884	0.9240	3.6669	0.0002	0.0009	UP
Hbegf	1751.8931	3.1319	0.2918	10.7324	0.0000	0.0000	UP

Il11	67.4325	3.4900	0.6793	5.1376	0.0000	0.0000	UP
Il17f	10.0814	3.3420	0.8862	3.7710	0.0002	0.0006	UP
Il1rn	447.7563	3.7498	0.6035	6.2134	0.0000	0.0000	UP
Inhba	195.4384	1.7741	0.3552	4.9953	0.0000	0.0000	UP
Inhbb	218.6645	3.5163	0.2137	16.4520	0.0000	0.0000	UP
Jag2	222.1416	1.7907	0.2988	5.9927	0.0000	0.0000	UP
Lif	550.8291	2.8882	0.4806	6.0090	0.0000	0.0000	UP
Lrsam1	224.0254	-1.1719	0.1721	-6.8111	0.0000	0.0000	DOWN
Ngf	18.4199	2.1160	0.5164	4.0979	0.0000	0.0002	UP
Nmb	17.1129	1.7814	0.4379	4.0679	0.0000	0.0002	UP
Ccn3	79.2027	1.1663	0.2974	3.9220	0.0001	0.0003	UP
Npy	116.8891	2.1337	0.3590	5.9432	0.0000	0.0000	UP
Nrg1	539.9510	2.0218	0.4463	4.5300	0.0000	0.0000	UP
Nrg3	8.8892	1.5139	0.7350	2.0598	0.0394	0.0764	UP
Nrg4	33.9914	-1.1272	0.3902	-2.8890	0.0039	0.0101	DOWN
Ntf3	23.6082	-1.4861	0.5759	-2.5805	0.0099	0.0231	DOWN
Nts	323.6583	-1.2322	0.5571	-2.2117	0.0270	0.0551	DOWN
Osm	61.3002	4.5065	0.7830	5.7552	0.0000	0.0000	UP
Endou	47.7751	2.1062	0.5093	4.1358	0.0000	0.0002	UP
Pdgfc	126.2196	-1.1134	0.3008	-3.7012	0.0002	0.0008	DOWN
Pgf	61.4975	2.6061	0.3035	8.5872	0.0000	0.0000	UP
Pthlh	23.4649	2.3045	0.4524	5.0939	0.0000	0.0000	UP
Rabep2	179.7080	-1.4699	0.2929	-5.0182	0.0000	0.0000	DOWN
Retn	108.4880	2.1428	0.7355	2.9135	0.0036	0.0095	UP
S100a6	1546.3193	1.2713	0.4175	3.0449	0.0023	0.0065	UP
Scg2	875.1652	1.3627	0.2618	5.2045	0.0000	0.0000	UP
Scgb3a1	44.4016	2.0936	0.3456	6.0579	0.0000	0.0000	UP
Sct	130.9670	-1.0906	0.1755	-6.2149	0.0000	0.0000	DOWN
Sst	890.9748	1.1284	0.1778	6.3471	0.0000	0.0000	UP
Stc1	241.3811	3.1377	0.3318	9.4577	0.0000	0.0000	UP
Tac1	242.1234	2.0739	0.2613	7.9358	0.0000	0.0000	UP
Tgfb1	545.7158	1.2942	0.1906	6.7917	0.0000	0.0000	UP
Tgfb2	142.0968	1.5772	0.2767	5.7009	0.0000	0.0000	UP
Tnfrsf11b	180.5629	1.9486	0.3929	4.9589	0.0000	0.0000	UP
Tnfsf13	94.8897	-1.0898	0.3507	-3.1072	0.0019	0.0054	DOWN
Tnfsf13b	191.6063	-1.0701	0.2804	-3.8167	0.0001	0.0005	DOWN
Tnfsf14	16.4798	1.8377	0.7586	2.4225	0.0154	0.0340	UP
Tnfsf15	88.5971	1.2334	0.4830	2.5538	0.0107	0.0247	UP
Tnfsf9	37.5178	2.1104	0.4092	5.1572	0.0000	0.0000	UP
Tslp	20.6206	2.2525	0.5689	3.9593	0.0001	0.0003	UP

Ucn2	4.3211	2.2037	0.8315	2.6502	0.0080	0.0193	UP
Vgf	58.6388	2.7196	0.3785	7.1860	0.0000	0.0000	UP
Vip	1202.1880	1.9179	0.3482	5.5086	0.0000	0.0000	UP
Acvr2b	183.1633	-1.8561	0.2115	-8.7763	0.0000	0.0000	DOWN
Adcyap1r1	119.0527	1.3329	0.3393	3.9279	0.0001	0.0003	UP
Adipor2	6206.3398	-1.6934	0.1287	-13.1572	0.0000	0.0000	DOWN
Adrb2	69.5692	1.8195	0.3967	4.5866	0.0000	0.0000	UP
Angpt4	4.8125	1.6776	0.8083	2.0754	0.0379	0.0740	UP
Avpr1a	165.7661	3.1083	0.2609	11.9142	0.0000	0.0000	UP
Cntfr	20.6249	1.7465	0.4083	4.2774	0.0000	0.0001	UP
Crlf2	174.0412	1.1630	0.2054	5.6615	0.0000	0.0000	UP
Csf2rb	656.8267	1.9821	0.3168	6.2576	0.0000	0.0000	UP
Csf3r	176.7796	2.5959	0.5258	4.9368	0.0000	0.0000	UP
Eng	784.5547	1.5220	0.1739	8.7501	0.0000	0.0000	UP
Esr1	17.2103	1.0446	0.4858	2.1503	0.0315	0.0630	UP
Esrra	2619.0510	-1.1208	0.2081	-5.3865	0.0000	0.0000	DOWN
Fgfr1	604.6687	1.8644	0.1706	10.9291	0.0000	0.0000	UP
Fgfr4	336.6915	2.3910	0.4348	5.4986	0.0000	0.0000	UP
Flt1	807.4785	1.5668	0.2523	6.2089	0.0000	0.0000	UP
Galr3	4.9462	-1.4399	0.7345	-1.9602	0.0500	0.0933	DOWN
Glp1r	6.3318	-2.2289	0.8395	-2.6550	0.0079	0.0191	DOWN
Hnf4a	13060.4574	-1.0576	0.1073	-9.8598	0.0000	0.0000	DOWN
Hnf4g	6758.1199	-2.9911	0.2466	-12.1307	0.0000	0.0000	DOWN
Htr3a	108.5433	1.5708	0.3346	4.6951	0.0000	0.0000	UP
Htr3b	15.0147	1.2297	0.6047	2.0336	0.0420	0.0806	UP
Ifngr2	3702.9410	-1.2968	0.1511	-8.5844	0.0000	0.0000	DOWN
Il10rb	1529.5440	-1.2298	0.2259	-5.4428	0.0000	0.0000	DOWN
Il12rb1	64.7338	-1.0981	0.5573	-1.9704	0.0488	0.0914	DOWN
Il2rb	378.9121	1.3957	0.3080	4.5316	0.0000	0.0000	UP
Il18rap	109.2781	1.9197	0.4540	4.2283	0.0000	0.0001	UP
Il1r1	1034.1220	2.9434	0.2913	10.1045	0.0000	0.0000	UP
Il1r2	407.4783	4.2911	0.3547	12.0995	0.0000	0.0000	UP
Il1rl1	491.7658	1.8832	0.5240	3.5936	0.0003	0.0011	UP
Il20rb	74.5648	1.5068	0.2068	7.2847	0.0000	0.0000	UP
Il22ra2	93.2288	1.1852	0.5046	2.3489	0.0188	0.0405	UP
Il23r	14.0864	1.5609	0.5634	2.7703	0.0056	0.0140	UP
Il2ra	39.5191	1.5007	0.3918	3.8301	0.0001	0.0005	UP
Il31ra	5.0028	1.9505	0.8614	2.2644	0.0235	0.0490	UP
Il9r	20.3517	-1.3699	0.4849	-2.8250	0.0047	0.0121	DOWN
Insr	1782.0276	-1.2318	0.1436	-8.5773	0.0000	0.0000	DOWN

Ngfr	205.1137	1.5135	0.2780	5.4445	0.0000	0.0000	UP
Nr1d1	1687.8695	-1.4853	0.3308	-4.4903	0.0000	0.0000	DOWN
Nr1h3	532.5942	-1.5086	0.2474	-6.0979	0.0000	0.0000	DOWN
Nr1i3	584.6145	-1.5333	0.4922	-3.1149	0.0018	0.0053	DOWN
Nr3c1	2659.1901	-1.2011	0.1577	-7.6144	0.0000	0.0000	DOWN
Nr4a1	1345.3037	4.5399	0.5112	8.8804	0.0000	0.0000	UP
Nr4a2	224.9731	1.7426	0.3996	4.3607	0.0000	0.0001	UP
Nr4a3	403.6485	3.9691	0.3918	10.1304	0.0000	0.0000	UP
Oprd1	28.2635	1.2631	0.5998	2.1060	0.0352	0.0694	UP
Osmr	707.7684	2.4932	0.2197	11.3503	0.0000	0.0000	UP
Pgrmc2	1235.2524	-1.0646	0.3207	-3.3196	0.0009	0.0028	DOWN
Prlr	2619.0739	-1.8102	0.1804	-10.0355	0.0000	0.0000	DOWN
Ptger2	59.3093	1.0663	0.3791	2.8126	0.0049	0.0125	UP
Rora	374.1600	1.8971	0.2721	6.9734	0.0000	0.0000	UP
Rorc	608.2115	-1.3224	0.2997	-4.4130	0.0000	0.0000	DOWN
S1pr1	655.4066	2.9328	0.2487	11.7913	0.0000	0.0000	UP
Sdc1	2816.8532	1.1152	0.1784	6.2515	0.0000	0.0000	UP
Sdc4	5282.1558	1.9142	0.2847	6.7245	0.0000	0.0000	UP
Sstr5	9.9927	-1.2578	0.5217	-2.4108	0.0159	0.0349	DOWN
Tacr1	189.1738	2.3210	0.4260	5.4488	0.0000	0.0000	UP
Tgfbr2	2425.1315	1.4596	0.0851	17.1590	0.0000	0.0000	UP
Tie1	397.1344	1.3349	0.2636	5.0650	0.0000	0.0000	UP
Tnfrsf12a	1399.3043	4.5505	0.3109	14.6378	0.0000	0.0000	UP
Tnfrsf18	38.4578	1.1907	0.4095	2.9078	0.0036	0.0096	UP
Tnfrsf19	117.5084	-1.0222	0.3544	-2.8845	0.0039	0.0103	DOWN
Tnfrsf1b	1041.5165	2.3037	0.2040	11.2921	0.0000	0.0000	UP
Tnfrsf4	51.5370	1.8572	0.3015	6.1591	0.0000	0.0000	UP
Tnfrsf9	39.0478	2.0438	0.4967	4.1145	0.0000	0.0002	UP
Tshr	16.5057	2.5312	0.8009	3.1602	0.0016	0.0046	UP
Tubb3	175.7552	1.4654	0.2929	5.0027	0.0000	0.0000	UP
Vipr1	4513.8981	-1.1301	0.2608	-4.3328	0.0000	0.0001	DOWN
Klrc1	11.6275	1.3909	0.5992	2.3214	0.0203	0.0432	UP
Icam1	1026.8552	3.2805	0.3443	9.5293	0.0000	0.0000	UP
Pik3r2	1129.2873	-1.1951	0.1341	-8.9091	0.0000	0.0000	DOWN
Shc2	41.6453	1.0496	0.3549	2.9575	0.0031	0.0084	UP
Shc4	20.0969	1.0319	0.4943	2.0876	0.0368	0.0721	UP
Fos	3204.6385	1.0598	0.3947	2.6852	0.0072	0.0176	UP
Nfkbia	3749.1397	2.3695	0.2555	9.2736	0.0000	0.0000	UP
Nfkbie	254.2081	1.5590	0.2904	5.3680	0.0000	0.0000	UP
Cd28	198.4327	1.1140	0.3791	2.9387	0.0033	0.0088	UP

Icos	96.2708	2.3271	0.2887	8.0595	0.0000	0.0000	UP
Map3k8	195.7764	3.3398	0.3212	10.3983	0.0000	0.0000	UP
Map3k14	281.8035	1.0699	0.2177	4.9139	0.0000	0.0000	UP
Ctla4	554.6045	5.0836	0.3328	15.2753	0.0000	0.0000	UP

Table S2 61 FRGs in mice after intestinal ischemia/reperfusion

Genes	log2FoldChange	pvalue	padj	change
Cs	-1.0861721	2.31E-09	2.14E-08	DOWN
Acsf2	-2.6450407	4.40E-80	1.17E-76	DOWN
Duox2	-1.4777547	0.00088474	0.00278425	DOWN
Scp2	-1.645005	6.34E-17	1.76E-15	DOWN
Acsl4	2.31805973	1.20E-19	4.40E-18	UP
Lpcat3	-1.0311657	8.37E-08	5.92E-07	DOWN
Hmox1	3.32433602	6.98E-10	7.11E-09	UP
Ncoa4	-1.0684909	4.98E-06	2.55E-05	DOWN
Alox15	-1.5687421	1.48E-08	1.21E-07	DOWN
Aloxe3	3.60880522	4.98E-08	3.69E-07	UP
Aco1	-1.3361637	3.93E-09	3.51E-08	DOWN
Atg4d	-1.0397795	8.31E-09	7.08E-08	DOWN
Atg13	-1.1055191	3.03E-20	1.20E-18	DOWN
Ulk2	-1.2744868	7.09E-07	4.24E-06	DOWN
Zeb1	1.34878272	2.02E-13	3.50E-12	UP
Dpp4	-2.5600692	4.89E-21	2.15E-19	DOWN
Cdo1	1.08233565	0.00143363	0.0042611	UP
Abcc1	1.7203088	4.81E-15	1.04E-13	UP
Hilpda	2.20899272	9.55E-10	9.49E-09	UP
Hif1a	1.75107446	7.14E-09	6.15E-08	UP
Ano6	-1.2093019	2.40E-10	2.63E-09	DOWN
Tnfaip3	1.76869422	9.18E-16	2.20E-14	UP
Atf3	1.83108078	0.00024854	0.00088936	UP
Idh1	-1.2357928	4.29E-08	3.23E-07	DOWN
Ptgs2	4.15867504	2.32E-40	5.70E-38	UP
Dusp1	4.74878517	1.04E-51	5.33E-49	UP
Mt3	2.12378104	4.09E-05	0.00017502	UP
Slc7a11	2.47986486	5.90E-06	2.98E-05	UP
Ddit4	1.45603412	5.63E-06	2.85E-05	UP
Jdp2	2.66335779	2.22E-22	1.10E-20	UP
Vldlr	1.32224035	0.00080661	0.00256112	UP
Slc7a5	1.2541165	7.03E-11	8.42E-10	UP

Klhl24	-1.6879971	5.31E-15	1.15E-13	DOWN
Trib3	-2.4521652	1.26E-07	8.57E-07	DOWN
Gdf15	3.53491871	1.10E-15	2.63E-14	UP
Rgs4	1.71372565	8.06E-06	3.97E-05	UP
Il6	7.70891185	4.56E-15	9.96E-14	UP
Cxcl2	8.07921167	2.08E-59	1.44E-56	UP
Rela	1.3273225	5.08E-20	1.95E-18	UP
Hsd17b11	-1.4613955	1.20E-09	1.17E-08	DOWN
Setd1b	-1.0379167	5.14E-16	1.28E-14	DOWN
Slc40a1	-2.2219733	1.45E-07	9.82E-07	DOWN
Hamp	3.38839342	0.0002455	0.00088026	UP
Hspb1	3.5894978	8.06E-20	3.03E-18	UP
Slc2a1	2.62267224	9.41E-16	2.25E-14	UP
Slc2a3	1.68484181	6.32E-06	3.17E-05	UP
Slc2a6	1.14121636	0.00706668	0.01725316	UP
Eif2ak4	1.15054431	8.46E-06	4.15E-05	UP
Nnmt	1.8769784	0.00025109	0.00089652	UP
Plin4	2.13824381	2.62E-06	1.41E-05	UP
Rrm2	1.4624116	2.20E-06	1.20E-05	UP
Capg	1.47037955	1.06E-07	7.32E-07	UP
Hnf4a	-1.0576266	6.22E-23	3.28E-21	DOWN
Gclc	2.0408031	8.94E-08	6.30E-07	UP
Sqstm1	1.09298194	1.04E-13	1.87E-12	UP
Hspa5	1.0396077	3.28E-15	7.33E-14	UP
Cd44	2.47558298	2.87E-42	8.65E-40	UP
Zfp36	1.60890505	1.09E-08	9.07E-08	UP
Chmp5	-1.1037975	1.85E-18	6.10E-17	DOWN
Gclm	-1.323224	8.73E-15	1.84E-13	DOWN
Cryab	2.01030589	2.61E-17	7.58E-16	UP

Table S3 294 IRGs in mice after intestinal ischemia/reperfusion

Genes	log2FoldChange	pvalue	padj	change
Cd8a	-1.447108	1.97E-05	8.97E-05	DOWN
Ctsl	1.12489734	1.63E-14	3.31E-13	UP
Fcer1g	1.1507313	2.80E-05	0.00012365	UP
Hspa1a	3.00172898	5.08E-09	4.46E-08	UP
Hspa1b	2.74237231	1.58E-07	1.06E-06	UP
Hspa2	1.86986864	3.78E-07	2.37E-06	UP
Hspa5	1.0396077	3.28E-15	7.33E-14	UP

Orm1	3.07893717	3.99E-05	0.00017093	UP
Tnf	1.88567287	5.46E-07	3.33E-06	UP
Aen	1.29053251	1.49E-12	2.28E-11	UP
Isg20	1.33556543	9.30E-07	5.44E-06	UP
Bcl3	1.76135837	1.01E-11	1.38E-10	UP
Duox2	-1.4777547	0.00088474	0.00278425	DOWN
Tlr3	-1.454561	4.46E-33	6.59E-31	DOWN
Ifih1	-1.4352704	5.50E-13	8.92E-12	DOWN
Trim5	-2.2981857	2.64E-26	1.99E-24	DOWN
Ido1	-4.2875318	1.68E-15	3.86E-14	DOWN
Gdf15	3.53491871	1.10E-15	2.63E-14	UP
Adipoq	2.27552807	0.00687799	0.01686668	UP
Stat1	-1.100738	0.00684533	0.0167995	DOWN
Socs3	3.42269564	1.54E-40	3.84E-38	UP
Tnfsf10	-2.3448026	8.71E-06	4.26E-05	DOWN
Il15	-2.1465997	6.23E-16	1.53E-14	DOWN
Cd40	1.36217394	5.94E-05	0.00024542	UP
Zyx	1.20045406	1.59E-09	1.51E-08	UP
Ikbke	-1.4938258	1.09E-20	4.61E-19	DOWN
Isg15	-2.0793811	5.45E-05	0.0002268	DOWN
Dhx58	-1.0567817	0.00099197	0.00307201	DOWN
Tnfaip3	1.76869422	9.18E-16	2.20E-14	UP
F2r	1.34481599	2.80E-10	3.03E-09	UP
Eln	1.67808246	0.00011615	0.00044981	UP
Il27	2.44224563	0.0002675	0.00094782	UP
Lep	6.42050934	9.75E-09	8.18E-08	UP
Klkb1	-1.8424371	0.00145618	0.00432167	DOWN
Csrp1	1.56114588	1.97E-09	1.86E-08	UP
Irf5	1.46884147	3.35E-15	7.47E-14	UP
Ccr6	1.34418524	0.02701384	0.0551049	UP
Tlr8	1.89883419	9.74E-08	6.80E-07	UP
Wnt5a	-1.4882917	6.04E-08	4.41E-07	DOWN
Tyk2	-1.0464308	4.44E-12	6.39E-11	DOWN
Tpm2	1.17807842	0.0002921	0.00102824	UP
Ahnak	1.07415466	1.33E-15	3.11E-14	UP
Fgf2	2.12976558	1.95E-05	8.89E-05	UP
Tkfc	-1.0821031	0.00128356	0.00385383	DOWN
Nfkbiz	1.04267424	0.00036597	0.00125927	UP
Robo3	1.25414015	0.03756033	0.07337282	UP
Slc11a1	2.05996515	5.78E-15	1.23E-13	UP
Sting1	1.78124211	1.05E-12	1.64E-11	UP

Des	1.2615283	5.15E-05	0.00021581	UP
Ccl4	1.84418717	0.00128812	0.00386606	UP
Tnfsf11	2.5993683	0.0004438	0.00150086	UP
Klrk1	1.40858098	0.00235606	0.00656717	UP
Jund	1.454659	8.67E-05	0.00034581	UP
Cldn4	1.78017475	1.42E-06	8.04E-06	UP
Irf7	-2.0770622	1.60E-15	3.70E-14	DOWN
Il18	-1.2620038	0.01195756	0.02725735	DOWN
Rela	1.3273225	5.08E-20	1.95E-18	UP
Ptx3	6.00726503	2.82E-32	3.81E-30	UP
Ptgs2	4.15867504	2.32E-40	5.70E-38	UP
Cd14	3.25620047	1.72E-67	2.28E-64	UP
Hmox1	3.32433602	6.98E-10	7.11E-09	UP
Hgf	1.66818349	1.65E-06	9.24E-06	UP
Plscr1	2.57342622	3.69E-08	2.81E-07	UP
Rsad2	-1.0783179	0.03706023	0.07252022	DOWN
Pdcd1	2.40625821	1.55E-05	7.23E-05	UP
Pcsk2	1.54826638	2.24E-06	1.22E-05	UP
Arg2	-1.8455028	9.07E-06	4.41E-05	DOWN
Vtn	1.37348909	0.00491089	0.01249818	UP
Vim	1.99463552	8.08E-26	5.75E-24	UP
Vcam1	2.13325895	2.39E-13	4.10E-12	UP
Gfap	4.99385565	2.73E-35	5.06E-33	UP
Ager	2.16215565	2.24E-14	4.46E-13	UP
Actg1	1.5157334	8.61E-16	2.08E-14	UP
Aco1	-1.3361637	3.93E-09	3.51E-08	DOWN
Ccl17	1.54912241	0.0221685	0.04664098	UP
Ccr3	-1.8671699	0.01127235	0.02588778	DOWN
Ackr2	1.96537798	2.83E-07	1.82E-06	UP
Ccr7	2.95748826	1.54E-09	1.47E-08	UP
Ccr8	3.26185429	0.0009756	0.00302953	UP
Ccl2	6.67466031	7.97E-28	7.14E-26	UP
Ccl7	5.36464318	4.27E-14	8.10E-13	UP
Ccl3	1.51629911	2.54E-05	0.00011297	UP
Ccl11	2.98817785	8.77E-16	2.11E-14	UP
Ccr5	1.38168513	0.00020664	0.00075172	UP
Xcl1	-1.86598	0.00863608	0.02057082	DOWN
Ccr1	2.19599106	2.88E-11	3.68E-10	UP
Cxcl1	8.13802891	6.41E-45	2.32E-42	UP
Cxcl10	1.51894164	0.0034325	0.00914568	UP
Cxcr4	1.55458281	4.23E-06	2.19E-05	UP

Cxcl2	8.07921167	2.08E-59	1.44E-56	UP
Tafa3	-2.8670101	0.00017305	0.00064035	DOWN
Tafa1	2.05443586	0.00094648	0.0029483	UP
Il6	7.70891185	4.56E-15	9.96E-14	UP
Il1b	4.05131742	4.12E-22	1.99E-20	UP
Il13	-3.0863183	0.01588274	0.03484894	DOWN
Il10	4.57589738	1.72E-24	1.07E-22	UP
Mif	1.0940852	3.81E-14	7.30E-13	UP
Ptgdr	-4.6161173	3.01E-12	4.43E-11	DOWN
Cd86	1.82882404	6.96E-08	5.01E-07	UP
Hck	-1.0379613	1.01E-05	4.90E-05	DOWN
Vdr	-1.4275168	1.20E-07	8.24E-07	DOWN
Txk	1.09227292	0.01319056	0.02967733	UP
Blnk	1.92324375	5.88E-09	5.12E-08	UP
Vav2	-1.1699223	5.42E-10	5.61E-09	DOWN
Chp2	-2.1076297	5.32E-09	4.66E-08	DOWN
Nfatc1	1.12586394	3.48E-13	5.79E-12	UP
Nfatc2	2.00031034	3.07E-28	2.83E-26	UP
Cxcl13	1.82568373	0.00082784	0.00262069	UP
Cxcl14	1.50334551	0.00057122	0.00188384	UP
Cxcl3	6.61682776	1.80E-09	1.71E-08	UP
Cxcl5	5.59526742	2.98E-09	2.72E-08	UP
Ccn1	3.72613956	1.86E-16	4.87E-15	UP
Edn2	-2.7714841	1.80E-06	1.00E-05	DOWN
Edn3	-2.6417506	1.14E-16	3.07E-15	DOWN
Fgf10	1.11965366	0.0055399	0.01390898	UP
Pf4	2.44637867	5.26E-13	8.56E-12	UP
Plau	1.96896708	5.44E-06	2.76E-05	UP
Ppbp	5.38763017	3.07E-06	1.64E-05	UP
Sema3c	1.63395998	3.44E-06	1.82E-05	UP
Sema3f	1.80074832	4.60E-17	1.30E-15	UP
Sema4a	-1.1522313	4.35E-08	3.26E-07	DOWN
Sema4c	3.14882256	2.03E-31	2.50E-29	UP
Sema4f	1.38221323	0.01048681	0.02433952	UP
Sema4g	-1.315352	1.06E-09	1.05E-08	DOWN
Sema6a	-2.4929241	1.17E-22	6.00E-21	DOWN
Sema6b	2.09849008	1.98E-13	3.44E-12	UP
Sema7a	2.02049107	1.50E-08	1.23E-07	UP
Tnc	1.4892001	5.10E-07	3.13E-06	UP
Tymp	-2.8504684	9.66E-08	6.75E-07	DOWN
C5ar1	1.7913419	2.32E-06	1.26E-05	UP

Ccrl2	2.88364302	7.28E-14	1.34E-12	UP
Cxcr5	1.99749118	0.02390093	0.04967657	UP
Ackr3	2.69853829	3.64E-23	2.01E-21	UP
Ednra	1.53702828	1.66E-07	1.11E-06	UP
Ednrb	1.61708261	1.60E-13	2.79E-12	UP
Fpr1	2.90240105	0.00099634	0.0030826	UP
Fpr2	3.95696347	1.16E-06	6.69E-06	UP
Cxcr2	5.20489902	4.55E-06	2.34E-05	UP
Ltb4r2	-3.0706779	3.06E-09	2.79E-08	DOWN
Plaur	5.42751698	1.57E-117	2.50E-113	UP
Plxna4	1.20029148	0.00017934	0.00066086	UP
Plxnb2	-1.0109764	9.87E-26	6.99E-24	DOWN
Adm	4.16661706	1.05E-35	2.01E-33	UP
Adm2	2.69138866	0.04071348	0.07846581	UP
Agt	1.00579298	1.72E-05	7.92E-05	UP
Areg	4.99981414	3.96E-25	2.64E-23	UP
Artn	1.45552633	0.00102384	0.00315479	UP
Bdnf	3.7068726	3.42E-06	1.81E-05	UP
Bmp8a	-4.3890291	5.56E-21	2.43E-19	DOWN
Btc	2.9397892	2.61E-10	2.84E-09	UP
Calca	6.45236441	2.05E-14	4.10E-13	UP
Calcb	1.17065572	0.00690455	0.01691101	UP
Cat	-1.5428846	3.32E-08	2.57E-07	DOWN
Clcf1	1.3816141	7.69E-07	4.57E-06	UP
Cmtm3	1.03141962	1.51E-07	1.01E-06	UP
Cmtm5	2.15445097	0.00682606	0.01675479	UP
Cntf	1.08257742	0.00047994	0.00161146	UP
Csf1	2.21427389	1.49E-11	1.98E-10	UP
Csf3	8.44295913	1.03E-17	3.16E-16	UP
Epgn	2.35210984	0.00168476	0.00491142	UP
Ereg	5.02812729	1.30E-38	2.91E-36	UP
Esm1	1.95213456	7.60E-05	0.00030715	UP
Fam3c	-1.4278846	2.19E-25	1.49E-23	DOWN
Fgf12	1.59214487	0.00895608	0.02124906	UP
Fgf13	1.31866162	0.00012335	0.00047527	UP
Fgf9	-1.4579549	9.62E-08	6.73E-07	DOWN
Gal	1.84198025	0.00026812	0.00094962	UP
Gdnf	2.41829371	3.62E-32	4.77E-30	UP
Hamp	3.38839342	0.0002455	0.00088026	UP
Hbegf	3.13192017	7.17E-27	5.72E-25	UP
Il11	3.48999668	2.78E-07	1.79E-06	UP

Il17f	3.34197653	0.00016262	0.0006061	UP
Il1rn	3.74977058	5.18E-10	5.40E-09	UP
Inhba	1.77408855	5.88E-07	3.56E-06	UP
Inhbb	3.51631567	8.12E-61	6.17E-58	UP
Jag2	1.79074051	2.06E-09	1.93E-08	UP
Lif	2.88819269	1.87E-09	1.76E-08	UP
Lrsam1	-1.1718928	9.68E-12	1.33E-10	DOWN
Ngf	2.1160209	4.17E-05	0.00017787	UP
Nmb	1.78138391	4.74E-05	0.00020007	UP
Ccn3	1.1663286	8.78E-05	0.00034988	UP
Npy	2.13366654	2.79E-09	2.56E-08	UP
Nrg1	2.02183922	5.90E-06	2.98E-05	UP
Nrg3	1.51391787	0.03942119	0.0764091	UP
Nrg4	-1.1272174	0.00386413	0.01014993	DOWN
Ntf3	-1.4861391	0.00986583	0.02312028	DOWN
Nts	-1.2322199	0.02698847	0.05506779	DOWN
Osm	4.50651364	8.65E-09	7.34E-08	UP
Endou	2.10623011	3.54E-05	0.00015302	UP
Pdgfc	-1.1134112	0.00021458	0.00077813	DOWN
Pgf	2.6060886	8.92E-18	2.77E-16	UP
Pthlh	2.3045305	3.51E-07	2.22E-06	UP
Rabep2	-1.4698559	5.22E-07	3.19E-06	DOWN
Retn	2.14284418	0.00357396	0.00947513	UP
S100a6	1.27130472	0.0023278	0.00649975	UP
Scg2	1.36265269	1.94E-07	1.28E-06	UP
Scgb3a1	2.09360011	1.38E-09	1.33E-08	UP
Sct	-1.0906231	5.13E-10	5.36E-09	DOWN
Sst	1.1283818	2.19E-10	2.42E-09	UP
Stc1	3.13766974	3.15E-21	1.42E-19	UP
Tac1	2.07385209	2.09E-15	4.77E-14	UP
Tgfb1	1.29420236	1.11E-11	1.51E-10	UP
Tgfb2	1.57722204	1.19E-08	9.89E-08	UP
Tnfrsf11b	1.94856112	7.09E-07	4.24E-06	UP
Tnfsf13	-1.089797	0.00188893	0.00541263	DOWN
Tnfsf13b	-1.0700675	0.00013524	0.00051524	DOWN
Tnfsf14	1.83769213	0.01541592	0.03397551	UP
Tnfsf15	1.23341675	0.01065402	0.02467736	UP
Tnfsf9	2.11042978	2.51E-07	1.62E-06	UP
Tslp	2.25246868	7.52E-05	0.00030404	UP
Ucn2	2.20367796	0.00804331	0.01933083	UP
Vgf	2.71960278	6.67E-13	1.07E-11	UP

Vip	1.91788372	3.62E-08	2.76E-07	UP
Acvr2b	-1.8560936	1.69E-18	5.63E-17	DOWN
Adcyap1r1	1.33288363	8.57E-05	0.00034231	UP
Adipor2	-1.6933974	1.55E-39	3.63E-37	DOWN
Adrb2	1.819509	4.51E-06	2.32E-05	UP
Angpt4	1.67763671	0.03794518	0.07399774	UP
Avpr1a	3.10829996	9.98E-33	1.41E-30	UP
Cntfr	1.74648068	1.89E-05	8.65E-05	UP
Crlf2	1.16297949	1.50E-08	1.23E-07	UP
Csf2rb	1.9821248	3.91E-10	4.13E-09	UP
Csf3r	2.59590998	7.94E-07	4.70E-06	UP
Eng	1.52198931	2.13E-18	7.01E-17	UP
Esr1	1.0446123	0.03153463	0.06298239	UP
Esrra	-1.120843	7.19E-08	5.16E-07	DOWN
Fgfr1	1.86443542	8.37E-28	7.38E-26	UP
Fgfr4	2.3909688	3.83E-08	2.91E-07	UP
Flt1	1.56675501	5.34E-10	5.54E-09	UP
Galr3	-1.4398569	0.04996739	0.09325843	DOWN
Glp1r	-2.2289255	0.00793135	0.01910615	DOWN
Hnf4a	-1.0576266	6.22E-23	3.28E-21	DOWN
Hnf4g	-2.9910909	7.26E-34	1.15E-31	DOWN
Htr3a	1.57077382	2.67E-06	1.43E-05	UP
Htr3b	1.22968273	0.04199154	0.08058443	UP
Ifngr2	-1.2967924	9.13E-18	2.83E-16	DOWN
Il10rb	-1.2297833	5.25E-08	3.87E-07	DOWN
Il12rb1	-1.0980608	0.04879207	0.09143694	DOWN
Il2rb	1.39567644	5.85E-06	2.96E-05	UP
Il18rap	1.91974212	2.36E-05	0.0001057	UP
Il1r1	2.94343195	5.27E-24	3.15E-22	UP
Il1r2	4.2910932	1.06E-33	1.61E-31	UP
Il1rl1	1.88319426	0.00032609	0.00113552	UP
Il20rb	1.50684531	3.22E-13	5.38E-12	UP
Il22ra2	1.18516399	0.01883047	0.04046661	UP
Il23r	1.56088061	0.00560019	0.01404406	UP
Il2ra	1.50072032	0.0001281	0.00049121	UP
Il31ra	1.95052037	0.02354757	0.04903157	UP
Il9r	-1.3699227	0.00472746	0.01209114	DOWN
Insr	-1.2317887	9.71E-18	2.99E-16	DOWN
Ngfr	1.51348752	5.19E-08	3.84E-07	UP
Nr1d1	-1.4853011	7.11E-06	3.54E-05	DOWN
Nr1h3	-1.5085937	1.07E-09	1.06E-08	DOWN

Nr1i3	-1.5332819	0.00183982	0.00529475	DOWN
Nr3c1	-1.2011314	2.65E-14	5.20E-13	DOWN
Nr4a1	4.53994412	6.66E-19	2.29E-17	UP
Nr4a2	1.74255379	1.30E-05	6.14E-05	UP
Nr4a3	3.96911073	4.05E-24	2.45E-22	UP
Oprd1	1.26309967	0.03520458	0.06936555	UP
Osmr	2.49319263	7.39E-30	8.07E-28	UP
Pgrmc2	-1.0646396	0.00090161	0.00282786	DOWN
Prlr	-1.8101503	1.06E-23	6.13E-22	DOWN
Ptger2	1.0662505	0.00491423	0.01250468	UP
Rora	1.89713005	3.09E-12	4.54E-11	UP
Rorc	-1.3224459	1.02E-05	4.92E-05	DOWN
S1pr1	2.93276446	4.33E-32	5.57E-30	UP
Sdc1	1.11516029	4.07E-10	4.29E-09	UP
Sdc4	1.91415693	1.76E-11	2.32E-10	UP
Sstr5	-1.2577698	0.01591962	0.03492159	DOWN
Tacr1	2.32100778	5.07E-08	3.75E-07	UP
Tgfbr2	1.4596238	5.38E-66	6.14E-63	UP
Tie1	1.33494589	4.08E-07	2.54E-06	UP
Tnfrsf12a	4.5504644	1.61E-48	7.35E-46	UP
Tnfrsf18	1.19065811	0.00364034	0.0096287	UP
Tnfrsf19	-1.0222224	0.00391988	0.01028621	DOWN
Tnfrsf1b	2.30367209	1.44E-29	1.53E-27	UP
Tnfrsf4	1.85720421	7.31E-10	7.43E-09	UP
Tnfrsf9	2.04382428	3.88E-05	0.00016679	UP
Tshr	2.53116751	0.00157647	0.00462616	UP
Tubb3	1.46540676	5.65E-07	3.43E-06	UP
Vipr1	-1.1301011	1.47E-05	6.90E-05	DOWN
Klrc1	1.39094219	0.02026488	0.04316536	UP
Icam1	3.28051472	1.58E-21	7.30E-20	UP
Pik3r2	-1.1950896	5.15E-19	1.78E-17	DOWN
Shc2	1.04957089	0.00310109	0.0083604	UP
Shc4	1.03192455	0.03683182	0.07210864	UP
Fos	1.05981923	0.00724829	0.01764994	UP
Nfkbia	2.36946252	1.80E-20	7.38E-19	UP
Nfkbie	1.55904593	7.96E-08	5.67E-07	UP
Cd28	1.114039	0.00329605	0.0088323	UP
Icos	2.32711197	7.66E-16	1.86E-14	UP
Map3k8	3.33982323	2.52E-25	1.69E-23	UP
Map3k14	1.06993626	8.93E-07	5.24E-06	UP
Ctla4	5.08359744	1.12E-52	6.36E-50	UP

Table S4 2245 DEGs obtained from the 5 human intestinal I/R injury samples and 5 control samples.

	log2FoldChange	pvalue	padj	regulated
NAMPT	4.3337	1.49E-32	3.65E-28	up
FOSL1	7.1198	1.04E-26	1.28E-22	up
IL1RAP	2.2960	6.64E-23	4.07E-19	up
ARG1	4.4361	2.13E-22	1.04E-18	up
NR4A3	5.7107	7.54E-22	3.08E-18	up
NAMPTP1	4.1244	1.68E-21	5.16E-18	up
PLAUR	3.8158	1.57E-21	5.16E-18	up
IL1R2	5.2641	2.31E-21	6.29E-18	up
CD177	6.5185	8.61E-21	2.11E-17	up
HIF1A	2.5263	1.80E-20	4.01E-17	up
FABP6	-11.7706	2.15E-20	4.39E-17	down
B4GALT5	1.3987	3.18E-20	6.00E-17	up
CXCL8	7.8820	1.50E-19	2.63E-16	up
ABL2	2.3757	8.24E-19	1.26E-15	up
SBNO2	2.2883	1.81E-18	2.62E-15	up
LOC100506403	3.0293	1.77E-17	2.41E-14	up
PUS7	1.2371	3.83E-17	4.95E-14	up
CXCL3	5.3143	1.02E-16	1.25E-13	up
ADAMTS4	6.4058	2.03E-16	2.37E-13	up
PTX3	6.0305	2.53E-16	2.82E-13	up
TIMP1	4.2746	2.99E-16	3.19E-13	up
ELL2	2.5908	4.95E-16	5.06E-13	up
PLK3	2.9420	8.79E-16	8.43E-13	up
MAP3K5	1.1146	8.94E-16	8.43E-13	up
PXMP4	-1.2697	1.16E-15	1.05E-12	down
COLCA1	-2.6777	1.29E-15	1.12E-12	down
PTPRE	1.5876	1.33E-15	1.12E-12	up
PANX1	1.9690	1.89E-15	1.55E-12	up
UPP1	3.0386	2.04E-15	1.61E-12	up
C14orf28	-1.5150	3.83E-15	2.93E-12	down
MCEMP1	6.9057	4.79E-15	3.56E-12	up
TEAD4	2.4786	8.68E-15	6.26E-12	up
GPR3	3.9856	1.05E-14	7.10E-12	up
C3orf86	4.2552	1.07E-14	7.10E-12	up
SOD2	3.9183	1.03E-14	7.10E-12	up

NFIL3	2.3462	1.35E-14	8.71E-12	up
CPO	-7.5957	2.16E-14	1.36E-11	down
SERPINE1	6.2407	5.72E-14	3.51E-11	up
DDX21	2.2459	7.02E-14	4.10E-11	up
EIF4A1	2.0731	6.86E-14	4.10E-11	up
MCL1	1.9555	7.27E-14	4.14E-11	up
CSRNP1	2.5193	9.94E-14	5.54E-11	up
EIF4A1P10	1.8757	1.30E-13	6.94E-11	up
ZNF345	-1.4030	1.30E-13	6.94E-11	down
ECHDC2	-1.8502	2.92E-13	1.49E-10	down
PLAU	3.0182	3.13E-13	1.56E-10	up
SLC2A3	3.2707	3.51E-13	1.72E-10	up
CIRBP	-1.2070	3.64E-13	1.75E-10	down
LIF	5.1461	5.57E-13	2.63E-10	up
RPL22L1	1.8910	6.39E-13	2.96E-10	up
ZER1	-1.1987	7.02E-13	3.19E-10	down
CSF3	7.6541	7.27E-13	3.24E-10	up
SLC38A2	1.5758	8.87E-13	3.88E-10	up
LINC01089	-1.7616	1.29E-12	5.55E-10	down
ADGRG3	3.0901	1.84E-12	7.79E-10	up
TUBB3	2.9723	1.96E-12	8.03E-10	up
HRH2	2.9904	2.00E-12	8.04E-10	up
DBP	-2.4706	2.24E-12	8.85E-10	down
PDE4B	2.3914	3.72E-12	1.45E-09	up
S100A3	2.2545	3.80E-12	1.46E-09	up
GNL3	1.6876	4.18E-12	1.58E-09	up
SLC5A12	-9.3622	4.88E-12	1.81E-09	down
NFKBIZ	2.4035	6.18E-12	2.26E-09	up
RRP12	2.0643	6.43E-12	2.32E-09	up
LOC101928674	4.2613	7.13E-12	2.53E-09	up
SNHG15	2.0724	8.67E-12	2.99E-09	up
ACSL4	2.3092	8.61E-12	2.99E-09	up
MAD2L2	1.5270	9.40E-12	3.20E-09	up
IL6	5.7008	1.12E-11	3.77E-09	up
ITPRIP	3.0823	1.39E-11	4.60E-09	up
CCDC71L	3.0663	1.48E-11	4.83E-09	up
LINC00954	-2.0720	1.50E-11	4.84E-09	down
ZNF606	-1.1946	1.59E-11	5.06E-09	down
GRWD1	1.0972	1.79E-11	5.62E-09	up
ING4	-1.2100	1.97E-11	6.11E-09	down
EIF4A3	1.2792	2.42E-11	7.43E-09	up

TMEM165	1.4024	2.66E-11	8.06E-09	up
PVR	1.7550	2.71E-11	8.11E-09	up
PHLDA1	3.0562	3.14E-11	9.28E-09	up
ICAM1	4.2061	3.51E-11	1.02E-08	up
OSM	4.3572	3.73E-11	1.08E-08	up
CEMIP	4.7917	4.51E-11	1.27E-08	up
IL1B	5.2089	5.10E-11	1.42E-08	up
SH2B1	-1.1155	6.44E-11	1.78E-08	down
MPZL2	2.4074	6.80E-11	1.85E-08	up
LOC91370	4.0297	7.80E-11	2.10E-08	up
CCL2	4.6146	1.03E-10	2.75E-08	up
SELE	6.2021	1.08E-10	2.82E-08	up
DYRK3	2.8630	1.07E-10	2.82E-08	up
PPP1R3E	-1.7962	1.09E-10	2.82E-08	down
FAM20C	1.6272	1.13E-10	2.89E-08	up
SERPINB2	6.6938	1.17E-10	2.92E-08	up
PPIF	1.4446	1.40E-10	3.47E-08	up
MYC	2.7522	1.44E-10	3.53E-08	up
SLED1	4.7376	1.49E-10	3.63E-08	up
NOP16	1.6784	2.26E-10	5.36E-08	up
TEX26-AS1	3.6197	2.30E-10	5.36E-08	up
LOC388813	2.5584	2.29E-10	5.36E-08	up
SDE2	1.2306	2.35E-10	5.45E-08	up
DUSP4	2.9447	2.67E-10	6.11E-08	up
MAP3K8	2.8058	2.88E-10	6.49E-08	up
HOXB7	-1.8748	2.99E-10	6.68E-08	down
PHC2	1.8281	3.11E-10	6.88E-08	up
IER3	3.7008	3.21E-10	7.03E-08	up
LIPN	4.2482	3.24E-10	7.03E-08	up
CHSY1	2.2890	3.30E-10	7.11E-08	up
THBS1	3.9364	3.52E-10	7.51E-08	up
S100A8	6.2247	4.21E-10	8.78E-08	up
KLHL33	-4.1548	4.22E-10	8.78E-08	down
IL1RL2	2.7381	4.74E-10	9.68E-08	up
FTSJ1	1.1056	4.78E-10	9.68E-08	up
PROCR	1.6222	4.90E-10	9.86E-08	up
PPRC1	2.0105	5.01E-10	9.99E-08	up
TNFAIP3	2.9043	5.98E-10	1.17E-07	up
RCAN1	2.6331	6.06E-10	1.18E-07	up
NOP56	1.1266	6.62E-10	1.28E-07	up
SRPRB	1.1105	7.64E-10	1.45E-07	up

HOXA-AS3	-2.4937	7.60E-10	1.45E-07	down
PPP1R15B	1.2593	8.13E-10	1.52E-07	up
TCEA3	-2.4400	8.72E-10	1.62E-07	down
RNF24	2.3766	9.29E-10	1.71E-07	up
MTHFD1L	1.9098	1.03E-09	1.88E-07	up
IL18R1	2.0821	1.07E-09	1.92E-07	up
PDPN	3.1506	1.13E-09	2.02E-07	up
CXCL2	3.8701	1.47E-09	2.61E-07	up
RLIM	1.0705	1.49E-09	2.61E-07	up
CDHR1	-6.8186	1.48E-09	2.61E-07	down
ALPL	4.4630	1.52E-09	2.62E-07	up
BDKRB1	3.7955	1.51E-09	2.62E-07	up
KCNJ13	-6.9406	1.64E-09	2.82E-07	down
EIF4A1P7	1.7517	1.76E-09	2.99E-07	up
NOLC1	1.5976	1.79E-09	3.03E-07	up
LOC220729	-1.3009	1.91E-09	3.20E-07	down
IL17RC	-1.2305	1.95E-09	3.22E-07	down
CH25H	3.7979	1.94E-09	3.22E-07	up
PIGA	1.8338	1.98E-09	3.25E-07	up
RTP4	-1.8174	2.02E-09	3.30E-07	down
HSPA6	6.6021	2.13E-09	3.46E-07	up
RN7SL368P	3.2342	2.19E-09	3.51E-07	up
IL1RL1	6.3236	2.33E-09	3.71E-07	up
SLC34A3	-6.9680	2.65E-09	4.16E-07	down
GTPBP4	1.5402	2.94E-09	4.57E-07	up
HAS1	5.5429	2.95E-09	4.57E-07	up
ANKMY2	-1.0846	3.06E-09	4.71E-07	down
S100A9	5.8742	3.43E-09	5.25E-07	up
C11orf96	3.5421	3.72E-09	5.66E-07	up
CBARP	3.2591	3.77E-09	5.70E-07	up
PLEKHG2	1.7697	4.32E-09	6.41E-07	up
INHBA	6.1003	4.37E-09	6.45E-07	up
P4HA1	2.0214	4.54E-09	6.66E-07	up
TFDP2	-1.4301	4.68E-09	6.75E-07	down
TMEM80	-1.4563	4.74E-09	6.75E-07	down
HMOX1	3.0108	4.74E-09	6.75E-07	up
PDCD11	1.1343	5.04E-09	7.14E-07	up
LOC101927837	-2.5533	5.18E-09	7.30E-07	down
SLC23A1	-5.8394	5.45E-09	7.64E-07	down
TPBG	1.3129	5.91E-09	8.22E-07	up
HOXA9	-3.9383	5.94E-09	8.22E-07	down

TSC22D1-AS1	-3.0716	6.05E-09	8.33E-07	down
H3-5	1.3637	6.23E-09	8.54E-07	up
OSMR	2.6402	6.97E-09	9.50E-07	up
BHLHE40	2.2986	7.29E-09	9.88E-07	up
EIF4E3	-1.2141	7.60E-09	1.02E-06	down
BYSL	1.6934	8.41E-09	1.13E-06	up
TMEM70	1.3486	8.62E-09	1.14E-06	up
SLC7A9	-6.7422	8.89E-09	1.16E-06	down
STC1	4.0874	9.16E-09	1.17E-06	up
ZNF540	-2.2274	9.06E-09	1.17E-06	down
ABCE1	1.2725	9.54E-09	1.20E-06	up
RNF122	2.0785	9.56E-09	1.20E-06	up
PNO1	1.6997	9.75E-09	1.21E-06	up
BZW1	1.0876	9.77E-09	1.21E-06	up
MATN2	-2.5067	9.68E-09	1.21E-06	down
ERFE	4.5828	9.90E-09	1.22E-06	up
C11orf91	4.9198	1.04E-08	1.27E-06	up
LOC105370854	-4.3074	1.04E-08	1.27E-06	down
ADAMTS9	4.4463	1.06E-08	1.28E-06	up
HSPA5	1.9688	1.14E-08	1.36E-06	up
NPM3	1.3328	1.18E-08	1.40E-06	up
EREG	4.0399	1.23E-08	1.44E-06	up
WDR43	1.4439	1.29E-08	1.50E-06	up
SNAPC1	1.3103	1.32E-08	1.52E-06	up
PTPN1	1.2831	1.34E-08	1.54E-06	up
TCEANC	-1.4421	1.36E-08	1.55E-06	down
HMGXB3	1.0335	1.40E-08	1.59E-06	up
FUT11	1.0342	1.41E-08	1.59E-06	up
CDKN2B-AS1	-5.1531	1.46E-08	1.64E-06	down
HEYL	3.0789	1.53E-08	1.72E-06	up
CHST2	1.8627	1.58E-08	1.75E-06	up
SERTAD1	1.8390	1.57E-08	1.75E-06	up
RND3	2.5014	1.60E-08	1.76E-06	up
NOP2	1.7830	1.89E-08	2.06E-06	up
TLR2	2.8602	1.91E-08	2.08E-06	up
ARID5B	1.8437	1.97E-08	2.12E-06	up
C9orf72	1.4426	2.00E-08	2.14E-06	up
FJX1	3.4371	2.00E-08	2.14E-06	up
PADI4	4.0269	2.04E-08	2.15E-06	up
IL11RA	-1.5297	2.04E-08	2.15E-06	down
EIF5A	1.1016	2.04E-08	2.15E-06	up

TPM4	1.5747	2.14E-08	2.25E-06	up
CCN1	3.2577	2.23E-08	2.34E-06	up
CLCF1	3.5169	2.30E-08	2.40E-06	up
ACBD4	-2.3194	2.31E-08	2.40E-06	down
ELK1	1.0624	2.34E-08	2.41E-06	up
SRGN	2.4769	2.34E-08	2.41E-06	up
HAS2	4.3169	2.35E-08	2.41E-06	up
ALDH1A1	-1.9386	2.68E-08	2.72E-06	down
AREG	4.3830	2.74E-08	2.76E-06	up
FSIP2	-4.5791	3.46E-08	3.44E-06	down
CDC42SE1	1.1319	3.68E-08	3.63E-06	up
TREM1	4.9510	3.73E-08	3.66E-06	up
LOC100506289	-3.0935	3.79E-08	3.68E-06	down
FOLR3	7.8897	3.79E-08	3.68E-06	up
SLC17A8	-7.3837	3.81E-08	3.69E-06	down
PGF	3.2700	3.93E-08	3.78E-06	up
GALT	-1.4621	3.97E-08	3.80E-06	down
KAT14	-1.4616	4.04E-08	3.86E-06	down
NAALADL1	-4.7407	4.21E-08	3.99E-06	down
PHEX	-4.6384	4.30E-08	4.04E-06	down
IL11	6.3573	4.30E-08	4.04E-06	up
SPHK1	2.7782	4.50E-08	4.21E-06	up
GPAT2	2.3952	4.58E-08	4.27E-06	up
HSD17B8	-1.7611	4.73E-08	4.39E-06	down
SERPINF2	1.7393	4.94E-08	4.54E-06	up
ATF3	2.1314	5.03E-08	4.55E-06	up
ZDHHC19	3.6204	5.01E-08	4.55E-06	up
C8orf44	-1.3075	5.03E-08	4.55E-06	down
TMEM252	-4.7958	4.98E-08	4.55E-06	down
KLHDC9	-2.5486	5.20E-08	4.65E-06	down
NIP7	1.1744	5.19E-08	4.65E-06	up
TRIB1	2.3836	5.24E-08	4.67E-06	up
HBEGF	2.7514	5.36E-08	4.76E-06	up
YRDC	1.6208	5.49E-08	4.84E-06	up
IRAK3	2.3617	5.48E-08	4.84E-06	up
CXCL1	5.1950	5.62E-08	4.94E-06	up
FAM200B	-1.0602	5.96E-08	5.22E-06	down
KLHDC2	-1.0305	6.02E-08	5.25E-06	down
TM4SF1	2.8853	6.37E-08	5.48E-06	up
ATP13A3	1.6075	6.33E-08	5.48E-06	up
EGR3	3.3597	6.37E-08	5.48E-06	up

ELL	1.3500	6.40E-08	5.49E-06	up
SLC25A23	-2.0380	6.43E-08	5.49E-06	down
CHAD	-4.8344	6.64E-08	5.65E-06	down
PPP1R15A	2.9673	6.76E-08	5.73E-06	up
LOC171391	-1.8566	6.79E-08	5.74E-06	down
ABCG2	-4.8913	6.93E-08	5.84E-06	down
SULT1A2	-5.2029	7.54E-08	6.33E-06	down
PUM3	1.4182	7.61E-08	6.37E-06	up
RHOQ-AS1	2.5302	8.11E-08	6.75E-06	up
GRAMD1A	1.6414	8.25E-08	6.83E-06	up
CCDC146	-1.6199	8.38E-08	6.91E-06	down
CCL3	3.2713	8.83E-08	7.24E-06	up
LOC102724788	-5.4835	8.94E-08	7.31E-06	down
MTHFD2	2.2239	9.00E-08	7.33E-06	up
PTGES	2.7933	9.24E-08	7.50E-06	up
CYTOR	2.2832	9.32E-08	7.54E-06	up
S100A12	6.7530	1.09E-07	8.70E-06	up
ATP11A	1.0816	1.11E-07	8.80E-06	up
GUCA2B	-7.7920	1.11E-07	8.81E-06	down
FAM151A	-6.3834	1.14E-07	8.98E-06	down
CLK4	-1.1267	1.17E-07	9.21E-06	down
NUP58	1.1255	1.18E-07	9.21E-06	up
CD44	1.7191	1.19E-07	9.29E-06	up
NNMT	3.4052	1.22E-07	9.48E-06	up
CUBN	-6.0892	1.22E-07	9.48E-06	down
TNFAIP6	4.2399	1.25E-07	9.68E-06	up
SLCO4A1	2.5885	1.34E-07	1.03E-05	up
SLC10A2	-8.2616	1.36E-07	1.05E-05	down
CSGALNACT2	1.5900	1.39E-07	1.06E-05	up
LOC100419170	4.3472	1.43E-07	1.09E-05	up
ZNF121	1.0115	1.47E-07	1.11E-05	up
ZBTB21	1.4913	1.47E-07	1.11E-05	up
ZNF436-AS1	-2.3430	1.51E-07	1.13E-05	down
LOC100134368	-2.1428	1.50E-07	1.13E-05	down
ATG101	1.1495	1.54E-07	1.15E-05	up
CEBPB	2.2712	1.57E-07	1.17E-05	up
CDHR3	-3.5203	1.60E-07	1.18E-05	down
PAPPA	2.0961	1.68E-07	1.24E-05	up
ZNF599	-1.0949	1.69E-07	1.24E-05	down
NME1	1.6698	1.76E-07	1.29E-05	up
SH3TC1	1.8476	1.80E-07	1.31E-05	up

GPR84	5.2385	1.80E-07	1.31E-05	up
THBD	2.8975	1.81E-07	1.31E-05	up
FCER1A	-3.4107	1.84E-07	1.32E-05	down
ADD3-AS1	-2.7388	1.88E-07	1.35E-05	down
LHPP	-1.6889	1.96E-07	1.39E-05	down
LINC01011	-1.4133	1.98E-07	1.40E-05	down
PTPRVP	-4.5834	2.16E-07	1.53E-05	down
MYBPC3	2.4873	2.21E-07	1.56E-05	up
EAF1	1.2655	2.23E-07	1.57E-05	up
KY	-4.9391	2.29E-07	1.61E-05	down
ARC	5.1021	2.35E-07	1.64E-05	up
LOC100130111	-6.3822	2.36E-07	1.64E-05	down
INO80E	-1.0618	2.34E-07	1.64E-05	down
DDX60	-1.3099	2.39E-07	1.65E-05	down
IFITM2	2.2252	2.38E-07	1.65E-05	up
GVQW3	-2.0205	2.44E-07	1.68E-05	down
FCAR	5.0834	2.45E-07	1.68E-05	up
MAFF	3.0177	2.44E-07	1.68E-05	up
CFAP45	3.5338	2.47E-07	1.69E-05	up
IL24	6.9909	2.48E-07	1.69E-05	up
H3-3B	1.2160	2.51E-07	1.70E-05	up
SEH1L	1.1070	2.53E-07	1.71E-05	up
TNFRSF12A	3.1700	2.60E-07	1.75E-05	up
DCUN1D3	1.9827	2.61E-07	1.75E-05	up
CYP2U1	-1.3115	2.69E-07	1.80E-05	down
MYORG	-2.3941	2.74E-07	1.81E-05	down
SERPINH1	3.2566	2.75E-07	1.81E-05	up
URB2	1.5323	2.79E-07	1.84E-05	up
DNASE1	-3.7959	2.90E-07	1.90E-05	down
SLC19A2	1.9557	3.08E-07	2.00E-05	up
LILRA5	4.1666	3.07E-07	2.00E-05	up
RGS16	4.2173	3.10E-07	2.00E-05	up
HSP90B2P	1.4035	3.14E-07	2.03E-05	up
DET1	-1.8157	3.20E-07	2.05E-05	down
SIGLEC17P	-1.8468	3.24E-07	2.07E-05	down
MB	-3.3835	3.26E-07	2.07E-05	down
GLIS3	1.8579	3.42E-07	2.17E-05	up
XIRP1	6.1239	3.43E-07	2.17E-05	up
ZNF281	1.3727	3.49E-07	2.21E-05	up
BATF3	2.0536	3.77E-07	2.37E-05	up
SLC25A25	2.0149	3.86E-07	2.40E-05	up

FAXDC2	-2.2388	3.95E-07	2.44E-05	down
ZNF780B	-1.3480	3.94E-07	2.44E-05	down
SLC7A5	3.5058	3.99E-07	2.47E-05	up
HOXC-AS2	-4.3548	4.12E-07	2.54E-05	down
FAM126A	1.1500	4.14E-07	2.55E-05	up
TGIF1	2.1817	4.19E-07	2.57E-05	up
RNASE2	5.4203	4.25E-07	2.60E-05	up
FPR1	4.4619	4.32E-07	2.64E-05	up
SLC28A1	-5.5422	4.50E-07	2.73E-05	down
DKC1	1.0305	4.57E-07	2.77E-05	up
HOXC-AS1	-4.5649	4.60E-07	2.78E-05	down
SLC26A3	-6.4467	4.64E-07	2.80E-05	down
WEE2-AS1	-1.4901	4.70E-07	2.83E-05	down
SLC11A1	4.6301	4.73E-07	2.84E-05	up
ITPKC	1.8454	4.78E-07	2.86E-05	up
CAMK2G	-2.1489	4.88E-07	2.91E-05	down
SERPINE2	2.6132	4.95E-07	2.94E-05	up
PLK2	1.6201	4.99E-07	2.95E-05	up
DAB1	-4.9544	5.01E-07	2.96E-05	down
SAP30L	-1.1597	5.07E-07	2.98E-05	down
RAB3C	1.3236	5.12E-07	3.00E-05	up
ZNF19	-1.4870	5.48E-07	3.18E-05	down
MEDAG	3.7394	5.51E-07	3.19E-05	up
IKBIP	1.7918	5.62E-07	3.24E-05	up
SERPINB8	1.7537	5.84E-07	3.36E-05	up
TNFAIP1	1.1261	5.88E-07	3.38E-05	up
RIPK2	1.7986	5.99E-07	3.42E-05	up
ARID5A	2.0781	6.29E-07	3.56E-05	up
EPOP	3.1905	6.29E-07	3.56E-05	up
FPR2	4.2210	6.34E-07	3.58E-05	up
POLA2	3.5808	6.87E-07	3.87E-05	up
PTGIR	2.6388	6.97E-07	3.91E-05	up
KLC4	-2.1999	7.17E-07	4.01E-05	down
RRP9	1.1664	7.19E-07	4.02E-05	up
BTBD19	2.0877	7.49E-07	4.16E-05	up
SRGAP1	1.0652	7.71E-07	4.26E-05	up
ADAMTSL4-AS1	3.2687	8.09E-07	4.46E-05	up
PAXIP1-DT	-1.3030	8.19E-07	4.49E-05	down
SOCS3	3.2166	8.21E-07	4.49E-05	up
CNGA1	-4.1418	8.37E-07	4.56E-05	down
PROK2	3.7293	8.53E-07	4.63E-05	up

DHRS1	-1.9636	8.51E-07	4.63E-05	down
SNAI1	3.4061	8.67E-07	4.69E-05	up
TDRD9	2.4462	8.70E-07	4.70E-05	up
ADAM17	1.1469	9.30E-07	4.98E-05	up
SPRY4	1.7701	9.32E-07	4.98E-05	up
ENPP3	-5.6074	9.34E-07	4.98E-05	down
UGCG	1.7220	9.33E-07	4.98E-05	up
DRAM1	2.1709	9.38E-07	4.99E-05	up
CLEC5A	5.2370	9.47E-07	5.03E-05	up
PAK1IP1	1.3415	9.54E-07	5.05E-05	up
TMEM161B-AS1	-2.4267	9.80E-07	5.18E-05	down
SPTBN5	2.2352	1.02E-06	5.40E-05	up
ZNF737	-1.0778	1.04E-06	5.45E-05	down
TTC30B	-1.3754	1.04E-06	5.48E-05	down
C2orf88	-3.2886	1.06E-06	5.54E-05	down
TNFRSF10D	2.3545	1.08E-06	5.63E-05	up
SLC6A4	-5.4714	1.11E-06	5.79E-05	down
SHC1	1.2595	1.12E-06	5.81E-05	up
ASGR1	2.1864	1.12E-06	5.81E-05	up
FBXW4	-1.0044	1.12E-06	5.81E-05	down
GLT1D1	3.1523	1.13E-06	5.83E-05	up
SCIN	-5.3551	1.14E-06	5.86E-05	down
AGTRAP	1.8463	1.18E-06	6.07E-05	up
KAZALD1	-2.7461	1.18E-06	6.07E-05	down
RAN	1.0398	1.19E-06	6.09E-05	up
CRISPLD2	2.7249	1.21E-06	6.19E-05	up
FAM167B	2.0653	1.24E-06	6.32E-05	up
ADH4	5.2873	1.26E-06	6.37E-05	up
MIEF2	-1.3325	1.31E-06	6.59E-05	down
EIF5AL1	1.3474	1.33E-06	6.65E-05	up
MRPL17	1.0543	1.34E-06	6.72E-05	up
NOL12	-1.2426	1.35E-06	6.73E-05	down
ACKR3	2.3477	1.38E-06	6.90E-05	up
RND1	4.9179	1.40E-06	6.98E-05	up
HOXC10	-3.6441	1.41E-06	6.99E-05	down
POLR1C	1.3383	1.41E-06	7.01E-05	up
PNP	2.4652	1.43E-06	7.06E-05	up
EIF4A1P2	2.0918	1.43E-06	7.06E-05	up
NUDT12	-1.2872	1.44E-06	7.08E-05	down
ZNF252P-AS1	-2.7387	1.47E-06	7.20E-05	down
E2F3	1.3552	1.50E-06	7.34E-05	up

FBXL22	-4.1552	1.52E-06	7.39E-05	down
OSGEPL1	-1.2374	1.53E-06	7.46E-05	down
GRHL1	2.8785	1.58E-06	7.69E-05	up
ZFP14	-1.6968	1.59E-06	7.71E-05	down
RPL32P32	2.4307	1.65E-06	7.95E-05	up
NXT1	1.4734	1.67E-06	8.04E-05	up
LOC100287896	-1.4575	1.71E-06	8.19E-05	down
USP31	1.1798	1.76E-06	8.42E-05	up
ACE2	-5.6182	1.78E-06	8.51E-05	down
LIN7B	-1.3316	1.81E-06	8.60E-05	down
ASXL3	-1.6670	1.82E-06	8.65E-05	down
NUDCD1	1.1573	1.84E-06	8.72E-05	up
EGR4	4.2977	1.86E-06	8.79E-05	up
SERTAD4	-2.6958	1.87E-06	8.81E-05	down
MTHFD2P7	2.2190	1.88E-06	8.81E-05	up
HLF	-2.8438	1.88E-06	8.81E-05	down
ZNF460	1.7937	1.88E-06	8.81E-05	up
FKBP1A	1.2682	1.93E-06	9.03E-05	up
METTL1	1.7398	2.00E-06	9.32E-05	up
JUNB	1.7304	2.01E-06	9.34E-05	up
PGLYRP1	4.2696	2.11E-06	9.76E-05	up
HYOU1	1.3855	2.15E-06	9.95E-05	up
BCL6B	2.6995	2.21E-06	0.00010197	up
SNHG16	1.4487	2.22E-06	0.00010228	up
LRRC59	1.3001	2.28E-06	0.00010447	up
HOXB6	-1.3585	2.29E-06	0.00010475	down
MAPKAPK2	1.1846	2.37E-06	0.00010805	up
STX18-AS1	-1.2225	2.40E-06	0.00010913	down
NCOA7	1.7219	2.43E-06	0.00011028	up
RELT	2.2202	2.45E-06	0.00011086	up
SNHG17	1.4436	2.45E-06	0.00011086	up
ACKR4	-2.2022	2.47E-06	0.00011151	down
HOXA7	-1.9097	2.55E-06	0.0001151	down
NR4A2	2.7533	2.62E-06	0.00011789	up
ETF1	1.2155	2.66E-06	0.00011909	up
LRRC19	-5.3561	2.67E-06	0.00011932	down
RAB13	1.5116	2.72E-06	0.00012112	up
C11orf54	-1.5590	2.72E-06	0.00012112	down
SOAT2	-4.9252	2.72E-06	0.00012112	down
MMP1	7.4673	2.78E-06	0.00012314	up
HDAC11	-1.2989	2.82E-06	0.00012439	down

RNF149	1.3605	2.84E-06	0.0001251	up
TMEM158	3.6406	2.91E-06	0.00012808	up
MCHR1	2.5021	2.91E-06	0.00012808	up
GPR4	3.5740	2.93E-06	0.00012845	up
LOC107987479	-4.5771	2.94E-06	0.00012845	down
WTAP	1.4227	2.94E-06	0.00012848	up
LITAF	1.6376	3.04E-06	0.00013224	up
GNL2	1.2889	3.07E-06	0.00013349	up
CARF	-1.3884	3.09E-06	0.00013389	down
RIOK1	1.1779	3.13E-06	0.00013445	up
FAM71F2	1.6596	3.13E-06	0.00013445	up
B4GALT1	1.6240	3.12E-06	0.00013445	up
KDM6B	1.7856	3.14E-06	0.00013445	up
DPF3	-2.0469	3.16E-06	0.00013542	down
STPG3-AS1	-4.0081	3.18E-06	0.00013556	down
SMOX	1.9859	3.18E-06	0.00013556	up
SPAG8	-2.2542	3.19E-06	0.00013564	down
PDZD7	-3.4792	3.19E-06	0.00013564	down
TMED9	1.0338	3.24E-06	0.00013721	up
NAPEPLD	-2.0313	3.26E-06	0.00013778	down
SLC9A3	-4.3356	3.30E-06	0.00013939	down
CHIC2	1.2403	3.40E-06	0.00014263	up
SBK3	3.7008	3.46E-06	0.00014509	up
APLN	3.6892	3.51E-06	0.00014643	up
SH3RF3	1.4535	3.53E-06	0.00014709	up
TUBAP2	1.8072	3.55E-06	0.00014737	up
ROGDI	-1.9757	3.54E-06	0.00014737	down
HERC2P7	-1.3629	3.66E-06	0.00015158	down
LINC01303	3.4213	3.81E-06	0.00015696	up
NFKB2	1.8583	3.85E-06	0.00015805	up
SLC5A9	-5.2243	3.86E-06	0.00015823	down
POP1	1.2357	4.00E-06	0.00016373	up
NAT8B	-6.2924	4.01E-06	0.00016375	down
KCTD7	-1.6272	4.02E-06	0.00016386	down
C10orf143	-1.4829	4.05E-06	0.00016495	down
NLRP3	2.2667	4.16E-06	0.00016843	up
TOB1-AS1	-2.5396	4.26E-06	0.00017194	down
GFPT2	3.2565	4.28E-06	0.00017248	up
R3HDM4	1.1955	4.40E-06	0.00017698	up
C5AR2	2.7231	4.66E-06	0.00018605	up
TAF1D	1.1267	4.78E-06	0.00019046	up

PUS1	1.1786	4.84E-06	0.00019248	up
TBX10	-6.2098	4.89E-06	0.00019385	down
LUCAT1	5.4148	4.89E-06	0.00019387	up
DMRTA1	-1.9455	5.11E-06	0.00020073	down
PAGR1	-1.2402	5.43E-06	0.00021233	down
AMPD2	1.0750	5.49E-06	0.0002144	up
KLF6	1.6792	5.58E-06	0.00021722	up
ARHGEF37	-2.0853	5.72E-06	0.00022209	down
CCN4	3.1573	5.74E-06	0.00022274	up
SUGCT	-2.3697	5.79E-06	0.0002241	down
CSF3R	3.1493	5.81E-06	0.00022439	up
USP30	-1.0723	5.84E-06	0.00022503	down
CKAP4	1.5623	5.94E-06	0.0002287	up
KLHL2	1.1248	6.04E-06	0.00023219	up
NIFK	1.1398	6.07E-06	0.00023294	up
HYKK	-2.0500	6.12E-06	0.00023418	down
FAS	1.0000	6.22E-06	0.00023702	up
HSP90B1	1.3927	6.31E-06	0.00023974	up
GNPNAT1	1.2480	6.39E-06	0.00024199	up
EIF3J-DT	-1.1146	6.52E-06	0.00024669	down
C17orf113	-2.2728	6.68E-06	0.00025215	down
RABL2A	-1.1900	6.76E-06	0.00025419	down
ZSWIM3	-1.1028	6.83E-06	0.00025555	down
LINC01534	-1.2475	6.82E-06	0.00025555	down
PAQR8	-3.1234	7.17E-06	0.00026763	down
LGALS2	-4.6595	7.29E-06	0.00027136	down
SEC14L5	-3.2916	7.32E-06	0.00027181	down
NOP58	1.4676	7.54E-06	0.00027914	up
LOC101927825	-3.8955	7.60E-06	0.00028119	down
ACOX2	-2.5117	7.62E-06	0.00028121	down
HOXC9	-2.8076	7.67E-06	0.00028293	down
MIR4435-2HG	1.5024	7.77E-06	0.00028576	up
ZNF331	1.8381	7.77E-06	0.00028576	up
RETN	6.3400	7.84E-06	0.0002878	up
DCUN1D5	1.0455	8.02E-06	0.00029304	up
ACE	-3.9799	8.01E-06	0.00029304	down
NR3C2	-2.2568	8.05E-06	0.0002936	down
FAM161B	-1.1174	8.30E-06	0.00030162	down
IQSEC2	-1.0948	8.39E-06	0.00030385	down
NMUR1	-1.9813	8.52E-06	0.00030688	down
SPAG4	2.5227	8.51E-06	0.00030688	up

ABCC6	-3.1323	8.62E-06	0.00030995	down
CYP2J2	-5.0952	8.83E-06	0.00031711	down
APOB	-6.1597	8.92E-06	0.00031827	down
LRRC8A	1.2691	8.91E-06	0.00031827	up
MAP2K3	1.6239	8.90E-06	0.00031827	up
LDLR	3.0275	8.93E-06	0.00031827	up
CLEC4D	3.3528	9.12E-06	0.00032352	up
NBR2	-1.3828	9.16E-06	0.00032403	down
LZTS1	2.3630	9.21E-06	0.00032537	up
P2RY4	-4.7189	9.25E-06	0.00032628	down
C3orf85	-6.6648	9.37E-06	0.00032984	down
NOL6	1.2131	9.38E-06	0.00032984	up
DUSP1	1.7462	9.44E-06	0.00033175	up
RNF145	1.0619	9.48E-06	0.00033244	up
LOC100996351	4.1297	9.49E-06	0.00033244	up
CYP4F11	-5.9894	9.50E-06	0.00033244	down
VIPR1	-3.6333	9.66E-06	0.00033758	down
KLHL15	1.0605	9.75E-06	0.00033944	up
MMP28	-2.2878	9.79E-06	0.00034056	down
RPARP-AS1	-1.6434	1.01E-05	0.00035174	down
MS4A10	-6.4303	1.03E-05	0.00035343	down
CYP4F2	-6.7244	1.03E-05	0.00035343	down
PPIEL	-1.0134	1.04E-05	0.00035826	down
NOD1	1.4197	1.04E-05	0.00035826	up
TMEM129	-1.0501	1.05E-05	0.00036052	down
HEXIM2	-1.4524	1.06E-05	0.00036278	down
MMP25	2.3433	1.07E-05	0.00036286	up
A4GALT	1.5177	1.07E-05	0.00036286	up
SPRY1	1.8846	1.08E-05	0.0003657	up
CCDC86	1.1912	1.08E-05	0.00036639	up
ZBTB3	-1.0465	1.08E-05	0.00036639	down
PBXIP1	-1.5057	1.09E-05	0.00036721	down
BTC	-3.3077	1.09E-05	0.00036724	down
TNFSF10	-1.8792	1.09E-05	0.0003677	down
TGFBI	1.4856	1.10E-05	0.00036803	up
TMEM132A	1.9827	1.11E-05	0.00037105	up
CCL4	2.5581	1.13E-05	0.00037543	up
MSX2	3.2963	1.16E-05	0.00038439	up
GABPB1	1.2879	1.20E-05	0.00039537	up
TEF	-1.6319	1.22E-05	0.00040016	down
CRLF1	2.7526	1.25E-05	0.00040916	up

LRRC66	-3.7292	1.25E-05	0.00040945	down
LINC01229	-4.7873	1.27E-05	0.00041514	down
CCDC191	-1.0868	1.28E-05	0.00041606	down
CAPN9	-4.9375	1.28E-05	0.00041613	down
TGM2	1.5853	1.29E-05	0.00041736	up
TNFSF9	3.5873	1.29E-05	0.00041741	up
RPL7P1	2.3598	1.32E-05	0.00042735	up
P4HA3	2.9347	1.32E-05	0.00042735	up
SCNN1D	-1.3836	1.34E-05	0.00043036	down
CNKSR2	-2.0615	1.35E-05	0.00043268	down
ABCB5	-3.6487	1.39E-05	0.00044468	down
LOC101930275	-2.2382	1.39E-05	0.00044468	down
GLUL	2.5824	1.43E-05	0.00045562	up
OARD1	-1.1667	1.43E-05	0.00045734	down
SLC5A11	-5.0374	1.44E-05	0.00045769	down
GRIA4	-4.5938	1.45E-05	0.00045978	down
LOC105371592	-2.3408	1.45E-05	0.00046043	down
LOC105370941	-2.3126	1.47E-05	0.0004659	down
KRT17	5.5141	1.48E-05	0.00046734	up
CREM	1.8805	1.51E-05	0.00047563	up
CCL14	-2.7453	1.52E-05	0.00047872	down
CASP16P	-4.7352	1.53E-05	0.00048121	down
AHR	1.0967	1.55E-05	0.00048552	up
IGF1	3.2903	1.56E-05	0.00048753	up
KHK	-4.0765	1.58E-05	0.00049146	down
SAMD14	1.9036	1.58E-05	0.00049146	up
RPS2P5	1.1179	1.61E-05	0.00050069	up
AEN	1.2865	1.63E-05	0.00050707	up
LOC107985216	-1.9404	1.64E-05	0.00050743	down
DUSP6	1.6581	1.64E-05	0.00050743	up
PIM3	1.5685	1.66E-05	0.00051158	up
LINC01954	-4.8740	1.69E-05	0.00051846	down
P3H1	1.6234	1.69E-05	0.00051942	up
PCBP3	1.8231	1.70E-05	0.00052131	up
COL18A1	1.8871	1.79E-05	0.00054593	up
C21orf62	-4.9105	1.82E-05	0.0005531	down
YBX3	1.7115	1.84E-05	0.00055682	up
PBLD	-3.8918	1.85E-05	0.00055944	down
TRMT6	1.2253	1.85E-05	0.00055944	up
PTRH2	1.5050	1.88E-05	0.0005659	up
RPF2	1.3433	1.88E-05	0.00056732	up

GPD1L	-1.6677	1.90E-05	0.0005706	down
SNHG3	1.5376	1.92E-05	0.0005762	up
SPRED3	2.7724	1.93E-05	0.00057774	up
VASN	2.3424	1.93E-05	0.00058	up
TRPM6	-4.1946	1.96E-05	0.00058592	down
DGAT1	-3.1213	1.96E-05	0.0005866	down
CDKN2D	1.1199	1.97E-05	0.00058729	up
CYP4F12	-4.1107	1.99E-05	0.00059332	down
SLC13A1	-7.4454	2.03E-05	0.0006024	down
LOC100129534	-1.2260	2.05E-05	0.00060789	down
COLCA2	-2.2633	2.06E-05	0.00061031	down
GNA15	2.5289	2.07E-05	0.00061284	up
C1orf220	-2.8361	2.09E-05	0.00061674	down
CASTOR3	-1.1928	2.12E-05	0.00062343	down
SMIM2-AS1	-3.4648	2.12E-05	0.00062343	down
DHRS12	-1.0215	2.16E-05	0.0006315	down
MARCHF8	-1.3975	2.16E-05	0.00063244	down
KDM8	-2.5481	2.17E-05	0.00063421	down
C2CD4B	3.1886	2.17E-05	0.00063483	up
ODC1	1.3522	2.24E-05	0.00065169	up
ZNF785	-1.0735	2.29E-05	0.00066491	down
LYAR	1.4059	2.30E-05	0.00066865	up
NXPE1	-5.5081	2.36E-05	0.0006821	down
LIAS	-1.0826	2.39E-05	0.00068653	down
KCNE1	3.6331	2.38E-05	0.00068653	up
EGR1	2.0973	2.39E-05	0.00068673	up
SLC17A4	-6.6221	2.41E-05	0.00068992	down
LTV1	1.0066	2.44E-05	0.00069676	up
TPRG1L	-1.0097	2.45E-05	0.00069946	down
MIR221	2.5948	2.47E-05	0.00070374	up
HSPA13	1.2791	2.49E-05	0.00070803	up
RNPC3	-1.2611	2.51E-05	0.00071271	down
TMEM217	2.4490	2.56E-05	0.00072103	up
DHRS11	-3.7383	2.56E-05	0.00072103	down
STPG3	-3.5899	2.57E-05	0.00072488	down
SLC22A5	-2.1108	2.61E-05	0.00073115	down
ALOX5AP	1.2155	2.61E-05	0.00073178	up
TDRD12	-4.1594	2.62E-05	0.00073222	down
ZSWIM4	2.1127	2.62E-05	0.00073222	up
SNORD83A	2.7060	2.65E-05	0.00073856	up
VNN3	3.0429	2.72E-05	0.00075623	up

NLRP12	3.6681	2.72E-05	0.00075623	up
NINJ1	1.6068	2.73E-05	0.00075763	up
FGF7	2.5318	2.73E-05	0.00075763	up
PTCSC1	3.2888	2.78E-05	0.00077029	up
GADD45B	2.0685	2.78E-05	0.00077029	up
VCAN	3.3335	2.79E-05	0.0007716	up
ZNF514	-1.0428	2.83E-05	0.00077946	down
ULBP1	3.8360	2.83E-05	0.00077946	up
SLC23A3	-4.0098	2.88E-05	0.00079139	down
EPHX2	-2.7447	2.88E-05	0.00079139	down
MBLAC1	-1.2906	2.94E-05	0.00080736	down
GUCA2A	-7.1553	2.96E-05	0.0008108	down
NFKB1	1.0319	2.96E-05	0.0008108	up
CMBL	-2.9466	2.99E-05	0.00081693	down
B4GALNT2	-6.1561	2.99E-05	0.00081693	down
OLR1	2.4516	3.01E-05	0.0008209	up
TAT	-4.0715	3.02E-05	0.00082244	down
TLNRD1	1.6261	3.05E-05	0.00082839	up
ADAMTS1	2.7766	3.06E-05	0.00082974	up
SEMA6B	2.5151	3.08E-05	0.00083287	up
DENND3	1.0583	3.09E-05	0.00083533	up
LOC105369614	-3.5621	3.11E-05	0.00084001	down
TCEAL9	1.7594	3.17E-05	0.00085314	up
LIMK2	1.1205	3.17E-05	0.00085314	up
HOMER1	2.6465	3.19E-05	0.000856	up
ACADSB	-1.0581	3.19E-05	0.000856	down
SDCBP	1.4689	3.20E-05	0.0008567	up
AMY2B	-1.1467	3.23E-05	0.00086372	down
MCTP1	1.9130	3.24E-05	0.00086682	up
PNPLA8	1.1861	3.25E-05	0.00086682	up
LOX	2.3372	3.31E-05	0.00087913	up
SMC2-AS1	-3.2262	3.36E-05	0.00089119	down
BID	1.1125	3.37E-05	0.0008922	up
HSP90AB2P	2.2283	3.39E-05	0.00089771	up
ZNF697	1.2451	3.41E-05	0.00090114	up
GSDMC	2.6499	3.46E-05	0.00091143	up
POLR3D	1.2608	3.46E-05	0.00091143	up
MS4A2	-2.5313	3.47E-05	0.00091143	down
CLSTN3	1.1568	3.46E-05	0.00091143	up
SYCP3	-2.5351	3.49E-05	0.00091567	down
MEP1B	-6.4007	3.56E-05	0.00093055	down

STPG1	-1.0261	3.57E-05	0.00093179	down
MEP1A	-6.2791	3.58E-05	0.00093427	down
IL13RA2	4.4363	3.59E-05	0.00093427	up
CLEC2B	1.5799	3.60E-05	0.00093689	up
CD160	-2.8308	3.61E-05	0.00093801	down
LINC01359	-1.6676	3.62E-05	0.00093864	down
IDNK	-2.0056	3.63E-05	0.00093963	down
MIR22HG	1.2608	3.64E-05	0.00094063	up
SLC39A1	1.4359	3.65E-05	0.00094101	up
NSUN5P1	-1.1302	3.65E-05	0.00094101	down
LINC01235	3.7315	3.65E-05	0.00094101	up
APOA1	-6.2975	3.66E-05	0.00094101	down
ANO5	-1.9661	3.68E-05	0.0009433	down
PTGER2	2.1931	3.68E-05	0.0009433	up
ARPC5L	1.2969	3.70E-05	0.00094805	up
SLC16A6	2.8950	3.75E-05	0.0009571	up
LRRC75B	-1.9460	3.76E-05	0.00095943	down
TRIB3	3.3374	3.79E-05	0.00096522	up
YARS1	1.2693	3.92E-05	0.00099161	up
GCA	1.6596	3.91E-05	0.00099161	up
BDNF-AS	-1.0305	3.95E-05	0.00099718	down
LRRC71	1.9971	3.96E-05	0.00099902	up
CASP4	1.0901	3.98E-05	0.00100347	up
HSPA5P1	2.9222	4.00E-05	0.00100732	up
CXCL5	6.0813	4.04E-05	0.00101505	up
TWNK	1.2837	4.11E-05	0.00103273	up
HSPH1	3.3101	4.14E-05	0.00103875	up
LOC100288073	2.6400	4.19E-05	0.00104714	up
HOXA3	-1.0185	4.26E-05	0.00105812	down
ACVR2B-AS1	-1.9383	4.29E-05	0.00106214	down
LINC00865	-1.9385	4.32E-05	0.0010689	down
ULBP2	3.5812	4.36E-05	0.00107658	up
DCAF13	1.1806	4.37E-05	0.00107905	up
ARL13B	1.0596	4.40E-05	0.00108444	up
LOC107985246	-1.3266	4.44E-05	0.00109162	down
SSH1	1.1617	4.47E-05	0.00109782	up
DAW1	5.0176	4.51E-05	0.00110596	up
SLC2A11	-1.2409	4.52E-05	0.0011066	down
CLEC12A	2.4924	4.65E-05	0.00113167	up
MROH7	-2.6405	4.69E-05	0.00114001	down
RWDD3	-1.0666	4.72E-05	0.0011441	down

PDZRN4	-4.5060	4.73E-05	0.0011441	down
KCNH6	-5.2199	4.73E-05	0.0011441	down
ZNF572	-1.7236	4.74E-05	0.00114499	down
RSRP1	-1.4083	4.76E-05	0.00114745	down
MPV17L	-1.6151	4.77E-05	0.00114839	down
LY6G6C	3.0385	4.85E-05	0.00116794	up
PLEKHM2	1.0142	4.87E-05	0.00116864	up
TREH	-4.6822	4.87E-05	0.00116864	down
SHBG	-3.9468	4.95E-05	0.00118356	down
COMP	4.6983	5.01E-05	0.00119561	up
MAK16	1.2915	5.03E-05	0.0011984	up
CTSL	2.5089	5.05E-05	0.00120033	up
SLC46A3	-2.6305	5.08E-05	0.00120338	down
MIR600HG	-1.9841	5.10E-05	0.00120426	down
RAB37	-1.8469	5.17E-05	0.00121759	down
BDKRB2	1.8256	5.24E-05	0.00123115	up
RAB8B	1.0364	5.31E-05	0.00124777	up
GLA	1.0288	5.39E-05	0.00126165	up
AQP11	-2.6278	5.39E-05	0.00126165	down
MFSD8	-1.0443	5.41E-05	0.00126288	down
FOXO4	-1.2321	5.43E-05	0.00126585	down
SMIM3	1.7934	5.46E-05	0.00127098	up
ZNF112	-1.0631	5.49E-05	0.00127775	down
MROH5	5.2108	5.54E-05	0.00128507	up
ZNF607	-1.3490	5.54E-05	0.00128507	down
TIGAR	1.3921	5.57E-05	0.00128931	up
CD300E	3.7903	5.57E-05	0.00128931	up
IER2	1.1209	5.60E-05	0.00129322	up
ARHGAP33	-1.1289	5.82E-05	0.00133868	down
C15orf39	1.1559	5.87E-05	0.00134805	up
MARCO	4.8519	5.91E-05	0.0013559	up
CLPB	1.2334	5.91E-05	0.0013559	up
HOXB8	-2.2839	5.92E-05	0.0013559	down
SULF2	1.6818	5.95E-05	0.00136067	up
NFKBIA	1.9998	5.99E-05	0.00136996	up
PIM1	1.7201	6.02E-05	0.00137038	up
SMPD3	-4.0451	6.01E-05	0.00137038	down
PLEKHA4	1.7361	6.01E-05	0.00137038	up
FSTL3	2.2156	6.03E-05	0.00137111	up
TKTL1	3.4251	6.08E-05	0.00138267	up
VEPH1	3.0921	6.10E-05	0.00138335	up

TMEM220	-2.6100	6.09E-05	0.00138335	down
ATG9B	3.0161	6.16E-05	0.00139336	up
COQ9	-1.1284	6.24E-05	0.00140821	down
CD55	2.1530	6.32E-05	0.00142458	up
QRFP	3.0990	6.37E-05	0.00143399	up
GATA6-AS1	-3.5674	6.41E-05	0.00143978	down
RN7SKP16	2.1984	6.47E-05	0.00144959	up
GDPD2	-5.6688	6.49E-05	0.00145183	down
IPO4	1.5197	6.52E-05	0.00145494	up
RNF207	-1.0635	6.61E-05	0.00147197	down
ADGRA3	-1.0028	6.64E-05	0.0014771	down
SH3GLB2	-1.0181	6.66E-05	0.00147871	down
OSCAR	3.0517	6.86E-05	0.00151867	up
TPBGL	2.1372	7.00E-05	0.00154643	up
HSP90B3P	1.4564	7.01E-05	0.00154725	up
LRRC15	3.5761	7.02E-05	0.00154725	up
LINC02829	-4.4524	7.03E-05	0.00154725	down
BCAS1	-4.8862	7.05E-05	0.00155121	down
CRAT	-1.0961	7.10E-05	0.00156105	down
LOC100507437	-1.2153	7.13E-05	0.00156438	down
RAPH1	1.6105	7.15E-05	0.00156531	up
REM2	2.4465	7.23E-05	0.00157914	up
JMJD6	1.2335	7.35E-05	0.00160286	up
SRXN1	1.6649	7.44E-05	0.0016149	up
INPP5J	-3.8732	7.46E-05	0.0016184	down
PCK2	-3.1547	7.48E-05	0.00162097	down
SLC16A9	-2.8619	7.60E-05	0.00164052	down
PPIP5K1	-1.3186	7.59E-05	0.00164052	down
IRF9	-1.1148	7.79E-05	0.00167586	down
PHF7	-1.2263	7.96E-05	0.0017054	down
CCDC151	1.6433	8.13E-05	0.00174144	up
PLB1	-3.9351	8.15E-05	0.00174146	down
CARNS1	-2.6648	8.14E-05	0.00174146	down
ENTPD5	-2.6618	8.17E-05	0.00174417	down
IGSF9	-4.4960	8.24E-05	0.00175842	down
PYY	-5.9456	8.26E-05	0.00176134	down
PIFO	-2.9695	8.34E-05	0.0017725	down
PRKAB2	-1.3938	8.33E-05	0.0017725	down
GPR75	1.7854	8.34E-05	0.0017725	up
SLC14A2	-3.5988	8.33E-05	0.0017725	down
CRIP3	-2.5727	8.39E-05	0.00178012	down

ABCC13	-4.5810	8.54E-05	0.00180786	down
SEMA3F	1.5866	8.61E-05	0.00181817	up
PDE5A	-2.2325	8.61E-05	0.00181817	down
SLC51B	-4.2672	8.60E-05	0.00181817	down
SNHG22	-1.4718	8.63E-05	0.00182017	down
RYR3	-2.1370	8.64E-05	0.00182152	down
ZC3H12A	2.2144	8.72E-05	0.00183619	up
ZNF519	-1.7739	8.74E-05	0.00183817	down
CEP44	-1.0970	8.76E-05	0.00184032	down
C9orf24	-2.8138	8.79E-05	0.00184522	down
FAM98C	-1.0779	8.81E-05	0.00184852	down
HES7	2.2846	8.89E-05	0.00186217	up
PROSER2	2.1447	8.91E-05	0.00186229	up
LINC00886	-1.7832	8.94E-05	0.00186678	down
KCNJ15	3.4322	8.95E-05	0.00186678	up
TSBP1-AS1	-2.4206	9.01E-05	0.00187716	down
MGAM	-4.6635	9.10E-05	0.00189194	down
ZNF488	-4.3064	9.18E-05	0.00190541	down
ZNF782	-1.3630	9.19E-05	0.00190561	down
RPS2P46	1.1782	9.22E-05	0.00190753	up
GRPEL1	1.1498	9.26E-05	0.00191145	up
CHRDL2	4.8748	9.27E-05	0.00191145	up
FNIP2	1.1970	9.28E-05	0.00191206	up
ZNF469	2.8502	9.33E-05	0.00192166	up
SLC4A10	-2.3015	9.41E-05	0.00193404	down
CD300H	3.1924	9.42E-05	0.00193445	up
CMTM2	2.6604	9.50E-05	0.00194833	up
LOC107987462	2.9584	9.52E-05	0.00195107	up
TMEM25	-2.5061	9.54E-05	0.0019546	down
MEFV	2.3923	9.76E-05	0.00199229	up
MMP19	3.6083	9.78E-05	0.00199406	up
ARNTL2	1.9733	9.83E-05	0.00200109	up
PRR7	1.8252	9.87E-05	0.00200633	up
IL27	3.7538	9.89E-05	0.00200933	up
CHD1	1.0503	9.91E-05	0.00201219	up
ASB16-AS1	-1.3815	9.95E-05	0.00201807	down
AMOT	-1.5286	9.96E-05	0.0020189	down
CCDC152	-3.0288	0.00010129	0.00204414	down
RCN1	1.4108	0.00010175	0.00205177	up
WIPI1	1.6532	0.00010386	0.00209078	up
CDH11	1.8235	0.00010411	0.00209416	up

CTHRC1	2.1225	0.00010665	0.00214006	up
ACADM	-1.1907	0.00010677	0.00214057	down
ZNRD1ASP	-1.3205	0.00010786	0.00215728	down
SIK1B	2.4946	0.00010798	0.00215786	up
GCKR	3.2546	0.00010852	0.00216692	up
ADGRE2	2.4677	0.00010895	0.00217372	up
MMP10	6.2202	0.00010952	0.00218142	up
HCK	2.5610	0.00010951	0.00218142	up
G6PC	-6.3673	0.00011012	0.0021917	down
GCNT4	-2.8934	0.0001103	0.00219226	down
AMIGO1	-1.7712	0.00011173	0.0022112	down
FADS1	1.6709	0.00011228	0.00221842	up
HOXA10	-3.8996	0.00011241	0.00221914	down
SEC23B	1.0791	0.00011431	0.00224954	up
PDK2	-1.6784	0.00011722	0.00229568	down
IFI27	-1.9148	0.00011815	0.00231214	down
CIRBP-AS1	1.1364	0.00011894	0.00232189	up
CCDC162P	-2.8657	0.00012018	0.00234441	down
PANK1	-2.5129	0.00012205	0.00237703	down
TLCD3A	1.3541	0.00012308	0.00239517	up
EXOC6B	-1.1134	0.00012385	0.00240832	down
KCNQ3	1.9201	0.00012425	0.00241409	up
LINC00473	2.0978	0.00012538	0.00243035	up
CCDC183	-1.9232	0.00012651	0.00244825	down
DNAAF1	2.2705	0.00012694	0.00245465	up
NGFR	2.2364	0.0001277	0.00246744	up
HYAL3	1.1974	0.000128	0.00247129	up
PDZK1	-4.5757	0.00012815	0.00247227	down
USP32	1.0245	0.00012843	0.00247569	up
LOC101927495	-4.0481	0.00012937	0.00248991	down
HMGB1P49	-3.3608	0.00012948	0.00249002	down
CD163	3.8533	0.00013113	0.00251594	up
CCDC9B	-2.3212	0.00013124	0.00251609	down
KBTBD7	-1.0136	0.00013452	0.00256888	down
APOM	-2.4446	0.00013489	0.00257397	down
SSH3	-1.1067	0.00013502	0.00257447	down
NTS	-4.5333	0.00013807	0.00262638	down
DNTTIP2	1.1282	0.00013902	0.00263788	up
TNNC2	-2.6940	0.0001391	0.00263788	down
LINC01748	-3.2795	0.00013954	0.0026441	down
NDUFV2	2.0067	0.00013987	0.00264838	up

MANEA-DT	-2.1980	0.00014003	0.00264936	down
LOC100129844	3.0150	0.00014058	0.0026557	up
PWP2	2.2455	0.00014054	0.0026557	up
TEX52	-1.9108	0.00014148	0.00266961	down
ZNF248	-1.2633	0.00014347	0.00270186	down
CA3	-2.1767	0.00014422	0.00271243	down
CCN2	2.0235	0.0001466	0.00274801	up
NOD2	1.6484	0.00014649	0.00274801	up
BRIX1	1.1643	0.00014735	0.00275385	up
PPIB	1.1759	0.00014746	0.00275385	up
ZNF827	-1.6296	0.00014791	0.00276006	down
NAP1L1P1	1.2371	0.00014932	0.0027842	up
SRP14P4	-3.2274	0.00015145	0.00281711	down
IL1R1	2.0430	0.00015181	0.00281711	up
NOCT	1.7136	0.00015182	0.00281711	up
PLN	-3.4518	0.000152	0.00281711	down
CHN2	-3.0419	0.00015194	0.00281711	down
FLT1	2.3229	0.00015231	0.00282081	up
LIPG	2.3306	0.0001528	0.00282765	up
GSTM4	-1.8760	0.00015319	0.00283283	down
TAF13	1.4790	0.00015407	0.00284513	up
HEPH	-2.6818	0.00015485	0.0028526	down
PARD3B	-1.4474	0.00015608	0.00286886	down
PPBP	3.9863	0.00015654	0.00287512	up
LCP2	1.3157	0.00015683	0.00287837	up
LINC01558	-2.5354	0.00015746	0.00288766	down
LINC01465	1.4399	0.00015802	0.00289369	up
MIR3936HG	-2.2411	0.00015914	0.00290768	down
FKBP10	1.8915	0.00016043	0.0029291	up
AGO2	1.0546	0.00016114	0.00293984	up
BCL6	2.2769	0.00016138	0.00294086	up
TM6SF2	-4.4616	0.00016276	0.00296065	down
LINC00574	-4.3846	0.00016325	0.00296726	down
TPST1	1.6199	0.00016534	0.00299859	up
STARD13-AS	2.3660	0.00016619	0.00301181	up
SLC7A4	-2.1865	0.00016677	0.00302017	down
HR	-1.3698	0.00016773	0.00303529	down
MFSD13B	-2.0747	0.00016798	0.0030376	down
TLCD4	-1.8054	0.00016855	0.00304327	down
CASR	-4.9147	0.00016849	0.00304327	down
LINC00923	-2.0895	0.00017018	0.00306976	down

NOP10	1.1323	0.00017039	0.00306976	up
LOC644656	-1.5882	0.00017376	0.00312135	down
ASTL	3.8429	0.00017449	0.00313117	up
ABRA	4.4043	0.00017456	0.00313117	up
EDNRB	1.5804	0.00017545	0.00314247	up
NKD2	2.4795	0.00017728	0.00316928	up
CYS1	-3.3075	0.00017776	0.00317463	down
PRKG2	-3.1163	0.0001788	0.0031818	down
RNF144B	1.9132	0.00018242	0.00324135	up
LYPLAL1-DT	-3.0727	0.00018278	0.00324526	down
HPGD	-2.9983	0.00018383	0.00325924	down
ACSS1	-1.6601	0.00018484	0.00327481	down
LBP	6.2829	0.00018547	0.00328125	up
RCL1	1.2472	0.0001869	0.00330175	up
ADGRG1	1.7643	0.00018807	0.00331764	up
TRANK1	-1.4356	0.00019232	0.00338519	down
CEBPD	1.6929	0.00019388	0.00341026	up
MLKL	1.5971	0.00019469	0.00342205	up
HNF1A-AS1	-5.0200	0.00019484	0.0034223	down
ERICH4	-4.1922	0.0001952	0.00342362	down
ACP6	-1.1592	0.00019722	0.00345421	down
PTGDR	-1.8650	0.00019884	0.00347505	down
DNAJB1	3.4954	0.00020184	0.00351757	up
LMCD1	2.7287	0.00020262	0.00352611	up
COL24A1	-2.5093	0.00020547	0.00356557	down
GSTM2	-1.8213	0.00020697	0.00358911	down
HILPDA	2.0094	0.00021189	0.00366406	up
LINC01778	-4.3880	0.0002132	0.00368406	down
IMPDH1P10	2.4609	0.0002141	0.00369437	up
MAT2A	1.1148	0.00021607	0.00372315	up
TLR3	-1.4925	0.00021731	0.00373657	down
IFI16	1.2800	0.0002191	0.00376208	up
C1QTNF7	-2.9332	0.00021943	0.00376508	down
ABCC6P2	-3.2255	0.00022017	0.00377519	down
HOXB-AS3	-1.4646	0.00022193	0.00380266	down
SLC52A1	-4.4501	0.00022237	0.00380767	down
LOC100505664	2.5450	0.00022286	0.00380828	up
LOC101928058	-3.2690	0.00022599	0.00385615	down
BCDIN3D-AS1	-1.8037	0.00022714	0.00387311	down
ITGA5	2.4085	0.00023184	0.00393956	up
UNC5A	2.3881	0.00023306	0.00395475	up

IL1A	5.3884	0.00023474	0.00397775	up
CLCN1	-3.2705	0.0002363	0.00399862	down
LOC102724330	-1.4315	0.00023993	0.0040461	down
CDK20	-1.3720	0.00024038	0.0040497	down
LOC554206	-1.4426	0.00024052	0.0040497	down
CCL3L3	3.1889	0.00024064	0.0040497	up
WDR3	1.0512	0.0002452	0.00410674	up
SLC7A2	1.7254	0.0002461	0.00411619	up
ZNF439	-1.5787	0.00024789	0.00414338	down
ZNF267	1.1941	0.00024818	0.00414532	up
LOC100133315	-1.3230	0.00025012	0.00416921	down
SNORD15B	3.0248	0.00025101	0.0041813	up
PKM	1.0524	0.00025122	0.00418182	up
LINC00242	-1.7694	0.00025211	0.00419099	down
CEBPB-AS1	-1.6483	0.00025371	0.00421473	down
STARD5	-2.2673	0.00025409	0.00421827	down
SLC35E2A	-1.4832	0.00025434	0.00421957	down
GNRHR2	-1.9179	0.00025807	0.00426295	down
ENPEP	-3.6725	0.00025934	0.0042793	down
MSX1	2.8029	0.00025979	0.00428227	up
LOC101927702	-2.3839	0.00025987	0.00428227	down
CD1C	-3.2417	0.00026121	0.00430071	down
PEAK3	1.7627	0.00026134	0.00430071	up
ACOXL	-1.5530	0.00026248	0.00431532	down
ARF4	1.3064	0.00026258	0.00431532	up
MS4A8	-5.4444	0.00026523	0.00435015	down
ARTN	2.2920	0.00026554	0.00435227	up
ITGA10	2.6107	0.00026743	0.00437455	up
FRMD1	-4.5150	0.00026784	0.00437837	down
BCL2A1	2.6962	0.00026934	0.00439697	up
ECI1	-1.0608	0.0002698	0.00440154	down
IL17RA	1.3742	0.00027065	0.00441254	up
SLC37A4	-2.4627	0.00027128	0.00441984	down
MROCKI	-3.0283	0.00027209	0.00442713	down
CDHR5	-5.2214	0.00027267	0.0044336	down
GGCT	1.0683	0.00027303	0.0044365	up
ACCS	-1.7001	0.0002736	0.00444285	down
GRTP1	-2.5108	0.00027613	0.00447796	down
LOC100506302	-2.1007	0.00027934	0.00452399	down
ZBED8	-1.6056	0.00028008	0.00453306	down
TMEM221	-1.7756	0.00028091	0.00454045	down

CYBRD1	-1.8250	0.00028491	0.00458648	down
ABHD6	-1.8682	0.0002848	0.00458648	down
CNGB3	-4.6300	0.0002847	0.00458648	down
SAXO2	-2.1183	0.000285	0.00458648	down
LOC107984142	-1.8333	0.00028497	0.00458648	down
LOC105372401	1.2348	0.00028507	0.00458648	up
KCNJ2	1.3007	0.0002855	0.0045905	up
FTH1P2	1.8721	0.0002867	0.00460365	up
LPCAT1	1.0834	0.0002884	0.00462492	up
DPY19L1	1.0161	0.00028923	0.0046352	up
FMO5	-3.2831	0.00028981	0.00464145	down
PNRC1	1.0722	0.00029065	0.00465196	up
ORM1	3.8864	0.00029223	0.00467419	up
NTM	-2.7035	0.00029384	0.00469114	down
SNORD19	3.1064	0.00029527	0.00470843	up
PRRG3	-2.0522	0.00029695	0.00473113	down
SUCLG1	-1.3480	0.00029786	0.00473639	down
CD93	2.1202	0.00029875	0.00474446	up
ACVRL1	1.3023	0.00029977	0.0047575	up
F5	2.3624	0.00030217	0.00478321	up
GRM2	2.9537	0.00030277	0.00478965	up
GABRD	2.2079	0.00030331	0.00479503	up
AADAC	-4.6063	0.00030698	0.00484097	down
REP15	-3.3811	0.00030686	0.00484097	down
BTN3A1	-1.1411	0.00030792	0.00485238	down
BCHE	-3.3235	0.0003091	0.0048678	down
CCL26	2.5374	0.00031267	0.00491762	up
LOC105378083	-1.0349	0.00031404	0.0049305	down
RAD51-AS1	-1.1591	0.00031409	0.0049305	down
PLD4	-3.1207	0.0003148	0.00493851	down
RPGR	1.3033	0.00031659	0.00496021	up
NDUFA6-DT	-1.8065	0.00031686	0.00496133	down
SLC35E4	1.5882	0.00031881	0.00498541	up
CYP2B6	-5.6715	0.00031903	0.00498569	down
MAGI3	-1.2797	0.0003215	0.00500736	down
LAMC1-AS1	1.7147	0.00032147	0.00500736	up
RMDN2	-1.6480	0.0003212	0.00500736	down
VSIG10	-2.0295	0.00032461	0.00504728	down
PLA2R1	-1.7469	0.0003252	0.00505004	down
CABCOCO1	-4.3435	0.00032609	0.00505733	down
SLC22A15	1.1024	0.00032749	0.00506628	up

SPTSSA	1.0287	0.00033263	0.00513928	up
TMEM229B	-1.5792	0.00033286	0.00513967	down
FLT1P1	2.5782	0.00033641	0.00518787	up
TTC23L-AS1	-2.0603	0.00034091	0.00525062	down
F2RL3	2.6329	0.00034152	0.00525675	up
PRRX2	2.2584	0.0003418	0.00525785	up
ABCA5	-1.9423	0.00034264	0.00526737	down
ECSCR	1.2882	0.00034563	0.00530007	up
ZNF823	-1.0416	0.00034767	0.00532801	down
GARS1	1.4302	0.00034887	0.00534304	up
BMP3	-4.0101	0.00035372	0.00540724	down
LINC02175	-1.3832	0.00035365	0.00540724	down
TPSG1	-3.1807	0.00035439	0.00541405	down
AP2S1	1.0907	0.00035516	0.0054196	up
XPNPEP2	-3.7081	0.00036006	0.0054803	down
COQ4	-1.1823	0.00036144	0.00549779	down
NOX1	-2.7827	0.00036208	0.00549836	down
RILPL2	1.4673	0.00036184	0.00549836	up
PHLPP2	-2.3923	0.0003639	0.00551476	down
LOC101928725	-3.3957	0.00036528	0.00553218	down
FKBP1C	1.6296	0.00036634	0.00554478	up
GOLT1B	1.3397	0.00037354	0.00563649	up
VSIG4	3.9005	0.00037408	0.00564112	up
PGM5-AS1	-3.5429	0.00037498	0.00564809	down
RHBDF2	1.6536	0.000375	0.00564809	up
TACR2	-3.8492	0.00037525	0.00564833	down
B3GALT6	1.0275	0.0003781	0.00568082	up
YBX2	-3.0410	0.00037846	0.00568262	down
NHSL1	-2.1736	0.00038008	0.0056965	down
C6orf136	-1.7050	0.00038066	0.00569831	down
TCTEX1D4	2.2286	0.00038112	0.00570176	up
PHLDA2	2.5025	0.00038335	0.00572547	up
STEAP1	2.4205	0.000389	0.00579004	up
AGBL2	-2.3973	0.00038939	0.00579004	down
HCG27	-1.7624	0.00039152	0.0058078	down
SMLR1	-5.7773	0.00039153	0.0058078	down
IGSF3	-2.0260	0.00039198	0.00581043	down
NIPAL3	-1.0080	0.00039319	0.00582185	down
TWIST1	2.9004	0.00039465	0.00583638	up
BPHL	-1.7968	0.00039781	0.00587613	down
ADAMTS3	1.9555	0.00039889	0.0058885	up

KLF16	1.1663	0.00040393	0.00595568	up
ZFP3	-1.0612	0.00040815	0.0060107	down
FAM177B	-2.9863	0.0004088	0.0060167	down
RALGPS1	-2.1655	0.00040949	0.00602314	down
COL4A2-AS1	2.0197	0.0004106	0.00603589	up
ZMAT1	-1.0414	0.00041188	0.00604744	down
ROR1-AS1	2.0153	0.00041329	0.00605714	up
IRAK2	2.0524	0.00041712	0.00608793	up
SH3PXD2B	1.6655	0.00041711	0.00608793	up
TMEM236	-3.5866	0.00041693	0.00608793	down
ABCC6P1	-3.8458	0.00041693	0.00608793	down
NR4A1	2.6127	0.00041871	0.00610424	up
DHRS4-AS1	-1.3785	0.00041873	0.00610424	down
PGM3	1.0343	0.00041947	0.00611141	up
TSPOAP1	-2.0024	0.00042007	0.00611242	down
PRND	-4.1310	0.00042028	0.00611242	down
KCNJ14	2.0731	0.00042054	0.00611242	up
ZNF91	-1.4806	0.00042601	0.0061772	down
SHD	-3.6445	0.00042671	0.00618371	down
GSTO1	1.1921	0.00042777	0.00619483	up
LOC400499	2.3183	0.0004282	0.00619483	up
ZFP36	1.4696	0.00043138	0.00623296	up
AGFG1	1.2084	0.00043382	0.00626263	up
CEBPA-DT	-2.0185	0.00043394	0.00626263	down
RAB9B	-2.4292	0.00043442	0.00626585	down
TNIP3	2.5734	0.00043558	0.00627547	up
DAAM2-AS1	1.1397	0.0004356	0.00627547	up
ECRG4	-2.3103	0.00043739	0.00629762	down
FCGR2A	2.7052	0.00044657	0.00641473	up
IGSF10	-2.6190	0.00044875	0.00644222	down
CCL8	2.1873	0.00045035	0.00646002	up
PHGR1	-6.0059	0.00045169	0.00646547	down
PF4	3.1783	0.00045267	0.00647574	up
HEATR4	-1.1495	0.00045403	0.00648904	down
GFER	-1.3312	0.00045413	0.00648904	down
CCT5P1	1.0474	0.00045686	0.00652051	up
GNA11	-1.8208	0.00045727	0.00652249	down
OLAH	3.7660	0.00045771	0.00652508	up
ST3GAL1	1.9818	0.00046341	0.00659857	up
ST8SIA1	-2.0128	0.0004653	0.00662168	down
CFAP44	-1.0285	0.00046808	0.00664965	down

PGK1	1.0232	0.00046836	0.0066498	up
MSN	1.4190	0.0004698	0.00666251	up
CCIN	3.2801	0.00047208	0.00668705	up
LINC00365	-3.3133	0.00047336	0.00669405	down
CROT	-1.4821	0.00047761	0.00674202	down
LINC00570	-3.2156	0.0004792	0.00675784	down
SEMA4G	-3.1702	0.00047928	0.00675784	down
TTLL6	-3.6595	0.00048148	0.0067772	down
ZBTB26	-1.1288	0.00048207	0.00678063	down
KLRK1-AS1	-1.5842	0.00048241	0.00678063	down
MARCHF3	1.6779	0.00048404	0.00679368	up
TMEM253	-3.3742	0.00048451	0.00679644	down
BTNL8	-4.3868	0.00048651	0.00680893	down
RAG1	-1.8721	0.0004865	0.00680893	down
IL10	3.2610	0.00049139	0.00686942	up
LILRB2	3.2195	0.00049316	0.0068823	up
LINC02747	-5.0051	0.00049389	0.00688856	down
HTR2B	-3.4695	0.00049513	0.00690199	down
SGTB	1.7376	0.0004968	0.00691745	up
HOXA6	-2.0617	0.00049662	0.00691745	down
PRDM16-DT	-1.2582	0.00049839	0.00693168	down
SIRT4	-1.4546	0.00050075	0.00696059	down
LRP8	2.0779	0.00050159	0.00696238	up
PARP3	-1.0379	0.00050148	0.00696238	down
MLPH	-2.9353	0.00050355	0.00697971	down
FOSL2	1.4602	0.00050842	0.00703521	up
SHMT2	1.3018	0.00050814	0.00703521	up
LINC00271	-2.0431	0.00051721	0.00713669	down
MIR6746	3.3103	0.00052106	0.00717366	up
RPS6KA5	-1.7853	0.00052088	0.00717366	down
FMO4	-2.0161	0.00052266	0.00719171	down
SLC2A6	1.8163	0.00052391	0.00720084	up
DPY19L2P2	-2.2692	0.00052666	0.00722646	down
LINC02777	-1.8565	0.00052917	0.0072569	down
C1orf115	-2.3965	0.00053169	0.00728728	down
ADAM9	1.1982	0.00053599	0.00733394	up
LOC105377623	-1.8161	0.00053712	0.00734129	down
LY6K	3.0629	0.00053688	0.00734129	up
TKFC	-2.5862	0.00053995	0.00734954	down
RPS6P1	2.1191	0.00053974	0.00734954	up
NRCAM	2.4605	0.00054395	0.00739342	up

FN3K	-1.2933	0.00054756	0.00743006	down
SNORD89	1.5559	0.00055279	0.00749281	up
PGM2L1	1.3154	0.00055272	0.00749281	up
PDZD3	-4.1790	0.00055845	0.00756533	down
ENO1	1.1662	0.00056037	0.00758713	up
TOMM34	1.0023	0.00056098	0.00759115	up
NECTIN2	1.0779	0.00056233	0.00759848	up
LOC100130950	-1.2880	0.00056303	0.00760218	down
ADA	1.4083	0.00056352	0.00760462	up
NPTX1	-4.4670	0.00056458	0.00761368	down
MMP14	1.3379	0.00056765	0.00763922	up
NFKBIE	1.8641	0.00057171	0.00768931	up
SLC2A1	2.5400	0.00057342	0.00769158	up
STAM-AS1	-2.2538	0.00057293	0.00769158	down
OAT	-2.2790	0.00057635	0.00772246	down
ZNF443	-1.1391	0.00057673	0.00772334	down
LINC01503	2.6502	0.0005786	0.00774413	up
HAPLN3	1.7065	0.00058059	0.00776225	up
AGAP2-AS1	1.2153	0.00058532	0.00781704	up
ACTG1P25	-2.8669	0.0005861	0.00782275	down
MEG9	2.0581	0.00058639	0.00782275	up
METRNL	1.2744	0.00059296	0.0078975	up
HLA-DMB	-2.1631	0.0005985	0.00794547	down
CYP4V2	-1.4488	0.00060294	0.00799577	down
LOC101928834	-2.9989	0.00060341	0.00799763	down
VPS13A	-1.4744	0.00060422	0.00800404	down
F3	1.5917	0.00060651	0.00803009	up
DNAJA1	1.4888	0.00060704	0.00803272	up
AMZ2P1	-1.0185	0.00060927	0.00804914	down
JRK	-1.0131	0.00061044	0.00805293	down
LOC102724684	-1.8351	0.00061135	0.00805929	down
CYB561D2	-2.5110	0.00061297	0.00806435	down
KYNU	2.4298	0.00061611	0.00808725	up
MANF	1.3738	0.00061695	0.00809392	up
LINC01482	2.8732	0.0006225	0.00816234	up
FRMD3	-1.3627	0.00062409	0.00817884	down
PIPOX	-2.4236	0.00062479	0.00818368	down
SERPINB9	1.5024	0.00062532	0.00818632	up
RBMS1	1.5230	0.00063012	0.00824031	up
IFNAR2	1.0173	0.00063128	0.00825103	up
ALDH3A2	-1.0388	0.00063236	0.00825641	down

NOC3L	1.1023	0.00063453	0.00827832	up
RTL1	3.5275	0.00063548	0.00828388	up
FKBP11	1.2726	0.00063725	0.00829366	up
TFPI2	4.0073	0.00063761	0.00829399	up
PPAT	1.0798	0.000638	0.00829466	up
SDS	3.0761	0.00063991	0.00831515	up
CYB5RL	-1.0228	0.00064069	0.00832087	down
PLPP6	-1.2711	0.00064234	0.00833343	down
GOLGA2P5	-2.3469	0.00064333	0.00833545	down
TMEM229A	-4.0159	0.00064559	0.00834907	down
UGT2B15	-5.2445	0.00064633	0.00835425	down
RAVER2	-1.7577	0.00064896	0.00837498	down
MRGPRF-AS1	-2.2485	0.00065801	0.00847398	down
IL18RAP	1.6574	0.00065845	0.00847441	up
FZD7	-1.6730	0.00065888	0.00847441	down
ACSM3	-1.6060	0.00065933	0.00847441	down
RELA-DT	-1.1664	0.00066002	0.00847753	down
COQ10B	1.0156	0.00066357	0.00851872	up
TDP2	-2.3101	0.00067345	0.00862744	down
ADGRE1	2.6758	0.0006762	0.0086582	up
RPSAP12	1.5669	0.00068383	0.00873781	up
CLEC4E	2.4400	0.00068472	0.0087444	up
PDE4D	2.1836	0.00068513	0.00874515	up
PTAFR	2.1932	0.00069177	0.00881149	up
RASGRF2-AS1	1.7233	0.00069301	0.00882279	up
SNORA3B	1.7487	0.00069381	0.00882375	up
RPL26P4	1.4621	0.00069429	0.00882523	up
RN7SL262P	-2.5620	0.00069635	0.00882989	down
RNY1P16	-3.0348	0.00069666	0.00882989	down
SLC43A3	1.4458	0.00069858	0.00884771	up
ZNF589	-1.2995	0.00070041	0.00886239	down
C5AR1	2.9531	0.00070118	0.00886239	up
NHLH1	2.0064	0.00070359	0.00888361	up
TRPV1	-1.3946	0.00070327	0.00888361	down
RPS2P31	3.7732	0.00070879	0.0089359	up
RRS1	1.2481	0.00070882	0.0089359	up
CCDC85B	1.2957	0.00071071	0.00895507	up
ZADH2	-1.0399	0.00071366	0.00897844	down
LRRC8B	1.2311	0.0007163	0.00900696	up
SLC7A11	4.1832	0.00071813	0.00902082	up
VWA3B	-2.5380	0.00072081	0.00904519	down

RFX8	3.6935	0.00072063	0.00904519	up
DPP4	-3.2097	0.00072291	0.00905475	down
SLC30A4	-1.6188	0.00072305	0.00905475	down
TRPV6	4.7558	0.00073338	0.00916076	up
IQCH	1.5653	0.00073594	0.00918328	up
C10orf55	2.3007	0.00073692	0.00919086	up
MMEL1	-2.4670	0.00073811	0.00919648	down
TGFB1	1.2556	0.00073812	0.00919648	up
ZSWIM5	-2.1646	0.00073858	0.00919755	down
RN7SKP127	-4.8905	0.00074037	0.00921518	down
LINC02207	2.0822	0.00074523	0.00926156	up
TNFRSF4	2.1334	0.00075015	0.00929751	up
C3orf36	3.0241	0.00075062	0.00929751	up
ABCB1	-3.1164	0.000749	0.00929751	down
ABO	-2.6991	0.00075078	0.00929751	down
ACR	1.7685	0.00075066	0.00929751	up
CRYZL2P-SEC16B	-2.6877	0.00075315	0.00931749	down
ZNF311	-1.0783	0.00075526	0.00933883	down
STRADB	-1.7242	0.00076171	0.00940439	down
HEXD	-1.1009	0.0007625	0.00940866	down
ARRDC3	1.2917	0.00076703	0.00944157	up
LINC01679	1.6995	0.00076829	0.00945226	up
RPL18AP6	1.0834	0.00077221	0.00947236	up
CDK2	1.1794	0.00077224	0.00947236	up
LINC00330	-4.2805	0.00077198	0.00947236	down
LOC101928414	-4.2166	0.00077513	0.009503	down
HSP90AA1	2.3665	0.00077738	0.00952111	up
KCNA2	-2.1747	0.00077825	0.00952704	down
MASP1	-3.0629	0.00078255	0.00955501	down
ZG16	-5.7965	0.00078249	0.00955501	down
SIGLEC9	3.0225	0.00078287	0.00955501	up
INSIG1	1.5868	0.00078553	0.00958265	up
LINC02613	-3.3640	0.00078642	0.00958757	down
TTC36	-2.5827	0.0007871	0.00958757	down
PHYH	-1.2408	0.00078673	0.00958757	down
ANGPT2	2.4898	0.00079224	0.00964535	up
HECW2	1.4017	0.00079402	0.00965269	up
KHDRBS2	-3.6144	0.0007939	0.00965269	down
FSIP1	1.6273	0.00079458	0.00965467	up
ZNF385D	1.5024	0.00080029	0.00971446	up
AKR1B1	1.0573	0.00080557	0.00977362	up

ASB16	-1.5664	0.00081286	0.00984398	down
IFIT3	-1.3948	0.00081637	0.00987052	down
PFDN2	1.2152	0.00082278	0.00993329	up
TRBV19	-2.7763	0.00082894	0.00999296	down
SLC26A9	3.1553	0.00083455	0.01004941	up
KAT2B	-1.0026	0.00083485	0.01004941	down
VEGFA	1.5154	0.00083869	0.0100753	up
XAF1	-1.8530	0.00083906	0.0100753	down
CBR1	-2.0344	0.00083892	0.0100753	down
WNT2	2.8602	0.00084111	0.01009492	up
NFE2	2.9146	0.00084444	0.01011898	up
PI15	3.8278	0.00084519	0.01011918	up
TOLLIP-AS1	-1.6386	0.00084714	0.01013266	down
LINC01550	-1.9752	0.00085217	0.01017785	down
PHACTR1	1.2327	0.00085276	0.01018003	up
SNHG26	1.0560	0.00085655	0.01022023	up
CEP43	-1.0875	0.00085782	0.01023044	down
PKLR	-4.1338	0.00086847	0.01033886	down
DIO2	2.7564	0.00087174	0.01037119	up
ADAMTS2	2.5232	0.00087531	0.01040217	up
IZUMO1	2.5036	0.000875	0.01040217	up
CYP3A7	-3.2065	0.00087784	0.01041848	down
HSD11B2	-3.8164	0.00087753	0.01041848	down
DNAH7	-2.5553	0.00088002	0.01041857	down
PLTP	3.4074	0.00088032	0.01041857	up
DNASE1L3	-3.0704	0.00088685	0.0104825	down
C8G	-3.7083	0.00088719	0.0104825	down
CLEC7A	1.5335	0.00088751	0.0104825	up
LOC105375166	-4.0479	0.000889	0.01049506	down
TGFB3	1.1858	0.00088967	0.01049793	up
GZMA	-2.5255	0.00089166	0.0105113	down
SCARNA9L	-2.2741	0.00089154	0.0105113	down
RHPN1	1.1042	0.00091485	0.01074336	up
RERG	-2.3752	0.00091834	0.01077256	down
PNPLA7	-1.1281	0.00092205	0.01080725	down
CLEC12B	2.3752	0.00092304	0.0108093	up
NKAPP1	-1.2594	0.00092502	0.01082654	down
RPL7AP52	-4.6472	0.00092863	0.01085842	down
NNAT	-2.5650	0.0009297	0.01086571	down
HAAO	-2.3644	0.0009318	0.01088505	down
MTARC2	-1.5640	0.00093586	0.01090073	down

PRORSD1P	-1.0041	0.00093459	0.01090073	down
TRPV4	2.2500	0.00093444	0.01090073	up
ETS2	1.7369	0.00093547	0.01090073	up
SEMA6A	-1.4043	0.00094151	0.01095668	down
SUCLG2	-1.0503	0.00095161	0.01104214	down
TMEM117	-1.2944	0.00095177	0.01104214	down
ZNF575	-1.4289	0.0009525	0.01104214	down
AANAT	1.9953	0.00095908	0.01110844	up
CES2	-2.9197	0.00096097	0.01111986	down
TMEM254	-1.0148	0.00096342	0.01114296	down
BTG3	1.3462	0.00096766	0.01118147	up
PDIA6	1.0693	0.00096876	0.01118883	up
PNPLA3	1.9412	0.00097532	0.01125404	up
IER5	2.0827	0.00098355	0.01133306	up
BARX1	3.7929	0.00098549	0.01133642	up
ACY3	-4.6500	0.0009879	0.01135116	down
SLC1A7	-2.0198	0.00099212	0.01139432	down
ABCA10	-2.0355	0.00099687	0.01144347	down
NT5DC2	1.0162	0.00100306	0.01150064	up
PLLP	-2.1336	0.00100504	0.01151186	down
LRRC26	-4.5997	0.00100754	0.01152086	down
LOC112268292	-1.8127	0.00100784	0.01152086	down
ADHFE1	-1.3720	0.00101028	0.01154342	down
MT1A	2.6279	0.00101153	0.01155227	up
TUBA1C	1.3930	0.00101208	0.01155317	up
SLC15A1	-4.9680	0.00101449	0.01157529	down
LINC00520	5.1575	0.00101659	0.01158846	up
GSTM5	-1.9272	0.00101878	0.01160809	down
S100A11	1.8582	0.00102809	0.01169992	up
NR1I3	-2.5190	0.00102828	0.01169992	down
MSC	2.2184	0.00102927	0.01170033	up
PRXL2C	1.2954	0.00102913	0.01170033	up
PYGB	-1.3223	0.00104315	0.01184168	down
C5orf63	-1.0863	0.00104474	0.01185082	down
SRP14-AS1	-1.1774	0.00104492	0.01185082	down
PLEKHG1	1.1982	0.00104614	0.01185367	up
EMP1	2.4820	0.00104567	0.01185367	up
LINC02177	-4.0887	0.00105899	0.01197157	down
OCEL1	-1.0726	0.00106664	0.01204144	down
TNFRSF10A	1.3709	0.00107546	0.01213537	up
BASP1	1.5504	0.00109724	0.01235275	up

LOC106660606	-1.8835	0.00109788	0.01235434	down
FAM20A	2.5645	0.00110246	0.01239443	up
RAB27B	-2.3281	0.00110707	0.01244054	down
PITPNC1	1.3053	0.00110777	0.01244277	up
QPRT	-1.7181	0.00110874	0.01244797	down
ABCD1	-1.3089	0.00110933	0.01244887	down
EPGN	4.2592	0.00111615	0.01249767	up
THY1	1.8436	0.00111486	0.01249767	up
LRRC75A	-3.0577	0.00111889	0.01251604	down
PXDC1	1.1190	0.00112105	0.01253452	up
LOC107987457	1.3616	0.00112369	0.01255254	up
USP36	1.0513	0.00112884	0.01259291	up
HSPD1	2.0769	0.00114546	0.01273775	up
LINC00654	-1.2452	0.0011569	0.01283587	down
FBP1	-2.9776	0.00116008	0.0128653	down
CXXC4-AS1	-2.5046	0.0011647	0.01290489	down
SEC1P	-2.3384	0.00116596	0.01291297	down
HIF1A-AS3	2.7098	0.00117123	0.01296548	up
SLC16A3	1.6686	0.0011719	0.01296709	up
CGAS	2.0298	0.00118506	0.01309006	up
ADAM1B	-2.2787	0.00118515	0.01309006	down
SH2B3	1.4471	0.00119064	0.01314475	up
SLC51A	-3.0243	0.00119493	0.01318025	down
SMIM38	-2.8821	0.00119654	0.01319204	down
RPLP0P2	1.0749	0.00119752	0.01319695	up
CREB5	1.5347	0.00119931	0.01321069	up
SOX7	1.9255	0.00121299	0.01334347	up
OSBPL7	-1.8695	0.00121371	0.01334347	down
SRM	1.2806	0.00121767	0.01336903	up
ANO7	-3.0076	0.00122072	0.01336903	down
SNORA33	1.5297	0.00121834	0.01336903	up
KBTBD11	-1.8958	0.00121983	0.01336903	down
CYP2C19	-5.1344	0.00121979	0.01336903	down
KCTD10	1.1831	0.00122053	0.01336903	up
PTN	-2.2530	0.00122744	0.0134205	down
LINC00294	-1.1867	0.00122702	0.0134205	down
ART5	-2.3151	0.00123714	0.01350012	down
ALDH5A1	-1.6009	0.00124494	0.01357315	down
SMIM24	-4.3925	0.00125062	0.01361691	down
RPL28P2	-3.4242	0.001258	0.01366687	down
PTGDS	-2.2326	0.00126016	0.01368425	down

NOXA1	-1.9138	0.00126853	0.01376303	down
EEF1AKMT4	1.5848	0.00127632	0.01381886	up
LINC00893	-1.3168	0.0012765	0.01381886	down
LINC00479	-4.1702	0.00128305	0.01385309	down
FAM157A	1.8607	0.00129353	0.01396007	up
BTNL3	-4.5074	0.00130403	0.01403851	down
LINC00173	-1.5238	0.00130327	0.01403851	down
SNORA31	1.9583	0.00130353	0.01403851	up
SKIDA1	-2.1027	0.0013078	0.01407073	down
CAMSAP2	1.1852	0.0013098	0.01408614	up
NEURL3	-3.0771	0.00131225	0.01410628	down
TMEM220-AS1	-2.1096	0.00131851	0.01416109	down
NPY6R	-4.1241	0.00131951	0.01416236	down
SERTAD2	1.0002	0.00132074	0.01416645	up
OPCML	-2.1371	0.0013306	0.01425973	down
FAM47E	-2.1533	0.00133954	0.01432575	down
RANGAP1	1.2103	0.00133968	0.01432575	up
LINC01625	-3.5642	0.00134156	0.01433407	down
RASGRP4	1.9183	0.00134163	0.01433407	up
C22orf34	1.4013	0.0013434	0.01434674	up
ARSJ	1.6867	0.00134996	0.01440428	up
LOC339874	-2.5110	0.00135281	0.01442208	down
LOC729558	-4.5167	0.0013528	0.01442208	down
SEPSECS	-1.4147	0.00135422	0.01443087	down
SATB2-AS1	-2.7758	0.00135669	0.01445094	down
PRDM1	1.5915	0.00136155	0.01449642	up
RAB17	-3.6779	0.00136374	0.01451336	down
FLVCR1	-2.2326	0.00138082	0.01466977	down
HGF	1.6564	0.00138198	0.01467571	up
RAB32	1.1540	0.00139094	0.01476447	up
CBX8	1.4156	0.00139156	0.01476465	up
SDR42E1	-2.2021	0.0013924	0.0147672	down
HAPLN2	-3.0048	0.00139878	0.01482034	down
TMSB4XP4	1.1547	0.00139826	0.01482034	up
FOSB	2.7989	0.00139923	0.01482034	up
LOC101929532	2.4029	0.00140054	0.01482781	up
ENTPD8	-4.5106	0.00140247	0.01483501	down
CAPS	-1.1299	0.0014045	0.01484408	down
KLHDC7A	-3.1454	0.00140764	0.01487093	down
FGF9	-2.2477	0.00141152	0.0149055	down
ZNF396	-1.0418	0.00141459	0.01493143	down

MDM1	-1.1325	0.00141814	0.01496253	down
CALU	1.5498	0.00142178	0.01499444	up
POLR1G	1.5338	0.0014275	0.01504181	up
PTK7	1.2822	0.00143244	0.01508088	up
SH2D5	5.2459	0.00143396	0.01508398	up
MPO	2.4312	0.00143727	0.0151123	up
H1-2	1.3972	0.00143832	0.01511687	up
MPST	-1.8465	0.00144807	0.0152063	down
ZNF821	-1.3196	0.00144939	0.01521367	down
IFITM3	1.5107	0.00145792	0.0152901	up
FREM2	-3.2199	0.00145943	0.01529937	down
ALG1L9P	-1.2794	0.00147046	0.0153952	down
LOC101928940	3.1240	0.00147698	0.0154569	up
LRRC28	-1.2806	0.00148098	0.01549212	down
CACFD1	-1.3904	0.00148774	0.01554297	down
GPR42	3.0962	0.00149465	0.01560191	up
CYP2C18	-5.3896	0.00149735	0.01562017	down
PDIA4	1.3969	0.00149983	0.01563601	up
MAP4K4	1.0594	0.00150484	0.01568153	up
PHETA1	-1.8360	0.00150653	0.01569247	down
MISP3	-2.2769	0.00150912	0.01569944	down
STING1	1.2003	0.00154542	0.0160256	up
MSANTD3	1.6200	0.00154942	0.01605744	up
CIB2	-1.5293	0.0015684	0.01621294	down
LOC100506725	-2.1754	0.00156923	0.01621474	down
MIR3682	1.9102	0.00157744	0.01626723	up
ACSM1	-2.0029	0.00157763	0.01626723	down
SLC1A1	-2.6550	0.00157865	0.01627091	down
ELOC	1.1467	0.00158144	0.01629281	up
FAM43A	1.5972	0.00158278	0.01629294	up
CLYBL	-1.4372	0.00158227	0.01629294	down
GK5	-1.1053	0.00158815	0.01631185	down
GDPD3	-1.3512	0.00158861	0.01631185	down
HSP90AA6P	2.6446	0.0015923	0.0163429	up
PRAP1	-4.1581	0.00159471	0.01635392	down
LOC101930370	-1.1669	0.00159929	0.01639402	down
ANGPTL7	-2.6912	0.00160716	0.01644728	down
FAM229A	-1.0877	0.00161267	0.01648986	down
TGFBR3L	-2.8900	0.00162044	0.01655547	down
ZNF491	-1.1533	0.00162167	0.01656114	down
AATK	-1.5521	0.00163844	0.0166976	down

SYT2	-1.0654	0.00164174	0.01671734	down
ITGBL1	2.5226	0.00164347	0.01672804	up
ANKRD23	-1.3396	0.00165008	0.01676283	down
GALNT18	1.8450	0.00164979	0.01676283	up
BEST4	-3.1092	0.00165374	0.01679073	down
KCTD21-AS1	-1.4173	0.00165567	0.01680343	down
ABCC2	-2.7165	0.00165712	0.01680687	down
EIF4A1P4	1.0881	0.00165784	0.01680687	up
COLGALT1	1.2178	0.00166388	0.01684489	up
CHST1	1.6844	0.00166636	0.01685612	up
RNF175	1.5417	0.0016676	0.01686172	up
CAPN10-DT	-1.3228	0.00166977	0.01687663	down
HERC6	-1.5434	0.00167319	0.01690428	down
CDC42EP1	1.0561	0.00168668	0.01697754	up
ERN1	1.2102	0.00169109	0.01700797	up
BGN	2.1604	0.00169594	0.01704482	up
SOWAHA	-4.3106	0.00170042	0.0170808	down
RIN1	1.6222	0.00171007	0.01715663	up
LONRF3	1.0582	0.00171418	0.01718197	up
CYP2C9	-4.5365	0.00171469	0.01718197	down
ELK3	1.3327	0.00171418	0.01718197	up
ZSCAN26	-1.0537	0.00171807	0.01720081	down
SLC47A2	-2.5386	0.00171877	0.01720081	down
SYT7	-1.1807	0.00172075	0.01720747	down
PROC	-2.7618	0.00172179	0.01721091	down
KRT80	4.4228	0.00172753	0.01725418	up
LOC101929657	-2.2611	0.00173378	0.01730957	down
ATP6V0C	1.3679	0.00173656	0.01733028	up
LINC01426	2.6373	0.0017396	0.01734413	up
SCAMP5	-2.1762	0.00174868	0.0174087	down
RILP	-1.3638	0.00175729	0.01748023	down
POM121L9P	1.8979	0.00176318	0.01752459	up
RPS4XP7	-2.7303	0.00177078	0.01759299	down
DNAJB11	1.0297	0.00178236	0.01769371	up
IGSF23	-3.8808	0.00178702	0.01772558	down
ATOH1	-5.1561	0.00178901	0.01773819	down
PTGR2	-1.3392	0.00179126	0.0177461	down
GRAMD1C	-3.0982	0.00180326	0.01782896	down
ERO1A	1.7868	0.00180547	0.01784366	up
ZNF763	-1.5903	0.00181439	0.01791739	down
ANGPTL4	2.2918	0.00181715	0.01793534	up

TAF1A-AS1	-1.5935	0.0018192	0.01794317	down
LOC100133286	-3.6056	0.00182161	0.01794532	down
SIRPB2	2.7023	0.00182301	0.0179519	up
LOC100507156	1.8175	0.00182504	0.01796383	up
DNAJC3-DT	-1.0419	0.00183441	0.01804245	down
DAND5	-3.0438	0.00183524	0.01804333	down
SFI1	-1.5370	0.00184623	0.01812233	down
LINC00937	2.6017	0.0018502	0.01814413	up
CYP1B1	2.6366	0.00185577	0.01817958	up
ACO2	-1.2090	0.00186611	0.01827359	down
SYTL2	-1.4213	0.00187956	0.01838327	down
MIDN	1.3244	0.00189027	0.01847331	up
FXYD3	-4.2742	0.00189412	0.01850355	down
ENTPD2	-2.6346	0.0018977	0.01851411	down
B3GALT5	-4.1393	0.00189685	0.01851411	down
ASRGL1	1.4446	0.00190614	0.01856912	up
LOC100506497	-1.9898	0.00190892	0.0185815	down
SHROOM4	1.8060	0.00190891	0.0185815	up
NT5DC1	-1.0877	0.00191524	0.01863562	down
DELEC1	2.8516	0.00192274	0.01869269	up
SLC25A45	-1.7014	0.0019234	0.01869269	down
CSF2RA	1.4001	0.00192907	0.01873376	up
CYP19A1	2.2915	0.00192932	0.01873376	up
NAALAD2	-1.2974	0.00193158	0.0187425	down
DCLRE1B	1.3053	0.0019347	0.01876533	up
HAGLR	-1.8059	0.00195086	0.01889971	down
MYL9	-2.5119	0.0019554	0.01893619	down
RN7SL600P	1.9502	0.0019574	0.01894807	up
RAI14	1.8862	0.001974	0.01907859	up
VWC2	-3.4394	0.00197557	0.01907879	down
ASB13	-1.4077	0.00197488	0.01907879	down
SEMA6D	-1.9531	0.00197719	0.01908691	down
KCNE4	2.6479	0.00199626	0.01921798	up
CD8B	-2.2367	0.00199808	0.01922803	down
CYP4F3	-3.2187	0.00200026	0.01923245	down
PRLR	-2.8574	0.00200331	0.01924058	down
IFITM10	1.6883	0.00201178	0.01928413	up
ACSF2	-2.0177	0.00201648	0.01931408	down
GPT	-2.6308	0.00203352	0.01943933	down
ZNF767P	-1.1244	0.00203557	0.01945132	down
EPHA2	2.3058	0.00203656	0.01945321	up

LOC100240735	-2.1279	0.00204488	0.01951754	down
SEC14L6	-1.8040	0.00204903	0.01954186	down
NCKAP5	-2.1952	0.00206146	0.01965281	down
TMEM98	-1.7917	0.00206238	0.01965391	down
PNMA3	-1.3623	0.00206712	0.0196838	down
CLIC6	1.6056	0.00207327	0.019727	up
NLRC4	2.1690	0.00208689	0.0198335	up
TMEM35A	-2.9641	0.00208641	0.0198335	down
TIAM2	-1.4322	0.00209034	0.01985865	down
GATM	-2.1336	0.00209267	0.01987311	down
RPS17	1.1050	0.00209369	0.01987505	up
ERVMER34-1	2.0923	0.0020972	0.01990072	up
FCER1G	2.3693	0.00211141	0.01998911	up
DOCK4	1.1923	0.00211116	0.01998911	up
SEC14L1	1.1769	0.00211106	0.01998911	up
FAM3D-AS1	-3.2393	0.00211433	0.01999971	down
SLC2A12	-2.3606	0.00211498	0.01999971	down
MIR145	-3.1719	0.00211779	0.02001528	down
NKX3-2	-2.3540	0.00212218	0.02004459	down
HLA-DRA	-1.7072	0.00212974	0.02009285	down
SLC10A5	-2.1170	0.00214117	0.02019287	down
CLEC1B	3.4266	0.0021446	0.0202175	up
GDF15	2.4101	0.00215121	0.02026417	up
LOXL2	1.6088	0.00216112	0.02033412	up
ZNF664	-1.0477	0.00216101	0.02033412	down
PECR	-1.6410	0.00216355	0.02033578	down
TACSTD2	1.8587	0.00217057	0.0203666	up
SLA	1.8298	0.0021722	0.0203666	up
CPNE8	1.1396	0.0021713	0.0203666	up
CHRNE	1.8541	0.00217487	0.02037749	up
LAMC3	1.6028	0.0021817	0.02043365	up
CD1E	-3.1400	0.0021891	0.02048728	down
CYP21A1P	1.3782	0.00218871	0.02048728	up
C1QTNF12	-2.4622	0.00219042	0.02049185	down
THEMIS2	1.9284	0.00219199	0.02049465	up
SAT2	-1.3121	0.00219768	0.02052056	down
HNF4G	-4.3572	0.00220354	0.02056746	down
PVT1	1.4511	0.00220853	0.02059055	up
PLCB4	-1.0258	0.00221337	0.02062786	down
ALDOB	-4.9252	0.002216	0.02064448	down
FRK	-2.6092	0.00221885	0.02064988	down

FOXH1	-3.3546	0.00223174	0.02074162	down
EXOC3L4	-2.8669	0.0022387	0.02078494	down
TUBA1B	1.1700	0.00224704	0.02085441	up
LINC01138	-1.1752	0.00224797	0.02085519	down
NKRF	1.5583	0.00226458	0.02096958	up
LOC102724064	-2.7623	0.00227708	0.02107738	down
MIR186	-1.4086	0.00228427	0.02112002	down
DRP2	-3.2836	0.00228525	0.02112112	down
ACOT11	-2.4829	0.0022884	0.02112245	down
GSDME	-1.7849	0.00228761	0.02112245	down
RPL23AP66	-2.5232	0.00228777	0.02112245	down
MDK	-1.6698	0.00229163	0.0211255	down
DLC1	1.6749	0.00229424	0.02113738	up
NAAA	-2.1281	0.00230218	0.02119538	down
LOC644135	2.4828	0.00231211	0.0212413	up
MAT1A	3.3802	0.00231802	0.0212876	up
CROCCP3	-1.1841	0.00232898	0.02134235	down
XKRX	-3.1323	0.00233104	0.02134321	down
TPM1	-2.5500	0.00233064	0.02134321	down
LRRC32	1.9812	0.00233997	0.02140098	up
KLK14	2.7340	0.00233962	0.02140098	up
ZNF784	-1.0572	0.00235002	0.02146086	down
ABCD3	-1.1506	0.00235422	0.02147074	down
HSD17B11	-1.7877	0.00235446	0.02147074	down
SELENOP	-2.6450	0.0023546	0.02147074	down
SLC25A5-AS1	-1.1242	0.00236128	0.02150312	down
RPL10P3	1.3002	0.00236039	0.02150312	up
IL15RA	1.0922	0.00236166	0.02150312	up
RNF208	-1.0582	0.00236587	0.02153347	down
PPP3CB-AS1	-1.0880	0.00237121	0.02156608	down
SALL2	-2.4854	0.00238007	0.02163062	down
MIA2	-1.9403	0.00240365	0.02182866	down
PIK3R5	1.9193	0.00240547	0.02183717	up
SLC38A5	1.5720	0.00241507	0.02189959	up
MTMR11	-2.3909	0.00241747	0.02190557	down
PKD1L2	-2.3030	0.00242142	0.02193326	down
ZZEF1	-1.4175	0.00242392	0.02193967	down
UGT1A10	-4.8814	0.00242799	0.02196842	down
PPP1R16A	-1.7008	0.00242939	0.02197294	down
ACTRT3	2.4849	0.00244779	0.02209787	up
TMEM106C	-1.5052	0.00244916	0.02209787	down

CILP2	1.9352	0.00245036	0.02209787	up
STIP1	1.1818	0.00246867	0.02223799	up
NKX3-1	1.9555	0.00247268	0.0222659	up
TYMP	1.5243	0.0024759	0.02228672	up
BDH2	-1.4234	0.00247871	0.02230383	down
CAPN6	-2.1783	0.00248527	0.02234648	down
LILRA6	2.7811	0.0024869	0.02235296	up
RASGRF1	-1.9090	0.00249278	0.02238938	down
KRT23	1.8809	0.00250207	0.02244814	up
LOC100507283	-1.0774	0.00250549	0.02246242	down
RHOXF1	-3.1925	0.00252681	0.02261215	down
GPC1	1.4876	0.00253572	0.02265058	up
TCTEX1D1	1.6607	0.00254799	0.02272706	up
B4GALT4	-1.4150	0.00255336	0.02276665	down
AKAP1	-1.1712	0.00256229	0.02283803	down
EFCAB5	-2.2367	0.00256929	0.02289208	down
LXN	1.4424	0.00259391	0.02305123	up
SAT1	1.2584	0.00259336	0.02305123	up
FCGR3A	3.0171	0.00260672	0.02313311	up
BEND5	-1.7345	0.00262068	0.02324023	down
TMEM116	-1.3670	0.0026235	0.02325675	down
RPL19P6	-1.3502	0.00262843	0.02329207	down
ZBED5-AS1	-1.4461	0.00263474	0.02332265	down
NR1H4	-4.5762	0.00263391	0.02332265	down
GALNT2	1.2888	0.0026535	0.02346332	up
UBA7	-1.1642	0.00266244	0.02352539	down
CRYL1	-1.8499	0.00266834	0.02356905	down
CCDC17	-1.1696	0.00267264	0.02358771	down
STAG3L5P	-1.0723	0.00267199	0.02358771	down
NOS3	1.9798	0.00268481	0.02363793	up
ENPP7P11	-3.4848	0.0026982	0.02373025	down
CD74	-1.5610	0.00270669	0.02378619	down
SDHAP2	-1.1202	0.00270999	0.02379127	down
GDA	-4.5256	0.00271526	0.02382044	down
LINC01668	-2.1433	0.00272101	0.02385387	down
LEAP2	-2.9754	0.00273639	0.02398011	down
GPR82	-2.7541	0.00273951	0.02399887	down
PLIN2	1.6030	0.00274184	0.0240021	up
FNDC3B	1.1788	0.00275042	0.02406863	up
CXXC4	-2.1334	0.00275751	0.02411348	down
ENDOU	2.3003	0.00275747	0.02411348	up

CYP27B1	1.9806	0.00276147	0.02413091	up
SUSD2	-2.4731	0.00276488	0.02414344	down
MYH11	-3.3208	0.0027665	0.02414431	down
LINC01940	3.0239	0.0027681	0.02414583	up
ZNF385D-AS1	2.2731	0.00277443	0.02419237	up
SNORA73B	2.1100	0.00278454	0.02427191	up
DUSP19	-1.3228	0.00278653	0.02427202	down
TUBAP14	3.3050	0.00278639	0.02427202	up
UGT2B7	-4.7343	0.00279009	0.02429435	down
C11orf80	-1.7377	0.00279867	0.02435181	down
ARSG	1.0783	0.00280344	0.02436735	up
MROH3P	-4.2787	0.00280727	0.02437473	down
MAP10	-1.0607	0.002811	0.02438295	down
TNFAIP2	2.1873	0.0028112	0.02438295	up
APOLD1	2.0550	0.00281723	0.02441798	up
TNN	-2.6801	0.00282868	0.02449839	down
NELL2	-2.5666	0.0028295	0.02449839	down
LOC441204	-1.7162	0.00284359	0.02458561	down
STAR	2.1681	0.00284821	0.02460821	up
SNORD46	1.7941	0.00285019	0.02461558	up
ANPEP	-3.4168	0.00286	0.02466659	down
KLHL32	-2.5691	0.00286692	0.02470028	down
PEPD	-1.5905	0.00288872	0.02484441	down
ADM	2.1654	0.0028907	0.0248527	up
SERPINA3	2.7241	0.00289536	0.02488406	up
CKB	-2.4790	0.00289751	0.02489385	down
A3GALT2	2.7869	0.00290384	0.02493069	up
KBTBD11-OT1	-4.0437	0.00290891	0.02494803	down
FAHD2A	-1.0092	0.00291274	0.02496087	down
ELL3	-2.7032	0.00291653	0.02497845	down
SLC9A3R1	-2.5167	0.00297794	0.02542449	down
ALB	-1.6420	0.00298219	0.02545193	down
MAFTRR	-2.1111	0.00298335	0.02545294	down
CELP	-4.4299	0.00298965	0.02548843	down
CYP2D7	-1.7360	0.00299117	0.02548843	down
PBX1	-1.3943	0.00299324	0.025493	down
GALM	-1.4778	0.00299771	0.0255133	down
RPS2P28	3.2593	0.00299694	0.0255133	up
EDN3	-3.5902	0.00300803	0.02557453	down
CTRB1	2.5762	0.00301259	0.02560441	up
TFRC	1.2864	0.00302017	0.02563927	up

TRIM2	-1.2498	0.00302017	0.02563927	down
BCKDHB	-1.1838	0.00302577	0.02566306	down
STK33	-2.3104	0.00302566	0.02566306	down
ANKRD9	-1.4300	0.0030309	0.02568877	down
TMEM92-AS1	-2.8200	0.00303005	0.02568877	down
FLVCR1-DT	-1.6743	0.00304761	0.02581261	down
BAZ1A	1.0229	0.00305564	0.02586269	up
MYBPC1	-2.7974	0.00305877	0.02588032	down
AMT	-1.8521	0.00306123	0.02589219	down
CYP3A4	-5.4948	0.00306393	0.02589717	down
SPEF2	-1.0093	0.00307023	0.02594146	down
ZNF33B	-1.4361	0.00307654	0.02598581	down
VAMP1	-1.2081	0.0030789	0.02598784	down
OLIG1	2.7611	0.00308384	0.02600267	up
DCST2	-1.7140	0.00309099	0.02604503	down
TREML2	1.9605	0.00310649	0.02615763	up
HADH	-1.3471	0.00311273	0.02620124	down
KIF19	1.2638	0.00311406	0.0262034	up
DCST1	-2.0385	0.0031197	0.02623285	down
DUSP2	1.7509	0.00311875	0.02623285	up
TUBB1	1.5944	0.00312145	0.02623856	up
ESRRG	-2.0371	0.00312354	0.02624119	down
ALDH2	-1.5016	0.00312513	0.02624119	down
ANG	-1.2426	0.00312604	0.02624119	down
GSDMA	3.4337	0.00312464	0.02624119	up
TAMALIN	1.3961	0.00313061	0.02627054	up
OXER1	-2.2287	0.0031506	0.02641117	down
EIF4A1P6	2.5542	0.00316169	0.02648464	up
CLIC5	-2.3239	0.00317135	0.02654262	down
SLC16A11	-1.2519	0.00317482	0.02655274	down
FER1L4	2.5615	0.00317615	0.02655274	up
PRR5L	-1.6559	0.00319961	0.02672157	down
ZNF594	-1.2661	0.00320882	0.02676196	down
FST	1.9957	0.00321611	0.0268137	up
EDNRA	1.3286	0.00322799	0.02687709	up
DCAF11	-1.2971	0.0032292	0.02687709	down
ANKRD63	-3.3564	0.00322815	0.02687709	down
AGMO	-3.2019	0.00323871	0.02692888	down
BATF	1.6696	0.00324197	0.02694684	up
ZNF704	-1.1962	0.00324339	0.0269495	down
SQLE	1.3895	0.00325723	0.02703696	up

PSD	-3.3727	0.0032594	0.02704589	down
SIGLEC6	-1.9579	0.00327079	0.02713118	down
SLC2A14	2.2847	0.00327388	0.02714766	up
CMA1	-3.0485	0.00328019	0.02718155	down
LOC107984265	-2.0557	0.00328788	0.02721766	down
TSPAN12	-1.8077	0.00329866	0.02728851	down
RN7SL473P	2.1012	0.00330946	0.02735018	up
REEP6	-3.2568	0.00331247	0.02735661	down
FSCN1	1.4028	0.00333566	0.0275018	up
CALR	1.0682	0.00333933	0.0275228	up
WDR87BP	-3.4029	0.00334437	0.02754586	down
MYH7	-3.2012	0.00336222	0.0276767	down
PART1	-3.8345	0.00337348	0.02773783	down
PODXL	1.3475	0.00337447	0.02773783	up
LOC105377663	1.6695	0.00338267	0.02779593	up
BEND7	-1.3814	0.00338418	0.02779906	down
IYD	-4.7812	0.00338902	0.02782018	down
NLRC3	-1.5641	0.00338859	0.02782018	down
ITM2C	-1.4559	0.00340158	0.02788589	down
PPARGC1B	-1.2584	0.0033996	0.02788589	down
CHAC1	3.0027	0.00340079	0.02788589	up
FAM186A	-1.4356	0.00340705	0.02792141	down
SLC22A23	-1.2418	0.00341533	0.02797057	down
TMEM19	-1.1906	0.00343166	0.02807618	down
FGR	2.1941	0.00343307	0.02807831	up
CHRFAM7A	-3.6347	0.0034409	0.02812359	down
DUSP5	1.7606	0.00344759	0.02814075	up
GPR12	-2.3301	0.00345357	0.02816871	down
EGR2	1.6022	0.00346347	0.02822345	up
ELFN1	1.7880	0.00346625	0.02823665	up
LINC00487	-2.4993	0.00346812	0.02824255	down
LOC100128059	3.1988	0.00347173	0.02824433	up
PTGR1	-1.7939	0.00347178	0.02824433	down
STYK1	-2.8579	0.00347908	0.02829424	down
ZNF214	-1.2211	0.00348796	0.02834765	down
AVIL	1.0448	0.00349409	0.02838804	up
TNNT1	2.8719	0.00351111	0.02850743	up
MSRA	-1.3300	0.00352012	0.02856169	down
SCP2	-1.1313	0.00352447	0.02857819	down
FOXD1	-2.4368	0.00352565	0.02857819	down
FCGBP	-3.1496	0.00354652	0.0286925	down

LRRC25	2.4214	0.00354908	0.0286925	up
PSMD12P1	1.1912	0.00355756	0.02872285	up
EXOSC4	1.0061	0.00356014	0.02873425	up
DEPDC7	-2.6106	0.00356852	0.02877346	down
STRIP2	2.9020	0.00358563	0.02889239	up
LINC01529	-1.7926	0.00359855	0.02896769	down
RPS26P23	3.2438	0.00360766	0.02899373	up
SLC20A1	1.2030	0.00361883	0.02907393	up
LINC01134	-2.3818	0.00362852	0.02911528	down
SNORD51	3.0517	0.00362978	0.02911528	up
XK	-2.5455	0.00362728	0.02911528	down
CTNNA3	-3.5380	0.00363089	0.02911528	down
PACRG	-2.5945	0.00363514	0.02912865	down
MYO1A	-4.3306	0.00363422	0.02912865	down
NAIP	1.8536	0.00365792	0.02929202	up
RPL7P6	2.2978	0.0036834	0.02945946	up
CCL18	2.7801	0.00369561	0.02951675	up
FABP3	1.4732	0.00371434	0.02964699	up
ANKRD29	-1.3512	0.00373072	0.0297584	down
LINC01798	-1.8983	0.00374921	0.02988028	down
CDK17	1.0528	0.00375464	0.02991026	up
PTP4A3	1.6997	0.00375783	0.02992591	up
RPL36A	1.5649	0.00376509	0.02995462	up
C13orf46	2.3536	0.00376428	0.02995462	up
XCL2	-2.1274	0.00377209	0.02997138	down
HSP90AB3P	1.2021	0.00377156	0.02997138	up
HDAC9	-1.1953	0.00377033	0.02997138	down
SECTM1	-1.9243	0.00377123	0.02997138	down
FLJ22447	2.3174	0.00377586	0.02998189	up
GCHFR	-2.1656	0.00378755	0.03005523	down
ESPN	-3.4325	0.00379482	0.03009343	down
SPOCD1	2.5929	0.00379707	0.03010158	up
TDRD5	-1.8094	0.00380884	0.03015587	down
PDXP	-1.5497	0.00381777	0.03020705	down
BCO1	-3.7142	0.0038269	0.03026958	down
FCGR1A	3.2912	0.00384035	0.03033183	up
TSPOAP1-AS1	-1.5205	0.00384096	0.03033183	down
LOC100996419	-1.3213	0.00384909	0.03038624	down
NEURL1	-2.3091	0.00385637	0.03043202	down
CSRNP3	-1.5931	0.00386639	0.03045416	down
ANK3	-1.7785	0.00386349	0.03045416	down

ZNF460-AS1	-1.2246	0.00386285	0.03045416	down
C19orf73	-1.6173	0.00386557	0.03045416	down
NRGN	1.5988	0.00386857	0.03046156	up
HOXC6	-1.7623	0.00390337	0.03067647	down
ATP8A1	-1.6956	0.00392349	0.03077796	down
IL3RA	1.1948	0.00392248	0.03077796	up
CRYZ	-1.0769	0.00394071	0.03084912	down
UGDH	1.1755	0.00394314	0.03085063	up
EXOC3L2	1.6087	0.0039686	0.03103991	up
IGHV4-61	3.4448	0.00397771	0.03110124	up
TESC	1.8802	0.00398075	0.03111137	up
DNAH3	-1.6226	0.00398155	0.03111137	down
PON3	-1.7939	0.00399955	0.03121224	down
CFAP161	2.2392	0.00400084	0.0312124	up
LGALS9C	-3.1231	0.00400812	0.03124934	down
ACTG1P14	1.3043	0.00401307	0.03126805	up
MMP15	-1.5431	0.00403045	0.03137357	down
LATS2	1.3691	0.00404138	0.03143869	up
HOXB3	-1.1691	0.00404434	0.03145169	down
AVPR1B	-2.7805	0.00405072	0.03148134	down
DECR2	-1.2326	0.00407574	0.03164398	down
EPS8L2	-2.7551	0.00408203	0.03165697	down
CMPK2	-1.5616	0.00408504	0.03166775	down
CCL13	3.0777	0.00409595	0.03170225	up
UAP1	1.1632	0.00410366	0.03173183	up
CTSB	2.3714	0.00410731	0.0317401	up
TNFSF14	2.6153	0.00413459	0.03191069	up
APOBEC2	-2.2813	0.00413655	0.03191576	down
ATP1A2	-2.5239	0.00414735	0.03196885	down
LINC00921	-1.2681	0.00415167	0.03199216	down
MPND	-1.0646	0.00416756	0.03207422	down
RANBP3L	-2.2204	0.00416941	0.03207839	down
SPATC1	1.7521	0.00417715	0.03212481	up
KLKB1	-2.3339	0.00419955	0.03225942	down
MYO1B	1.3360	0.00421266	0.032324	up
CASP6	-1.3519	0.00421319	0.032324	down
INSYN2B	2.5711	0.00421595	0.03233507	up
BCO2	-1.1930	0.00422313	0.03237997	down
DUSP14	1.8849	0.00423452	0.03243688	up
FGFR3	-2.9725	0.00423679	0.03244416	down
AMN	-4.1436	0.00424629	0.03249659	down

CCR1	2.5163	0.00425387	0.03253428	up
DICER1-AS1	-1.1003	0.00426599	0.03261683	down
RPL15P18	1.4369	0.00427053	0.03264136	up
GJA4	2.0352	0.00427351	0.03265391	up
TUBAL3	-4.2838	0.00427918	0.0326769	down
FOS	1.1064	0.0042841	0.03270424	up
IL17RE	-2.1614	0.00429393	0.03273856	down
ACY1	-2.1802	0.00429915	0.03275956	down
GPLD1	-2.1329	0.00431878	0.03286708	down
ITIH2	-1.5242	0.00431883	0.03286708	down
CTRB2	3.1733	0.00431737	0.03286708	up
CCDC121	-1.2002	0.0043296	0.03291839	down
SOX15	-1.6187	0.00433146	0.03292229	down
LOC100506098	-3.4618	0.00434191	0.03299151	down
RHCG	2.9122	0.00434585	0.03301123	up
KLHL34	-3.6544	0.00436351	0.03309413	down
MYO15B	-1.7644	0.00436798	0.03310925	down
CEACAM3	2.4229	0.00437609	0.03313829	up
GLULP4	1.7213	0.00437913	0.03315103	up
GDPD1	-1.4854	0.00438906	0.03321594	down
NPC1	1.0409	0.00440087	0.033254	up
CAP2	-2.2527	0.00440535	0.03327761	down
LINC00933	-2.2394	0.00442054	0.03337179	down
B3GALT2	-2.2207	0.00442526	0.03338688	down
LINC01198	2.2268	0.0044305	0.03339557	up
CTSG	-2.1647	0.00442893	0.03339557	down
ATE1-AS1	-2.1522	0.00445249	0.03354069	down
THSD4	-2.0061	0.00446626	0.03359716	down
LOC105373100	2.1493	0.00447074	0.03360593	up
LOC101927124	-1.4775	0.00448138	0.03367396	down
HPN-AS1	2.5044	0.00448254	0.03367396	up
PHOSPHO2	-1.0908	0.00448499	0.03368122	down
MIR4257	1.7117	0.00449068	0.03370415	up
RPL13AP20	1.4752	0.00449568	0.03372103	up
TUBB2A	1.0585	0.00450503	0.03377049	up
CEP170P1	1.1051	0.00451938	0.03383673	up
PLD1	-1.3860	0.00451868	0.03383673	down
ZNF483	-1.6428	0.00451923	0.03383673	down
TMPRSS15	-4.3347	0.00452811	0.0338917	down
NDUFA4L2	2.0204	0.00453607	0.03394094	up
LOC100132857	1.5065	0.00457242	0.03417121	up

BRINP3	-3.4493	0.00458729	0.03426145	down
CEACAM22P	-2.5113	0.0045869	0.03426145	down
MOGAT2	-4.4173	0.00459692	0.03430202	down
RPS16P1	1.2545	0.00460345	0.03434034	up
LINC00942	3.0115	0.00463398	0.03450506	up
KLRC1	-2.0284	0.00464736	0.0345732	down
SLC35G1	-1.8183	0.00465372	0.03457858	down
STRCP1	-2.3841	0.00465768	0.0345975	down
CATIP	2.2946	0.00467248	0.03468641	up
RNU6-415P	2.2137	0.00470084	0.03486527	up
WDR54	1.2046	0.00472282	0.03500149	up
FLJ12825	-2.6539	0.00472349	0.03500149	down
FADS6	-4.5708	0.00472717	0.03501816	down
MCRIP2	-1.2759	0.0047329	0.03504425	down
HLA-DRB6	-1.4338	0.00473811	0.03506746	down
ACAA1	-1.2264	0.00476531	0.03521558	down
FLJ46284	-1.4015	0.00476929	0.0352344	down
LINC01133	-2.8845	0.00480015	0.03537012	down
ST6GAL2	-2.5567	0.0047942	0.03537012	down
SLC3A2	1.1003	0.00480064	0.03537012	up
SPHK2	-1.0854	0.00479582	0.03537012	down
CSNK1E	1.1939	0.00479786	0.03537012	up
EVA1C	1.2386	0.0047971	0.03537012	up
CATSPER2	-1.3106	0.00482362	0.03548606	down
LOC105373334	-1.7047	0.00484026	0.03555514	down
TMEM120A	-1.3590	0.00484234	0.03555982	down
FAM219A	1.0310	0.00484818	0.03557069	up
STX19	-2.9257	0.00485483	0.03560884	down
MFSD3	-1.0541	0.00487553	0.03569608	down
BMS1P1	-1.5333	0.00487691	0.03569608	down
LINC00857	-1.2175	0.00487907	0.03570122	down
PGAP3	-1.1870	0.00488372	0.03572456	down
BACE2	1.4290	0.00488529	0.03572539	up
TAS2R4	-1.4603	0.00489994	0.03578984	down
SOCS2	1.1925	0.00489869	0.03578984	up
SI	-5.1595	0.00490788	0.03583718	down
VMP1	1.2157	0.00491532	0.0358808	up
CD63	1.0998	0.00491833	0.03589208	up
STOX1	-1.5741	0.00493324	0.03595812	down
FAM166B	-1.3456	0.00494234	0.03601374	down
PYCR1	1.7049	0.00494733	0.03603939	up

MFSD4B	-1.2570	0.00494882	0.03603949	down
TLR8	2.5174	0.00495231	0.03605421	up
GCATP1	1.7817	0.00495658	0.0360746	up
ZNF273	-1.4935	0.00496743	0.03614282	down
LOC100507516	-2.0949	0.00497271	0.03614544	down
LINC01224	-4.0473	0.0049703	0.03614544	down
ASB2	-2.6995	0.00498809	0.03621792	down
LYPD3	1.5854	0.00499179	0.03622336	up
MEX3A	1.2184	0.00499348	0.03622486	up
ZNF223	-1.1802	0.00500507	0.0362769	down
LINC01686	2.7582	0.00501509	0.03633276	up
ADCY3	1.3656	0.00501576	0.03633276	up
CCL28	-2.3105	0.00503813	0.03646238	down
CES1	-2.3113	0.0050396	0.03646238	down
NEIL1	-1.1760	0.00504351	0.03647988	down
RPF2P1	1.4768	0.00505208	0.03653113	up
PPFIA2	1.5898	0.00505723	0.03655756	up
HCP5B	-2.6898	0.00508381	0.03669546	down
RGCC	2.1947	0.00508655	0.03669546	up
LOC105378819	1.5587	0.00511124	0.03683942	up
RPS3AP6	1.4687	0.00511107	0.03683942	up
HINT2	-1.0215	0.00516355	0.03715092	down
FUT7	1.7857	0.00516304	0.03715092	up
BAIAP2L2	-2.8855	0.00517088	0.03719275	down
HLA-DPA1	-1.5800	0.00517672	0.03722382	down
PRTFDC1	-1.3033	0.00518216	0.03725203	down
RPSAP15	3.1231	0.00519031	0.03728871	up
HELB	1.1048	0.0052118	0.03743217	up
DAZL	2.9071	0.00522211	0.03746427	up
MKRN2OS	-2.2433	0.00522151	0.03746427	down
METTL7B	-3.1410	0.00522057	0.03746427	down
CAPN3	-1.3630	0.00524291	0.03757851	down
TMSB15A	2.2166	0.00525217	0.03762289	up
ADGRB2	-1.2202	0.00525649	0.03764284	down
NUDT16L2P	-1.9922	0.00526087	0.03766324	down
CFAP157	1.0085	0.005267	0.03769613	up
ABAT	-1.4303	0.00530651	0.03793455	down
RPL21P1	1.4224	0.0053135	0.03796242	up
ECM1	1.3416	0.0053285	0.03804585	up
LOC105375624	-1.0836	0.00533667	0.03806801	down
LOC100419831	-1.0408	0.00534205	0.03808868	down

STEAP2	1.0917	0.00534388	0.03809069	up
AKR7L	-3.3270	0.00535281	0.03813213	down
USH2A	-1.6890	0.00536621	0.03821652	down
CD14	2.5073	0.00537056	0.03823637	up
ZNF385C	-1.4236	0.00537497	0.03824694	down
RORC	-3.0901	0.00539538	0.03836711	down
SLC3A1	-2.5995	0.00541017	0.03844024	down
PP2D1	1.4933	0.00542123	0.03849657	up
CCL23	2.6429	0.00542959	0.03853358	up
EVA1A	1.6836	0.00544599	0.03859411	up
DOLPP1	-1.6311	0.00544515	0.03859411	down
FAP	2.2116	0.00545853	0.03866062	up
IMPG1	-1.8854	0.00552114	0.03900269	down
ULBP3	1.4879	0.00552908	0.03903626	up
DYRK2	-1.3254	0.00552859	0.03903626	down
HSP90AB1	1.1551	0.00554502	0.03911502	up
LINC01238	-1.9968	0.00555565	0.03916751	down
LINC01554	1.9282	0.00556123	0.03919557	up
ASTE1	-1.0820	0.00557176	0.03923423	down
KIF17	1.2303	0.00558678	0.03930788	up
ARL5B	1.0546	0.00559393	0.03933556	up
ZDHHC23	-1.7429	0.00559896	0.03935969	down
GPR137B	1.5211	0.00561074	0.03939737	up
SMAP2	1.0778	0.0056067	0.03939737	up
HLA-DPB1	-1.4356	0.00561075	0.03939737	down
TMEM184A	-3.4075	0.00564353	0.03954825	down
PXMP2	-1.9563	0.0056431	0.03954825	down
TMEM72	-3.2658	0.00564724	0.03955705	down
PYGM	-1.9212	0.00567376	0.03964851	down
SCNN1A	-3.2385	0.0056715	0.03964851	down
PREX1	1.4298	0.00570344	0.03982012	up
CLEC2L	-2.0246	0.00570908	0.03983683	down
ABCA1	1.4983	0.00570778	0.03983683	up
H3C6	-1.9704	0.00572783	0.0399449	down
PDLIM2	-1.1705	0.00575041	0.04009104	down
POLR1F	1.1438	0.00576092	0.04015286	up
COBL	-2.4114	0.00576585	0.04017582	down
COL3A1	2.6927	0.00578281	0.04025967	up
SULT1B1	-3.0270	0.00578702	0.04027754	down
EEF1B2P6	1.3422	0.0058134	0.0404267	up
RERGL	-1.5891	0.00586624	0.04070179	down

LINC02432	2.8039	0.00587356	0.04071802	up
MPP7	-1.6540	0.0058728	0.04071802	down
ASIC1	-1.7557	0.00587334	0.04071802	down
TMEM178A	-1.5542	0.00589881	0.0408469	down
PPFIBP2	-1.4053	0.00590475	0.04087644	down
CDH15	2.2486	0.00591533	0.04092144	up
EVPL	-2.6980	0.00592172	0.04094773	down
ETV5	1.5830	0.00593387	0.04098548	up
PAFAH2	-1.3266	0.00594794	0.04103355	down
BTNL2	-3.4873	0.00594635	0.04103355	down
MIR25	-1.5993	0.00594459	0.04103355	down
LINC00484	-1.9542	0.00595149	0.04103355	down
OIT3	-3.5777	0.00594886	0.04103355	down
ACSL5	-2.4323	0.00595215	0.04103355	down
ETV2	-1.3237	0.00595628	0.04103627	down
CYP3A5	-3.3527	0.00597178	0.04113145	down
SEPTIN6	-1.0108	0.00598318	0.0411984	down
CHRM2	-3.8637	0.00599554	0.04126038	down
OR2B11	3.4808	0.00600064	0.04127231	up
MYBPH	3.0372	0.00600856	0.04130359	up
KCNK7	1.7873	0.00604316	0.04145225	up
FES	1.2835	0.00604187	0.04145225	up
SIGLEC16	2.2721	0.00604371	0.04145225	up
LOC105370969	-2.0775	0.00608109	0.04165035	down
BMF	-1.4830	0.00608777	0.04167282	down
PRR16	1.5864	0.0061199	0.0418177	up
PTPN12	1.0008	0.00613828	0.04192496	up
RNASE4	-1.6751	0.0061455	0.04196256	down
LRP5	-1.0419	0.00615116	0.04197789	down
LOC257396	-1.2265	0.00616603	0.04202084	down
RAP1GAP	-2.6597	0.00618135	0.04210186	down
C19orf38	1.7176	0.00619242	0.04215387	up
ATP6V0D2	-3.1364	0.00620399	0.04219749	down
ZBTB7B	-1.5645	0.00621665	0.04223518	down
FOXC1	1.6935	0.00621815	0.04223518	up
ETS1	1.3114	0.00621354	0.04223518	up
BCYRN1	1.8959	0.00623194	0.04230539	up
LINC00649	-1.4021	0.00623566	0.04231893	down
PGAP2	-1.0886	0.00623979	0.04233529	down
RNF224	-2.6881	0.00624606	0.04236612	down
SLC39A8	2.4307	0.00624843	0.04237046	up

SRPK3	-1.6540	0.00625427	0.04239828	down
NGF	1.9412	0.00625825	0.04241356	up
C9orf40	-1.1738	0.0062916	0.04260427	down
LOC100505501	-1.7968	0.00629482	0.04261432	down
ENPP7	-4.5425	0.00630187	0.04262674	down
CEACAM4	2.1381	0.00630676	0.04263629	up
SLC35D1	-1.2202	0.00632561	0.04274014	down
RCC1	1.0455	0.00633001	0.04274634	up
RGL3	1.6503	0.00632927	0.04274634	up
PGR	-2.1972	0.0063389	0.04279453	down
LBX2-AS1	-1.5240	0.00634078	0.04279544	down
ACADS	-1.5528	0.0064177	0.04327888	down
COL4A1	1.9209	0.00642819	0.04331392	up
TBXAS1	1.6238	0.00643047	0.04331733	up
LMNA	1.5746	0.00643478	0.04332356	up
CHST11	1.1385	0.00643981	0.04333265	up
STAP2	-2.7858	0.00646535	0.04345676	down
FAM151B	1.2644	0.00646937	0.04346573	up
CMYA5	-1.4645	0.00647023	0.04346573	down
RPL7P18	1.9690	0.00647649	0.04349587	up
ASB9	1.0743	0.00650606	0.0436586	up
C1orf162	2.1419	0.00651935	0.04372388	up
CBX7	-1.3158	0.00655033	0.04390761	down
LACTB2-AS1	-1.8910	0.00655374	0.04391851	down
HDAC4-AS1	-1.3173	0.00658265	0.04409873	down
HOXB5	-1.6428	0.00658613	0.04409938	down
EEF1GP5	1.3858	0.00663242	0.04434874	up
FAM43B	2.0420	0.00665348	0.04445322	up
MFSD9	-1.1326	0.00665952	0.04448143	down
ANKRD33	3.0230	0.00666364	0.04449688	up
BBS12	-1.0505	0.00667059	0.04450888	down
SNORD14A	1.6090	0.00667129	0.04450888	up
TRDV1	-3.9520	0.00666901	0.04450888	down
KIAA0040	1.2893	0.00669124	0.04460825	up
DCLK3	1.4732	0.00670456	0.0446728	up
RPS2P20	1.3258	0.0067141	0.0447242	up
CDC14A	-1.2935	0.00671921	0.04474606	down
AKR1B10	-3.6088	0.00673462	0.04481216	down
DNAJB4	1.7553	0.00674606	0.04486812	up
CACNB2	-1.8527	0.00677196	0.04497518	down
CASZ1	-1.6474	0.00677914	0.04501067	down

SORBS2	-1.8573	0.00678172	0.04501562	down
PANX2	2.0781	0.00678648	0.04501619	up
FAAH	-1.7965	0.00683498	0.04519532	down
DENND1B	-1.6723	0.00682823	0.04519532	down
LCORL	-1.1984	0.00683151	0.04519532	down
F13A1	2.9795	0.00683384	0.04519532	up
DPEP1	-4.9287	0.00684331	0.04519532	down
PRO1804	-2.6223	0.00683852	0.04519532	down
C1QL3	-1.4331	0.00684797	0.0452106	down
LGR4	-1.2939	0.00687551	0.04534357	down
DUBR	-1.3212	0.00688719	0.04540842	down
GPR15	-3.6020	0.00689689	0.04546017	down
AKR1B15	-2.8407	0.00691327	0.04553137	down
LINC02313	-3.4999	0.00691609	0.04553776	down
LINC00426	-2.0813	0.00692009	0.04555187	down
TAPT1-AS1	-1.0776	0.00697744	0.0458894	down
UGT2A3	-4.5864	0.00698334	0.04590658	down
C3orf18	-1.3505	0.00699143	0.04593792	down
CYTL1	1.7162	0.00701218	0.04604557	up
PDE9A	-2.1477	0.00704185	0.04616742	down
CKMT1B	-2.7600	0.00706477	0.04629297	down
TMIGD2	-2.5455	0.0070753	0.04634956	down
HTRA3	1.7379	0.00710714	0.04644648	up
LINC00339	-1.0515	0.00712083	0.04651114	down
HEBP1	-1.2007	0.00713156	0.04655637	down
FREM1	-1.9327	0.00714236	0.04657731	down
IL20RA	-1.3879	0.00714674	0.0465935	down
SLC4A4	-1.8040	0.00715233	0.04661752	down
RHEX	-1.8598	0.0071782	0.04672405	down
NAGS	-2.4389	0.00717737	0.04672405	down
BTD	-1.2630	0.00718452	0.04672797	down
LHFPL3-AS2	-3.4843	0.00718349	0.04672797	down
MT2A	1.6421	0.00718254	0.04672797	up
CLDN1	1.9561	0.00719345	0.04676121	up
STAB2	-1.9482	0.00721177	0.0468431	down
RNF150	-1.6933	0.00722255	0.04688828	down
LRG1	2.0547	0.00722691	0.04690411	up
GALNT12	-1.6388	0.00723477	0.04691953	down
C2CD4A	3.3633	0.00723159	0.04691953	up
SELL	1.9534	0.00727058	0.04710033	up
KIAA2013	-1.1225	0.00727711	0.0471177	down

LOC100420899	2.0348	0.00729661	0.04723146	up
RPL21P72	2.1474	0.00733233	0.04741148	up
EML6	-2.4935	0.00733792	0.047413	down
PCDH17	1.5019	0.00737218	0.04758249	up
PLAAT4	-1.6059	0.00742384	0.04781414	down
PCAT19	1.5305	0.00742871	0.04781414	up
SIGLEC7	2.4222	0.00742668	0.04781414	up
VPREB3	-3.6464	0.00742395	0.04781414	down
LOC442517	2.4642	0.00743855	0.04785965	up
MPL	-1.2321	0.00744295	0.04787542	down
LOC340090	-2.7843	0.00746589	0.04799782	down
PLEK	1.6871	0.00747766	0.04806087	up
KCNN3	-1.9004	0.00749718	0.04813554	down
CCL4L1	1.5072	0.0074955	0.04813554	up
SGK2	-2.1047	0.00749745	0.04813554	down
RPL23P7	1.3534	0.00751176	0.04820425	up
SNORD69	1.2153	0.00754031	0.04833683	up
LOC613206	-2.0660	0.0075429	0.0483408	down
CTNND1	-1.0410	0.00754993	0.04837291	down
CA14	-2.6357	0.00756772	0.0484619	down
KLF2	1.4660	0.00760616	0.04869528	up
LRRC70	1.4950	0.00766949	0.0489984	up
MIGA2	-1.1311	0.00767312	0.04900884	down
GALNT8	-1.5373	0.00770169	0.04914844	down
ANKS4B	-3.8266	0.007703	0.04914844	down
OSTN-AS1	-3.6200	0.00772146	0.04924303	down
EPB41L4B	-2.3116	0.00772318	0.04924303	down
DMD	-1.4196	0.00772852	0.04926001	down
NCF2	1.8439	0.00778218	0.04957626	up
RPS3AP19	-2.7070	0.00779432	0.0496407	down
METTL24	-1.8789	0.00780401	0.0496761	down
DGKB	-2.9450	0.0078057	0.0496761	down
S100B	-2.1286	0.00782578	0.04975062	down
PLEKHA7	-1.6829	0.00782945	0.04975304	down
ERVFRD-1	-2.0260	0.007858	0.04986649	down
IMPDH1	1.4267	0.00786028	0.04986649	up
ADAMTS7P4	-1.5916	0.00788209	0.04996607	down

Table S5 45 FRGs in human after intestinal ischemia/reperfusion

Genes	log2FoldChange	pvalue	padj	regulated
Acsf2	-2.0176516	0.00201648	0.01931408	down
Nox1	-2.7827104	0.00036208	0.00549836	down
Scp2	-1.1313064	0.00352447	0.02857819	down
Acsl4	2.30924202	8.61E-12	2.99E-09	up
Tfrc	1.28638114	0.00302017	0.02563927	up
Hmox1	3.01077673	4.74E-09	6.75E-07	up
Wipi1	1.6531891	0.00010386	0.00209078	up
Sat1	1.25844082	0.00259336	0.02305123	up
Bid	1.1124967	3.37E-05	0.0008922	up
Dpp4	-3.2096671	0.00072291	0.00905475	down
Chac1	3.00274634	0.00340079	0.02788589	up
Hilpda	2.0093699	0.00021189	0.00366406	up
Hif1a	2.52630806	1.80E-20	4.01E-17	up
Tnfaip3	2.90434654	5.98E-10	1.17E-07	up
Atf3	2.13140328	5.03E-08	4.55E-06	up
Panx1	1.96895057	1.89E-15	1.55E-12	up
Dusp1	1.74622131	9.44E-06	0.00033175	up
Ncf2	1.84390702	0.00778218	0.04957626	up
Alb	-1.6420041	0.00298219	0.02545193	down
Srxn1	1.66493872	7.44E-05	0.0016149	up
Angptl7	-2.6912218	0.00160716	0.01644728	down
Slc7a11	4.18321519	0.00071813	0.00902082	up
Pck2	-3.1547425	7.48E-05	0.00162097	down
Slc7a5	3.5058468	3.99E-07	2.47E-05	up
Slc3a2	1.10033076	0.00480064	0.03537012	up
Trib3	3.33739598	3.79E-05	0.00096522	up
Vegfa	1.51542615	0.00083869	0.0100753	up
Gdf15	2.41009407	0.00215121	0.02026417	up
Arrdc3	1.29165882	0.00076703	0.00944157	up
Il6	5.70080342	1.12E-11	3.77E-09	up
Cxcl2	3.87008077	1.47E-09	2.61E-07	up
Hsd17b11	-1.7877427	0.00235446	0.02147074	down
Map3k5	1.11462892	8.94E-16	8.43E-13	up
Slc2a1	2.53999817	0.00057342	0.00769158	up
Slc2a3	3.27070965	3.51E-13	1.72E-10	up
Slc2a6	1.81633074	0.00052391	0.00720084	up
Slc2a12	-2.3605809	0.00211498	0.01999971	down
Slc2a14	2.28470666	0.00327388	0.02714766	up

Nnmt	3.40516886	1.22E-07	9.48E-06	up
Gabpb1	1.28786866	1.20E-05	0.00039537	up
Hspa5	1.96879059	1.14E-08	1.36E-06	up
Cd44	1.71907931	1.19E-07	9.29E-06	up
Plin2	1.60300513	0.00274184	0.0240021	up
Zfp36	1.46958971	0.00043138	0.00623296	up
Sqle	1.38945017	0.00325723	0.02703696	up

Table S6 200 FRGs in human after intestinal ischemia/reperfusion

Genes	log2FoldChange	pvalue	padj	regulated
Calr	1.06820021	0.00333933	0.0275228	up
Cd1c	-3.2416877	0.00026121	0.00430071	down
Cd1e	-3.1400321	0.0021891	0.02048728	down
Cd8b	-2.236737	0.00199808	0.01922803	down
Cd74	-1.5610183	0.00270669	0.02378619	down
Ctsb	2.3714353	0.00410731	0.0317401	up
Ctsl	2.50886073	5.05E-05	0.00120033	up
Fcer1g	2.36932999	0.00211141	0.01998911	up
Hla-Dmb	-2.1631002	0.0005985	0.00794547	down
Hla-Dpa1	-1.5800265	0.00517672	0.03722382	down
Hla-Dpb1	-1.4355878	0.00561075	0.03939737	down
Hla-Dra	-1.7072297	0.00212974	0.02009285	down
Hspa5	1.96879059	1.14E-08	1.36E-06	up
Hspa6	6.60212484	2.13E-09	3.46E-07	up
Orm1	3.88641119	0.00029223	0.00467419	up
Ctsg	-2.1646855	0.00442893	0.03339557	down
Aen	1.2865195	1.63E-05	0.00050707	up
Tlr3	-1.4924951	0.00021731	0.00373657	down
Tfrc	1.28638114	0.00302017	0.02563927	up
Gdf15	2.41009407	0.00215121	0.02026417	up
Socs3	3.21656761	8.21E-07	4.49E-05	up
Tnfsf10	-1.8791618	1.09E-05	0.0003677	down
Plaat4	-1.6058979	0.00742384	0.04781414	down
Vegfa	1.51542615	0.00083869	0.0100753	up
Tnfaip3	2.90434654	5.98E-10	1.17E-07	up
Il27	3.7537736	9.89E-05	0.00200933	up

Klkb1	-2.3338728	0.00419955	0.03225942	down
Tlr8	2.51744614	0.00495231	0.03605421	up
Apom	-2.4445853	0.00013489	0.00257397	down
Nod1	1.41970595	1.04E-05	0.00035826	up
Bphl	-1.7967506	0.00039781	0.00587613	down
Tkfc	-2.5862038	0.00053995	0.00734954	down
Nfkbiz	2.40351823	6.18E-12	2.26E-09	up
Mpo	2.43123526	0.00143727	0.0151123	up
Slc11a1	4.63014349	4.73E-07	2.84E-05	up
Sting1	1.20026876	0.00154542	0.0160256	up
Tnfrsf10a	1.37088511	0.00107546	0.01213537	up
Ccl4	2.55806409	1.13E-05	0.00037543	up
Marco	4.85194532	5.91E-05	0.0013559	up
Ccl28	-2.3105458	0.00503813	0.03646238	down
Il1a	5.38842117	0.00023474	0.00397775	up
Ptx3	6.03051239	2.53E-16	2.82E-13	up
Ifnar2	1.01725104	0.00063128	0.00825103	up
Cd14	2.50726246	0.00537056	0.03823637	up
Masp1	-3.0629047	0.00078255	0.00955501	down
Proc	-2.761756	0.00172179	0.01721091	down
Irf9	-1.114809	7.79E-05	0.00167586	down
Hmox1	3.01077673	4.74E-09	6.75E-07	up
Hgf	1.65644268	0.00138198	0.01467571	up
Stab2	-1.9482246	0.00721177	0.0468431	down
Alb	-1.6420041	0.00298219	0.02545193	down
Serpina3	2.72405066	0.00289536	0.02488406	up
Ccl14	-2.7453167	1.52E-05	0.00047872	down
Ccl13	3.07773376	0.00409595	0.03170225	up
Ccl18	2.78006284	0.00369561	0.02951675	up
Ccl26	2.53736487	0.00031267	0.00491762	up
Ccl4l1	1.50720923	0.0074955	0.04813554	up
Ackr4	-2.2022466	2.47E-06	0.00011151	down
Ccl2	4.61460708	1.03E-10	2.75E-08	up
Ccl3	3.27127092	8.83E-08	7.24E-06	up
Ccl23	2.64285191	0.00542959	0.03853358	up
Ccl3l3	3.18891818	0.00024064	0.0040497	up
Ccl8	2.18734281	0.00045035	0.00646002	up
Ccr1	2.51632464	0.00425387	0.03253428	up
Xcl2	-2.1274197	0.00377209	0.02997138	down
Cxcl1	5.19501555	5.62E-08	4.94E-06	up
Cxcl2	3.87008077	1.47E-09	2.61E-07	up

Il6	5.70080342	1.12E-11	3.77E-09	up
Il1b	5.20891648	5.10E-11	1.42E-08	up
Il10	3.26097635	0.00049139	0.00686942	up
Fgr	2.19413376	0.00343307	0.02807831	up
Ptgdr	-1.8650323	0.00019884	0.00347505	down
Hck	2.56103574	0.00010951	0.00218142	up
Olr1	2.45159977	3.01E-05	0.0008209	up
Rnase2	5.42032668	4.25E-07	2.60E-05	up
Ighv4-61	3.4447533	0.00397771	0.03110124	up
Cma1	-3.0484701	0.00328019	0.02718155	down
Cxcl3	5.31434741	1.02E-16	1.25E-13	up
Cxcl5	6.08132413	4.04E-05	0.00101505	up
Ccn1	3.25770024	2.23E-08	2.34E-06	up
Edn3	-3.5902304	0.00300803	0.02557453	down
Cxcl8	7.88200103	1.50E-19	2.63E-16	up
Pf4	3.17826989	0.00045267	0.00647574	up
Plau	3.01820605	3.13E-13	1.56E-10	up
Ppbp	3.98629082	0.00015654	0.00287512	up
Prok2	3.72928329	8.53E-07	4.63E-05	up
Sema3f	1.58657407	8.61E-05	0.00181817	up
Sema4g	-3.1702269	0.00047928	0.00675784	down
Sema6a	-1.4042987	0.00094151	0.01095668	down
Sema6b	2.51511215	3.08E-05	0.00083287	up
Sema6d	-1.9531334	0.00197719	0.01908691	down
Tymp	1.52426486	0.0024759	0.02228672	up
C5ar1	2.95311446	0.00070118	0.00886239	up
Ackr3	2.34767481	1.38E-06	6.90E-05	up
Ednra	1.32859207	0.00322799	0.02687709	up
Ednrb	1.58038952	0.00017545	0.00314247	up
Fpr1	4.46188403	4.32E-07	2.64E-05	up
Fpr2	4.22102825	6.34E-07	3.58E-05	up
C5ar2	2.7231254	4.66E-06	0.00018605	up
Plaur	3.81578711	1.57E-21	5.16E-18	up
Ptafr	2.19318772	0.00069177	0.00881149	up
Adm	2.16541334	0.0028907	0.0248527	up
Angptl7	-2.6912218	0.00160716	0.01644728	down
Apln	3.68924337	3.51E-06	0.00014643	up
Areg	4.38299695	2.74E-08	2.76E-06	up
Manf	1.37380813	0.00061695	0.00809392	up
Artn	2.2920014	0.00026554	0.00435227	up
Bmp3	-4.010105	0.00035372	0.00540724	down

Btc	-3.3076983	1.09E-05	0.00036724	down
Clcf1	3.51694494	2.30E-08	2.40E-06	up
Cmtm2	2.6604154	9.50E-05	0.00194833	up
Csf3	7.65407211	7.27E-13	3.24E-10	up
Ccn2	2.02352286	0.0001466	0.00274801	up
Epgn	4.25923765	0.00111615	0.01249767	up
Ereg	4.03986913	1.23E-08	1.44E-06	up
Fgf7	2.53175998	2.73E-05	0.00075763	up
Fgf9	-2.2476665	0.00141152	0.0149055	down
Guca2a	-7.1552501	2.96E-05	0.0008108	down
Hbegf	2.75142125	5.36E-08	4.76E-06	up
Igf1	3.29026986	1.56E-05	0.00048753	up
Il11	6.35729966	4.30E-08	4.04E-06	up
Il24	6.99090382	2.48E-07	1.69E-05	up
Inhba	6.10031644	4.37E-09	6.45E-07	up
Lif	5.14612036	5.57E-13	2.63E-10	up
Mdk	-1.6697955	0.00229163	0.0211255	down
Nampt	4.33366817	1.49E-32	3.65E-28	up
Ngf	1.94122716	0.00625825	0.04241356	up
Nts	-4.533267	0.00013807	0.00262638	down
Osm	4.35715131	3.73E-11	1.08E-08	up
Endou	2.30034561	0.00275747	0.02411348	up
Pgf	3.26999224	3.93E-08	3.78E-06	up
Ptn	-2.2530032	0.00122744	0.0134205	down
Pyy	-5.9456247	8.26E-05	0.00176134	down
Qrfp	3.09904007	6.37E-05	0.00143399	up
Retn	6.33997974	7.84E-06	0.0002878	up
Sectm1	-1.9242669	0.00377123	0.02997138	down
Stc1	4.08737319	9.16E-09	1.17E-06	up
Tgfb1	1.25558826	0.00073812	0.00919648	up
Tgfb3	1.18582311	0.00088967	0.01049793	up
Tnfsf14	2.61525756	0.00413459	0.03191069	up
Tnfsf9	3.58727688	1.29E-05	0.00041741	up
Acvrl1	1.30225159	0.00029977	0.0047575	up
Angptl4	2.29180889	0.00181715	0.01793534	up
Avpr1b	-2.7805225	0.00405072	0.03148134	down
Crlf1	2.75263125	1.25E-05	0.00040916	up
Csf2ra	1.40013508	0.00192907	0.01873376	up
Csf3r	3.14933957	5.81E-06	0.00022439	up
Esrrg	-2.0370773	0.00312354	0.02624119	down
Fgfr3	-2.9725117	0.00423679	0.03244416	down

Flt1	2.32291657	0.00015231	0.00282081	up
Hnf4g	-4.3571792	0.00220354	0.02056746	down
Il11ra	-1.529746	2.04E-08	2.15E-06	down
Il13ra2	4.43627514	3.59E-05	0.00093427	up
Il15ra	1.09222368	0.00236166	0.02150312	up
Il17ra	1.37416224	0.00027065	0.00441254	up
Il17rc	-1.2305088	1.95E-09	3.22E-07	down
Il17re	-2.1613897	0.00429393	0.03273856	down
Il18r1	2.08209552	1.07E-09	1.92E-07	up
Il18rap	1.6574332	0.00065845	0.00847441	up
Il1r1	2.04301401	0.00015181	0.00281711	up
Il1r2	5.26409733	2.31E-21	6.29E-18	up
Il1rap	2.29595623	6.64E-23	4.07E-19	up
Il1rl1	6.32359363	2.33E-09	3.71E-07	up
Il1rl2	2.73811094	4.74E-10	9.68E-08	up
Il20ra	-1.3879352	0.00714674	0.0465935	down
Il3ra	1.1947581	0.00392248	0.03077796	up
Lgr4	-1.2938959	0.00687551	0.04534357	down
Mchr1	2.50209466	2.91E-06	0.00012808	up
Mpl	-1.232087	0.00744295	0.04787542	down
Ngfr	2.23642765	0.0001277	0.00246744	up
Nr1h4	-4.5762417	0.00263391	0.02332265	down
Nr1i3	-2.5190007	0.00102828	0.01169992	down
Nr3c2	-2.2567669	8.05E-06	0.0002936	down
Nr4a1	2.61267692	0.00041871	0.00610424	up
Nr4a2	2.75326387	2.62E-06	0.00011789	up
Nr4a3	5.71073417	7.54E-22	3.08E-18	up
Osmr	2.64019085	6.97E-09	9.50E-07	up
Pgr	-2.1971614	0.0063389	0.04279453	down
Prlr	-2.8573673	0.00200331	0.01924058	down
Ptgds	-2.2325875	0.00126016	0.01368425	down
Ptger2	2.19313663	3.68E-05	0.0009433	up
Rorc	-3.0900764	0.00539538	0.03836711	down
Tnfrsf10d	2.35450201	1.08E-06	5.63E-05	up
Tnfrsf12a	3.17002872	2.60E-07	1.75E-05	up
Tnfrsf4	2.13337804	0.00075015	0.00929751	up
Tubb3	2.97230958	1.96E-12	8.03E-10	up
Vipr1	-3.6333384	9.66E-06	0.00033758	down
Klrc1	-2.0283864	0.00464736	0.0345732	down
Icam1	4.2060724	3.51E-11	1.02E-08	up
Fcgr3a	3.0171136	0.00260672	0.02313311	up

Lcp2	1.31568582	0.00015683	0.00287837	up
Pik3r5	1.91931398	0.00240547	0.02183717	up
Shc1	1.25954354	1.12E-06	5.81E-05	up
Fos	1.10643494	0.0042841	0.03270424	up
Nfkb1	1.0318553	2.96E-05	0.0008108	up
Nfkbia	1.99977174	5.99E-05	0.00136996	up
Nfkbie	1.86407789	0.00057171	0.00768931	up
Map3k8	2.80582493	2.88E-10	6.49E-08	up
Trbv19	-2.7763408	0.00082894	0.00999296	down
Trdv1	-3.9519606	0.00666901	0.04450888	down

Table S7

Significant Enrichment Results of GO Analysis of FRGs

Ontology	ID	Description	GeneRatio	BgRatio	pvalue	qvalue	Count
BP	GO:0006979	response to oxidative stress	14/60	409/23328	0.0000	0.0000	14
BP	GO:0062012	regulation of small molecule metabolic process	11/60	358/23328	0.0000	0.0000	11
BP	GO:0009611	response to wounding	11/60	492/23328	0.0000	0.0000	11
BP	GO:0048872	homeostasis of number of cells	10/60	330/23328	0.0000	0.0000	10
BP	GO:0050727	regulation of inflammatory response	10/60	372/23328	0.0000	0.0000	10
BP	GO:0031331	positive regulation of cellular catabolic process	10/60	396/23328	0.0000	0.0000	10
BP	GO:2001233	regulation of apoptotic signaling pathway	10/60	413/23328	0.0000	0.0000	10
BP	GO:0070997	neuron death	10/60	416/23328	0.0000	0.0000	10
BP	GO:0006914	autophagy	10/60	425/23328	0.0000	0.0000	10
BP	GO:0061919	process utilizing autophagic mechanism	10/60	425/23328	0.0000	0.0000	10
BP	GO:0009896	positive regulation of catabolic process	10/60	463/23328	0.0000	0.0000	10
BP	GO:2001234	negative regulation of apoptotic signaling pathway	9/60	231/23328	0.0000	0.0000	9
BP	GO:0006790	sulfur compound metabolic process	9/60	279/23328	0.0000	0.0000	9
BP	GO:0062197	cellular response to chemical stress	9/60	332/23328	0.0000	0.0000	9
BP	GO:1901214	regulation of neuron death	9/60	377/23328	0.0000	0.0000	9
BP	GO:0009991	response to extracellular stimulus	9/60	378/23328	0.0000	0.0000	9
BP	GO:0015711	organic anion transport	9/60	463/23328	0.0000	0.0001	9
BP	GO:0048732	gland development	9/60	471/23328	0.0000	0.0001	9

BP	GO:1901615	organic hydroxy compound metabolic process	9/60	498/23328	0.0000	0.0002	9
BP	GO:1901215	negative regulation of neuron death	8/60	251/23328	0.0000	0.0000	8
BP	GO:0034599	cellular response to oxidative stress	8/60	276/23328	0.0000	0.0000	8
BP	GO:0031667	response to nutrient levels	8/60	346/23328	0.0000	0.0001	8
BP	GO:0042060	wound healing	8/60	349/23328	0.0000	0.0001	8
BP	GO:0006631	fatty acid metabolic process	8/60	408/23328	0.0000	0.0003	8
BP	GO:0010876	lipid localization	8/60	413/23328	0.0000	0.0003	8
BP	GO:0001933	negative regulation of protein phosphorylation	8/60	425/23328	0.0000	0.0004	8
BP	GO:0009117	nucleotide metabolic process	8/60	427/23328	0.0000	0.0004	8
BP	GO:0006753	nucleoside phosphate metabolic process	8/60	436/23328	0.0000	0.0004	8
BP	GO:0042326	negative regulation of phosphorylation	8/60	471/23328	0.0000	0.0005	8
CC	GO:0045177	apical part of cell	8/61	454/23271	0.0000	0.0015	8
BP	GO:0046916	cellular transition metal ion homeostasis	7/60	104/23328	0.0000	0.0000	7
BP	GO:0055076	transition metal ion homeostasis	7/60	134/23328	0.0000	0.0000	7
BP	GO:0002262	myeloid cell homeostasis	7/60	187/23328	0.0000	0.0000	7
BP	GO:0010506	regulation of autophagy	7/60	278/23328	0.0000	0.0002	7
BP	GO:0097193	intrinsic apoptotic signaling pathway	7/60	295/23328	0.0000	0.0003	7
BP	GO:0071216	cellular response to biotic stimulus	7/60	320/23328	0.0000	0.0004	7
BP	GO:0009150	purine ribonucleotide metabolic process	7/60	324/23328	0.0000	0.0004	7
BP	GO:0009259	ribonucleotide metabolic process	7/60	334/23328	0.0000	0.0005	7
BP	GO:0019693	ribose phosphate metabolic process	7/60	345/23328	0.0000	0.0006	7
BP	GO:0006163	purine nucleotide metabolic process	7/60	354/23328	0.0000	0.0006	7
BP	GO:0019216	regulation of lipid metabolic process	7/60	363/23328	0.0000	0.0007	7
BP	GO:0006869	lipid transport	7/60	364/23328	0.0000	0.0007	7
BP	GO:0032496	response to lipopolysaccharide	7/60	368/23328	0.0000	0.0007	7
BP	GO:0022411	cellular component disassembly	7/60	383/23328	0.0001	0.0008	7
BP	GO:0032102	negative regulation of response to external stimulus	7/60	384/23328	0.0001	0.0008	7

BP	GO:0002237	response to molecule of bacterial origin	7/60	389/23328	0.0001	0.0009	7
BP	GO:0072521	purine-containing compound metabolic process	7/60	396/23328	0.0001	0.0009	7
BP	GO:0006091	generation of precursor metabolites and energy	7/60	400/23328	0.0001	0.0009	7
BP	GO:1901652	response to peptide	7/60	400/23328	0.0001	0.0009	7
BP	GO:0001819	positive regulation of cytokine production	7/60	449/23328	0.0001	0.0015	7
BP	GO:0002683	negative regulation of immune system process	7/60	462/23328	0.0002	0.0017	7
BP	GO:0006879	cellular iron ion homeostasis	6/60	64/23328	0.0000	0.0000	6
BP	GO:0055072	iron ion homeostasis	6/60	92/23328	0.0000	0.0000	6
BP	GO:0001776	leukocyte homeostasis	6/60	115/23328	0.0000	0.0000	6
BP	GO:0006575	cellular modified amino acid metabolic process	6/60	165/23328	0.0000	0.0002	6
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	6/60	165/23328	0.0000	0.0002	6
BP	GO:0098739	import across plasma membrane	6/60	166/23328	0.0000	0.0002	6
BP	GO:0042594	response to starvation	6/60	178/23328	0.0000	0.0002	6
BP	GO:0046890	regulation of lipid biosynthetic process	6/60	184/23328	0.0000	0.0002	6
BP	GO:0001666	response to hypoxia	6/60	208/23328	0.0000	0.0004	6
BP	GO:0042180	cellular ketone metabolic process	6/60	211/23328	0.0000	0.0004	6
BP	GO:0002819	regulation of adaptive immune response	6/60	213/23328	0.0000	0.0004	6
BP	GO:0098656	anion transmembrane transport	6/60	221/23328	0.0000	0.0005	6
BP	GO:0097191	extrinsic apoptotic signaling pathway	6/60	233/23328	0.0000	0.0006	6
BP	GO:0036293	response to decreased oxygen levels	6/60	234/23328	0.0000	0.0006	6
BP	GO:1903320	regulation of protein modification by small protein conjugation or removal	6/60	240/23328	0.0000	0.0006	6
BP	GO:0034976	response to endoplasmic reticulum stress	6/60	249/23328	0.0000	0.0007	6
BP	GO:0098657	import into cell	6/60	251/23328	0.0000	0.0007	6
BP	GO:0051348	negative regulation of transferase activity	6/60	260/23328	0.0001	0.0008	6
BP	GO:0045926	negative regulation of growth	6/60	264/23328	0.0001	0.0009	6

BP	GO:0071222	cellular response to lipopolysaccharide	6/60	285/23328	0.0001	0.0011	6
BP	GO:0070482	response to oxygen levels	6/60	287/23328	0.0001	0.0011	6
BP	GO:0072593	reactive oxygen species metabolic process	6/60	292/23328	0.0001	0.0012	6
BP	GO:0071219	cellular response to molecule of bacterial origin	6/60	295/23328	0.0001	0.0012	6
BP	GO:0060326	cell chemotaxis	6/60	303/23328	0.0001	0.0013	6
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	6/60	308/23328	0.0001	0.0014	6
BP	GO:0009895	negative regulation of catabolic process	6/60	311/23328	0.0001	0.0015	6
BP	GO:0070371	ERK1 and ERK2 cascade	6/60	325/23328	0.0002	0.0018	6
BP	GO:0046942	carboxylic acid transport	6/60	333/23328	0.0002	0.0020	6
BP	GO:0015849	organic acid transport	6/60	337/23328	0.0002	0.0020	6
BP	GO:0050878	regulation of body fluid levels	6/60	354/23328	0.0003	0.0024	6
BP	GO:0001503	ossification	6/60	394/23328	0.0005	0.0038	6
BP	GO:0034248	regulation of cellular amide metabolic process	6/60	410/23328	0.0006	0.0043	6
BP	GO:0051090	regulation of DNA-binding transcription factor activity	6/60	415/23328	0.0007	0.0045	6
BP	GO:0072594	establishment of protein localization to organelle	6/60	426/23328	0.0008	0.0049	6
BP	GO:0022407	regulation of cell-cell adhesion	6/60	427/23328	0.0008	0.0049	6
BP	GO:0090407	organophosphate biosynthetic process	6/60	427/23328	0.0008	0.0049	6
BP	GO:0001558	regulation of cell growth	6/60	438/23328	0.0009	0.0053	6
MF	GO:0008509	anion transmembrane transporter activity	6/58	336/22669	0.0002	0.0080	6
MF	GO:0033218	amide binding	6/58	391/22669	0.0005	0.0103	6
BP	GO:0043648	dicarboxylic acid metabolic process	5/60	85/23328	0.0000	0.0001	5
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	5/60	101/23328	0.0000	0.0002	5
BP	GO:0030282	bone mineralization	5/60	120/23328	0.0000	0.0004	5
BP	GO:0042542	response to hydrogen peroxide	5/60	121/23328	0.0000	0.0004	5
BP	GO:1905039	carboxylic acid transmembrane transport	5/60	124/23328	0.0000	0.0004	5
BP	GO:1903825	organic acid transmembrane transport	5/60	125/23328	0.0000	0.0004	5
BP	GO:0001889	liver development	5/60	126/23328	0.0000	0.0004	5

BP	GO:0061008	hepaticobiliary system development	5/60	129/23328	0.0000	0.0004	5
BP	GO:0010565	regulation of cellular ketone metabolic process	5/60	139/23328	0.0000	0.0006	5
BP	GO:1902652	secondary alcohol metabolic process	5/60	141/23328	0.0000	0.0006	5
BP	GO:0006633	fatty acid biosynthetic process	5/60	145/23328	0.0000	0.0006	5
BP	GO:0050728	negative regulation of inflammatory response	5/60	156/23328	0.0001	0.0008	5
BP	GO:0031214	biomineral tissue development	5/60	162/23328	0.0001	0.0009	5
BP	GO:0110148	biomineralization	5/60	162/23328	0.0001	0.0009	5
BP	GO:0048660	regulation of smooth muscle cell proliferation	5/60	165/23328	0.0001	0.0009	5
BP	GO:0048659	smooth muscle cell proliferation	5/60	170/23328	0.0001	0.0009	5
BP	GO:1901605	alpha-amino acid metabolic process	5/60	180/23328	0.0001	0.0012	5
BP	GO:0043524	negative regulation of neuron apoptotic process	5/60	182/23328	0.0001	0.0012	5
BP	GO:0006109	regulation of carbohydrate metabolic process	5/60	195/23328	0.0001	0.0015	5
BP	GO:0072330	monocarboxylic acid biosynthetic process	5/60	196/23328	0.0001	0.0015	5
BP	GO:0000302	response to reactive oxygen species	5/60	202/23328	0.0002	0.0017	5
BP	GO:0031396	regulation of protein ubiquitination	5/60	206/23328	0.0002	0.0018	5
BP	GO:0006469	negative regulation of protein kinase activity	5/60	207/23328	0.0002	0.0018	5
BP	GO:0043542	endothelial cell migration	5/60	212/23328	0.0002	0.0020	5
BP	GO:0031668	cellular response to extracellular stimulus	5/60	217/23328	0.0002	0.0021	5
BP	GO:0048545	response to steroid hormone	5/60	218/23328	0.0002	0.0021	5
BP	GO:0033673	negative regulation of kinase activity	5/60	227/23328	0.0003	0.0024	5
BP	GO:0031348	negative regulation of defense response	5/60	228/23328	0.0003	0.0025	5
BP	GO:0033002	muscle cell proliferation	5/60	236/23328	0.0004	0.0028	5
BP	GO:0015980	energy derivation by oxidation of organic compounds	5/60	248/23328	0.0004	0.0034	5
BP	GO:0006520	cellular amino acid metabolic process	5/60	250/23328	0.0005	0.0034	5
BP	GO:0045444	fat cell differentiation	5/60	252/23328	0.0005	0.0035	5

BP	GO:0005996	monosaccharide metabolic process	5/60	261/23328	0.0006	0.0040	5
BP	GO:0022409	positive regulation of cell-cell adhesion	5/60	265/23328	0.0006	0.0042	5
BP	GO:0043523	regulation of neuron apoptotic process	5/60	270/23328	0.0007	0.0044	5
BP	GO:0010038	response to metal ion	5/60	274/23328	0.0007	0.0045	5
BP	GO:0071496	cellular response to external stimulus	5/60	280/23328	0.0008	0.0048	5
BP	GO:0044262	cellular carbohydrate metabolic process	5/60	292/23328	0.0009	0.0054	5
BP	GO:0010631	epithelial cell migration	5/60	295/23328	0.0010	0.0056	5
BP	GO:0090132	epithelium migration	5/60	297/23328	0.0010	0.0057	5
BP	GO:0051402	neuron apoptotic process	5/60	298/23328	0.0010	0.0058	5
BP	GO:0046394	carboxylic acid biosynthetic process	5/60	299/23328	0.0010	0.0058	5
BP	GO:0090130	tissue migration	5/60	299/23328	0.0010	0.0058	5
BP	GO:1901653	cellular response to peptide	5/60	299/23328	0.0010	0.0058	5
BP	GO:0016053	organic acid biosynthetic process	5/60	300/23328	0.0010	0.0058	5
BP	GO:0008202	steroid metabolic process	5/60	309/23328	0.0012	0.0062	5
BP	GO:0006066	alcohol metabolic process	5/60	323/23328	0.0014	0.0070	5
BP	GO:0032386	regulation of intracellular transport	5/60	329/23328	0.0016	0.0075	5
BP	GO:0019221	cytokine-mediated signaling pathway	5/60	369/23328	0.0026	0.0103	5
BP	GO:0009914	hormone transport	5/60	372/23328	0.0027	0.0106	5
BP	GO:0042176	regulation of protein catabolic process	5/60	395/23328	0.0035	0.0124	5
BP	GO:0009314	response to radiation	5/60	401/23328	0.0037	0.0130	5
BP	GO:0032103	positive regulation of response to external stimulus	5/60	418/23328	0.0044	0.0151	5
BP	GO:1903706	regulation of hemopoiesis	5/60	424/23328	0.0047	0.0157	5
BP	GO:0001667	ameboidal-type cell migration	5/60	427/23328	0.0048	0.0160	5
BP	GO:0010959	regulation of metal ion transport	5/60	427/23328	0.0048	0.0160	5
BP	GO:0045785	positive regulation of cell adhesion	5/60	435/23328	0.0052	0.0170	5
BP	GO:0002697	regulation of immune effector process	5/60	440/23328	0.0054	0.0176	5
BP	GO:1901361	organic cyclic compound catabolic process	5/60	442/23328	0.0055	0.0177	5

BP	GO:0045666	positive regulation of neuron differentiation	5/60	472/23328	0.0073	0.0216	5
BP	GO:0007005	mitochondrion organization	5/60	481/23328	0.0079	0.0227	5
CC	GO:0005811	lipid droplet	5/61	89/23271	0.0000	0.0005	5
CC	GO:0016323	basolateral plasma membrane	5/61	259/23271	0.0006	0.0109	5
CC	GO:0016324	apical plasma membrane	5/61	350/23271	0.0022	0.0289	5
CC	GO:0000323	lytic vacuole	5/61	460/23271	0.0071	0.0510	5
CC	GO:0005764	lysosome	5/61	460/23271	0.0071	0.0510	5
MF	GO:0008514	organic anion transmembrane transporter activity	5/58	220/22669	0.0002	0.0080	5
MF	GO:0031625	ubiquitin protein ligase binding	5/58	306/22669	0.0011	0.0132	5
MF	GO:0044389	ubiquitin-like protein ligase binding	5/58	324/22669	0.0014	0.0132	5
MF	GO:0048018	receptor ligand activity	5/58	499/22669	0.0089	0.0373	5
BP	GO:0006534	cysteine metabolic process	4/60	12/23328	0.0000	0.0000	4
BP	GO:0000096	sulfur amino acid metabolic process	4/60	34/23328	0.0000	0.0001	4
BP	GO:0009069	serine family amino acid metabolic process	4/60	34/23328	0.0000	0.0001	4
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	4/60	51/23328	0.0000	0.0003	4
BP	GO:0006749	glutathione metabolic process	4/60	57/23328	0.0000	0.0004	4
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	4/60	57/23328	0.0000	0.0004	4
BP	GO:0009060	aerobic respiration	4/60	74/23328	0.0000	0.0007	4
BP	GO:0006094	gluconeogenesis	4/60	76/23328	0.0000	0.0007	4
BP	GO:0002260	lymphocyte homeostasis	4/60	79/23328	0.0001	0.0008	4
BP	GO:0019319	hexose biosynthetic process	4/60	79/23328	0.0001	0.0008	4
BP	GO:0006637	acyl-CoA metabolic process	4/60	83/23328	0.0001	0.0009	4
BP	GO:0035383	thioester metabolic process	4/60	83/23328	0.0001	0.0009	4
BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	4/60	84/23328	0.0001	0.0009	4
BP	GO:0051384	response to glucocorticoid	4/60	84/23328	0.0001	0.0009	4
BP	GO:0046364	monosaccharide biosynthetic process	4/60	85/23328	0.0001	0.0009	4
BP	GO:0044272	sulfur compound biosynthetic process	4/60	86/23328	0.0001	0.0009	4
BP	GO:0031960	response to corticosteroid	4/60	88/23328	0.0001	0.0010	4

BP	GO:1903321	negative regulation of protein modification by small protein conjugation or removal	4/60	88/23328	0.0001	0.0010	4
BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	4/60	91/23328	0.0001	0.0011	4
BP	GO:0043535	regulation of blood vessel endothelial cell migration	4/60	94/23328	0.0001	0.0012	4
BP	GO:1904035	regulation of epithelial cell apoptotic process	4/60	94/23328	0.0001	0.0012	4
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	4/60	95/23328	0.0001	0.0012	4
BP	GO:0019217	regulation of fatty acid metabolic process	4/60	97/23328	0.0001	0.0012	4
BP	GO:0033865	nucleoside bisphosphate metabolic process	4/60	99/23328	0.0001	0.0013	4
BP	GO:0033875	ribonucleoside bisphosphate metabolic process	4/60	99/23328	0.0001	0.0013	4
BP	GO:0034032	purine nucleoside bisphosphate metabolic process	4/60	99/23328	0.0001	0.0013	4
BP	GO:0010595	positive regulation of endothelial cell migration	4/60	103/23328	0.0001	0.0015	4
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	4/60	108/23328	0.0002	0.0017	4
BP	GO:0001676	long-chain fatty acid metabolic process	4/60	111/23328	0.0002	0.0018	4
BP	GO:0009636	response to toxic substance	4/60	116/23328	0.0002	0.0020	4
BP	GO:0006986	response to unfolded protein	4/60	117/23328	0.0002	0.0021	4
BP	GO:1904019	epithelial cell apoptotic process	4/60	118/23328	0.0002	0.0021	4
BP	GO:0043534	blood vessel endothelial cell migration	4/60	119/23328	0.0003	0.0022	4
BP	GO:0120254	olefinic compound metabolic process	4/60	126/23328	0.0003	0.0026	4
BP	GO:0008203	cholesterol metabolic process	4/60	130/23328	0.0004	0.0028	4
BP	GO:0071887	leukocyte apoptotic process	4/60	138/23328	0.0004	0.0034	4
BP	GO:0016125	sterol metabolic process	4/60	139/23328	0.0005	0.0034	4
BP	GO:0035966	response to topologically incorrect protein	4/60	141/23328	0.0005	0.0035	4
BP	GO:0010508	positive regulation of autophagy	4/60	144/23328	0.0005	0.0038	4
BP	GO:1903364	positive regulation of cellular protein catabolic process	4/60	145/23328	0.0005	0.0038	4
BP	GO:0045598	regulation of fat cell differentiation	4/60	146/23328	0.0005	0.0039	4

BP	GO:0010634	positive regulation of epithelial cell migration	4/60	150/23328	0.0006	0.0042	4
BP	GO:0008643	carbohydrate transport	4/60	151/23328	0.0006	0.0043	4
BP	GO:0022612	gland morphogenesis	4/60	154/23328	0.0007	0.0044	4
BP	GO:1901568	fatty acid derivative metabolic process	4/60	154/23328	0.0007	0.0044	4
BP	GO:0009267	cellular response to starvation	4/60	156/23328	0.0007	0.0045	4
BP	GO:0071248	cellular response to metal ion	4/60	156/23328	0.0007	0.0045	4
BP	GO:0045333	cellular respiration	4/60	157/23328	0.0007	0.0046	4
BP	GO:0062013	positive regulation of small molecule metabolic process	4/60	157/23328	0.0007	0.0046	4
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	4/60	162/23328	0.0008	0.0050	4
BP	GO:0033135	regulation of peptidyl-serine phosphorylation	4/60	164/23328	0.0008	0.0051	4
BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	4/60	164/23328	0.0008	0.0051	4
BP	GO:1905952	regulation of lipid localization	4/60	165/23328	0.0009	0.0051	4
BP	GO:0010594	regulation of endothelial cell migration	4/60	166/23328	0.0009	0.0052	4
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	4/60	167/23328	0.0009	0.0053	4
BP	GO:0043271	negative regulation of ion transport	4/60	174/23328	0.0011	0.0058	4
BP	GO:0007612	learning	4/60	175/23328	0.0011	0.0058	4
BP	GO:0035296	regulation of tube diameter	4/60	176/23328	0.0011	0.0058	4
BP	GO:0097746	regulation of blood vessel diameter	4/60	176/23328	0.0011	0.0058	4
BP	GO:0035150	regulation of tube size	4/60	177/23328	0.0011	0.0059	4
BP	GO:0010951	negative regulation of endopeptidase activity	4/60	182/23328	0.0012	0.0064	4
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	4/60	185/23328	0.0013	0.0066	4
BP	GO:0031669	cellular response to nutrient levels	4/60	188/23328	0.0014	0.0069	4
BP	GO:0045766	positive regulation of angiogenesis	4/60	188/23328	0.0014	0.0069	4
BP	GO:0050796	regulation of insulin secretion	4/60	190/23328	0.0015	0.0070	4
BP	GO:0042445	hormone metabolic process	4/60	196/23328	0.0016	0.0077	4
BP	GO:0016051	carbohydrate biosynthetic process	4/60	197/23328	0.0017	0.0078	4

BP	GO:0030308	negative regulation of cell growth	4/60	199/23328	0.0017	0.0080	4
BP	GO:0006006	glucose metabolic process	4/60	202/23328	0.0018	0.0083	4
BP	GO:0016236	macroautophagy	4/60	205/23328	0.0019	0.0086	4
BP	GO:0030522	intracellular receptor signaling pathway	4/60	207/23328	0.0020	0.0088	4
BP	GO:2000377	regulation of reactive oxygen species metabolic process	4/60	207/23328	0.0020	0.0088	4
BP	GO:1904018	positive regulation of vasculature development	4/60	208/23328	0.0020	0.0088	4
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	4/60	209/23328	0.0021	0.0088	4
BP	GO:0050866	negative regulation of cell activation	4/60	210/23328	0.0021	0.0089	4
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	4/60	215/23328	0.0023	0.0095	4
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	4/60	216/23328	0.0023	0.0097	4
BP	GO:0030595	leukocyte chemotaxis	4/60	219/23328	0.0024	0.0100	4
BP	GO:0097529	myeloid leukocyte migration	4/60	219/23328	0.0024	0.0100	4
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	4/60	221/23328	0.0025	0.0102	4
BP	GO:0045732	positive regulation of protein catabolic process	4/60	222/23328	0.0026	0.0103	4
BP	GO:0003018	vascular process in circulatory system	4/60	224/23328	0.0027	0.0105	4
BP	GO:0050920	regulation of chemotaxis	4/60	224/23328	0.0027	0.0105	4
BP	GO:1901617	organic hydroxy compound biosynthetic process	4/60	225/23328	0.0027	0.0106	4
BP	GO:0071241	cellular response to inorganic substance	4/60	227/23328	0.0028	0.0108	4
BP	GO:0030073	insulin secretion	4/60	229/23328	0.0029	0.0109	4
BP	GO:0019318	hexose metabolic process	4/60	231/23328	0.0030	0.0111	4
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	4/60	234/23328	0.0031	0.0115	4
BP	GO:0010632	regulation of epithelial cell migration	4/60	235/23328	0.0031	0.0116	4
BP	GO:0090276	regulation of peptide hormone secretion	4/60	235/23328	0.0031	0.0116	4
BP	GO:0010466	negative regulation of peptidase activity	4/60	246/23328	0.0037	0.0131	4

BP	GO:0031330	negative regulation of cellular catabolic process	4/60	250/23328	0.0039	0.0137	4
BP	GO:1903362	regulation of cellular protein catabolic process	4/60	254/23328	0.0042	0.0143	4
BP	GO:0001818	negative regulation of cytokine production	4/60	260/23328	0.0045	0.0153	4
BP	GO:0043588	skin development	4/60	275/23328	0.0055	0.0176	4
BP	GO:0002366	leukocyte activation involved in immune response	4/60	285/23328	0.0062	0.0193	4
BP	GO:0030072	peptide hormone secretion	4/60	285/23328	0.0062	0.0193	4
BP	GO:0009615	response to virus	4/60	286/23328	0.0063	0.0194	4
BP	GO:0002263	cell activation involved in immune response	4/60	289/23328	0.0065	0.0199	4
BP	GO:0009416	response to light stimulus	4/60	298/23328	0.0073	0.0216	4
BP	GO:0007611	learning or memory	4/60	299/23328	0.0073	0.0216	4
BP	GO:0046883	regulation of hormone secretion	4/60	303/23328	0.0077	0.0224	4
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	4/60	309/23328	0.0082	0.0233	4
BP	GO:0044282	small molecule catabolic process	4/60	320/23328	0.0093	0.0248	4
BP	GO:0045765	regulation of angiogenesis	4/60	320/23328	0.0093	0.0248	4
BP	GO:0050863	regulation of T cell activation	4/60	321/23328	0.0094	0.0250	4
BP	GO:0016042	lipid catabolic process	4/60	324/23328	0.0097	0.0255	4
BP	GO:0018105	peptidyl-serine phosphorylation	4/60	331/23328	0.0104	0.0270	4
BP	GO:0043434	response to peptide hormone	4/60	336/23328	0.0109	0.0280	4
BP	GO:0050890	cognition	4/60	336/23328	0.0109	0.0280	4
BP	GO:0007159	leukocyte cell-cell adhesion	4/60	345/23328	0.0120	0.0301	4
BP	GO:0052548	regulation of endopeptidase activity	4/60	346/23328	0.0121	0.0303	4
BP	GO:0051222	positive regulation of protein transport	4/60	348/23328	0.0123	0.0308	4
BP	GO:0045861	negative regulation of proteolysis	4/60	350/23328	0.0126	0.0311	4
BP	GO:0006417	regulation of translation	4/60	355/23328	0.0132	0.0321	4
BP	GO:0050806	positive regulation of synaptic transmission	4/60	355/23328	0.0132	0.0321	4
BP	GO:1901342	regulation of vasculature development	4/60	356/23328	0.0133	0.0323	4
BP	GO:0018209	peptidyl-serine modification	4/60	357/23328	0.0134	0.0325	4
BP	GO:0050900	leukocyte migration	4/60	360/23328	0.0138	0.0330	4

BP	GO:1904062	regulation of cation transmembrane transport	4/60	361/23328	0.0139	0.0332	4
BP	GO:0046879	hormone secretion	4/60	364/23328	0.0143	0.0337	4
BP	GO:1904951	positive regulation of establishment of protein localization	4/60	364/23328	0.0143	0.0337	4
BP	GO:0050708	regulation of protein secretion	4/60	365/23328	0.0145	0.0337	4
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	4/60	368/23328	0.0149	0.0344	4
BP	GO:1902903	regulation of supramolecular fiber organization	4/60	370/23328	0.0151	0.0350	4
BP	GO:0010976	positive regulation of neuron projection development	4/60	372/23328	0.0154	0.0355	4
BP	GO:0050678	regulation of epithelial cell proliferation	4/60	372/23328	0.0154	0.0355	4
BP	GO:0044403	symbiotic process	4/60	374/23328	0.0157	0.0359	4
BP	GO:0010721	negative regulation of cell development	4/60	387/23328	0.0175	0.0393	4
BP	GO:0051346	negative regulation of hydrolase activity	4/60	405/23328	0.0204	0.0441	4
BP	GO:0002791	regulation of peptide secretion	4/60	406/23328	0.0205	0.0444	4
BP	GO:0030098	lymphocyte differentiation	4/60	409/23328	0.0210	0.0452	4
BP	GO:0032535	regulation of cellular component size	4/60	413/23328	0.0217	0.0460	4
BP	GO:0007517	muscle organ development	4/60	420/23328	0.0229	0.0483	4
BP	GO:0052547	regulation of peptidase activity	4/60	421/23328	0.0231	0.0483	4
BP	GO:0060249	anatomical structure homeostasis	4/60	422/23328	0.0233	0.0486	4
BP	GO:0050673	epithelial cell proliferation	4/60	438/23328	0.0262	0.0515	4
BP	GO:0045860	positive regulation of protein kinase activity	4/60	440/23328	0.0266	0.0520	4
BP	GO:0071900	regulation of protein serine/threonine kinase activity	4/60	442/23328	0.0270	0.0525	4
BP	GO:0042391	regulation of membrane potential	4/60	450/23328	0.0286	0.0535	4
BP	GO:0045786	negative regulation of cell cycle	4/60	451/23328	0.0288	0.0538	4
BP	GO:0070838	divalent metal ion transport	4/60	467/23328	0.0321	0.0553	4
BP	GO:0009306	protein secretion	4/60	470/23328	0.0327	0.0553	4
BP	GO:0072511	divalent inorganic cation transport	4/60	470/23328	0.0327	0.0553	4

BP	GO:0035592	establishment of protein localization to extracellular region	4/60	471/23328	0.0330	0.0553	4
BP	GO:0031346	positive regulation of cell projection organization	4/60	478/23328	0.0345	0.0566	4
BP	GO:0071692	protein localization to extracellular region	4/60	478/23328	0.0345	0.0566	4
BP	GO:0034765	regulation of ion transmembrane transport	4/60	489/23328	0.0370	0.0583	4
CC	GO:0005901	caveola	4/61	97/23271	0.0001	0.0040	4
CC	GO:0044853	plasma membrane raft	4/61	130/23271	0.0004	0.0095	4
CC	GO:0031253	cell projection membrane	4/61	304/23271	0.0083	0.0566	4
CC	GO:0045121	membrane raft	4/61	379/23271	0.0174	0.0842	4
CC	GO:0098857	membrane microdomain	4/61	380/23271	0.0176	0.0842	4
CC	GO:0098589	membrane region	4/61	393/23271	0.0196	0.0866	4
MF	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	4/58	28/22669	0.0000	0.0001	4
MF	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4/58	29/22669	0.0000	0.0001	4
MF	GO:0051213	dioxygenase activity	4/58	92/22669	0.0001	0.0044	4
MF	GO:0005319	lipid transporter activity	4/58	138/22669	0.0004	0.0103	4
MF	GO:0016874	ligase activity	4/58	163/22669	0.0008	0.0132	4
MF	GO:0005506	iron ion binding	4/58	167/22669	0.0009	0.0132	4
MF	GO:0031406	carboxylic acid binding	4/58	226/22669	0.0027	0.0166	4
MF	GO:0043177	organic acid binding	4/58	241/22669	0.0034	0.0197	4
MF	GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	4/58	284/22669	0.0060	0.0311	4
MF	GO:0042277	peptide binding	4/58	318/22669	0.0089	0.0373	4
MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	4/58	344/22669	0.0116	0.0435	4
MF	GO:0001217	DNA-binding transcription repressor activity	4/58	345/22669	0.0117	0.0435	4
MF	GO:0140297	DNA-binding transcription factor binding	4/58	365/22669	0.0142	0.0506	4
BP	GO:0006750	glutathione biosynthetic process	3/60	12/23328	0.0000	0.0001	3

BP	GO:0001781	neutrophil apoptotic process	3/60	13/23328	0.0000	0.0002	3
BP	GO:0019184	nonribosomal peptide biosynthetic process	3/60	14/23328	0.0000	0.0002	3
BP	GO:0072350	tricarboxylic acid metabolic process	3/60	15/23328	0.0000	0.0002	3
BP	GO:0090594	inflammatory response to wounding	3/60	15/23328	0.0000	0.0002	3
BP	GO:0032495	response to muramyl dipeptide	3/60	20/23328	0.0000	0.0004	3
BP	GO:0010039	response to iron ion	3/60	21/23328	0.0000	0.0004	3
BP	GO:0034114	regulation of heterotypic cell-cell adhesion	3/60	25/23328	0.0000	0.0006	3
BP	GO:0001780	neutrophil homeostasis	3/60	26/23328	0.0000	0.0007	3
BP	GO:0010575	positive regulation of vascular endothelial growth factor production	3/60	26/23328	0.0000	0.0007	3
BP	GO:0006925	inflammatory cell apoptotic process	3/60	27/23328	0.0000	0.0007	3
BP	GO:0042908	xenobiotic transport	3/60	27/23328	0.0000	0.0007	3
BP	GO:0006536	glutamate metabolic process	3/60	28/23328	0.0001	0.0008	3
BP	GO:0006099	tricarboxylic acid cycle	3/60	32/23328	0.0001	0.0009	3
BP	GO:0010574	regulation of vascular endothelial growth factor production	3/60	32/23328	0.0001	0.0009	3
BP	GO:0120255	olefinic compound biosynthetic process	3/60	34/23328	0.0001	0.0011	3
BP	GO:0010573	vascular endothelial growth factor production	3/60	36/23328	0.0001	0.0012	3
BP	GO:0001782	B cell homeostasis	3/60	37/23328	0.0001	0.0013	3
BP	GO:0033028	myeloid cell apoptotic process	3/60	39/23328	0.0001	0.0014	3
BP	GO:0042398	cellular modified amino acid biosynthetic process	3/60	39/23328	0.0001	0.0014	3
BP	GO:0042304	regulation of fatty acid biosynthetic process	3/60	43/23328	0.0002	0.0018	3
BP	GO:0089718	amino acid import across plasma membrane	3/60	45/23328	0.0002	0.0020	3
BP	GO:0006636	unsaturated fatty acid biosynthetic process	3/60	46/23328	0.0002	0.0020	3
BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	3/60	46/23328	0.0002	0.0020	3
BP	GO:0006110	regulation of glycolytic process	3/60	48/23328	0.0003	0.0022	3
BP	GO:0043090	amino acid import	3/60	49/23328	0.0003	0.0023	3

BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	3/60	49/23328	0.0003	0.0023	3
BP	GO:1902475	L-alpha-amino acid transmembrane transport	3/60	50/23328	0.0003	0.0024	3
BP	GO:1903202	negative regulation of oxidative stress-induced cell death	3/60	52/23328	0.0003	0.0027	3
BP	GO:0006111	regulation of gluconeogenesis	3/60	53/23328	0.0003	0.0028	3
BP	GO:1900408	negative regulation of cellular response to oxidative stress	3/60	53/23328	0.0003	0.0028	3
BP	GO:0034113	heterotypic cell-cell adhesion	3/60	54/23328	0.0004	0.0029	3
BP	GO:1902883	negative regulation of response to oxidative stress	3/60	56/23328	0.0004	0.0032	3
BP	GO:0140115	export across plasma membrane	3/60	57/23328	0.0004	0.0033	3
BP	GO:0043470	regulation of carbohydrate catabolic process	3/60	58/23328	0.0005	0.0034	3
BP	GO:0009064	glutamine family amino acid metabolic process	3/60	64/23328	0.0006	0.0042	3
BP	GO:0015807	L-amino acid transport	3/60	65/23328	0.0006	0.0043	3
BP	GO:1901570	fatty acid derivative biosynthetic process	3/60	67/23328	0.0007	0.0045	3
BP	GO:0000422	autophagy of mitochondrion	3/60	68/23328	0.0007	0.0046	3
BP	GO:0030968	endoplasmic reticulum unfolded protein response	3/60	68/23328	0.0007	0.0046	3
BP	GO:0061726	mitochondrion disassembly	3/60	68/23328	0.0007	0.0046	3
BP	GO:0019369	arachidonic acid metabolic process	3/60	70/23328	0.0008	0.0049	3
BP	GO:0010507	negative regulation of autophagy	3/60	75/23328	0.0010	0.0056	3
BP	GO:0042306	regulation of protein import into nucleus	3/60	75/23328	0.0010	0.0056	3
BP	GO:0031397	negative regulation of protein ubiquitination	3/60	77/23328	0.0010	0.0058	3
BP	GO:1903201	regulation of oxidative stress-induced cell death	3/60	77/23328	0.0010	0.0058	3
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	3/60	78/23328	0.0011	0.0058	3
BP	GO:0032651	regulation of interleukin-1 beta production	3/60	80/23328	0.0012	0.0061	3
BP	GO:1900542	regulation of purine nucleotide metabolic process	3/60	80/23328	0.0012	0.0061	3

BP	GO:0006140	regulation of nucleotide metabolic process	3/60	81/23328	0.0012	0.0062	3
BP	GO:1904589	regulation of protein import	3/60	81/23328	0.0012	0.0062	3
BP	GO:0015914	phospholipid transport	3/60	82/23328	0.0012	0.0064	3
BP	GO:0003333	amino acid transmembrane transport	3/60	83/23328	0.0013	0.0065	3
BP	GO:1901379	regulation of potassium ion transmembrane transport	3/60	86/23328	0.0014	0.0070	3
BP	GO:0034620	cellular response to unfolded protein	3/60	88/23328	0.0015	0.0073	3
BP	GO:0070301	cellular response to hydrogen peroxide	3/60	89/23328	0.0016	0.0075	3
BP	GO:0032611	interleukin-1 beta production	3/60	91/23328	0.0017	0.0078	3
BP	GO:1900407	regulation of cellular response to oxidative stress	3/60	91/23328	0.0017	0.0078	3
BP	GO:0006096	glycolytic process	3/60	92/23328	0.0017	0.0080	3
BP	GO:0006757	ATP generation from ADP	3/60	93/23328	0.0018	0.0082	3
BP	GO:0015908	fatty acid transport	3/60	94/23328	0.0018	0.0084	3
BP	GO:1903578	regulation of ATP metabolic process	3/60	96/23328	0.0020	0.0087	3
BP	GO:0032652	regulation of interleukin-1 production	3/60	98/23328	0.0021	0.0088	3
BP	GO:0036473	cell death in response to oxidative stress	3/60	98/23328	0.0021	0.0088	3
BP	GO:1903008	organelle disassembly	3/60	98/23328	0.0021	0.0088	3
BP	GO:0046031	ADP metabolic process	3/60	99/23328	0.0021	0.0090	3
BP	GO:0062014	negative regulation of small molecule metabolic process	3/60	99/23328	0.0021	0.0090	3
BP	GO:0046889	positive regulation of lipid biosynthetic process	3/60	100/23328	0.0022	0.0092	3
BP	GO:1902882	regulation of response to oxidative stress	3/60	100/23328	0.0022	0.0092	3
BP	GO:0015748	organophosphate ester transport	3/60	103/23328	0.0024	0.0098	3
BP	GO:0009135	purine nucleoside diphosphate metabolic process	3/60	104/23328	0.0024	0.0100	3
BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	3/60	104/23328	0.0024	0.0100	3
BP	GO:1905954	positive regulation of lipid localization	3/60	105/23328	0.0025	0.0102	3
BP	GO:0000041	transition metal ion transport	3/60	106/23328	0.0026	0.0103	3
BP	GO:0006165	nucleoside diphosphate phosphorylation	3/60	106/23328	0.0026	0.0103	3

BP	GO:0009185	ribonucleoside diphosphate metabolic process	3/60	108/23328	0.0027	0.0106	3
BP	GO:0043255	regulation of carbohydrate biosynthetic process	3/60	108/23328	0.0027	0.0106	3
BP	GO:0043266	regulation of potassium ion transport	3/60	108/23328	0.0027	0.0106	3
BP	GO:0046939	nucleotide phosphorylation	3/60	108/23328	0.0027	0.0106	3
BP	GO:0002526	acute inflammatory response	3/60	110/23328	0.0029	0.0109	3
BP	GO:0032612	interleukin-1 production	3/60	110/23328	0.0029	0.0109	3
BP	GO:0035967	cellular response to topologically incorrect protein	3/60	110/23328	0.0029	0.0109	3
BP	GO:2000106	regulation of leukocyte apoptotic process	3/60	110/23328	0.0029	0.0109	3
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	3/60	111/23328	0.0029	0.0111	3
BP	GO:1904659	glucose transmembrane transport	3/60	111/23328	0.0029	0.0111	3
BP	GO:0008645	hexose transmembrane transport	3/60	112/23328	0.0030	0.0113	3
BP	GO:0015749	monosaccharide transmembrane transport	3/60	114/23328	0.0032	0.0117	3
BP	GO:0034219	carbohydrate transmembrane transport	3/60	115/23328	0.0033	0.0119	3
BP	GO:0006090	pyruvate metabolic process	3/60	120/23328	0.0037	0.0130	3
BP	GO:0033559	unsaturated fatty acid metabolic process	3/60	120/23328	0.0037	0.0130	3
BP	GO:0002688	regulation of leukocyte chemotaxis	3/60	121/23328	0.0038	0.0132	3
BP	GO:0009132	nucleoside diphosphate metabolic process	3/60	123/23328	0.0039	0.0137	3
BP	GO:1903409	reactive oxygen species biosynthetic process	3/60	125/23328	0.0041	0.0142	3
BP	GO:0046822	regulation of nucleocytoplasmic transport	3/60	126/23328	0.0042	0.0145	3
BP	GO:0010906	regulation of glucose metabolic process	3/60	128/23328	0.0044	0.0151	3
BP	GO:0006690	icosanoid metabolic process	3/60	129/23328	0.0045	0.0153	3
BP	GO:0033138	positive regulation of peptidyl-serine phosphorylation	3/60	129/23328	0.0045	0.0153	3
BP	GO:0032368	regulation of lipid transport	3/60	130/23328	0.0046	0.0155	3
BP	GO:0048640	negative regulation of developmental growth	3/60	131/23328	0.0047	0.0157	3

BP	GO:0045995	regulation of embryonic development	3/60	134/23328	0.0050	0.0165	3
BP	GO:0043467	regulation of generation of precursor metabolites and energy	3/60	135/23328	0.0051	0.0167	3
BP	GO:1900180	regulation of protein localization to nucleus	3/60	139/23328	0.0055	0.0177	3
BP	GO:0016052	carbohydrate catabolic process	3/60	142/23328	0.0059	0.0185	3
BP	GO:0035270	endocrine system development	3/60	147/23328	0.0065	0.0199	3
BP	GO:0034101	erythrocyte homeostasis	3/60	149/23328	0.0067	0.0204	3
BP	GO:0034614	cellular response to reactive oxygen species	3/60	150/23328	0.0068	0.0206	3
BP	GO:0050729	positive regulation of inflammatory response	3/60	152/23328	0.0071	0.0211	3
BP	GO:0002821	positive regulation of adaptive immune response	3/60	154/23328	0.0073	0.0216	3
BP	GO:0006457	protein folding	3/60	155/23328	0.0075	0.0218	3
BP	GO:0034250	positive regulation of cellular amide metabolic process	3/60	158/23328	0.0079	0.0227	3
BP	GO:0050777	negative regulation of immune response	3/60	158/23328	0.0079	0.0227	3
BP	GO:0002700	regulation of production of molecular mediator of immune response	3/60	159/23328	0.0080	0.0228	3
BP	GO:0009266	response to temperature stimulus	3/60	159/23328	0.0080	0.0228	3
BP	GO:0045580	regulation of T cell differentiation	3/60	159/23328	0.0080	0.0228	3
BP	GO:0006694	steroid biosynthetic process	3/60	161/23328	0.0083	0.0233	3
BP	GO:0006865	amino acid transport	3/60	162/23328	0.0084	0.0237	3
BP	GO:0045017	glycerolipid biosynthetic process	3/60	164/23328	0.0087	0.0242	3
BP	GO:0006606	protein import into nucleus	3/60	165/23328	0.0089	0.0242	3
BP	GO:0051147	regulation of muscle cell differentiation	3/60	165/23328	0.0089	0.0242	3
BP	GO:0007596	blood coagulation	3/60	166/23328	0.0090	0.0245	3
BP	GO:0045834	positive regulation of lipid metabolic process	3/60	167/23328	0.0091	0.0246	3
BP	GO:0007599	hemostasis	3/60	168/23328	0.0093	0.0248	3
BP	GO:0050817	coagulation	3/60	169/23328	0.0094	0.0250	3
BP	GO:0051170	import into nucleus	3/60	169/23328	0.0094	0.0250	3

BP	GO:0071356	cellular response to tumor necrosis factor	3/60	169/23328	0.0094	0.0250	3
BP	GO:0008654	phospholipid biosynthetic process	3/60	172/23328	0.0099	0.0258	3
BP	GO:0007033	vacuole organization	3/60	174/23328	0.0102	0.0266	3
BP	GO:0015718	monocarboxylic acid transport	3/60	174/23328	0.0102	0.0266	3
BP	GO:0007369	gastrulation	3/60	176/23328	0.0105	0.0272	3
BP	GO:0032388	positive regulation of intracellular transport	3/60	184/23328	0.0119	0.0299	3
BP	GO:0034612	response to tumor necrosis factor	3/60	188/23328	0.0126	0.0311	3
BP	GO:0002695	negative regulation of leukocyte activation	3/60	189/23328	0.0128	0.0315	3
BP	GO:0007259	receptor signaling pathway via JAK-STAT	3/60	191/23328	0.0131	0.0321	3
BP	GO:0045619	regulation of lymphocyte differentiation	3/60	192/23328	0.0133	0.0323	3
BP	GO:1903531	negative regulation of secretion by cell	3/60	193/23328	0.0135	0.0327	3
BP	GO:0048771	tissue remodeling	3/60	196/23328	0.0141	0.0333	3
BP	GO:0097696	receptor signaling pathway via STAT	3/60	196/23328	0.0141	0.0333	3
BP	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/60	197/23328	0.0143	0.0337	3
BP	GO:0050714	positive regulation of protein secretion	3/60	199/23328	0.0147	0.0341	3
BP	GO:0051216	cartilage development	3/60	200/23328	0.0149	0.0344	3
BP	GO:0071805	potassium ion transmembrane transport	3/60	200/23328	0.0149	0.0344	3
BP	GO:0002285	lymphocyte activation involved in immune response	3/60	203/23328	0.0154	0.0355	3
BP	GO:0050679	positive regulation of epithelial cell proliferation	3/60	208/23328	0.0165	0.0375	3
BP	GO:0002685	regulation of leukocyte migration	3/60	217/23328	0.0184	0.0409	3
BP	GO:0017038	protein import	3/60	217/23328	0.0184	0.0409	3
BP	GO:0044242	cellular lipid catabolic process	3/60	219/23328	0.0189	0.0416	3
BP	GO:0016054	organic acid catabolic process	3/60	223/23328	0.0198	0.0432	3

BP	GO:0046395	carboxylic acid catabolic process	3/60	223/23328	0.0198	0.0432	3
BP	GO:0051048	negative regulation of secretion	3/60	223/23328	0.0198	0.0432	3
BP	GO:0002793	positive regulation of peptide secretion	3/60	230/23328	0.0214	0.0460	3
BP	GO:0033157	regulation of intracellular protein transport	3/60	232/23328	0.0219	0.0465	3
BP	GO:0051607	defense response to virus	3/60	239/23328	0.0237	0.0495	3
BP	GO:0006813	potassium ion transport	3/60	240/23328	0.0239	0.0499	3
BP	GO:0030278	regulation of ossification	3/60	241/23328	0.0242	0.0503	3
BP	GO:0032147	activation of protein kinase activity	3/60	242/23328	0.0245	0.0503	3
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	3/60	247/23328	0.0258	0.0509	3
BP	GO:1903522	regulation of blood circulation	3/60	248/23328	0.0261	0.0513	3
BP	GO:0030258	lipid modification	3/60	250/23328	0.0266	0.0520	3
BP	GO:0046034	ATP metabolic process	3/60	253/23328	0.0274	0.0526	3
BP	GO:0071375	cellular response to peptide hormone stimulus	3/60	253/23328	0.0274	0.0526	3
BP	GO:0051403	stress-activated MAPK cascade	3/60	257/23328	0.0285	0.0535	3
BP	GO:0001894	tissue homeostasis	3/60	261/23328	0.0297	0.0541	3
BP	GO:0002703	regulation of leukocyte mediated immunity	3/60	261/23328	0.0297	0.0541	3
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	3/60	263/23328	0.0303	0.0541	3
BP	GO:0048588	developmental cell growth	3/60	267/23328	0.0314	0.0553	3
BP	GO:0031098	stress-activated protein kinase signaling cascade	3/60	272/23328	0.0330	0.0553	3
BP	GO:0042593	glucose homeostasis	3/60	273/23328	0.0333	0.0554	3
BP	GO:0071695	anatomical structure maturation	3/60	273/23328	0.0333	0.0554	3
BP	GO:0110053	regulation of actin filament organization	3/60	273/23328	0.0333	0.0554	3
BP	GO:0033500	carbohydrate homeostasis	3/60	274/23328	0.0336	0.0558	3
BP	GO:0061448	connective tissue development	3/60	276/23328	0.0342	0.0566	3
BP	GO:0030336	negative regulation of cell migration	3/60	278/23328	0.0348	0.0566	3
BP	GO:0031349	positive regulation of defense response	3/60	278/23328	0.0348	0.0566	3
BP	GO:0090287	regulation of cellular response to growth factor stimulus	3/60	281/23328	0.0358	0.0571	3

BP	GO:0030217	T cell differentiation	3/60	282/23328	0.0361	0.0574	3
BP	GO:0007162	negative regulation of cell adhesion	3/60	290/23328	0.0387	0.0594	3
BP	GO:2000146	negative regulation of cell motility	3/60	291/23328	0.0390	0.0594	3
BP	GO:0034504	protein localization to nucleus	3/60	293/23328	0.0397	0.0594	3
BP	GO:0071214	cellular response to abiotic stimulus	3/60	294/23328	0.0401	0.0594	3
BP	GO:0104004	cellular response to environmental stimulus	3/60	294/23328	0.0401	0.0594	3
BP	GO:0043405	regulation of MAP kinase activity	3/60	301/23328	0.0425	0.0609	3
BP	GO:0006913	nucleocytoplasmic transport	3/60	308/23328	0.0449	0.0625	3
BP	GO:0051169	nuclear transport	3/60	308/23328	0.0449	0.0625	3
BP	GO:0016032	viral process	3/60	309/23328	0.0453	0.0625	3
BP	GO:1902105	regulation of leukocyte differentiation	3/60	309/23328	0.0453	0.0625	3
BP	GO:0008544	epidermis development	3/60	313/23328	0.0468	0.0639	3
BP	GO:1903829	positive regulation of cellular protein localization	3/60	317/23328	0.0482	0.0644	3
BP	GO:0018108	peptidyl-tyrosine phosphorylation	3/60	322/23328	0.0501	0.0657	3
BP	GO:0018212	peptidyl-tyrosine modification	3/60	325/23328	0.0513	0.0669	3
BP	GO:0040013	negative regulation of locomotion	3/60	326/23328	0.0516	0.0671	3
BP	GO:0051271	negative regulation of cellular component movement	3/60	326/23328	0.0516	0.0671	3
BP	GO:0021700	developmental maturation	3/60	327/23328	0.0520	0.0671	3
BP	GO:0050768	negative regulation of neurogenesis	3/60	337/23328	0.0560	0.0693	3
BP	GO:0042063	gliogenesis	3/60	338/23328	0.0564	0.0696	3
BP	GO:0045862	positive regulation of proteolysis	3/60	344/23328	0.0588	0.0714	3
BP	GO:0046486	glycerolipid metabolic process	3/60	360/23328	0.0655	0.0757	3
BP	GO:0002440	production of molecular mediator of immune response	3/60	361/23328	0.0660	0.0760	3
BP	GO:0032956	regulation of actin cytoskeleton organization	3/60	361/23328	0.0660	0.0760	3
BP	GO:0048167	regulation of synaptic plasticity	3/60	365/23328	0.0677	0.0764	3
BP	GO:0051961	negative regulation of nervous system development	3/60	365/23328	0.0677	0.0764	3
BP	GO:0043010	camera-type eye development	3/60	370/23328	0.0699	0.0777	3

BP	GO:0006644	phospholipid metabolic process	3/60	374/23328	0.0717	0.0785	3
BP	GO:0051656	establishment of organelle localization	3/60	382/23328	0.0753	0.0806	3
BP	GO:1903532	positive regulation of secretion by cell	3/60	388/23328	0.0781	0.0820	3
BP	GO:0044270	cellular nitrogen compound catabolic process	3/60	391/23328	0.0795	0.0823	3
BP	GO:0030900	forebrain development	3/60	393/23328	0.0805	0.0832	3
BP	GO:0046700	heterocycle catabolic process	3/60	397/23328	0.0824	0.0843	3
BP	GO:0042692	muscle cell differentiation	3/60	399/23328	0.0834	0.0848	3
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	3/60	405/23328	0.0863	0.0855	3
BP	GO:0048638	regulation of developmental growth	3/60	409/23328	0.0882	0.0871	3
BP	GO:0010256	endomembrane system organization	3/60	410/23328	0.0887	0.0871	3
BP	GO:0032970	regulation of actin filament-based process	3/60	410/23328	0.0887	0.0871	3
BP	GO:0019439	aromatic compound catabolic process	3/60	411/23328	0.0892	0.0875	3
BP	GO:0001654	eye development	3/60	418/23328	0.0927	0.0894	3
BP	GO:0006816	calcium ion transport	3/60	420/23328	0.0937	0.0897	3
BP	GO:0150063	visual system development	3/60	422/23328	0.0947	0.0905	3
BP	GO:0048880	sensory system development	3/60	426/23328	0.0968	0.0915	3
BP	GO:0007015	actin filament organization	3/60	437/23328	0.1025	0.0944	3
BP	GO:0043254	regulation of protein-containing complex assembly	3/60	438/23328	0.1030	0.0948	3
BP	GO:0051047	positive regulation of secretion	3/60	440/23328	0.1041	0.0954	3
BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/60	445/23328	0.1067	0.0964	3
BP	GO:0010498	proteasomal protein catabolic process	3/60	470/23328	0.1204	0.1042	3
BP	GO:0048608	reproductive structure development	3/60	477/23328	0.1244	0.1061	3
BP	GO:0002696	positive regulation of leukocyte activation	3/60	479/23328	0.1255	0.1062	3
BP	GO:0061458	reproductive system development	3/60	481/23328	0.1267	0.1070	3

BP	GO:0015672	monovalent inorganic cation transport	3/60	489/23328	0.1313	0.1088	3
BP	GO:0050867	positive regulation of cell activation	3/60	496/23328	0.1353	0.1106	3
CC	GO:0000407	phagophore assembly site	3/61	29/23271	0.0001	0.0026	3
CC	GO:0030018	Z disc	3/61	125/23271	0.0043	0.0482	3
CC	GO:0031674	I band	3/61	138/23271	0.0057	0.0510	3
CC	GO:0005777	peroxisome	3/61	145/23271	0.0065	0.0510	3
CC	GO:0042579	microbody	3/61	145/23271	0.0065	0.0510	3
CC	GO:0030496	midbody	3/61	147/23271	0.0068	0.0510	3
CC	GO:0030017	sarcomere	3/61	188/23271	0.0133	0.0817	3
CC	GO:0019867	outer membrane	3/61	196/23271	0.0148	0.0834	3
CC	GO:0031968	organelle outer membrane	3/61	196/23271	0.0148	0.0834	3
CC	GO:0030016	myofibril	3/61	212/23271	0.0182	0.0842	3
CC	GO:0043292	contractile fiber	3/61	226/23271	0.0215	0.0899	3
CC	GO:0008021	synaptic vesicle	3/61	239/23271	0.0249	0.0959	3
CC	GO:0070382	exocytic vesicle	3/61	261/23271	0.0312	0.0961	3
CC	GO:0019898	extrinsic component of membrane	3/61	320/23271	0.0517	0.1286	3
CC	GO:0030133	transport vesicle	3/61	339/23271	0.0594	0.1296	3
CC	GO:0031252	cell leading edge	3/61	395/23271	0.0851	0.1537	3
CC	GO:0043235	receptor complex	3/61	403/23271	0.0891	0.1537	3
CC	GO:0097060	synaptic membrane	3/61	470/23271	0.1255	0.1847	3
CC	GO:0015629	actin cytoskeleton	3/61	497/23271	0.1416	0.2036	3
MF	GO:0042910	xenobiotic transmembrane transporter activity	3/58	26/22669	0.0000	0.0025	3
MF	GO:0043130	ubiquitin binding	3/58	75/22669	0.0009	0.0132	3
MF	GO:0032182	ubiquitin-like protein binding	3/58	95/22669	0.0019	0.0133	3
MF	GO:0031072	heat shock protein binding	3/58	146/22669	0.0062	0.0311	3
MF	GO:0019887	protein kinase regulator activity	3/58	170/22669	0.0095	0.0387	3
MF	GO:0019207	kinase regulator activity	3/58	202/22669	0.0150	0.0518	3
MF	GO:0005125	cytokine activity	3/58	231/22669	0.0214	0.0675	3
MF	GO:0016746	transferase activity, transferring acyl groups	3/58	268/22669	0.0313	0.0763	3
MF	GO:0005126	cytokine receptor binding	3/58	314/22669	0.0465	0.0869	3
BP	GO:0015911	long-chain fatty acid import across plasma membrane	2/60	10/23328	0.0003	0.0024	2
BP	GO:0033029	regulation of neutrophil apoptotic process	2/60	10/23328	0.0003	0.0024	2
BP	GO:0019372	lipoxygenase pathway	2/60	11/23328	0.0004	0.0028	2

BP	GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	2/60	11/23328	0.0004	0.0028	2
BP	GO:0097421	liver regeneration	2/60	12/23328	0.0004	0.0033	2
BP	GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	2/60	13/23328	0.0005	0.0036	2
BP	GO:0071281	cellular response to iron ion	2/60	13/23328	0.0005	0.0036	2
BP	GO:0006857	oligopeptide transport	2/60	14/23328	0.0006	0.0041	2
BP	GO:0034116	positive regulation of heterotypic cell-cell adhesion	2/60	14/23328	0.0006	0.0041	2
BP	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	2/60	14/23328	0.0006	0.0041	2
BP	GO:1902001	fatty acid transmembrane transport	2/60	14/23328	0.0006	0.0041	2
BP	GO:0010715	regulation of extracellular matrix disassembly	2/60	15/23328	0.0007	0.0044	2
BP	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	2/60	15/23328	0.0007	0.0044	2
BP	GO:0044068	modulation by symbiont of host cellular process	2/60	16/23328	0.0008	0.0048	2
BP	GO:0002689	negative regulation of leukocyte chemotaxis	2/60	17/23328	0.0009	0.0051	2
BP	GO:0034755	iron ion transmembrane transport	2/60	17/23328	0.0009	0.0051	2
BP	GO:0035729	cellular response to hepatocyte growth factor stimulus	2/60	17/23328	0.0009	0.0051	2
BP	GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	2/60	17/23328	0.0009	0.0051	2
BP	GO:0032740	positive regulation of interleukin-17 production	2/60	18/23328	0.0010	0.0056	2
BP	GO:0045779	negative regulation of bone resorption	2/60	18/23328	0.0010	0.0056	2
BP	GO:0035728	response to hepatocyte growth factor	2/60	19/23328	0.0011	0.0058	2
BP	GO:0044539	long-chain fatty acid import into cell	2/60	19/23328	0.0011	0.0058	2
BP	GO:0045540	regulation of cholesterol biosynthetic process	2/60	19/23328	0.0011	0.0058	2

BP	GO:0060099	regulation of phagocytosis, engulfment	2/60	19/23328	0.0011	0.0058	2
BP	GO:0106118	regulation of sterol biosynthetic process	2/60	19/23328	0.0011	0.0058	2
BP	GO:0140354	lipid import into cell	2/60	19/23328	0.0011	0.0058	2
BP	GO:0045722	positive regulation of gluconeogenesis	2/60	20/23328	0.0012	0.0062	2
BP	GO:0046851	negative regulation of bone remodeling	2/60	20/23328	0.0012	0.0062	2
BP	GO:1905153	regulation of membrane invagination	2/60	20/23328	0.0012	0.0062	2
BP	GO:0035357	peroxisome proliferator activated receptor signaling pathway	2/60	21/23328	0.0013	0.0066	2
BP	GO:0042759	long-chain fatty acid biosynthetic process	2/60	21/23328	0.0013	0.0066	2
BP	GO:0046716	muscle cell cellular homeostasis	2/60	21/23328	0.0013	0.0066	2
BP	GO:0051900	regulation of mitochondrial depolarization	2/60	21/23328	0.0013	0.0066	2
BP	GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	2/60	21/23328	0.0013	0.0066	2
BP	GO:0043651	linoleic acid metabolic process	2/60	22/23328	0.0015	0.0070	2
BP	GO:0098780	response to mitochondrial depolarisation	2/60	22/23328	0.0015	0.0070	2
BP	GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	2/60	22/23328	0.0015	0.0070	2
BP	GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	2/60	22/23328	0.0015	0.0070	2
BP	GO:0002313	mature B cell differentiation involved in immune response	2/60	23/23328	0.0016	0.0075	2
BP	GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	2/60	23/23328	0.0016	0.0075	2
BP	GO:0071276	cellular response to cadmium ion	2/60	23/23328	0.0016	0.0075	2
BP	GO:0051882	mitochondrial depolarization	2/60	24/23328	0.0017	0.0080	2

BP	GO:0070498	interleukin-1-mediated signaling pathway	2/60	24/23328	0.0017	0.0080	2
BP	GO:1903204	negative regulation of oxidative stress-induced neuron death	2/60	24/23328	0.0017	0.0080	2
BP	GO:0000423	mitophagy	2/60	25/23328	0.0019	0.0084	2
BP	GO:0006706	steroid catabolic process	2/60	25/23328	0.0019	0.0084	2
BP	GO:0032703	negative regulation of interleukin-2 production	2/60	25/23328	0.0019	0.0084	2
BP	GO:0044003	modulation by symbiont of host process	2/60	25/23328	0.0019	0.0084	2
BP	GO:0046685	response to arsenic-containing substance	2/60	25/23328	0.0019	0.0084	2
BP	GO:0031100	animal organ regeneration	2/60	26/23328	0.0020	0.0088	2
BP	GO:0034104	negative regulation of tissue remodeling	2/60	26/23328	0.0020	0.0088	2
BP	GO:0045723	positive regulation of fatty acid biosynthetic process	2/60	26/23328	0.0020	0.0088	2
BP	GO:0072337	modified amino acid transport	2/60	26/23328	0.0020	0.0088	2
BP	GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	2/60	26/23328	0.0020	0.0088	2
BP	GO:2000637	positive regulation of gene silencing by miRNA	2/60	26/23328	0.0020	0.0088	2
BP	GO:0060148	positive regulation of posttranscriptional gene silencing	2/60	27/23328	0.0022	0.0092	2
BP	GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	2/60	27/23328	0.0022	0.0092	2
BP	GO:0090025	regulation of monocyte chemotaxis	2/60	28/23328	0.0024	0.0097	2
BP	GO:1900273	positive regulation of long-term synaptic potentiation	2/60	28/23328	0.0024	0.0097	2
BP	GO:0035094	response to nicotine	2/60	29/23328	0.0025	0.0102	2
BP	GO:0002335	mature B cell differentiation	2/60	30/23328	0.0027	0.0106	2
BP	GO:0032373	positive regulation of sterol transport	2/60	31/23328	0.0029	0.0109	2
BP	GO:0032376	positive regulation of cholesterol transport	2/60	31/23328	0.0029	0.0109	2
BP	GO:0072574	hepatocyte proliferation	2/60	31/23328	0.0029	0.0109	2
BP	GO:0072575	epithelial cell proliferation involved in liver morphogenesis	2/60	31/23328	0.0029	0.0109	2

BP	GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	2/60	31/23328	0.0029	0.0109	2
BP	GO:0071354	cellular response to interleukin-6	2/60	32/23328	0.0031	0.0114	2
BP	GO:0022617	extracellular matrix disassembly	2/60	33/23328	0.0033	0.0119	2
BP	GO:0032891	negative regulation of organic acid transport	2/60	33/23328	0.0033	0.0119	2
BP	GO:0072576	liver morphogenesis	2/60	33/23328	0.0033	0.0119	2
BP	GO:0033032	regulation of myeloid cell apoptotic process	2/60	34/23328	0.0035	0.0124	2
BP	GO:0051180	vitamin transport	2/60	34/23328	0.0035	0.0124	2
BP	GO:0070741	response to interleukin-6	2/60	34/23328	0.0035	0.0124	2
BP	GO:0071634	regulation of transforming growth factor beta production	2/60	34/23328	0.0035	0.0124	2
BP	GO:0090181	regulation of cholesterol metabolic process	2/60	34/23328	0.0035	0.0124	2
BP	GO:0032660	regulation of interleukin-17 production	2/60	35/23328	0.0037	0.0130	2
BP	GO:0046686	response to cadmium ion	2/60	35/23328	0.0037	0.0130	2
BP	GO:1903203	regulation of oxidative stress-induced neuron death	2/60	35/23328	0.0037	0.0130	2
BP	GO:0036475	neuron death in response to oxidative stress	2/60	36/23328	0.0039	0.0136	2
BP	GO:0071604	transforming growth factor beta production	2/60	36/23328	0.0039	0.0136	2
BP	GO:0002675	positive regulation of acute inflammatory response	2/60	37/23328	0.0041	0.0142	2
BP	GO:0014823	response to activity	2/60	37/23328	0.0041	0.0142	2
BP	GO:0050892	intestinal absorption	2/60	39/23328	0.0045	0.0153	2
BP	GO:0090049	regulation of cell migration involved in sprouting angiogenesis	2/60	39/23328	0.0045	0.0153	2
BP	GO:1905710	positive regulation of membrane permeability	2/60	39/23328	0.0045	0.0153	2
BP	GO:0006984	ER-nucleus signaling pathway	2/60	40/23328	0.0048	0.0159	2
BP	GO:0015804	neutral amino acid transport	2/60	40/23328	0.0048	0.0159	2
BP	GO:0002686	negative regulation of leukocyte migration	2/60	41/23328	0.0050	0.0165	2
BP	GO:0006953	acute-phase response	2/60	41/23328	0.0050	0.0165	2
BP	GO:0010470	regulation of gastrulation	2/60	41/23328	0.0050	0.0165	2
BP	GO:0072348	sulfur compound transport	2/60	42/23328	0.0052	0.0171	2

BP	GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	2/60	43/23328	0.0055	0.0176	2
BP	GO:0032007	negative regulation of TOR signaling	2/60	43/23328	0.0055	0.0176	2
BP	GO:0032620	interleukin-17 production	2/60	43/23328	0.0055	0.0176	2
BP	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	2/60	43/23328	0.0055	0.0176	2
BP	GO:1903053	regulation of extracellular matrix organization	2/60	43/23328	0.0055	0.0176	2
BP	GO:1903792	negative regulation of anion transport	2/60	43/23328	0.0055	0.0176	2
BP	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	2/60	44/23328	0.0057	0.0181	2
BP	GO:0034198	cellular response to amino acid starvation	2/60	44/23328	0.0057	0.0181	2
BP	GO:0071385	cellular response to glucocorticoid stimulus	2/60	44/23328	0.0057	0.0181	2
BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	2/60	44/23328	0.0057	0.0181	2
BP	GO:1903672	positive regulation of sprouting angiogenesis	2/60	44/23328	0.0057	0.0181	2
BP	GO:0010907	positive regulation of glucose metabolic process	2/60	45/23328	0.0060	0.0187	2
BP	GO:0042149	cellular response to glucose starvation	2/60	45/23328	0.0060	0.0187	2
BP	GO:0045923	positive regulation of fatty acid metabolic process	2/60	45/23328	0.0060	0.0187	2
BP	GO:0061756	leukocyte adhesion to vascular endothelial cell	2/60	45/23328	0.0060	0.0187	2
BP	GO:0003254	regulation of membrane depolarization	2/60	46/23328	0.0063	0.0194	2
BP	GO:0071384	cellular response to corticosteroid stimulus	2/60	46/23328	0.0063	0.0194	2
BP	GO:0045332	phospholipid translocation	2/60	47/23328	0.0065	0.0199	2
BP	GO:0060964	regulation of gene silencing by miRNA	2/60	47/23328	0.0065	0.0199	2
BP	GO:0072666	establishment of protein localization to vacuole	2/60	47/23328	0.0065	0.0199	2
BP	GO:0038066	p38MAPK cascade	2/60	48/23328	0.0068	0.0206	2

BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2/60	48/23328	0.0068	0.0206	2
BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	2/60	48/23328	0.0068	0.0206	2
BP	GO:1990928	response to amino acid starvation	2/60	48/23328	0.0068	0.0206	2
BP	GO:0006695	cholesterol biosynthetic process	2/60	49/23328	0.0071	0.0211	2
BP	GO:0034204	lipid translocation	2/60	49/23328	0.0071	0.0211	2
BP	GO:1902653	secondary alcohol biosynthetic process	2/60	49/23328	0.0071	0.0211	2
BP	GO:1904407	positive regulation of nitric oxide metabolic process	2/60	49/23328	0.0071	0.0211	2
BP	GO:0010677	negative regulation of cellular carbohydrate metabolic process	2/60	50/23328	0.0074	0.0216	2
BP	GO:0045646	regulation of erythrocyte differentiation	2/60	50/23328	0.0074	0.0216	2
BP	GO:0060147	regulation of posttranscriptional gene silencing	2/60	50/23328	0.0074	0.0216	2
BP	GO:0060966	regulation of gene silencing by RNA	2/60	50/23328	0.0074	0.0216	2
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	2/60	50/23328	0.0074	0.0216	2
BP	GO:0098754	detoxification	2/60	51/23328	0.0076	0.0223	2
BP	GO:0032731	positive regulation of interleukin-1 beta production	2/60	52/23328	0.0079	0.0227	2
BP	GO:0032757	positive regulation of interleukin-8 production	2/60	52/23328	0.0079	0.0227	2
BP	GO:0042307	positive regulation of protein import into nucleus	2/60	52/23328	0.0079	0.0227	2
BP	GO:0045124	regulation of bone resorption	2/60	52/23328	0.0079	0.0227	2
BP	GO:1904036	negative regulation of epithelial cell apoptotic process	2/60	52/23328	0.0079	0.0227	2
BP	GO:0032371	regulation of sterol transport	2/60	53/23328	0.0082	0.0233	2
BP	GO:0032374	regulation of cholesterol transport	2/60	53/23328	0.0082	0.0233	2
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	2/60	53/23328	0.0082	0.0233	2
BP	GO:0046456	icosanoid biosynthetic process	2/60	54/23328	0.0085	0.0238	2
BP	GO:0061077	chaperone-mediated protein folding	2/60	54/23328	0.0085	0.0238	2

BP	GO:1900271	regulation of long-term synaptic potentiation	2/60	54/23328	0.0085	0.0238	2
BP	GO:1902930	regulation of alcohol biosynthetic process	2/60	54/23328	0.0085	0.0238	2
BP	GO:0002042	cell migration involved in sprouting angiogenesis	2/60	55/23328	0.0089	0.0242	2
BP	GO:0002673	regulation of acute inflammatory response	2/60	55/23328	0.0089	0.0242	2
BP	GO:0006826	iron ion transport	2/60	55/23328	0.0089	0.0242	2
BP	GO:0016126	sterol biosynthetic process	2/60	55/23328	0.0089	0.0242	2
BP	GO:0045912	negative regulation of carbohydrate metabolic process	2/60	55/23328	0.0089	0.0242	2
BP	GO:0050922	negative regulation of chemotaxis	2/60	55/23328	0.0089	0.0242	2
BP	GO:0097035	regulation of membrane lipid distribution	2/60	55/23328	0.0089	0.0242	2
BP	GO:2000351	regulation of endothelial cell apoptotic process	2/60	55/23328	0.0089	0.0242	2
BP	GO:0035924	cellular response to vascular endothelial growth factor stimulus	2/60	56/23328	0.0092	0.0246	2
BP	GO:0042446	hormone biosynthetic process	2/60	56/23328	0.0092	0.0246	2
BP	GO:0045599	negative regulation of fat cell differentiation	2/60	56/23328	0.0092	0.0246	2
BP	GO:0071675	regulation of mononuclear cell migration	2/60	56/23328	0.0092	0.0246	2
BP	GO:0071715	icosanoid transport	2/60	56/23328	0.0092	0.0246	2
BP	GO:1901571	fatty acid derivative transport	2/60	56/23328	0.0092	0.0246	2
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	2/60	56/23328	0.0092	0.0246	2
BP	GO:0002548	monocyte chemotaxis	2/60	57/23328	0.0095	0.0250	2
BP	GO:0051591	response to cAMP	2/60	57/23328	0.0095	0.0250	2
BP	GO:0032663	regulation of interleukin-2 production	2/60	58/23328	0.0098	0.0256	2
BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	2/60	58/23328	0.0098	0.0256	2
BP	GO:0072577	endothelial cell apoptotic process	2/60	58/23328	0.0098	0.0256	2
BP	GO:1904591	positive regulation of protein import	2/60	58/23328	0.0098	0.0256	2
BP	GO:0007595	lactation	2/60	60/23328	0.0105	0.0270	2

BP	GO:0090303	positive regulation of wound healing	2/60	60/23328	0.0105	0.0270	2
BP	GO:0032732	positive regulation of interleukin-1 production	2/60	61/23328	0.0108	0.0277	2
BP	GO:0061912	selective autophagy	2/60	61/23328	0.0108	0.0277	2
BP	GO:0019080	viral gene expression	2/60	62/23328	0.0111	0.0282	2
BP	GO:0031018	endocrine pancreas development	2/60	62/23328	0.0111	0.0282	2
BP	GO:0032387	negative regulation of intracellular transport	2/60	62/23328	0.0111	0.0282	2
BP	GO:0046850	regulation of bone remodeling	2/60	62/23328	0.0111	0.0282	2
BP	GO:0072665	protein localization to vacuole	2/60	62/23328	0.0111	0.0282	2
BP	GO:0098930	axonal transport	2/60	62/23328	0.0111	0.0282	2
BP	GO:1903428	positive regulation of reactive oxygen species biosynthetic process	2/60	63/23328	0.0115	0.0290	2
BP	GO:0015909	long-chain fatty acid transport	2/60	64/23328	0.0118	0.0299	2
BP	GO:0045454	cell redox homeostasis	2/60	65/23328	0.0122	0.0305	2
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	2/60	65/23328	0.0122	0.0305	2
BP	GO:0032623	interleukin-2 production	2/60	66/23328	0.0126	0.0311	2
BP	GO:0042440	pigment metabolic process	2/60	66/23328	0.0126	0.0311	2
BP	GO:0090559	regulation of membrane permeability	2/60	66/23328	0.0126	0.0311	2
BP	GO:0097006	regulation of plasma lipoprotein particle levels	2/60	66/23328	0.0126	0.0311	2
BP	GO:0000768	syncytium formation by plasma membrane fusion	2/60	67/23328	0.0129	0.0317	2
BP	GO:0010676	positive regulation of cellular carbohydrate metabolic process	2/60	67/23328	0.0129	0.0317	2
BP	GO:0140253	cell-cell fusion	2/60	67/23328	0.0129	0.0317	2
BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	2/60	68/23328	0.0133	0.0323	2
BP	GO:0006949	syncytium formation	2/60	69/23328	0.0137	0.0327	2
BP	GO:0008542	visual learning	2/60	69/23328	0.0137	0.0327	2
BP	GO:0016239	positive regulation of macroautophagy	2/60	69/23328	0.0137	0.0327	2
BP	GO:0032677	regulation of interleukin-8 production	2/60	69/23328	0.0137	0.0327	2
BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/60	69/23328	0.0137	0.0327	2

BP	GO:0045600	positive regulation of fat cell differentiation	2/60	69/23328	0.0137	0.0327	2
BP	GO:1990868	response to chemokine	2/60	70/23328	0.0140	0.0333	2
BP	GO:1990869	cellular response to chemokine	2/60	70/23328	0.0140	0.0333	2
BP	GO:2000107	negative regulation of leukocyte apoptotic process	2/60	70/23328	0.0140	0.0333	2
BP	GO:0007040	lysosome organization	2/60	71/23328	0.0144	0.0337	2
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	2/60	71/23328	0.0144	0.0337	2
BP	GO:0055081	anion homeostasis	2/60	71/23328	0.0144	0.0337	2
BP	GO:0080171	lytic vacuole organization	2/60	71/23328	0.0144	0.0337	2
BP	GO:0007632	visual behavior	2/60	73/23328	0.0152	0.0351	2
BP	GO:0046824	positive regulation of nucleocytoplasmic transport	2/60	74/23328	0.0156	0.0358	2
BP	GO:0007260	tyrosine phosphorylation of STAT protein	2/60	75/23328	0.0160	0.0365	2
BP	GO:0032637	interleukin-8 production	2/60	75/23328	0.0160	0.0365	2
BP	GO:1903670	regulation of sprouting angiogenesis	2/60	75/23328	0.0160	0.0365	2
BP	GO:0006809	nitric oxide biosynthetic process	2/60	77/23328	0.0168	0.0382	2
BP	GO:0045453	bone resorption	2/60	77/23328	0.0168	0.0382	2
BP	GO:0002066	columnar/cuboidal epithelial cell development	2/60	78/23328	0.0172	0.0387	2
BP	GO:0019229	regulation of vasoconstriction	2/60	78/23328	0.0172	0.0387	2
BP	GO:0050810	regulation of steroid biosynthetic process	2/60	78/23328	0.0172	0.0387	2
BP	GO:0070228	regulation of lymphocyte apoptotic process	2/60	78/23328	0.0172	0.0387	2
BP	GO:0070373	negative regulation of ERK1 and ERK2 cascade	2/60	78/23328	0.0172	0.0387	2
BP	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	2/60	78/23328	0.0172	0.0387	2
BP	GO:1903036	positive regulation of response to wounding	2/60	78/23328	0.0172	0.0387	2
BP	GO:0002637	regulation of immunoglobulin production	2/60	79/23328	0.0177	0.0394	2
BP	GO:0048635	negative regulation of muscle organ development	2/60	79/23328	0.0177	0.0394	2
BP	GO:0008088	axo-dendritic transport	2/60	80/23328	0.0181	0.0403	2
BP	GO:0060968	regulation of gene silencing	2/60	80/23328	0.0181	0.0403	2
BP	GO:0046209	nitric oxide metabolic process	2/60	81/23328	0.0185	0.0409	2

BP	GO:0051881	regulation of mitochondrial membrane potential	2/60	81/23328	0.0185	0.0409	2
BP	GO:0071347	cellular response to interleukin-1	2/60	81/23328	0.0185	0.0409	2
BP	GO:0030500	regulation of bone mineralization	2/60	82/23328	0.0189	0.0416	2
BP	GO:0032370	positive regulation of lipid transport	2/60	82/23328	0.0189	0.0416	2
BP	GO:0046323	glucose import	2/60	83/23328	0.0194	0.0425	2
BP	GO:0051899	membrane depolarization	2/60	83/23328	0.0194	0.0425	2
BP	GO:0051817	modulation of process of other organism involved in symbiotic interaction	2/60	84/23328	0.0198	0.0432	2
BP	GO:0002718	regulation of cytokine production involved in immune response	2/60	85/23328	0.0203	0.0440	2
BP	GO:0030301	cholesterol transport	2/60	85/23328	0.0203	0.0440	2
BP	GO:0015918	sterol transport	2/60	86/23328	0.0207	0.0446	2
BP	GO:0031646	positive regulation of nervous system process	2/60	86/23328	0.0207	0.0446	2
BP	GO:2001057	reactive nitrogen species metabolic process	2/60	86/23328	0.0207	0.0446	2
BP	GO:0034103	regulation of tissue remodeling	2/60	87/23328	0.0212	0.0455	2
BP	GO:0002312	B cell activation involved in immune response	2/60	88/23328	0.0216	0.0460	2
BP	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	2/60	88/23328	0.0216	0.0460	2
BP	GO:0045913	positive regulation of carbohydrate metabolic process	2/60	88/23328	0.0216	0.0460	2
BP	GO:0046683	response to organophosphorus	2/60	88/23328	0.0216	0.0460	2
BP	GO:1900182	positive regulation of protein localization to nucleus	2/60	88/23328	0.0216	0.0460	2
BP	GO:1904063	negative regulation of cation transmembrane transport	2/60	88/23328	0.0216	0.0460	2
BP	GO:0071674	mononuclear cell migration	2/60	89/23328	0.0221	0.0467	2
BP	GO:0032024	positive regulation of insulin secretion	2/60	90/23328	0.0225	0.0476	2
BP	GO:0014015	positive regulation of gliogenesis	2/60	91/23328	0.0230	0.0483	2

BP	GO:0032890	regulation of organic acid transport	2/60	91/23328	0.0230	0.0483	2
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	2/60	91/23328	0.0230	0.0483	2
BP	GO:1903524	positive regulation of blood circulation	2/60	91/23328	0.0230	0.0483	2
BP	GO:0071774	response to fibroblast growth factor	2/60	93/23328	0.0240	0.0499	2
BP	GO:0009408	response to heat	2/60	94/23328	0.0244	0.0503	2
BP	GO:0031016	pancreas development	2/60	96/23328	0.0254	0.0503	2
BP	GO:0070555	response to interleukin-1	2/60	96/23328	0.0254	0.0503	2
BP	GO:0002709	regulation of T cell mediated immunity	2/60	97/23328	0.0259	0.0511	2
BP	GO:0060395	SMAD protein signal transduction	2/60	98/23328	0.0264	0.0518	2
BP	GO:0030593	neutrophil chemotaxis	2/60	99/23328	0.0269	0.0524	2
BP	GO:0070167	regulation of biomineral tissue development	2/60	99/23328	0.0269	0.0524	2
BP	GO:0110149	regulation of biomineralization	2/60	99/23328	0.0269	0.0524	2
BP	GO:0032006	regulation of TOR signaling	2/60	100/23328	0.0274	0.0526	2
BP	GO:0050795	regulation of behavior	2/60	100/23328	0.0274	0.0526	2
BP	GO:0007041	lysosomal transport	2/60	101/23328	0.0279	0.0526	2
BP	GO:0071456	cellular response to hypoxia	2/60	101/23328	0.0279	0.0526	2
BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	2/60	101/23328	0.0279	0.0526	2
BP	GO:0070227	lymphocyte apoptotic process	2/60	102/23328	0.0284	0.0534	2
BP	GO:0042310	vasoconstriction	2/60	103/23328	0.0289	0.0540	2
BP	GO:0046427	positive regulation of receptor signaling pathway via JAK-STAT	2/60	103/23328	0.0289	0.0540	2
BP	GO:0014074	response to purine-containing compound	2/60	104/23328	0.0295	0.0541	2
BP	GO:0034766	negative regulation of ion transmembrane transport	2/60	104/23328	0.0295	0.0541	2
BP	GO:0045778	positive regulation of ossification	2/60	104/23328	0.0295	0.0541	2
BP	GO:0046849	bone remodeling	2/60	104/23328	0.0295	0.0541	2
BP	GO:0048525	negative regulation of viral process	2/60	104/23328	0.0295	0.0541	2
BP	GO:0046634	regulation of alpha-beta T cell activation	2/60	105/23328	0.0300	0.0541	2

BP	GO:0035710	CD4-positive, alpha-beta T cell activation	2/60	106/23328	0.0305	0.0541	2
BP	GO:0002367	cytokine production involved in immune response	2/60	107/23328	0.0310	0.0549	2
BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	2/60	107/23328	0.0310	0.0549	2
BP	GO:1904894	positive regulation of receptor signaling pathway via STAT	2/60	107/23328	0.0310	0.0549	2
BP	GO:0008306	associative learning	2/60	108/23328	0.0316	0.0553	2
BP	GO:0034754	cellular hormone metabolic process	2/60	108/23328	0.0316	0.0553	2
BP	GO:0051897	positive regulation of protein kinase B signaling	2/60	109/23328	0.0321	0.0553	2
BP	GO:0097756	negative regulation of blood vessel diameter	2/60	109/23328	0.0321	0.0553	2
BP	GO:1901800	positive regulation of proteasomal protein catabolic process	2/60	109/23328	0.0321	0.0553	2
BP	GO:0009410	response to xenobiotic stimulus	2/60	110/23328	0.0327	0.0553	2
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	2/60	110/23328	0.0327	0.0553	2
BP	GO:0022600	digestive system process	2/60	110/23328	0.0327	0.0553	2
BP	GO:0008637	apoptotic mitochondrial changes	2/60	111/23328	0.0332	0.0554	2
BP	GO:0016241	regulation of macroautophagy	2/60	111/23328	0.0332	0.0554	2
BP	GO:0019218	regulation of steroid metabolic process	2/60	111/23328	0.0332	0.0554	2
BP	GO:0032963	collagen metabolic process	2/60	111/23328	0.0332	0.0554	2
BP	GO:0007589	body fluid secretion	2/60	112/23328	0.0338	0.0560	2
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	2/60	112/23328	0.0338	0.0560	2
BP	GO:0001942	hair follicle development	2/60	113/23328	0.0343	0.0566	2
BP	GO:0050764	regulation of phagocytosis	2/60	113/23328	0.0343	0.0566	2
BP	GO:0034440	lipid oxidation	2/60	114/23328	0.0349	0.0566	2
BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	2/60	114/23328	0.0349	0.0566	2
BP	GO:0018958	phenol-containing compound metabolic process	2/60	115/23328	0.0354	0.0566	2
BP	GO:0030216	keratinocyte differentiation	2/60	115/23328	0.0354	0.0566	2

BP	GO:0031398	positive regulation of protein ubiquitination	2/60	115/23328	0.0354	0.0566	2
BP	GO:0022404	molting cycle process	2/60	116/23328	0.0360	0.0573	2
BP	GO:0022405	hair cycle process	2/60	116/23328	0.0360	0.0573	2
BP	GO:0098773	skin epidermis development	2/60	116/23328	0.0360	0.0573	2
BP	GO:0002286	T cell activation involved in immune response	2/60	117/23328	0.0365	0.0580	2
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	2/60	117/23328	0.0365	0.0580	2
BP	GO:0032680	regulation of tumor necrosis factor production	2/60	120/23328	0.0383	0.0588	2
BP	GO:0003158	endothelium development	2/60	122/23328	0.0394	0.0594	2
BP	GO:0031929	TOR signaling	2/60	122/23328	0.0394	0.0594	2
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	2/60	122/23328	0.0394	0.0594	2
BP	GO:0002040	sprouting angiogenesis	2/60	123/23328	0.0400	0.0594	2
BP	GO:0046474	glycerophospholipid biosynthetic process	2/60	123/23328	0.0400	0.0594	2
BP	GO:0051153	regulation of striated muscle cell differentiation	2/60	124/23328	0.0406	0.0595	2
BP	GO:0090277	positive regulation of peptide hormone secretion	2/60	124/23328	0.0406	0.0595	2
BP	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	2/60	124/23328	0.0406	0.0595	2
BP	GO:1990266	neutrophil migration	2/60	124/23328	0.0406	0.0595	2
BP	GO:0007586	digestion	2/60	126/23328	0.0418	0.0609	2
BP	GO:0032640	tumor necrosis factor production	2/60	126/23328	0.0418	0.0609	2
BP	GO:0036294	cellular response to decreased oxygen levels	2/60	126/23328	0.0418	0.0609	2
BP	GO:0071621	granulocyte chemotaxis	2/60	126/23328	0.0418	0.0609	2
BP	GO:0045727	positive regulation of translation	2/60	128/23328	0.0430	0.0610	2
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	2/60	128/23328	0.0430	0.0610	2
BP	GO:0007631	feeding behavior	2/60	130/23328	0.0442	0.0625	2
BP	GO:0042752	regulation of circadian rhythm	2/60	130/23328	0.0442	0.0625	2
BP	GO:0090305	nucleic acid phosphodiester bond hydrolysis	2/60	130/23328	0.0442	0.0625	2

BP	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	2/60	131/23328	0.0448	0.0625	2
BP	GO:0002456	T cell mediated immunity	2/60	132/23328	0.0454	0.0626	2
BP	GO:0034763	negative regulation of transmembrane transport	2/60	132/23328	0.0454	0.0626	2
BP	GO:0042303	molting cycle	2/60	133/23328	0.0461	0.0632	2
BP	GO:0042633	hair cycle	2/60	133/23328	0.0461	0.0632	2
BP	GO:0044070	regulation of anion transport	2/60	133/23328	0.0461	0.0632	2
BP	GO:0002698	negative regulation of immune effector process	2/60	134/23328	0.0467	0.0639	2
BP	GO:0051701	interaction with host	2/60	135/23328	0.0473	0.0639	2
BP	GO:0072331	signal transduction by p53 class mediator	2/60	135/23328	0.0473	0.0639	2
BP	GO:0035195	gene silencing by miRNA	2/60	136/23328	0.0479	0.0640	2
BP	GO:0035821	modulation of process of other organism	2/60	137/23328	0.0486	0.0648	2
BP	GO:0009411	response to UV	2/60	138/23328	0.0492	0.0654	2
BP	GO:0030218	erythrocyte differentiation	2/60	138/23328	0.0492	0.0654	2
BP	GO:0046165	alcohol biosynthetic process	2/60	138/23328	0.0492	0.0654	2
BP	GO:1903322	positive regulation of protein modification by small protein conjugation or removal	2/60	139/23328	0.0498	0.0657	2
BP	GO:0007034	vacuolar transport	2/60	140/23328	0.0505	0.0659	2
BP	GO:0071453	cellular response to oxygen levels	2/60	140/23328	0.0505	0.0659	2
BP	GO:0010821	regulation of mitochondrion organization	2/60	142/23328	0.0518	0.0671	2
BP	GO:0035194	post-transcriptional gene silencing by RNA	2/60	142/23328	0.0518	0.0671	2
BP	GO:0035725	sodium ion transmembrane transport	2/60	143/23328	0.0524	0.0671	2
BP	GO:0001837	epithelial to mesenchymal transition	2/60	144/23328	0.0531	0.0675	2
BP	GO:0090316	positive regulation of intracellular protein transport	2/60	144/23328	0.0531	0.0675	2
BP	GO:0017148	negative regulation of translation	2/60	145/23328	0.0537	0.0683	2
BP	GO:0016441	posttranscriptional gene silencing	2/60	146/23328	0.0544	0.0683	2
BP	GO:0019233	sensory perception of pain	2/60	146/23328	0.0544	0.0683	2
BP	GO:0061041	regulation of wound healing	2/60	146/23328	0.0544	0.0683	2

BP	GO:0031333	negative regulation of protein-containing complex assembly	2/60	147/23328	0.0551	0.0683	2
BP	GO:0002221	pattern recognition receptor signaling pathway	2/60	149/23328	0.0564	0.0696	2
BP	GO:0007613	memory	2/60	149/23328	0.0564	0.0696	2
BP	GO:0050921	positive regulation of chemotaxis	2/60	149/23328	0.0564	0.0696	2
BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	2/60	150/23328	0.0571	0.0700	2
BP	GO:0031099	regeneration	2/60	150/23328	0.0571	0.0700	2
BP	GO:0048593	camera-type eye morphogenesis	2/60	151/23328	0.0577	0.0702	2
BP	GO:0030183	B cell differentiation	2/60	153/23328	0.0591	0.0716	2
BP	GO:0071478	cellular response to radiation	2/60	153/23328	0.0591	0.0716	2
BP	GO:0014013	regulation of gliogenesis	2/60	154/23328	0.0598	0.0717	2
BP	GO:0097530	granulocyte migration	2/60	155/23328	0.0604	0.0722	2
BP	GO:0030856	regulation of epithelial cell differentiation	2/60	156/23328	0.0611	0.0729	2
BP	GO:0032675	regulation of interleukin-6 production	2/60	156/23328	0.0611	0.0729	2
BP	GO:1903707	negative regulation of hemopoiesis	2/60	157/23328	0.0618	0.0732	2
BP	GO:0051250	negative regulation of lymphocyte activation	2/60	158/23328	0.0625	0.0733	2
BP	GO:0071383	cellular response to steroid hormone stimulus	2/60	159/23328	0.0632	0.0740	2
BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	2/60	159/23328	0.0632	0.0740	2
BP	GO:1902904	negative regulation of supramolecular fiber organization	2/60	163/23328	0.0660	0.0760	2
BP	GO:0010970	transport along microtubule	2/60	164/23328	0.0667	0.0760	2
BP	GO:0030879	mammary gland development	2/60	164/23328	0.0667	0.0760	2
BP	GO:0034249	negative regulation of cellular amide metabolic process	2/60	164/23328	0.0667	0.0760	2
BP	GO:0046887	positive regulation of hormone secretion	2/60	164/23328	0.0667	0.0760	2
BP	GO:0051224	negative regulation of protein transport	2/60	164/23328	0.0667	0.0760	2
BP	GO:0007565	female pregnancy	2/60	166/23328	0.0681	0.0767	2
BP	GO:0046631	alpha-beta T cell activation	2/60	166/23328	0.0681	0.0767	2

BP	GO:0051896	regulation of protein kinase B signaling	2/60	166/23328	0.0681	0.0767	2
BP	GO:0032635	interleukin-6 production	2/60	167/23328	0.0689	0.0775	2
BP	GO:0046425	regulation of receptor signaling pathway via JAK-STAT	2/60	168/23328	0.0696	0.0775	2
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	2/60	169/23328	0.0703	0.0780	2
BP	GO:0031047	gene silencing by RNA	2/60	169/23328	0.0703	0.0780	2
BP	GO:1904950	negative regulation of establishment of protein localization	2/60	169/23328	0.0703	0.0780	2
BP	GO:0030833	regulation of actin filament polymerization	2/60	171/23328	0.0717	0.0785	2
BP	GO:0043409	negative regulation of MAPK cascade	2/60	173/23328	0.0732	0.0797	2
BP	GO:1904892	regulation of receptor signaling pathway via STAT	2/60	173/23328	0.0732	0.0797	2
BP	GO:0001890	placenta development	2/60	174/23328	0.0739	0.0797	2
BP	GO:0042129	regulation of T cell proliferation	2/60	175/23328	0.0747	0.0799	2
BP	GO:0048634	regulation of muscle organ development	2/60	181/23328	0.0791	0.0820	2
BP	GO:0048592	eye morphogenesis	2/60	182/23328	0.0799	0.0826	2
BP	GO:0009749	response to glucose	2/60	185/23328	0.0821	0.0841	2
BP	GO:0031644	regulation of nervous system process	2/60	185/23328	0.0821	0.0841	2
BP	GO:1903034	regulation of response to wounding	2/60	186/23328	0.0829	0.0848	2
BP	GO:0030041	actin filament polymerization	2/60	187/23328	0.0837	0.0848	2
BP	GO:0043200	response to amino acid	2/60	187/23328	0.0837	0.0848	2
BP	GO:0008064	regulation of actin polymerization or depolymerization	2/60	188/23328	0.0844	0.0852	2
BP	GO:0009746	response to hexose	2/60	188/23328	0.0844	0.0852	2
BP	GO:0034284	response to monosaccharide	2/60	189/23328	0.0852	0.0855	2
BP	GO:0061136	regulation of proteasomal protein catabolic process	2/60	189/23328	0.0852	0.0855	2
BP	GO:0030832	regulation of actin filament length	2/60	191/23328	0.0867	0.0859	2
BP	GO:0022408	negative regulation of cell-cell adhesion	2/60	192/23328	0.0875	0.0866	2
BP	GO:0009913	epidermal cell differentiation	2/60	193/23328	0.0883	0.0871	2

BP	GO:0030705	cytoskeleton-dependent intracellular transport	2/60	194/23328	0.0891	0.0874	2
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	2/60	195/23328	0.0898	0.0879	2
BP	GO:0099111	microtubule-based transport	2/60	195/23328	0.0898	0.0879	2
BP	GO:1905475	regulation of protein localization to membrane	2/60	195/23328	0.0898	0.0879	2
BP	GO:0002706	regulation of lymphocyte mediated immunity	2/60	196/23328	0.0906	0.0886	2
BP	GO:0043491	protein kinase B signaling	2/60	196/23328	0.0906	0.0886	2
BP	GO:0006911	phagocytosis, engulfment	2/60	197/23328	0.0914	0.0889	2
BP	GO:0044706	multi-multicellular organism process	2/60	197/23328	0.0914	0.0889	2
BP	GO:1990138	neuron projection extension	2/60	198/23328	0.0922	0.0894	2
BP	GO:0050870	positive regulation of T cell activation	2/60	200/23328	0.0938	0.0897	2
BP	GO:0032869	cellular response to insulin stimulus	2/60	201/23328	0.0946	0.0903	2
BP	GO:0050792	regulation of viral process	2/60	201/23328	0.0946	0.0903	2
BP	GO:0009743	response to carbohydrate	2/60	203/23328	0.0961	0.0909	2
BP	GO:0009165	nucleotide biosynthetic process	2/60	204/23328	0.0969	0.0915	2
BP	GO:0099024	plasma membrane invagination	2/60	206/23328	0.0985	0.0920	2
BP	GO:0001101	response to acid chemical	2/60	207/23328	0.0993	0.0927	2
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	2/60	208/23328	0.1001	0.0928	2
BP	GO:0008217	regulation of blood pressure	2/60	209/23328	0.1009	0.0933	2
BP	GO:1901293	nucleoside phosphate biosynthetic process	2/60	209/23328	0.1009	0.0933	2
BP	GO:0043112	receptor metabolic process	2/60	212/23328	0.1034	0.0950	2
BP	GO:0071559	response to transforming growth factor beta	2/60	212/23328	0.1034	0.0950	2
BP	GO:0008361	regulation of cell size	2/60	213/23328	0.1042	0.0954	2
BP	GO:0010324	membrane invagination	2/60	213/23328	0.1042	0.0954	2
BP	GO:0042098	T cell proliferation	2/60	213/23328	0.1042	0.0954	2
BP	GO:0032984	protein-containing complex disassembly	2/60	214/23328	0.1050	0.0954	2
BP	GO:0008154	actin polymerization or depolymerization	2/60	215/23328	0.1058	0.0960	2
BP	GO:0048839	inner ear development	2/60	215/23328	0.1058	0.0960	2
BP	GO:0035264	multicellular organism growth	2/60	216/23328	0.1066	0.0964	2

BP	GO:0007623	circadian rhythm	2/60	217/23328	0.1075	0.0966	2
BP	GO:0043903	regulation of symbiotic process	2/60	218/23328	0.1083	0.0972	2
BP	GO:0019058	viral life cycle	2/60	221/23328	0.1108	0.0989	2
BP	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	2/60	221/23328	0.1108	0.0989	2
BP	GO:0030100	regulation of endocytosis	2/60	222/23328	0.1116	0.0992	2
BP	GO:0061138	morphogenesis of a branching epithelium	2/60	222/23328	0.1116	0.0992	2
BP	GO:0045637	regulation of myeloid cell differentiation	2/60	224/23328	0.1133	0.1003	2
BP	GO:1903708	positive regulation of hemopoiesis	2/60	224/23328	0.1133	0.1003	2
BP	GO:0048762	mesenchymal cell differentiation	2/60	225/23328	0.1141	0.1003	2
BP	GO:0032271	regulation of protein polymerization	2/60	227/23328	0.1158	0.1017	2
BP	GO:0002274	myeloid leukocyte activation	2/60	231/23328	0.1191	0.1034	2
BP	GO:0050670	regulation of lymphocyte proliferation	2/60	231/23328	0.1191	0.1034	2
BP	GO:0006814	sodium ion transport	2/60	234/23328	0.1217	0.1047	2
BP	GO:0032944	regulation of mononuclear cell proliferation	2/60	234/23328	0.1217	0.1047	2
BP	GO:0032868	response to insulin	2/60	235/23328	0.1225	0.1051	2
BP	GO:0001763	morphogenesis of a branching structure	2/60	241/23328	0.1276	0.1070	2
BP	GO:0046777	protein autophosphorylation	2/60	241/23328	0.1276	0.1070	2
BP	GO:0006260	DNA replication	2/60	244/23328	0.1302	0.1080	2
BP	GO:0090257	regulation of muscle system process	2/60	244/23328	0.1302	0.1080	2
BP	GO:0043583	ear development	2/60	246/23328	0.1320	0.1091	2
BP	GO:0060291	long-term synaptic potentiation	2/60	248/23328	0.1337	0.1100	2
BP	GO:0010001	glial cell differentiation	2/60	249/23328	0.1346	0.1100	2
BP	GO:0015850	organic hydroxy compound transport	2/60	249/23328	0.1346	0.1100	2
BP	GO:0070663	regulation of leukocyte proliferation	2/60	251/23328	0.1363	0.1108	2
BP	GO:0021537	telencephalon development	2/60	252/23328	0.1372	0.1112	2
BP	GO:0002064	epithelial cell development	2/60	257/23328	0.1416	0.1140	2
BP	GO:0006650	glycerophospholipid metabolic process	2/60	257/23328	0.1416	0.1140	2

BP	GO:0045665	negative regulation of neuron differentiation	2/60	259/23328	0.1433	0.1147	2
BP	GO:0042493	response to drug	2/60	260/23328	0.1442	0.1153	2
BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	2/60	260/23328	0.1442	0.1153	2
BP	GO:0002377	immunoglobulin production	2/60	262/23328	0.1460	0.1163	2
BP	GO:0050864	regulation of B cell activation	2/60	270/23328	0.1531	0.1201	2
BP	GO:0006605	protein targeting	2/60	271/23328	0.1540	0.1207	2
BP	GO:0002699	positive regulation of immune effector process	2/60	273/23328	0.1558	0.1218	2
BP	GO:0016050	vesicle organization	2/60	275/23328	0.1576	0.1228	2
BP	GO:0051924	regulation of calcium ion transport	2/60	275/23328	0.1576	0.1228	2
BP	GO:0060560	developmental growth involved in morphogenesis	2/60	275/23328	0.1576	0.1228	2
BP	GO:0016458	gene silencing	2/60	279/23328	0.1612	0.1241	2
BP	GO:0060485	mesenchyme development	2/60	281/23328	0.1630	0.1248	2
BP	GO:0002831	regulation of response to biotic stimulus	2/60	291/23328	0.1721	0.1301	2
BP	GO:0051258	protein polymerization	2/60	293/23328	0.1740	0.1311	2
BP	GO:0072659	protein localization to plasma membrane	2/60	295/23328	0.1758	0.1319	2
BP	GO:0048511	rhythmic process	2/60	301/23328	0.1813	0.1351	2
BP	GO:0030198	extracellular matrix organization	2/60	302/23328	0.1822	0.1354	2
BP	GO:0043062	extracellular structure organization	2/60	303/23328	0.1832	0.1360	2
BP	GO:0016358	dendrite development	2/60	306/23328	0.1859	0.1375	2
BP	GO:0090596	sensory organ morphogenesis	2/60	311/23328	0.1906	0.1401	2
BP	GO:0046651	lymphocyte proliferation	2/60	317/23328	0.1962	0.1430	2
BP	GO:0051146	striated muscle cell differentiation	2/60	317/23328	0.1962	0.1430	2
BP	GO:0032943	mononuclear cell proliferation	2/60	320/23328	0.1990	0.1441	2
BP	GO:0051235	maintenance of location	2/60	320/23328	0.1990	0.1441	2
BP	GO:0048562	embryonic organ morphogenesis	2/60	328/23328	0.2065	0.1485	2
BP	GO:0009100	glycoprotein metabolic process	2/60	332/23328	0.2102	0.1501	2
BP	GO:0070661	leukocyte proliferation	2/60	344/23328	0.2216	0.1562	2
BP	GO:0032259	methylation	2/60	349/23328	0.2263	0.1588	2

BP	GO:0034655	nucleobase-containing compound catabolic process	2/60	352/23328	0.2292	0.1600	2
BP	GO:0006909	phagocytosis	2/60	358/23328	0.2349	0.1627	2
BP	GO:1990778	protein localization to cell periphery	2/60	363/23328	0.2396	0.1651	2
BP	GO:0018205	peptidyl-lysine modification	2/60	364/23328	0.2406	0.1657	2
BP	GO:0051052	regulation of DNA metabolic process	2/60	379/23328	0.2549	0.1724	2
BP	GO:0007018	microtubule-based movement	2/60	385/23328	0.2606	0.1751	2
BP	GO:0060562	epithelial tube morphogenesis	2/60	387/23328	0.2625	0.1758	2
BP	GO:0051098	regulation of binding	2/60	390/23328	0.2654	0.1773	2
BP	GO:0003012	muscle system process	2/60	408/23328	0.2826	0.1858	2
BP	GO:0030099	myeloid cell differentiation	2/60	414/23328	0.2883	0.1888	2
BP	GO:0051251	positive regulation of lymphocyte activation	2/60	416/23328	0.2902	0.1897	2
BP	GO:0042113	B cell activation	2/60	417/23328	0.2912	0.1901	2
BP	GO:0010639	negative regulation of organelle organization	2/60	420/23328	0.2940	0.1916	2
BP	GO:0016055	Wnt signaling pathway	2/60	430/23328	0.3035	0.1963	2
BP	GO:0002449	lymphocyte mediated immunity	2/60	432/23328	0.3055	0.1972	2
BP	GO:0198738	cell-cell signaling by wnt	2/60	432/23328	0.3055	0.1972	2
BP	GO:0034660	ncRNA metabolic process	2/60	444/23328	0.3169	0.2029	2
BP	GO:0014706	striated muscle tissue development	2/60	447/23328	0.3197	0.2045	2
BP	GO:0016570	histone modification	2/60	448/23328	0.3206	0.2050	2
BP	GO:0016569	covalent chromatin modification	2/60	462/23328	0.3339	0.2117	2
BP	GO:0060537	muscle tissue development	2/60	470/23328	0.3414	0.2159	2
BP	GO:0007389	pattern specification process	2/60	478/23328	0.3489	0.2201	2
CC	GO:0044754	autolysosome	2/61	12/23271	0.0004	0.0095	2
CC	GO:0005767	secondary lysosome	2/61	16/23271	0.0008	0.0128	2
CC	GO:0031430	M band	2/61	19/23271	0.0011	0.0162	2
CC	GO:0031672	A band	2/61	38/23271	0.0045	0.0482	2
CC	GO:0009925	basal plasma membrane	2/61	60/23271	0.0109	0.0702	2
CC	GO:0005776	autophagosome	2/61	73/23271	0.0158	0.0842	2
CC	GO:0000932	P-body	2/61	76/23271	0.0170	0.0842	2
CC	GO:0045178	basal part of cell	2/61	83/23271	0.0201	0.0866	2
CC	GO:0005902	microvillus	2/61	101/23271	0.0289	0.0961	2
CC	GO:1990204	oxidoreductase complex	2/61	110/23271	0.0338	0.1018	2
CC	GO:0043204	perikaryon	2/61	140/23271	0.0522	0.1286	2
CC	GO:0030027	lamellipodium	2/61	171/23271	0.0741	0.1500	2

CC	GO:0005741	mitochondrial outer membrane	2/61	175/23271	0.0772	0.1513	2
CC	GO:0030139	endocytic vesicle	2/61	200/23271	0.0968	0.1587	2
CC	GO:0043209	myelin sheath	2/61	213/23271	0.1075	0.1740	2
CC	GO:0036464	cytoplasmic ribonucleoprotein granule	2/61	218/23271	0.1117	0.1754	2
CC	GO:0098858	actin-based cell projection	2/61	221/23271	0.1143	0.1754	2
CC	GO:0031514	motile cilium	2/61	222/23271	0.1151	0.1754	2
CC	GO:0035770	ribonucleoprotein granule	2/61	229/23271	0.1212	0.1824	2
CC	GO:0014069	postsynaptic density	2/61	400/23271	0.2822	0.2978	2
CC	GO:0030141	secretory granule	2/61	401/23271	0.2832	0.2978	2
CC	GO:0032279	asymmetric synapse	2/61	405/23271	0.2871	0.2978	2
CC	GO:0005635	nuclear envelope	2/61	421/23271	0.3027	0.3011	2
CC	GO:0098984	neuron to neuron synapse	2/61	433/23271	0.3143	0.3037	2
CC	GO:0099572	postsynaptic specialization	2/61	439/23271	0.3201	0.3055	2
CC	GO:0005667	transcription regulator complex	2/61	460/23271	0.3403	0.3142	2
MF	GO:0031956	medium-chain fatty acid-CoA ligase activity	2/58	11/22669	0.0003	0.0096	2
MF	GO:0005324	long-chain fatty acid transporter activity	2/58	19/22669	0.0011	0.0132	2
MF	GO:0036041	long-chain fatty acid binding	2/58	20/22669	0.0012	0.0132	2
MF	GO:0015645	fatty acid ligase activity	2/58	21/22669	0.0013	0.0132	2
MF	GO:0005355	glucose transmembrane transporter activity	2/58	22/22669	0.0014	0.0132	2
MF	GO:0015149	hexose transmembrane transporter activity	2/58	22/22669	0.0014	0.0132	2
MF	GO:0016881	acid-amino acid ligase activity	2/58	22/22669	0.0014	0.0132	2
MF	GO:0070530	K63-linked polyubiquitin modification-dependent protein binding	2/58	22/22669	0.0014	0.0132	2
MF	GO:0090482	vitamin transmembrane transporter activity	2/58	23/22669	0.0016	0.0133	2
MF	GO:0015145	monosaccharide transmembrane transporter activity	2/58	24/22669	0.0017	0.0133	2
MF	GO:0000062	fatty-acyl-CoA binding	2/58	25/22669	0.0019	0.0133	2
MF	GO:0016405	CoA-ligase activity	2/58	25/22669	0.0019	0.0133	2
MF	GO:0051119	sugar transmembrane transporter activity	2/58	25/22669	0.0019	0.0133	2
MF	GO:0044183	protein folding chaperone	2/58	26/22669	0.0020	0.0138	2
MF	GO:0016878	acid-thiol ligase activity	2/58	28/22669	0.0023	0.0150	2
MF	GO:0120227	acyl-CoA binding	2/58	28/22669	0.0023	0.0150	2
MF	GO:0071889	14-3-3 protein binding	2/58	31/22669	0.0029	0.0172	2

MF	GO:1901567	fatty acid derivative binding	2/58	35/22669	0.0036	0.0205	2
MF	GO:0015144	carbohydrate transmembrane transporter activity	2/58	36/22669	0.0038	0.0211	2
MF	GO:0016877	ligase activity, forming carbon-sulfur bonds	2/58	39/22669	0.0045	0.0240	2
MF	GO:0005548	phospholipid transporter activity	2/58	47/22669	0.0065	0.0311	2
MF	GO:0070888	E-box binding	2/58	47/22669	0.0065	0.0311	2
MF	GO:0016879	ligase activity, forming carbon-nitrogen bonds	2/58	49/22669	0.0070	0.0329	2
MF	GO:0005504	fatty acid binding	2/58	52/22669	0.0079	0.0360	2
MF	GO:0004860	protein kinase inhibitor activity	2/58	54/22669	0.0085	0.0373	2
MF	GO:0031593	polyubiquitin modification-dependent protein binding	2/58	55/22669	0.0088	0.0373	2
MF	GO:0019210	kinase inhibitor activity	2/58	59/22669	0.0100	0.0402	2
MF	GO:0015179	L-amino acid transmembrane transporter activity	2/58	61/22669	0.0107	0.0420	2
MF	GO:0005080	protein kinase C binding	2/58	63/22669	0.0114	0.0435	2
MF	GO:0043621	protein self-association	2/58	66/22669	0.0124	0.0452	2
MF	GO:0070491	repressing transcription factor binding	2/58	73/22669	0.0151	0.0518	2
MF	GO:0033293	monocarboxylic acid binding	2/58	82/22669	0.0187	0.0633	2
MF	GO:0015171	amino acid transmembrane transporter activity	2/58	84/22669	0.0196	0.0640	2
MF	GO:0051082	unfolded protein binding	2/58	84/22669	0.0196	0.0640	2
MF	GO:0033613	activating transcription factor binding	2/58	85/22669	0.0201	0.0644	2
MF	GO:0005546	phosphatidylinositol-4,5-bisphosphate binding	2/58	90/22669	0.0223	0.0693	2
MF	GO:0008170	N-methyltransferase activity	2/58	92/22669	0.0232	0.0704	2
MF	GO:0042826	histone deacetylase binding	2/58	123/22669	0.0396	0.0798	2
MF	GO:1902936	phosphatidylinositol bisphosphate binding	2/58	123/22669	0.0396	0.0798	2
MF	GO:0019955	cytokine binding	2/58	136/22669	0.0475	0.0872	2
MF	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	2/58	142/22669	0.0513	0.0915	2
MF	GO:0008083	growth factor activity	2/58	147/22669	0.0545	0.0920	2
MF	GO:0070851	growth factor receptor binding	2/58	149/22669	0.0558	0.0920	2
MF	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	2/58	151/22669	0.0572	0.0920	2

MF	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	2/58	151/22669	0.0572	0.0920	2
MF	GO:0002020	protease binding	2/58	152/22669	0.0578	0.0920	2
MF	GO:0016853	isomerase activity	2/58	153/22669	0.0585	0.0920	2
MF	GO:0020037	heme binding	2/58	159/22669	0.0626	0.0920	2
MF	GO:0008234	cysteine-type peptidase activity	2/58	160/22669	0.0633	0.0920	2
MF	GO:0046943	carboxylic acid transmembrane transporter activity	2/58	160/22669	0.0633	0.0920	2
MF	GO:0005342	organic acid transmembrane transporter activity	2/58	161/22669	0.0640	0.0920	2
MF	GO:0046906	tetrapyrrole binding	2/58	168/22669	0.0689	0.0953	2
MF	GO:1901981	phosphatidylinositol phosphate binding	2/58	184/22669	0.0806	0.1035	2
MF	GO:0016829	lyase activity	2/58	188/22669	0.0837	0.1060	2
MF	GO:0140030	modification-dependent protein binding	2/58	192/22669	0.0867	0.1085	2
MF	GO:0000287	magnesium ion binding	2/58	197/22669	0.0906	0.1104	2
MF	GO:0008168	methyltransferase activity	2/58	205/22669	0.0969	0.1124	2
MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2/58	213/22669	0.1033	0.1155	2
MF	GO:0016741	transferase activity, transferring one-carbon groups	2/58	216/22669	0.1057	0.1155	2
MF	GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	2/58	233/22669	0.1198	0.1240	2
MF	GO:1901681	sulfur compound binding	2/58	260/22669	0.1430	0.1370	2
MF	GO:0035091	phosphatidylinositol binding	2/58	266/22669	0.1483	0.1387	2
MF	GO:0046982	protein heterodimerization activity	2/58	290/22669	0.1698	0.1514	2
MF	GO:0022804	active transmembrane transporter activity	2/58	341/22669	0.2170	0.1802	2
MF	GO:0003729	mRNA binding	2/58	345/22669	0.2208	0.1816	2
MF	GO:0042578	phosphoric ester hydrolase activity	2/58	357/22669	0.2321	0.1855	2
MF	GO:0004857	enzyme inhibitor activity	2/58	392/22669	0.2653	0.2078	2
MF	GO:0016887	ATPase activity	2/58	404/22669	0.2767	0.2149	2
MF	GO:0004674	protein serine/threonine kinase activity	2/58	439/22669	0.3099	0.2351	2
MF	GO:0003712	transcription coregulator activity	2/58	441/22669	0.3118	0.2354	2

MF	GO:0005543	phospholipid binding	2/58	448/22669	0.3184	0.2378	2
BP	GO:0002315	marginal zone B cell differentiation	1/60	10/23328	0.0254	0.0503	1
BP	GO:0002634	regulation of germinal center formation	1/60	10/23328	0.0254	0.0503	1
BP	GO:0006591	ornithine metabolic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:0006707	cholesterol catabolic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:0015801	aromatic amino acid transport	1/60	10/23328	0.0254	0.0503	1
BP	GO:0016127	sterol catabolic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:0030300	regulation of intestinal cholesterol absorption	1/60	10/23328	0.0254	0.0503	1
BP	GO:0031620	regulation of fever generation	1/60	10/23328	0.0254	0.0503	1
BP	GO:0033234	negative regulation of protein sumoylation	1/60	10/23328	0.0254	0.0503	1
BP	GO:0035871	protein K11-linked deubiquitination	1/60	10/23328	0.0254	0.0503	1
BP	GO:0036462	TRAIL-activated apoptotic signaling pathway	1/60	10/23328	0.0254	0.0503	1
BP	GO:0043301	negative regulation of leukocyte degranulation	1/60	10/23328	0.0254	0.0503	1
BP	GO:0045542	positive regulation of cholesterol biosynthetic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:0048671	negative regulation of collateral sprouting	1/60	10/23328	0.0254	0.0503	1
BP	GO:0051340	regulation of ligase activity	1/60	10/23328	0.0254	0.0503	1
BP	GO:0051775	response to redox state	1/60	10/23328	0.0254	0.0503	1
BP	GO:0051971	positive regulation of transmission of nerve impulse	1/60	10/23328	0.0254	0.0503	1
BP	GO:0061635	regulation of protein complex stability	1/60	10/23328	0.0254	0.0503	1
BP	GO:0070244	negative regulation of thymocyte apoptotic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:0070391	response to lipoteichoic acid	1/60	10/23328	0.0254	0.0503	1
BP	GO:0070417	cellular response to cold	1/60	10/23328	0.0254	0.0503	1
BP	GO:0071223	cellular response to lipoteichoic acid	1/60	10/23328	0.0254	0.0503	1
BP	GO:0090091	positive regulation of extracellular matrix disassembly	1/60	10/23328	0.0254	0.0503	1
BP	GO:0090269	fibroblast growth factor production	1/60	10/23328	0.0254	0.0503	1
BP	GO:0090270	regulation of fibroblast growth factor production	1/60	10/23328	0.0254	0.0503	1

BP	GO:0106049	regulation of cellular response to osmotic stress	1/60	10/23328	0.0254	0.0503	1
BP	GO:0106120	positive regulation of sterol biosynthetic process	1/60	10/23328	0.0254	0.0503	1
BP	GO:1990253	cellular response to leucine starvation	1/60	10/23328	0.0254	0.0503	1
BP	GO:2000192	negative regulation of fatty acid transport	1/60	10/23328	0.0254	0.0503	1
BP	GO:2000489	regulation of hepatic stellate cell activation	1/60	10/23328	0.0254	0.0503	1
BP	GO:2000551	regulation of T-helper 2 cell cytokine production	1/60	10/23328	0.0254	0.0503	1
BP	GO:0002676	regulation of chronic inflammatory response	1/60	11/23328	0.0279	0.0526	1
BP	GO:0006107	oxaloacetate metabolic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:0031053	primary miRNA processing	1/60	11/23328	0.0279	0.0526	1
BP	GO:0032959	inositol trisphosphate biosynthetic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:0033700	phospholipid efflux	1/60	11/23328	0.0279	0.0526	1
BP	GO:0034115	negative regulation of heterotypic cell-cell adhesion	1/60	11/23328	0.0279	0.0526	1
BP	GO:0035336	long-chain fatty-acyl-CoA metabolic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:0036490	regulation of translation in response to endoplasmic reticulum stress	1/60	11/23328	0.0279	0.0526	1
BP	GO:0042762	regulation of sulfur metabolic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:0045602	negative regulation of endothelial cell differentiation	1/60	11/23328	0.0279	0.0526	1
BP	GO:0045647	negative regulation of erythrocyte differentiation	1/60	11/23328	0.0279	0.0526	1
BP	GO:0070587	regulation of cell-cell adhesion involved in gastrulation	1/60	11/23328	0.0279	0.0526	1
BP	GO:0071864	positive regulation of cell proliferation in bone marrow	1/60	11/23328	0.0279	0.0526	1
BP	GO:0090205	positive regulation of cholesterol metabolic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:1902166	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1/60	11/23328	0.0279	0.0526	1

BP	GO:1904729	regulation of intestinal lipid absorption	1/60	11/23328	0.0279	0.0526	1
BP	GO:1990440	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	1/60	11/23328	0.0279	0.0526	1
BP	GO:2001280	positive regulation of unsaturated fatty acid biosynthetic process	1/60	11/23328	0.0279	0.0526	1
BP	GO:0009071	serine family amino acid catabolic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0010870	positive regulation of receptor biosynthetic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	1/60	12/23328	0.0304	0.0541	1
BP	GO:0031392	regulation of prostaglandin biosynthetic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0033004	negative regulation of mast cell activation	1/60	12/23328	0.0304	0.0541	1
BP	GO:0033210	leptin-mediated signaling pathway	1/60	12/23328	0.0304	0.0541	1
BP	GO:0033632	regulation of cell-cell adhesion mediated by integrin	1/60	12/23328	0.0304	0.0541	1
BP	GO:0035376	sterol import	1/60	12/23328	0.0304	0.0541	1
BP	GO:0035437	maintenance of protein localization in endoplasmic reticulum	1/60	12/23328	0.0304	0.0541	1
BP	GO:0035733	hepatic stellate cell activation	1/60	12/23328	0.0304	0.0541	1
BP	GO:0042447	hormone catabolic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0043455	regulation of secondary metabolic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0045717	negative regulation of fatty acid biosynthetic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0048021	regulation of melanin biosynthetic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:0051024	positive regulation of immunoglobulin secretion	1/60	12/23328	0.0304	0.0541	1
BP	GO:0060159	regulation of dopamine receptor signaling pathway	1/60	12/23328	0.0304	0.0541	1

BP	GO:0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	1/60	12/23328	0.0304	0.0541	1
BP	GO:0060586	multicellular organismal iron ion homeostasis	1/60	12/23328	0.0304	0.0541	1
BP	GO:0060872	semicircular canal development	1/60	12/23328	0.0304	0.0541	1
BP	GO:0061744	motor behavior	1/60	12/23328	0.0304	0.0541	1
BP	GO:0070508	cholesterol import	1/60	12/23328	0.0304	0.0541	1
BP	GO:0070586	cell-cell adhesion involved in gastrulation	1/60	12/23328	0.0304	0.0541	1
BP	GO:0071863	regulation of cell proliferation in bone marrow	1/60	12/23328	0.0304	0.0541	1
BP	GO:0097113	AMPA glutamate receptor clustering	1/60	12/23328	0.0304	0.0541	1
BP	GO:0097709	connective tissue replacement	1/60	12/23328	0.0304	0.0541	1
BP	GO:1900376	regulation of secondary metabolite biosynthetic process	1/60	12/23328	0.0304	0.0541	1
BP	GO:1902510	regulation of apoptotic DNA fragmentation	1/60	12/23328	0.0304	0.0541	1
BP	GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA	1/60	12/23328	0.0304	0.0541	1
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	1/60	12/23328	0.0304	0.0541	1
BP	GO:0001660	fever generation	1/60	13/23328	0.0329	0.0553	1
BP	GO:0006521	regulation of cellular amino acid metabolic process	1/60	13/23328	0.0329	0.0553	1
BP	GO:0006983	ER overload response	1/60	13/23328	0.0329	0.0553	1
BP	GO:0009263	deoxyribonucleotide biosynthetic process	1/60	13/23328	0.0329	0.0553	1
BP	GO:0010998	regulation of translational initiation by eIF2 alpha phosphorylation	1/60	13/23328	0.0329	0.0553	1
BP	GO:0015816	glycine transport	1/60	13/23328	0.0329	0.0553	1
BP	GO:0031652	positive regulation of heat generation	1/60	13/23328	0.0329	0.0553	1
BP	GO:0032060	bleb assembly	1/60	13/23328	0.0329	0.0553	1
BP	GO:0034497	protein localization to phagophore assembly site	1/60	13/23328	0.0329	0.0553	1
BP	GO:0035630	bone mineralization involved in bone maturation	1/60	13/23328	0.0329	0.0553	1

BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	1/60	13/23328	0.0329	0.0553	1
BP	GO:0042541	hemoglobin biosynthetic process	1/60	13/23328	0.0329	0.0553	1
BP	GO:0045628	regulation of T-helper 2 cell differentiation	1/60	13/23328	0.0329	0.0553	1
BP	GO:0045906	negative regulation of vasoconstriction	1/60	13/23328	0.0329	0.0553	1
BP	GO:0048102	autophagic cell death	1/60	13/23328	0.0329	0.0553	1
BP	GO:0055091	phospholipid homeostasis	1/60	13/23328	0.0329	0.0553	1
BP	GO:0061052	negative regulation of cell growth involved in cardiac muscle cell development	1/60	13/23328	0.0329	0.0553	1
BP	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	1/60	13/23328	0.0329	0.0553	1
BP	GO:0070091	glucagon secretion	1/60	13/23328	0.0329	0.0553	1
BP	GO:0070092	regulation of glucagon secretion	1/60	13/23328	0.0329	0.0553	1
BP	GO:0071294	cellular response to zinc ion	1/60	13/23328	0.0329	0.0553	1
BP	GO:0071838	cell proliferation in bone marrow	1/60	13/23328	0.0329	0.0553	1
BP	GO:0072540	T-helper 17 cell lineage commitment	1/60	13/23328	0.0329	0.0553	1
BP	GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	1/60	13/23328	0.0329	0.0553	1
BP	GO:0097688	glutamate receptor clustering	1/60	13/23328	0.0329	0.0553	1
BP	GO:0110154	RNA decapping	1/60	13/23328	0.0329	0.0553	1
BP	GO:0110156	methylguanosine-cap decapping	1/60	13/23328	0.0329	0.0553	1
BP	GO:2001054	negative regulation of mesenchymal cell apoptotic process	1/60	13/23328	0.0329	0.0553	1
BP	GO:0008298	intracellular mRNA localization	1/60	14/23328	0.0354	0.0566	1
BP	GO:0019896	axonal transport of mitochondrion	1/60	14/23328	0.0354	0.0566	1
BP	GO:0021984	adenohypophysis development	1/60	14/23328	0.0354	0.0566	1
BP	GO:0031915	positive regulation of synaptic plasticity	1/60	14/23328	0.0354	0.0566	1
BP	GO:0032494	response to peptidoglycan	1/60	14/23328	0.0354	0.0566	1
BP	GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	1/60	14/23328	0.0354	0.0566	1

BP	GO:0036498	IRE1-mediated unfolded protein response	1/60	14/23328	0.0354	0.0566	1
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	1/60	14/23328	0.0354	0.0566	1
BP	GO:0043558	regulation of translational initiation in response to stress	1/60	14/23328	0.0354	0.0566	1
BP	GO:0044804	autophagy of nucleus	1/60	14/23328	0.0354	0.0566	1
BP	GO:0045188	regulation of circadian sleep/wake cycle, non-REM sleep	1/60	14/23328	0.0354	0.0566	1
BP	GO:0046642	negative regulation of alpha-beta T cell proliferation	1/60	14/23328	0.0354	0.0566	1
BP	GO:0046886	positive regulation of hormone biosynthetic process	1/60	14/23328	0.0354	0.0566	1
BP	GO:0051290	protein heterotetramerization	1/60	14/23328	0.0354	0.0566	1
BP	GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail shortening	1/60	14/23328	0.0354	0.0566	1
BP	GO:0070365	hepatocyte differentiation	1/60	14/23328	0.0354	0.0566	1
BP	GO:0097012	response to granulocyte macrophage colony-stimulating factor	1/60	14/23328	0.0354	0.0566	1
BP	GO:1903624	regulation of DNA catabolic process	1/60	14/23328	0.0354	0.0566	1
BP	GO:2000347	positive regulation of hepatocyte proliferation	1/60	14/23328	0.0354	0.0566	1
BP	GO:2001279	regulation of unsaturated fatty acid biosynthetic process	1/60	14/23328	0.0354	0.0566	1
BP	GO:0010958	regulation of amino acid import across plasma membrane	1/60	15/23328	0.0379	0.0583	1
BP	GO:0019081	viral translation	1/60	15/23328	0.0379	0.0583	1
BP	GO:0023035	CD40 signaling pathway	1/60	15/23328	0.0379	0.0583	1
BP	GO:0030299	intestinal cholesterol absorption	1/60	15/23328	0.0379	0.0583	1
BP	GO:0031650	regulation of heat generation	1/60	15/23328	0.0379	0.0583	1
BP	GO:0032511	late endosome to vacuole transport via multivesicular body sorting pathway	1/60	15/23328	0.0379	0.0583	1
BP	GO:0032530	regulation of microvillus organization	1/60	15/23328	0.0379	0.0583	1
BP	GO:0032933	SREBP signaling pathway	1/60	15/23328	0.0379	0.0583	1

BP	GO:0035745	T-helper 2 cell cytokine production	1/60	15/23328	0.0379	0.0583	1
BP	GO:0042748	circadian sleep/wake cycle, non-REM sleep	1/60	15/23328	0.0379	0.0583	1
BP	GO:0042976	activation of Janus kinase activity	1/60	15/23328	0.0379	0.0583	1
BP	GO:0044793	negative regulation by host of viral process	1/60	15/23328	0.0379	0.0583	1
BP	GO:0047484	regulation of response to osmotic stress	1/60	15/23328	0.0379	0.0583	1
BP	GO:0060049	regulation of protein glycosylation	1/60	15/23328	0.0379	0.0583	1
BP	GO:0060396	growth hormone receptor signaling pathway	1/60	15/23328	0.0379	0.0583	1
BP	GO:0060442	branching involved in prostate gland morphogenesis	1/60	15/23328	0.0379	0.0583	1
BP	GO:0071280	cellular response to copper ion	1/60	15/23328	0.0379	0.0583	1
BP	GO:0071378	cellular response to growth hormone stimulus	1/60	15/23328	0.0379	0.0583	1
BP	GO:0098712	L-glutamate import across plasma membrane	1/60	15/23328	0.0379	0.0583	1
BP	GO:0099527	postsynapse to nucleus signaling pathway	1/60	15/23328	0.0379	0.0583	1
BP	GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	1/60	15/23328	0.0379	0.0583	1
BP	GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1/60	15/23328	0.0379	0.0583	1
BP	GO:1903587	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	1/60	15/23328	0.0379	0.0583	1
BP	GO:1903789	regulation of amino acid transmembrane transport	1/60	15/23328	0.0379	0.0583	1
BP	GO:1903799	negative regulation of production of miRNAs involved in gene silencing by miRNA	1/60	15/23328	0.0379	0.0583	1
BP	GO:1904478	regulation of intestinal absorption	1/60	15/23328	0.0379	0.0583	1
BP	GO:0002070	epithelial cell maturation	1/60	16/23328	0.0404	0.0594	1

BP	GO:0002295	T-helper cell lineage commitment	1/60	16/23328	0.0404	0.0594	1
BP	GO:0002407	dendritic cell chemotaxis	1/60	16/23328	0.0404	0.0594	1
BP	GO:0002467	germinal center formation	1/60	16/23328	0.0404	0.0594	1
BP	GO:0002830	positive regulation of type 2 immune response	1/60	16/23328	0.0404	0.0594	1
BP	GO:0006103	2-oxoglutarate metabolic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:0006620	posttranslational protein targeting to endoplasmic reticulum membrane	1/60	16/23328	0.0404	0.0594	1
BP	GO:0006658	phosphatidylserine metabolic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:0010224	response to UV-B	1/60	16/23328	0.0404	0.0594	1
BP	GO:0035337	fatty-acyl-CoA metabolic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:0035590	purinergic nucleotide receptor signaling pathway	1/60	16/23328	0.0404	0.0594	1
BP	GO:0035641	locomotory exploration behavior	1/60	16/23328	0.0404	0.0594	1
BP	GO:0042308	negative regulation of protein import into nucleus	1/60	16/23328	0.0404	0.0594	1
BP	GO:0042640	anagen	1/60	16/23328	0.0404	0.0594	1
BP	GO:0043518	negative regulation of DNA damage response, signal transduction by p53 class mediator	1/60	16/23328	0.0404	0.0594	1
BP	GO:0044827	modulation by host of viral genome replication	1/60	16/23328	0.0404	0.0594	1
BP	GO:0045820	negative regulation of glycolytic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:0045947	negative regulation of translational initiation	1/60	16/23328	0.0404	0.0594	1
BP	GO:0050862	positive regulation of T cell receptor signaling pathway	1/60	16/23328	0.0404	0.0594	1
BP	GO:0051938	L-glutamate import	1/60	16/23328	0.0404	0.0594	1
BP	GO:0060100	positive regulation of phagocytosis, engulfment	1/60	16/23328	0.0404	0.0594	1
BP	GO:0070486	leukocyte aggregation	1/60	16/23328	0.0404	0.0594	1
BP	GO:0071243	cellular response to arsenic-containing substance	1/60	16/23328	0.0404	0.0594	1

BP	GO:0071498	cellular response to fluid shear stress	1/60	16/23328	0.0404	0.0594	1
BP	GO:0071501	cellular response to sterol depletion	1/60	16/23328	0.0404	0.0594	1
BP	GO:0072537	fibroblast activation	1/60	16/23328	0.0404	0.0594	1
BP	GO:0072673	lamellipodium morphogenesis	1/60	16/23328	0.0404	0.0594	1
BP	GO:1904590	negative regulation of protein import	1/60	16/23328	0.0404	0.0594	1
BP	GO:1905155	positive regulation of membrane invagination	1/60	16/23328	0.0404	0.0594	1
BP	GO:2000628	regulation of miRNA metabolic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:2001053	regulation of mesenchymal cell apoptotic process	1/60	16/23328	0.0404	0.0594	1
BP	GO:0006991	response to sterol depletion	1/60	17/23328	0.0429	0.0609	1
BP	GO:0010713	negative regulation of collagen metabolic process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0019048	modulation by virus of host process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0032225	regulation of synaptic transmission, dopaminergic	1/60	17/23328	0.0429	0.0609	1
BP	GO:0032306	regulation of prostaglandin secretion	1/60	17/23328	0.0429	0.0609	1
BP	GO:0032957	inositol trisphosphate metabolic process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0032966	negative regulation of collagen biosynthetic process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0040015	negative regulation of multicellular organism growth	1/60	17/23328	0.0429	0.0609	1
BP	GO:0044320	cellular response to leptin stimulus	1/60	17/23328	0.0429	0.0609	1
BP	GO:0045064	T-helper 2 cell differentiation	1/60	17/23328	0.0429	0.0609	1
BP	GO:0046755	viral budding	1/60	17/23328	0.0429	0.0609	1
BP	GO:0048853	forebrain morphogenesis	1/60	17/23328	0.0429	0.0609	1
BP	GO:0050665	hydrogen peroxide biosynthetic process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0051014	actin filament severing	1/60	17/23328	0.0429	0.0609	1
BP	GO:0060644	mammary gland epithelial cell differentiation	1/60	17/23328	0.0429	0.0609	1
BP	GO:0061952	midbody abscission	1/60	17/23328	0.0429	0.0609	1
BP	GO:0070243	regulation of thymocyte apoptotic process	1/60	17/23328	0.0429	0.0609	1

BP	GO:0070262	peptidyl-serine dephosphorylation	1/60	17/23328	0.0429	0.0609	1
BP	GO:0071636	positive regulation of transforming growth factor beta production	1/60	17/23328	0.0429	0.0609	1
BP	GO:0090336	positive regulation of brown fat cell differentiation	1/60	17/23328	0.0429	0.0609	1
BP	GO:0097152	mesenchymal cell apoptotic process	1/60	17/23328	0.0429	0.0609	1
BP	GO:0099640	axo-dendritic protein transport	1/60	17/23328	0.0429	0.0609	1
BP	GO:1900119	positive regulation of execution phase of apoptosis	1/60	17/23328	0.0429	0.0609	1
BP	GO:1902894	negative regulation of pri-miRNA transcription by RNA polymerase II	1/60	17/23328	0.0429	0.0609	1
BP	GO:2001028	positive regulation of endothelial cell chemotaxis	1/60	17/23328	0.0429	0.0609	1
BP	GO:0000188	inactivation of MAPK activity	1/60	18/23328	0.0453	0.0625	1
BP	GO:0006700	C21-steroid hormone biosynthetic process	1/60	18/23328	0.0453	0.0625	1
BP	GO:0010801	negative regulation of peptidyl-threonine phosphorylation	1/60	18/23328	0.0453	0.0625	1
BP	GO:0021756	striatum development	1/60	18/23328	0.0453	0.0625	1
BP	GO:0030033	microvillus assembly	1/60	18/23328	0.0453	0.0625	1
BP	GO:0033631	cell-cell adhesion mediated by integrin	1/60	18/23328	0.0453	0.0625	1
BP	GO:0035633	maintenance of blood-brain barrier	1/60	18/23328	0.0453	0.0625	1
BP	GO:0042026	protein refolding	1/60	18/23328	0.0453	0.0625	1
BP	GO:0042448	progesterone metabolic process	1/60	18/23328	0.0453	0.0625	1
BP	GO:0044241	lipid digestion	1/60	18/23328	0.0453	0.0625	1
BP	GO:0050710	negative regulation of cytokine secretion	1/60	18/23328	0.0453	0.0625	1
BP	GO:0060416	response to growth hormone	1/60	18/23328	0.0453	0.0625	1
BP	GO:0060576	intestinal epithelial cell development	1/60	18/23328	0.0453	0.0625	1
BP	GO:0061158	3'-UTR-mediated mRNA destabilization	1/60	18/23328	0.0453	0.0625	1
BP	GO:0070102	interleukin-6-mediated signaling pathway	1/60	18/23328	0.0453	0.0625	1
BP	GO:0098856	intestinal lipid absorption	1/60	18/23328	0.0453	0.0625	1

BP	GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1/60	18/23328	0.0453	0.0625	1
BP	GO:1901673	regulation of mitotic spindle assembly	1/60	18/23328	0.0453	0.0625	1
BP	GO:1904706	negative regulation of vascular associated smooth muscle cell proliferation	1/60	18/23328	0.0453	0.0625	1
BP	GO:1990000	amyloid fibril formation	1/60	18/23328	0.0453	0.0625	1
BP	GO:0002544	chronic inflammatory response	1/60	19/23328	0.0478	0.0639	1
BP	GO:0002726	positive regulation of T cell cytokine production	1/60	19/23328	0.0478	0.0639	1
BP	GO:0006027	glycosaminoglycan catabolic process	1/60	19/23328	0.0478	0.0639	1
BP	GO:0006089	lactate metabolic process	1/60	19/23328	0.0478	0.0639	1
BP	GO:0006309	apoptotic DNA fragmentation	1/60	19/23328	0.0478	0.0639	1
BP	GO:0006622	protein targeting to lysosome	1/60	19/23328	0.0478	0.0639	1
BP	GO:0006656	phosphatidylcholine biosynthetic process	1/60	19/23328	0.0478	0.0639	1
BP	GO:0017121	plasma membrane phospholipid scrambling	1/60	19/23328	0.0478	0.0639	1
BP	GO:0020027	hemoglobin metabolic process	1/60	19/23328	0.0478	0.0639	1
BP	GO:0030502	negative regulation of bone mineralization	1/60	19/23328	0.0478	0.0639	1
BP	GO:0032352	positive regulation of hormone metabolic process	1/60	19/23328	0.0478	0.0639	1
BP	GO:0034138	toll-like receptor 3 signaling pathway	1/60	19/23328	0.0478	0.0639	1
BP	GO:0035994	response to muscle stretch	1/60	19/23328	0.0478	0.0639	1
BP	GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	1/60	19/23328	0.0478	0.0639	1
BP	GO:0043652	engulfment of apoptotic cell	1/60	19/23328	0.0478	0.0639	1
BP	GO:0045721	negative regulation of gluconeogenesis	1/60	19/23328	0.0478	0.0639	1
BP	GO:0045837	negative regulation of membrane potential	1/60	19/23328	0.0478	0.0639	1
BP	GO:0060965	negative regulation of gene silencing by miRNA	1/60	19/23328	0.0478	0.0639	1
BP	GO:0071071	regulation of phospholipid biosynthetic process	1/60	19/23328	0.0478	0.0639	1

BP	GO:0072578	neurotransmitter-gated ion channel clustering	1/60	19/23328	0.0478	0.0639	1
BP	GO:0097623	potassium ion export across plasma membrane	1/60	19/23328	0.0478	0.0639	1
BP	GO:1903599	positive regulation of autophagy of mitochondrion	1/60	19/23328	0.0478	0.0639	1
BP	GO:1903960	negative regulation of anion transmembrane transport	1/60	19/23328	0.0478	0.0639	1
BP	GO:0008209	androgen metabolic process	1/60	20/23328	0.0502	0.0657	1
BP	GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	1/60	20/23328	0.0502	0.0657	1
BP	GO:0032095	regulation of response to food	1/60	20/23328	0.0502	0.0657	1
BP	GO:0032310	prostaglandin secretion	1/60	20/23328	0.0502	0.0657	1
BP	GO:0035970	peptidyl-threonine dephosphorylation	1/60	20/23328	0.0502	0.0657	1
BP	GO:0043555	regulation of translation in response to stress	1/60	20/23328	0.0502	0.0657	1
BP	GO:0044321	response to leptin	1/60	20/23328	0.0502	0.0657	1
BP	GO:0045986	negative regulation of smooth muscle contraction	1/60	20/23328	0.0502	0.0657	1
BP	GO:0060252	positive regulation of glial cell proliferation	1/60	20/23328	0.0502	0.0657	1
BP	GO:0060547	negative regulation of necrotic cell death	1/60	20/23328	0.0502	0.0657	1
BP	GO:0070935	3'-UTR-mediated mRNA stabilization	1/60	20/23328	0.0502	0.0657	1
BP	GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1/60	20/23328	0.0502	0.0657	1
BP	GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	1/60	20/23328	0.0502	0.0657	1
BP	GO:1903909	regulation of receptor clustering	1/60	20/23328	0.0502	0.0657	1
BP	GO:1904385	cellular response to angiotensin	1/60	20/23328	0.0502	0.0657	1
BP	GO:0002043	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	1/60	21/23328	0.0527	0.0671	1
BP	GO:0002363	alpha-beta T cell lineage commitment	1/60	21/23328	0.0527	0.0671	1

BP	GO:0010869	regulation of receptor biosynthetic process	1/60	21/23328	0.0527	0.0671	1
BP	GO:0031065	positive regulation of histone deacetylation	1/60	21/23328	0.0527	0.0671	1
BP	GO:0032332	positive regulation of chondrocyte differentiation	1/60	21/23328	0.0527	0.0671	1
BP	GO:0034643	establishment of mitochondrion localization, microtubule-mediated	1/60	21/23328	0.0527	0.0671	1
BP	GO:0036336	dendritic cell migration	1/60	21/23328	0.0527	0.0671	1
BP	GO:0043931	ossification involved in bone maturation	1/60	21/23328	0.0527	0.0671	1
BP	GO:0045948	positive regulation of translational initiation	1/60	21/23328	0.0527	0.0671	1
BP	GO:0046697	decidualization	1/60	21/23328	0.0527	0.0671	1
BP	GO:0047497	mitochondrion transport along microtubule	1/60	21/23328	0.0527	0.0671	1
BP	GO:0051023	regulation of immunoglobulin secretion	1/60	21/23328	0.0527	0.0671	1
BP	GO:0051956	negative regulation of amino acid transport	1/60	21/23328	0.0527	0.0671	1
BP	GO:0060149	negative regulation of posttranscriptional gene silencing	1/60	21/23328	0.0527	0.0671	1
BP	GO:0060456	positive regulation of digestive system process	1/60	21/23328	0.0527	0.0671	1
BP	GO:0060967	negative regulation of gene silencing by RNA	1/60	21/23328	0.0527	0.0671	1
BP	GO:0090026	positive regulation of monocyte chemotaxis	1/60	21/23328	0.0527	0.0671	1
BP	GO:1902004	positive regulation of amyloid-beta formation	1/60	21/23328	0.0527	0.0671	1
BP	GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	1/60	21/23328	0.0527	0.0671	1
BP	GO:2000726	negative regulation of cardiac muscle cell differentiation	1/60	21/23328	0.0527	0.0671	1
BP	GO:0003323	type B pancreatic cell development	1/60	22/23328	0.0551	0.0683	1
BP	GO:0014850	response to muscle activity	1/60	22/23328	0.0551	0.0683	1
BP	GO:0015813	L-glutamate transmembrane transport	1/60	22/23328	0.0551	0.0683	1

BP	GO:0031649	heat generation	1/60	22/23328	0.0551	0.0683	1
BP	GO:0032366	intracellular sterol transport	1/60	22/23328	0.0551	0.0683	1
BP	GO:0032367	intracellular cholesterol transport	1/60	22/23328	0.0551	0.0683	1
BP	GO:0034377	plasma lipoprotein particle assembly	1/60	22/23328	0.0551	0.0683	1
BP	GO:0042438	melanin biosynthetic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:0044273	sulfur compound catabolic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:0044851	hair cycle phase	1/60	22/23328	0.0551	0.0683	1
BP	GO:0045624	positive regulation of T-helper cell differentiation	1/60	22/23328	0.0551	0.0683	1
BP	GO:0046337	phosphatidylethanolamine metabolic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:0048532	anatomical structure arrangement	1/60	22/23328	0.0551	0.0683	1
BP	GO:0060749	mammary gland alveolus development	1/60	22/23328	0.0551	0.0683	1
BP	GO:0061377	mammary gland lobule development	1/60	22/23328	0.0551	0.0683	1
BP	GO:0070242	thymocyte apoptotic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:1900543	negative regulation of purine nucleotide metabolic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:1901223	negative regulation of NIK/NF-kappaB signaling	1/60	22/23328	0.0551	0.0683	1
BP	GO:1901741	positive regulation of myoblast fusion	1/60	22/23328	0.0551	0.0683	1
BP	GO:1903055	positive regulation of extracellular matrix organization	1/60	22/23328	0.0551	0.0683	1
BP	GO:1990776	response to angiotensin	1/60	22/23328	0.0551	0.0683	1
BP	GO:2000353	positive regulation of endothelial cell apoptotic process	1/60	22/23328	0.0551	0.0683	1
BP	GO:2001026	regulation of endothelial cell chemotaxis	1/60	22/23328	0.0551	0.0683	1
BP	GO:0002719	negative regulation of cytokine production involved in immune response	1/60	23/23328	0.0575	0.0700	1
BP	GO:0023019	signal transduction involved in regulation of gene expression	1/60	23/23328	0.0575	0.0700	1
BP	GO:0034405	response to fluid shear stress	1/60	23/23328	0.0575	0.0700	1

BP	GO:0035278	miRNA mediated inhibition of translation	1/60	23/23328	0.0575	0.0700	1
BP	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	1/60	23/23328	0.0575	0.0700	1
BP	GO:0045980	negative regulation of nucleotide metabolic process	1/60	23/23328	0.0575	0.0700	1
BP	GO:0046931	pore complex assembly	1/60	23/23328	0.0575	0.0700	1
BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	1/60	23/23328	0.0575	0.0700	1
BP	GO:0051291	protein heterooligomerization	1/60	23/23328	0.0575	0.0700	1
BP	GO:0051969	regulation of transmission of nerve impulse	1/60	23/23328	0.0575	0.0700	1
BP	GO:0070977	bone maturation	1/60	23/23328	0.0575	0.0700	1
BP	GO:1901626	regulation of postsynaptic membrane organization	1/60	23/23328	0.0575	0.0700	1
BP	GO:1902410	mitotic cytokinetic process	1/60	23/23328	0.0575	0.0700	1
BP	GO:1903306	negative regulation of regulated secretory pathway	1/60	23/23328	0.0575	0.0700	1
BP	GO:2000345	regulation of hepatocyte proliferation	1/60	23/23328	0.0575	0.0700	1
BP	GO:0002903	negative regulation of B cell apoptotic process	1/60	24/23328	0.0600	0.0717	1
BP	GO:0006582	melanin metabolic process	1/60	24/23328	0.0600	0.0717	1
BP	GO:0015732	prostaglandin transport	1/60	24/23328	0.0600	0.0717	1
BP	GO:0021544	subpallium development	1/60	24/23328	0.0600	0.0717	1
BP	GO:0030728	ovulation	1/60	24/23328	0.0600	0.0717	1
BP	GO:0032691	negative regulation of interleukin-1 beta production	1/60	24/23328	0.0600	0.0717	1
BP	GO:0035743	CD4-positive, alpha-beta T cell cytokine production	1/60	24/23328	0.0600	0.0717	1
BP	GO:0040033	negative regulation of translation, ncRNA-mediated	1/60	24/23328	0.0600	0.0717	1
BP	GO:0044550	secondary metabolite biosynthetic process	1/60	24/23328	0.0600	0.0717	1
BP	GO:0045324	late endosome to vacuole transport	1/60	24/23328	0.0600	0.0717	1
BP	GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	1/60	24/23328	0.0600	0.0717	1

BP	GO:0045974	regulation of translation, ncRNA-mediated	1/60	24/23328	0.0600	0.0717	1
BP	GO:0046823	negative regulation of nucleocytoplasmic transport	1/60	24/23328	0.0600	0.0717	1
BP	GO:0048670	regulation of collateral sprouting	1/60	24/23328	0.0600	0.0717	1
BP	GO:0051654	establishment of mitochondrion localization	1/60	24/23328	0.0600	0.0717	1
BP	GO:0090335	regulation of brown fat cell differentiation	1/60	24/23328	0.0600	0.0717	1
BP	GO:0010884	positive regulation of lipid storage	1/60	25/23328	0.0624	0.0732	1
BP	GO:0010954	positive regulation of protein processing	1/60	25/23328	0.0624	0.0732	1
BP	GO:0019068	virion assembly	1/60	25/23328	0.0624	0.0732	1
BP	GO:0032753	positive regulation of interleukin-4 production	1/60	25/23328	0.0624	0.0732	1
BP	GO:0032897	negative regulation of viral transcription	1/60	25/23328	0.0624	0.0732	1
BP	GO:0035384	thioester biosynthetic process	1/60	25/23328	0.0624	0.0732	1
BP	GO:0046426	negative regulation of receptor signaling pathway via JAK-STAT	1/60	25/23328	0.0624	0.0732	1
BP	GO:0046688	response to copper ion	1/60	25/23328	0.0624	0.0732	1
BP	GO:0060575	intestinal epithelial cell differentiation	1/60	25/23328	0.0624	0.0732	1
BP	GO:0070633	transepithelial transport	1/60	25/23328	0.0624	0.0732	1
BP	GO:0071108	protein K48-linked deubiquitination	1/60	25/23328	0.0624	0.0732	1
BP	GO:0071616	acyl-CoA biosynthetic process	1/60	25/23328	0.0624	0.0732	1
BP	GO:0090169	regulation of spindle assembly	1/60	25/23328	0.0624	0.0732	1
BP	GO:1901739	regulation of myoblast fusion	1/60	25/23328	0.0624	0.0732	1
BP	GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	1/60	25/23328	0.0624	0.0732	1
BP	GO:1902993	positive regulation of amyloid precursor protein catabolic process	1/60	25/23328	0.0624	0.0732	1
BP	GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	1/60	25/23328	0.0624	0.0732	1

BP	GO:1905208	negative regulation of cardiocyte differentiation	1/60	25/23328	0.0624	0.0732	1
BP	GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	1/60	26/23328	0.0648	0.0749	1
BP	GO:0000737	DNA catabolic process, endonucleolytic	1/60	26/23328	0.0648	0.0749	1
BP	GO:0032104	regulation of response to extracellular stimulus	1/60	26/23328	0.0648	0.0749	1
BP	GO:0032107	regulation of response to nutrient levels	1/60	26/23328	0.0648	0.0749	1
BP	GO:0032303	regulation of icosanoid secretion	1/60	26/23328	0.0648	0.0749	1
BP	GO:0032800	receptor biosynthetic process	1/60	26/23328	0.0648	0.0749	1
BP	GO:0065005	protein-lipid complex assembly	1/60	26/23328	0.0648	0.0749	1
BP	GO:0070168	negative regulation of biomineral tissue development	1/60	26/23328	0.0648	0.0749	1
BP	GO:0070233	negative regulation of T cell apoptotic process	1/60	26/23328	0.0648	0.0749	1
BP	GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	1/60	26/23328	0.0648	0.0749	1
BP	GO:0071549	cellular response to dexamethasone stimulus	1/60	26/23328	0.0648	0.0749	1
BP	GO:0110150	negative regulation of biomineralization	1/60	26/23328	0.0648	0.0749	1
BP	GO:1901380	negative regulation of potassium ion transmembrane transport	1/60	26/23328	0.0648	0.0749	1
BP	GO:1904030	negative regulation of cyclin-dependent protein kinase activity	1/60	26/23328	0.0648	0.0749	1
BP	GO:1904893	negative regulation of receptor signaling pathway via STAT	1/60	26/23328	0.0648	0.0749	1
BP	GO:0002052	positive regulation of neuroblast proliferation	1/60	27/23328	0.0672	0.0760	1
BP	GO:0002068	glandular epithelial cell development	1/60	27/23328	0.0672	0.0760	1
BP	GO:0006882	cellular zinc ion homeostasis	1/60	27/23328	0.0672	0.0760	1
BP	GO:0030194	positive regulation of blood coagulation	1/60	27/23328	0.0672	0.0760	1
BP	GO:0030212	hyaluronan metabolic process	1/60	27/23328	0.0672	0.0760	1
BP	GO:0032528	microvillus organization	1/60	27/23328	0.0672	0.0760	1

BP	GO:0046885	regulation of hormone biosynthetic process	1/60	27/23328	0.0672	0.0760	1
BP	GO:0048305	immunoglobulin secretion	1/60	27/23328	0.0672	0.0760	1
BP	GO:0048799	animal organ maturation	1/60	27/23328	0.0672	0.0760	1
BP	GO:0051443	positive regulation of ubiquitin-protein transferase activity	1/60	27/23328	0.0672	0.0760	1
BP	GO:0060343	trabecula formation	1/60	27/23328	0.0672	0.0760	1
BP	GO:0061298	retina vasculature development in camera-type eye	1/60	27/23328	0.0672	0.0760	1
BP	GO:0071677	positive regulation of mononuclear cell migration	1/60	27/23328	0.0672	0.0760	1
BP	GO:0090103	cochlea morphogenesis	1/60	27/23328	0.0672	0.0760	1
BP	GO:0150077	regulation of neuroinflammatory response	1/60	27/23328	0.0672	0.0760	1
BP	GO:1900017	positive regulation of cytokine production involved in inflammatory response	1/60	27/23328	0.0672	0.0760	1
BP	GO:1900048	positive regulation of hemostasis	1/60	27/23328	0.0672	0.0760	1
BP	GO:1903319	positive regulation of protein maturation	1/60	27/23328	0.0672	0.0760	1
BP	GO:0006026	aminoglycan catabolic process	1/60	28/23328	0.0696	0.0775	1
BP	GO:0010460	positive regulation of heart rate	1/60	28/23328	0.0696	0.0775	1
BP	GO:0030878	thyroid gland development	1/60	28/23328	0.0696	0.0775	1
BP	GO:0033233	regulation of protein sumoylation	1/60	28/23328	0.0696	0.0775	1
BP	GO:0045648	positive regulation of erythrocyte differentiation	1/60	28/23328	0.0696	0.0775	1
BP	GO:0045922	negative regulation of fatty acid metabolic process	1/60	28/23328	0.0696	0.0775	1
BP	GO:0048596	embryonic camera-type eye morphogenesis	1/60	28/23328	0.0696	0.0775	1
BP	GO:0048820	hair follicle maturation	1/60	28/23328	0.0696	0.0775	1
BP	GO:0051016	barbed-end actin filament capping	1/60	28/23328	0.0696	0.0775	1
BP	GO:0055069	zinc ion homeostasis	1/60	28/23328	0.0696	0.0775	1
BP	GO:0060445	branching involved in salivary gland morphogenesis	1/60	28/23328	0.0696	0.0775	1
BP	GO:0061436	establishment of skin barrier	1/60	28/23328	0.0696	0.0775	1
BP	GO:0071480	cellular response to gamma radiation	1/60	28/23328	0.0696	0.0775	1

BP	GO:0001516	prostaglandin biosynthetic process	1/60	29/23328	0.0720	0.0785	1
BP	GO:0001919	regulation of receptor recycling	1/60	29/23328	0.0720	0.0785	1
BP	GO:0002507	tolerance induction	1/60	29/23328	0.0720	0.0785	1
BP	GO:0010586	miRNA metabolic process	1/60	29/23328	0.0720	0.0785	1
BP	GO:0010893	positive regulation of steroid biosynthetic process	1/60	29/23328	0.0720	0.0785	1
BP	GO:0030262	apoptotic nuclear changes	1/60	29/23328	0.0720	0.0785	1
BP	GO:0031063	regulation of histone deacetylation	1/60	29/23328	0.0720	0.0785	1
BP	GO:0031295	T cell costimulation	1/60	29/23328	0.0720	0.0785	1
BP	GO:0042403	thyroid hormone metabolic process	1/60	29/23328	0.0720	0.0785	1
BP	GO:0043032	positive regulation of macrophage activation	1/60	29/23328	0.0720	0.0785	1
BP	GO:0045109	intermediate filament organization	1/60	29/23328	0.0720	0.0785	1
BP	GO:0045187	regulation of circadian sleep/wake cycle, sleep	1/60	29/23328	0.0720	0.0785	1
BP	GO:0045589	regulation of regulatory T cell differentiation	1/60	29/23328	0.0720	0.0785	1
BP	GO:0046457	prostanoid biosynthetic process	1/60	29/23328	0.0720	0.0785	1
BP	GO:0060571	morphogenesis of an epithelial fold	1/60	29/23328	0.0720	0.0785	1
BP	GO:0061050	regulation of cell growth involved in cardiac muscle cell development	1/60	29/23328	0.0720	0.0785	1
BP	GO:0071353	cellular response to interleukin-4	1/60	29/23328	0.0720	0.0785	1
BP	GO:0071548	response to dexamethasone	1/60	29/23328	0.0720	0.0785	1
BP	GO:0090312	positive regulation of protein deacetylation	1/60	29/23328	0.0720	0.0785	1
BP	GO:0097345	mitochondrial outer membrane permeabilization	1/60	29/23328	0.0720	0.0785	1
BP	GO:0002360	T cell lineage commitment	1/60	30/23328	0.0744	0.0797	1
BP	GO:0002724	regulation of T cell cytokine production	1/60	30/23328	0.0744	0.0797	1
BP	GO:0003309	type B pancreatic cell differentiation	1/60	30/23328	0.0744	0.0797	1
BP	GO:0006767	water-soluble vitamin metabolic process	1/60	30/23328	0.0744	0.0797	1
BP	GO:0006829	zinc ion transport	1/60	30/23328	0.0744	0.0797	1

BP	GO:0006921	cellular component disassembly involved in execution phase of apoptosis	1/60	30/23328	0.0744	0.0797	1
BP	GO:0009262	deoxyribonucleotide metabolic process	1/60	30/23328	0.0744	0.0797	1
BP	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	1/60	30/23328	0.0744	0.0797	1
BP	GO:0035162	embryonic hemopoiesis	1/60	30/23328	0.0744	0.0797	1
BP	GO:0035767	endothelial cell chemotaxis	1/60	30/23328	0.0744	0.0797	1
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	1/60	30/23328	0.0744	0.0797	1
BP	GO:0043457	regulation of cellular respiration	1/60	30/23328	0.0744	0.0797	1
BP	GO:0050802	circadian sleep/wake cycle, sleep	1/60	30/23328	0.0744	0.0797	1
BP	GO:0050820	positive regulation of coagulation	1/60	30/23328	0.0744	0.0797	1
BP	GO:0051085	chaperone cofactor-dependent protein refolding	1/60	30/23328	0.0744	0.0797	1
BP	GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	1/60	30/23328	0.0744	0.0797	1
BP	GO:0061082	myeloid leukocyte cytokine production	1/60	30/23328	0.0744	0.0797	1
BP	GO:0072539	T-helper 17 cell differentiation	1/60	30/23328	0.0744	0.0797	1
BP	GO:0120178	steroid hormone biosynthetic process	1/60	30/23328	0.0744	0.0797	1
BP	GO:1903579	negative regulation of ATP metabolic process	1/60	30/23328	0.0744	0.0797	1
BP	GO:0001963	synaptic transmission, dopaminergic	1/60	31/23328	0.0768	0.0809	1
BP	GO:0002230	positive regulation of defense response to virus by host	1/60	31/23328	0.0768	0.0809	1
BP	GO:0002828	regulation of type 2 immune response	1/60	31/23328	0.0768	0.0809	1
BP	GO:0031294	lymphocyte costimulation	1/60	31/23328	0.0768	0.0809	1
BP	GO:0032365	intracellular lipid transport	1/60	31/23328	0.0768	0.0809	1
BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	1/60	31/23328	0.0768	0.0809	1
BP	GO:0035640	exploration behavior	1/60	31/23328	0.0768	0.0809	1
BP	GO:0042168	heme metabolic process	1/60	31/23328	0.0768	0.0809	1

BP	GO:0044319	wound healing, spreading of cells	1/60	31/23328	0.0768	0.0809	1
BP	GO:0044788	modulation by host of viral process	1/60	31/23328	0.0768	0.0809	1
BP	GO:0045920	negative regulation of exocytosis	1/60	31/23328	0.0768	0.0809	1
BP	GO:0045932	negative regulation of muscle contraction	1/60	31/23328	0.0768	0.0809	1
BP	GO:0048011	neurotrophin TRK receptor signaling pathway	1/60	31/23328	0.0768	0.0809	1
BP	GO:0061036	positive regulation of cartilage development	1/60	31/23328	0.0768	0.0809	1
BP	GO:0070670	response to interleukin-4	1/60	31/23328	0.0768	0.0809	1
BP	GO:0090505	epiboly involved in wound healing	1/60	31/23328	0.0768	0.0809	1
BP	GO:1900117	regulation of execution phase of apoptosis	1/60	31/23328	0.0768	0.0809	1
BP	GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	1/60	31/23328	0.0768	0.0809	1
BP	GO:1902932	positive regulation of alcohol biosynthetic process	1/60	31/23328	0.0768	0.0809	1
BP	GO:0001893	maternal placenta development	1/60	32/23328	0.0792	0.0820	1
BP	GO:0002902	regulation of B cell apoptotic process	1/60	32/23328	0.0792	0.0820	1
BP	GO:0008206	bile acid metabolic process	1/60	32/23328	0.0792	0.0820	1
BP	GO:0010043	response to zinc ion	1/60	32/23328	0.0792	0.0820	1
BP	GO:0010614	negative regulation of cardiac muscle hypertrophy	1/60	32/23328	0.0792	0.0820	1
BP	GO:0010939	regulation of necrotic cell death	1/60	32/23328	0.0792	0.0820	1
BP	GO:0016242	negative regulation of macroautophagy	1/60	32/23328	0.0792	0.0820	1
BP	GO:0032673	regulation of interleukin-4 production	1/60	32/23328	0.0792	0.0820	1
BP	GO:0032692	negative regulation of interleukin-1 production	1/60	32/23328	0.0792	0.0820	1
BP	GO:0032958	inositol phosphate biosynthetic process	1/60	32/23328	0.0792	0.0820	1
BP	GO:0042749	regulation of circadian sleep/wake cycle	1/60	32/23328	0.0792	0.0820	1
BP	GO:0048668	collateral sprouting	1/60	32/23328	0.0792	0.0820	1

BP	GO:0051150	regulation of smooth muscle cell differentiation	1/60	32/23328	0.0792	0.0820	1
BP	GO:0055022	negative regulation of cardiac muscle tissue growth	1/60	32/23328	0.0792	0.0820	1
BP	GO:0060561	apoptotic process involved in morphogenesis	1/60	32/23328	0.0792	0.0820	1
BP	GO:0061117	negative regulation of heart growth	1/60	32/23328	0.0792	0.0820	1
BP	GO:0070536	protein K63-linked deubiquitination	1/60	32/23328	0.0792	0.0820	1
BP	GO:0090504	epiboly	1/60	32/23328	0.0792	0.0820	1
BP	GO:1901797	negative regulation of signal transduction by p53 class mediator	1/60	32/23328	0.0792	0.0820	1
BP	GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	1/60	32/23328	0.0792	0.0820	1
BP	GO:2000352	negative regulation of endothelial cell apoptotic process	1/60	32/23328	0.0792	0.0820	1
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	1/60	32/23328	0.0792	0.0820	1
BP	GO:0006084	acetyl-CoA metabolic process	1/60	33/23328	0.0815	0.0836	1
BP	GO:0022410	circadian sleep/wake cycle process	1/60	33/23328	0.0815	0.0836	1
BP	GO:0032369	negative regulation of lipid transport	1/60	33/23328	0.0815	0.0836	1
BP	GO:0033081	regulation of T cell differentiation in thymus	1/60	33/23328	0.0815	0.0836	1
BP	GO:0033561	regulation of water loss via skin	1/60	33/23328	0.0815	0.0836	1
BP	GO:0045066	regulatory T cell differentiation	1/60	33/23328	0.0815	0.0836	1
BP	GO:0045616	regulation of keratinocyte differentiation	1/60	33/23328	0.0815	0.0836	1
BP	GO:0060740	prostate gland epithelium morphogenesis	1/60	33/23328	0.0815	0.0836	1
BP	GO:0060969	negative regulation of gene silencing	1/60	33/23328	0.0815	0.0836	1
BP	GO:0061157	mRNA destabilization	1/60	33/23328	0.0815	0.0836	1
BP	GO:0002021	response to dietary excess	1/60	34/23328	0.0839	0.0848	1
BP	GO:0006884	cell volume homeostasis	1/60	34/23328	0.0839	0.0848	1

BP	GO:0014741	negative regulation of muscle hypertrophy	1/60	34/23328	0.0839	0.0848	1
BP	GO:0021591	ventricular system development	1/60	34/23328	0.0839	0.0848	1
BP	GO:0032509	endosome transport via multivesicular body sorting pathway	1/60	34/23328	0.0839	0.0848	1
BP	GO:0035883	enteroendocrine cell differentiation	1/60	34/23328	0.0839	0.0848	1
BP	GO:0048048	embryonic eye morphogenesis	1/60	34/23328	0.0839	0.0848	1
BP	GO:0060512	prostate gland morphogenesis	1/60	34/23328	0.0839	0.0848	1
BP	GO:0090022	regulation of neutrophil chemotaxis	1/60	34/23328	0.0839	0.0848	1
BP	GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	1/60	34/23328	0.0839	0.0848	1
BP	GO:1903146	regulation of autophagy of mitochondrion	1/60	34/23328	0.0839	0.0848	1
BP	GO:1904646	cellular response to amyloid-beta	1/60	34/23328	0.0839	0.0848	1
BP	GO:2000108	positive regulation of leukocyte apoptotic process	1/60	34/23328	0.0839	0.0848	1
BP	GO:0006308	DNA catabolic process	1/60	35/23328	0.0863	0.0855	1
BP	GO:0006458	de novo' protein folding	1/60	35/23328	0.0863	0.0855	1
BP	GO:0006623	protein targeting to vacuole	1/60	35/23328	0.0863	0.0855	1
BP	GO:0007031	peroxisome organization	1/60	35/23328	0.0863	0.0855	1
BP	GO:0010837	regulation of keratinocyte proliferation	1/60	35/23328	0.0863	0.0855	1
BP	GO:0032094	response to food	1/60	35/23328	0.0863	0.0855	1
BP	GO:0033866	nucleoside bisphosphate biosynthetic process	1/60	35/23328	0.0863	0.0855	1
BP	GO:0034030	ribonucleoside bisphosphate biosynthetic process	1/60	35/23328	0.0863	0.0855	1
BP	GO:0034033	purine nucleoside bisphosphate biosynthetic process	1/60	35/23328	0.0863	0.0855	1
BP	GO:0034122	negative regulation of toll-like receptor signaling pathway	1/60	35/23328	0.0863	0.0855	1
BP	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	1/60	35/23328	0.0863	0.0855	1
BP	GO:0045987	positive regulation of smooth muscle contraction	1/60	35/23328	0.0863	0.0855	1
BP	GO:0046677	response to antibiotic	1/60	35/23328	0.0863	0.0855	1

BP	GO:0050832	defense response to fungus	1/60	35/23328	0.0863	0.0855	1
BP	GO:0050869	negative regulation of B cell activation	1/60	35/23328	0.0863	0.0855	1
BP	GO:0051084	de novo' posttranslational protein folding	1/60	35/23328	0.0863	0.0855	1
BP	GO:0055090	acylglycerol homeostasis	1/60	35/23328	0.0863	0.0855	1
BP	GO:0060142	regulation of syncytium formation by plasma membrane fusion	1/60	35/23328	0.0863	0.0855	1
BP	GO:0060236	regulation of mitotic spindle organization	1/60	35/23328	0.0863	0.0855	1
BP	GO:0070328	triglyceride homeostasis	1/60	35/23328	0.0863	0.0855	1
BP	GO:0072538	T-helper 17 type immune response	1/60	35/23328	0.0863	0.0855	1
BP	GO:1900181	negative regulation of protein localization to nucleus	1/60	35/23328	0.0863	0.0855	1
BP	GO:1902003	regulation of amyloid-beta formation	1/60	35/23328	0.0863	0.0855	1
BP	GO:0002701	negative regulation of production of molecular mediator of immune response	1/60	36/23328	0.0886	0.0871	1
BP	GO:0034381	plasma lipoprotein particle clearance	1/60	36/23328	0.0886	0.0871	1
BP	GO:0042745	circadian sleep/wake cycle	1/60	36/23328	0.0886	0.0871	1
BP	GO:0042832	defense response to protozoan	1/60	36/23328	0.0886	0.0871	1
BP	GO:0050779	RNA destabilization	1/60	36/23328	0.0886	0.0871	1
BP	GO:2000191	regulation of fatty acid transport	1/60	36/23328	0.0886	0.0871	1
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	1/60	36/23328	0.0886	0.0871	1
BP	GO:0007435	salivary gland morphogenesis	1/60	37/23328	0.0910	0.0886	1
BP	GO:0021680	cerebellar Purkinje cell layer development	1/60	37/23328	0.0910	0.0886	1
BP	GO:0035794	positive regulation of mitochondrial membrane permeability	1/60	37/23328	0.0910	0.0886	1
BP	GO:0045047	protein targeting to ER	1/60	37/23328	0.0910	0.0886	1
BP	GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	1/60	37/23328	0.0910	0.0886	1
BP	GO:0001706	endoderm formation	1/60	38/23328	0.0933	0.0894	1

BP	GO:0010831	positive regulation of myotube differentiation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0014002	astrocyte development	1/60	38/23328	0.0933	0.0894	1
BP	GO:0019432	triglyceride biosynthetic process	1/60	38/23328	0.0933	0.0894	1
BP	GO:0032733	positive regulation of interleukin-10 production	1/60	38/23328	0.0933	0.0894	1
BP	GO:0033238	regulation of cellular amine metabolic process	1/60	38/23328	0.0933	0.0894	1
BP	GO:0035335	peptidyl-tyrosine dephosphorylation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0038084	vascular endothelial growth factor signaling pathway	1/60	38/23328	0.0933	0.0894	1
BP	GO:0043267	negative regulation of potassium ion transport	1/60	38/23328	0.0933	0.0894	1
BP	GO:0043304	regulation of mast cell degranulation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0045601	regulation of endothelial cell differentiation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0045622	regulation of T-helper cell differentiation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0045940	positive regulation of steroid metabolic process	1/60	38/23328	0.0933	0.0894	1
BP	GO:0046627	negative regulation of insulin receptor signaling pathway	1/60	38/23328	0.0933	0.0894	1
BP	GO:0046640	regulation of alpha-beta T cell proliferation	1/60	38/23328	0.0933	0.0894	1
BP	GO:0051953	negative regulation of amine transport	1/60	38/23328	0.0933	0.0894	1
BP	GO:0051968	positive regulation of synaptic transmission, glutamatergic	1/60	38/23328	0.0933	0.0894	1
BP	GO:0071985	multivesicular body sorting pathway	1/60	38/23328	0.0933	0.0894	1
BP	GO:1904037	positive regulation of epithelial cell apoptotic process	1/60	38/23328	0.0933	0.0894	1
BP	GO:2000463	positive regulation of excitatory postsynaptic potential	1/60	38/23328	0.0933	0.0894	1
BP	GO:0006739	NADP metabolic process	1/60	39/23328	0.0956	0.0905	1
BP	GO:0006778	porphyrin-containing compound metabolic process	1/60	39/23328	0.0956	0.0905	1
BP	GO:0007212	dopamine receptor signaling pathway	1/60	39/23328	0.0956	0.0905	1
BP	GO:0021983	pituitary gland development	1/60	39/23328	0.0956	0.0905	1

BP	GO:0032506	cytokinetic process	1/60	39/23328	0.0956	0.0905	1
BP	GO:0032735	positive regulation of interleukin-12 production	1/60	39/23328	0.0956	0.0905	1
BP	GO:0033006	regulation of mast cell activation involved in immune response	1/60	39/23328	0.0956	0.0905	1
BP	GO:0042554	superoxide anion generation	1/60	39/23328	0.0956	0.0905	1
BP	GO:0060251	regulation of glial cell proliferation	1/60	39/23328	0.0956	0.0905	1
BP	GO:0061462	protein localization to lysosome	1/60	39/23328	0.0956	0.0905	1
BP	GO:0071827	plasma lipoprotein particle organization	1/60	39/23328	0.0956	0.0905	1
BP	GO:0090224	regulation of spindle organization	1/60	39/23328	0.0956	0.0905	1
BP	GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	1/60	39/23328	0.0956	0.0905	1
BP	GO:0001562	response to protozoan	1/60	40/23328	0.0980	0.0915	1
BP	GO:0001881	receptor recycling	1/60	40/23328	0.0980	0.0915	1
BP	GO:0007616	long-term memory	1/60	40/23328	0.0980	0.0915	1
BP	GO:0009409	response to cold	1/60	40/23328	0.0980	0.0915	1
BP	GO:0030431	sleep	1/60	40/23328	0.0980	0.0915	1
BP	GO:0031076	embryonic camera-type eye development	1/60	40/23328	0.0980	0.0915	1
BP	GO:0032633	interleukin-4 production	1/60	40/23328	0.0980	0.0915	1
BP	GO:0038179	neurotrophin signaling pathway	1/60	40/23328	0.0980	0.0915	1
BP	GO:0040019	positive regulation of embryonic development	1/60	40/23328	0.0980	0.0915	1
BP	GO:0042092	type 2 immune response	1/60	40/23328	0.0980	0.0915	1
BP	GO:0043368	positive T cell selection	1/60	40/23328	0.0980	0.0915	1
BP	GO:0060259	regulation of feeding behavior	1/60	40/23328	0.0980	0.0915	1
BP	GO:0071542	dopaminergic neuron differentiation	1/60	40/23328	0.0980	0.0915	1
BP	GO:1902692	regulation of neuroblast proliferation	1/60	40/23328	0.0980	0.0915	1
BP	GO:1903959	regulation of anion transmembrane transport	1/60	40/23328	0.0980	0.0915	1
BP	GO:1904645	response to amyloid-beta	1/60	40/23328	0.0980	0.0915	1
BP	GO:0002369	T cell cytokine production	1/60	41/23328	0.1003	0.0928	1
BP	GO:0007431	salivary gland development	1/60	41/23328	0.1003	0.0928	1
BP	GO:0008207	C21-steroid hormone metabolic process	1/60	41/23328	0.1003	0.0928	1

BP	GO:0014037	Schwann cell differentiation	1/60	41/23328	0.1003	0.0928	1
BP	GO:0034205	amyloid-beta formation	1/60	41/23328	0.1003	0.0928	1
BP	GO:0046164	alcohol catabolic process	1/60	41/23328	0.1003	0.0928	1
BP	GO:0051693	actin filament capping	1/60	41/23328	0.1003	0.0928	1
BP	GO:0071364	cellular response to epidermal growth factor stimulus	1/60	41/23328	0.1003	0.0928	1
BP	GO:0072595	maintenance of protein localization in organelle	1/60	41/23328	0.1003	0.0928	1
BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	1/60	41/23328	0.1003	0.0928	1
BP	GO:1900744	regulation of p38MAPK cascade	1/60	41/23328	0.1003	0.0928	1
BP	GO:1902991	regulation of amyloid precursor protein catabolic process	1/60	41/23328	0.1003	0.0928	1
BP	GO:0030501	positive regulation of bone mineralization	1/60	42/23328	0.1026	0.0944	1
BP	GO:0046633	alpha-beta T cell proliferation	1/60	42/23328	0.1026	0.0944	1
BP	GO:0051154	negative regulation of striated muscle cell differentiation	1/60	42/23328	0.1026	0.0944	1
BP	GO:1900077	negative regulation of cellular response to insulin stimulus	1/60	42/23328	0.1026	0.0944	1
BP	GO:2000279	negative regulation of DNA biosynthetic process	1/60	42/23328	0.1026	0.0944	1
BP	GO:0001783	B cell apoptotic process	1/60	43/23328	0.1049	0.0954	1
BP	GO:0003298	physiological muscle hypertrophy	1/60	43/23328	0.1049	0.0954	1
BP	GO:0003301	physiological cardiac muscle hypertrophy	1/60	43/23328	0.1049	0.0954	1
BP	GO:0035774	positive regulation of insulin secretion involved in cellular response to glucose stimulus	1/60	43/23328	0.1049	0.0954	1
BP	GO:0046636	negative regulation of alpha-beta T cell activation	1/60	43/23328	0.1049	0.0954	1
BP	GO:0046782	regulation of viral transcription	1/60	43/23328	0.1049	0.0954	1
BP	GO:0055026	negative regulation of cardiac muscle tissue development	1/60	43/23328	0.1049	0.0954	1
BP	GO:0061049	cell growth involved in cardiac muscle cell development	1/60	43/23328	0.1049	0.0954	1
BP	GO:0070232	regulation of T cell apoptotic process	1/60	43/23328	0.1049	0.0954	1

BP	GO:0071825	protein-lipid complex subunit organization	1/60	43/23328	0.1049	0.0954	1
BP	GO:1901381	positive regulation of potassium ion transmembrane transport	1/60	43/23328	0.1049	0.0954	1
BP	GO:1902742	apoptotic process involved in development	1/60	43/23328	0.1049	0.0954	1
BP	GO:0007080	mitotic metaphase plate congression	1/60	44/23328	0.1072	0.0964	1
BP	GO:0010559	regulation of glycoprotein biosynthetic process	1/60	44/23328	0.1072	0.0964	1
BP	GO:0016925	protein sumoylation	1/60	44/23328	0.1072	0.0964	1
BP	GO:0032350	regulation of hormone metabolic process	1/60	44/23328	0.1072	0.0964	1
BP	GO:0033628	regulation of cell adhesion mediated by integrin	1/60	44/23328	0.1072	0.0964	1
BP	GO:0045823	positive regulation of heart contraction	1/60	44/23328	0.1072	0.0964	1
BP	GO:0046621	negative regulation of organ growth	1/60	44/23328	0.1072	0.0964	1
BP	GO:0048854	brain morphogenesis	1/60	44/23328	0.1072	0.0964	1
BP	GO:0050691	regulation of defense response to virus by host	1/60	44/23328	0.1072	0.0964	1
BP	GO:0070849	response to epidermal growth factor	1/60	44/23328	0.1072	0.0964	1
BP	GO:1901998	toxin transport	1/60	44/23328	0.1072	0.0964	1
BP	GO:1903523	negative regulation of blood circulation	1/60	44/23328	0.1072	0.0964	1
BP	GO:0010464	regulation of mesenchymal cell proliferation	1/60	45/23328	0.1095	0.0979	1
BP	GO:0010824	regulation of centrosome duplication	1/60	45/23328	0.1095	0.0979	1
BP	GO:0032873	negative regulation of stress-activated MAPK cascade	1/60	45/23328	0.1095	0.0979	1
BP	GO:0042181	ketone biosynthetic process	1/60	45/23328	0.1095	0.0979	1
BP	GO:0050856	regulation of T cell receptor signaling pathway	1/60	45/23328	0.1095	0.0979	1
BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	1/60	45/23328	0.1095	0.0979	1
BP	GO:1902743	regulation of lamellipodium organization	1/60	45/23328	0.1095	0.0979	1

BP	GO:0010799	regulation of peptidyl-threonine phosphorylation	1/60	46/23328	0.1118	0.0992	1
BP	GO:0019083	viral transcription	1/60	46/23328	0.1118	0.0992	1
BP	GO:0030835	negative regulation of actin filament depolymerization	1/60	46/23328	0.1118	0.0992	1
BP	GO:0043616	keratinocyte proliferation	1/60	46/23328	0.1118	0.0992	1
BP	GO:0045740	positive regulation of DNA replication	1/60	46/23328	0.1118	0.0992	1
BP	GO:0048536	spleen development	1/60	46/23328	0.1118	0.0992	1
BP	GO:0090317	negative regulation of intracellular protein transport	1/60	46/23328	0.1118	0.0992	1
BP	GO:0098926	postsynaptic signal transduction	1/60	46/23328	0.1118	0.0992	1
BP	GO:0001941	postsynaptic membrane organization	1/60	47/23328	0.1141	0.1003	1
BP	GO:0002820	negative regulation of adaptive immune response	1/60	47/23328	0.1141	0.1003	1
BP	GO:0010718	positive regulation of epithelial to mesenchymal transition	1/60	47/23328	0.1141	0.1003	1
BP	GO:0033013	tetrapyrrole metabolic process	1/60	47/23328	0.1141	0.1003	1
BP	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	1/60	47/23328	0.1141	0.1003	1
BP	GO:0043277	apoptotic cell clearance	1/60	47/23328	0.1141	0.1003	1
BP	GO:0045581	negative regulation of T cell differentiation	1/60	47/23328	0.1141	0.1003	1
BP	GO:0046460	neutral lipid biosynthetic process	1/60	47/23328	0.1141	0.1003	1
BP	GO:0046463	acylglycerol biosynthetic process	1/60	47/23328	0.1141	0.1003	1
BP	GO:0051646	mitochondrion localization	1/60	47/23328	0.1141	0.1003	1
BP	GO:0060135	maternal process involved in female pregnancy	1/60	47/23328	0.1141	0.1003	1
BP	GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	1/60	48/23328	0.1164	0.1018	1
BP	GO:0010883	regulation of lipid storage	1/60	48/23328	0.1164	0.1018	1
BP	GO:0032965	regulation of collagen biosynthetic process	1/60	48/23328	0.1164	0.1018	1
BP	GO:0044848	biological phase	1/60	48/23328	0.1164	0.1018	1
BP	GO:0045907	positive regulation of vasoconstriction	1/60	48/23328	0.1164	0.1018	1
BP	GO:0070527	platelet aggregation	1/60	48/23328	0.1164	0.1018	1

BP	GO:1902622	regulation of neutrophil migration	1/60	48/23328	0.1164	0.1018	1
BP	GO:0006692	prostanoid metabolic process	1/60	49/23328	0.1187	0.1031	1
BP	GO:0006693	prostaglandin metabolic process	1/60	49/23328	0.1187	0.1031	1
BP	GO:0010332	response to gamma radiation	1/60	49/23328	0.1187	0.1031	1
BP	GO:0035196	production of miRNAs involved in gene silencing by miRNA	1/60	49/23328	0.1187	0.1031	1
BP	GO:0042755	eating behavior	1/60	49/23328	0.1187	0.1031	1
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	1/60	49/23328	0.1187	0.1031	1
BP	GO:0048255	mRNA stabilization	1/60	49/23328	0.1187	0.1031	1
BP	GO:0090102	cochlea development	1/60	49/23328	0.1187	0.1031	1
BP	GO:1903018	regulation of glycoprotein metabolic process	1/60	49/23328	0.1187	0.1031	1
BP	GO:1905953	negative regulation of lipid localization	1/60	49/23328	0.1187	0.1031	1
BP	GO:2000725	regulation of cardiac muscle cell differentiation	1/60	49/23328	0.1187	0.1031	1
BP	GO:0007032	endosome organization	1/60	50/23328	0.1209	0.1042	1
BP	GO:0007520	myoblast fusion	1/60	50/23328	0.1209	0.1042	1
BP	GO:0008333	endosome to lysosome transport	1/60	50/23328	0.1209	0.1042	1
BP	GO:0032309	icosanoid secretion	1/60	50/23328	0.1209	0.1042	1
BP	GO:0032715	negative regulation of interleukin-6 production	1/60	50/23328	0.1209	0.1042	1
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	1/60	50/23328	0.1209	0.1042	1
BP	GO:0043392	negative regulation of DNA binding	1/60	50/23328	0.1209	0.1042	1
BP	GO:0051438	regulation of ubiquitin-protein transferase activity	1/60	50/23328	0.1209	0.1042	1
BP	GO:0070169	positive regulation of biomineral tissue development	1/60	50/23328	0.1209	0.1042	1
BP	GO:0110151	positive regulation of biomineralization	1/60	50/23328	0.1209	0.1042	1
BP	GO:1903573	negative regulation of response to endoplasmic reticulum stress	1/60	50/23328	0.1209	0.1042	1
BP	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1/60	51/23328	0.1232	0.1051	1
BP	GO:0008089	anterograde axonal transport	1/60	51/23328	0.1232	0.1051	1
BP	GO:0031050	dsRNA processing	1/60	51/23328	0.1232	0.1051	1

BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	1/60	51/23328	0.1232	0.1051	1
BP	GO:0032330	regulation of chondrocyte differentiation	1/60	51/23328	0.1232	0.1051	1
BP	GO:0032722	positive regulation of chemokine production	1/60	51/23328	0.1232	0.1051	1
BP	GO:0042987	amyloid precursor protein catabolic process	1/60	51/23328	0.1232	0.1051	1
BP	GO:0043303	mast cell degranulation	1/60	51/23328	0.1232	0.1051	1
BP	GO:0046189	phenol-containing compound biosynthetic process	1/60	51/23328	0.1232	0.1051	1
BP	GO:0046470	phosphatidylcholine metabolic process	1/60	51/23328	0.1232	0.1051	1
BP	GO:0070918	production of small RNA involved in gene silencing by RNA	1/60	51/23328	0.1232	0.1051	1
BP	GO:0071470	cellular response to osmotic stress	1/60	51/23328	0.1232	0.1051	1
BP	GO:0090311	regulation of protein deacetylation	1/60	51/23328	0.1232	0.1051	1
BP	GO:0002279	mast cell activation involved in immune response	1/60	52/23328	0.1255	0.1062	1
BP	GO:0002448	mast cell mediated immunity	1/60	52/23328	0.1255	0.1062	1
BP	GO:0002639	positive regulation of immunoglobulin production	1/60	52/23328	0.1255	0.1062	1
BP	GO:0009620	response to fungus	1/60	52/23328	0.1255	0.1062	1
BP	GO:0030857	negative regulation of epithelial cell differentiation	1/60	52/23328	0.1255	0.1062	1
BP	GO:0043268	positive regulation of potassium ion transport	1/60	52/23328	0.1255	0.1062	1
BP	GO:0045104	intermediate filament cytoskeleton organization	1/60	52/23328	0.1255	0.1062	1
BP	GO:0045933	positive regulation of muscle contraction	1/60	52/23328	0.1255	0.1062	1
BP	GO:0061014	positive regulation of mRNA catabolic process	1/60	52/23328	0.1255	0.1062	1
BP	GO:0065002	intracellular protein transmembrane transport	1/60	52/23328	0.1255	0.1062	1
BP	GO:0140353	lipid export from cell	1/60	52/23328	0.1255	0.1062	1
BP	GO:1900015	regulation of cytokine production involved in inflammatory response	1/60	52/23328	0.1255	0.1062	1

BP	GO:0001662	behavioral fear response	1/60	53/23328	0.1277	0.1070	1
BP	GO:0001960	negative regulation of cytokine-mediated signaling pathway	1/60	53/23328	0.1277	0.1070	1
BP	GO:0009395	phospholipid catabolic process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0030850	prostate gland development	1/60	53/23328	0.1277	0.1070	1
BP	GO:0032720	negative regulation of tumor necrosis factor production	1/60	53/23328	0.1277	0.1070	1
BP	GO:0034605	cellular response to heat	1/60	53/23328	0.1277	0.1070	1
BP	GO:0044058	regulation of digestive system process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0045103	intermediate filament-based process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0046148	pigment biosynthetic process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0046902	regulation of mitochondrial membrane permeability	1/60	53/23328	0.1277	0.1070	1
BP	GO:0050435	amyloid-beta metabolic process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0051055	negative regulation of lipid biosynthetic process	1/60	53/23328	0.1277	0.1070	1
BP	GO:0051955	regulation of amino acid transport	1/60	53/23328	0.1277	0.1070	1
BP	GO:0061383	trabecula morphogenesis	1/60	53/23328	0.1277	0.1070	1
BP	GO:0002209	behavioral defense response	1/60	54/23328	0.1300	0.1079	1
BP	GO:0010823	negative regulation of mitochondrion organization	1/60	54/23328	0.1300	0.1079	1
BP	GO:0014009	glial cell proliferation	1/60	54/23328	0.1300	0.1079	1
BP	GO:0035272	exocrine system development	1/60	54/23328	0.1300	0.1079	1
BP	GO:0042743	hydrogen peroxide metabolic process	1/60	54/23328	0.1300	0.1079	1
BP	GO:0043300	regulation of leukocyte degranulation	1/60	54/23328	0.1300	0.1079	1
BP	GO:0045687	positive regulation of glial cell differentiation	1/60	54/23328	0.1300	0.1079	1
BP	GO:0048546	digestive tract morphogenesis	1/60	54/23328	0.1300	0.1079	1
BP	GO:0071806	protein transmembrane transport	1/60	54/23328	0.1300	0.1079	1
BP	GO:1902476	chloride transmembrane transport	1/60	54/23328	0.1300	0.1079	1
BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	1/60	54/23328	0.1300	0.1079	1

BP	GO:1904705	regulation of vascular associated smooth muscle cell proliferation	1/60	54/23328	0.1300	0.1079	1
BP	GO:1990874	vascular associated smooth muscle cell proliferation	1/60	54/23328	0.1300	0.1079	1
BP	GO:2000649	regulation of sodium ion transmembrane transporter activity	1/60	54/23328	0.1300	0.1079	1
BP	GO:0002534	cytokine production involved in inflammatory response	1/60	55/23328	0.1322	0.1091	1
BP	GO:0002720	positive regulation of cytokine production involved in immune response	1/60	55/23328	0.1322	0.1091	1
BP	GO:0010712	regulation of collagen metabolic process	1/60	55/23328	0.1322	0.1091	1
BP	GO:0030834	regulation of actin filament depolymerization	1/60	55/23328	0.1322	0.1091	1
BP	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	1/60	55/23328	0.1322	0.1091	1
BP	GO:0045604	regulation of epidermal cell differentiation	1/60	55/23328	0.1322	0.1091	1
BP	GO:0050891	multicellular organismal water homeostasis	1/60	55/23328	0.1322	0.1091	1
BP	GO:0002704	negative regulation of leukocyte mediated immunity	1/60	56/23328	0.1344	0.1100	1
BP	GO:0021587	cerebellum morphogenesis	1/60	56/23328	0.1344	0.1100	1
BP	GO:0043647	inositol phosphate metabolic process	1/60	56/23328	0.1344	0.1100	1
BP	GO:0045620	negative regulation of lymphocyte differentiation	1/60	56/23328	0.1344	0.1100	1
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	1/60	56/23328	0.1344	0.1100	1
BP	GO:0050873	brown fat cell differentiation	1/60	56/23328	0.1344	0.1100	1
BP	GO:0051568	histone H3-K4 methylation	1/60	56/23328	0.1344	0.1100	1
BP	GO:0070265	necrotic cell death	1/60	56/23328	0.1344	0.1100	1
BP	GO:0098586	cellular response to virus	1/60	56/23328	0.1344	0.1100	1
BP	GO:0098815	modulation of excitatory postsynaptic potential	1/60	56/23328	0.1344	0.1100	1
BP	GO:1900449	regulation of glutamate receptor signaling pathway	1/60	56/23328	0.1344	0.1100	1
BP	GO:1903350	response to dopamine	1/60	56/23328	0.1344	0.1100	1

BP	GO:1903351	cellular response to dopamine	1/60	56/23328	0.1344	0.1100	1
BP	GO:0002067	glandular epithelial cell differentiation	1/60	57/23328	0.1367	0.1108	1
BP	GO:0010463	mesenchymal cell proliferation	1/60	57/23328	0.1367	0.1108	1
BP	GO:0019748	secondary metabolic process	1/60	57/23328	0.1367	0.1108	1
BP	GO:0032964	collagen biosynthetic process	1/60	57/23328	0.1367	0.1108	1
BP	GO:0033003	regulation of mast cell activation	1/60	57/23328	0.1367	0.1108	1
BP	GO:0043030	regulation of macrophage activation	1/60	57/23328	0.1367	0.1108	1
BP	GO:0043489	RNA stabilization	1/60	57/23328	0.1367	0.1108	1
BP	GO:0045058	T cell selection	1/60	57/23328	0.1367	0.1108	1
BP	GO:0060761	negative regulation of response to cytokine stimulus	1/60	57/23328	0.1367	0.1108	1
BP	GO:0071622	regulation of granulocyte chemotaxis	1/60	57/23328	0.1367	0.1108	1
BP	GO:1902373	negative regulation of mRNA catabolic process	1/60	57/23328	0.1367	0.1108	1
BP	GO:2000648	positive regulation of stem cell proliferation	1/60	57/23328	0.1367	0.1108	1
BP	GO:0001755	neural crest cell migration	1/60	58/23328	0.1389	0.1122	1
BP	GO:0010656	negative regulation of muscle cell apoptotic process	1/60	58/23328	0.1389	0.1122	1
BP	GO:0032653	regulation of interleukin-10 production	1/60	58/23328	0.1389	0.1122	1
BP	GO:0032655	regulation of interleukin-12 production	1/60	58/23328	0.1389	0.1122	1
BP	GO:0042596	fear response	1/60	58/23328	0.1389	0.1122	1
BP	GO:0045071	negative regulation of viral genome replication	1/60	58/23328	0.1389	0.1122	1
BP	GO:0002011	morphogenesis of an epithelial sheet	1/60	59/23328	0.1411	0.1138	1
BP	GO:0007164	establishment of tissue polarity	1/60	59/23328	0.1411	0.1138	1
BP	GO:0030042	actin filament depolymerization	1/60	59/23328	0.1411	0.1138	1
BP	GO:0021517	ventral spinal cord development	1/60	60/23328	0.1433	0.1147	1
BP	GO:0021575	hindbrain morphogenesis	1/60	60/23328	0.1433	0.1147	1
BP	GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	1/60	60/23328	0.1433	0.1147	1
BP	GO:0046605	regulation of centrosome cycle	1/60	60/23328	0.1433	0.1147	1
BP	GO:0051310	metaphase plate congression	1/60	60/23328	0.1433	0.1147	1

BP	GO:0070098	chemokine-mediated signaling pathway	1/60	60/23328	0.1433	0.1147	1
BP	GO:0070231	T cell apoptotic process	1/60	60/23328	0.1433	0.1147	1
BP	GO:1901016	regulation of potassium ion transmembrane transporter activity	1/60	60/23328	0.1433	0.1147	1
BP	GO:1901616	organic hydroxy compound catabolic process	1/60	60/23328	0.1433	0.1147	1
BP	GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	1/60	60/23328	0.1433	0.1147	1
BP	GO:0006446	regulation of translational initiation	1/60	61/23328	0.1456	0.1160	1
BP	GO:0032615	interleukin-12 production	1/60	61/23328	0.1456	0.1160	1
BP	GO:0045824	negative regulation of innate immune response	1/60	61/23328	0.1456	0.1160	1
BP	GO:0048286	lung alveolus development	1/60	61/23328	0.1456	0.1160	1
BP	GO:0051851	modulation by host of symbiont process	1/60	61/23328	0.1456	0.1160	1
BP	GO:0006081	cellular aldehyde metabolic process	1/60	62/23328	0.1478	0.1168	1
BP	GO:0006900	vesicle budding from membrane	1/60	62/23328	0.1478	0.1168	1
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	1/60	62/23328	0.1478	0.1168	1
BP	GO:0031640	killing of cells of other organism	1/60	62/23328	0.1478	0.1168	1
BP	GO:0032613	interleukin-10 production	1/60	62/23328	0.1478	0.1168	1
BP	GO:0046513	ceramide biosynthetic process	1/60	62/23328	0.1478	0.1168	1
BP	GO:0048512	circadian behavior	1/60	62/23328	0.1478	0.1168	1
BP	GO:0050854	regulation of antigen receptor-mediated signaling pathway	1/60	62/23328	0.1478	0.1168	1
BP	GO:0051148	negative regulation of muscle cell differentiation	1/60	62/23328	0.1478	0.1168	1
BP	GO:0051926	negative regulation of calcium ion transport	1/60	62/23328	0.1478	0.1168	1
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	1/60	62/23328	0.1478	0.1168	1
BP	GO:1903078	positive regulation of protein localization to plasma membrane	1/60	62/23328	0.1478	0.1168	1
BP	GO:1905207	regulation of cardiocyte differentiation	1/60	62/23328	0.1478	0.1168	1

BP	GO:0001947	heart looping	1/60	63/23328	0.1500	0.1182	1
BP	GO:0010830	regulation of myotube differentiation	1/60	63/23328	0.1500	0.1182	1
BP	GO:0030104	water homeostasis	1/60	63/23328	0.1500	0.1182	1
BP	GO:0050994	regulation of lipid catabolic process	1/60	63/23328	0.1500	0.1182	1
BP	GO:0070936	protein K48-linked ubiquitination	1/60	63/23328	0.1500	0.1182	1
BP	GO:0071479	cellular response to ionizing radiation	1/60	63/23328	0.1500	0.1182	1
BP	GO:0001658	branching involved in ureteric bud morphogenesis	1/60	64/23328	0.1521	0.1194	1
BP	GO:0007622	rhythmic behavior	1/60	64/23328	0.1521	0.1194	1
BP	GO:0046173	polyol biosynthetic process	1/60	64/23328	0.1521	0.1194	1
BP	GO:0050707	regulation of cytokine secretion	1/60	64/23328	0.1521	0.1194	1
BP	GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	1/60	64/23328	0.1521	0.1194	1
BP	GO:1902305	regulation of sodium ion transmembrane transport	1/60	64/23328	0.1521	0.1194	1
BP	GO:1903510	mucopolysaccharide metabolic process	1/60	64/23328	0.1521	0.1194	1
BP	GO:0034121	regulation of toll-like receptor signaling pathway	1/60	65/23328	0.1543	0.1207	1
BP	GO:0042093	T-helper cell differentiation	1/60	65/23328	0.1543	0.1207	1
BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	1/60	65/23328	0.1543	0.1207	1
BP	GO:0098840	protein transport along microtubule	1/60	65/23328	0.1543	0.1207	1
BP	GO:0099118	microtubule-based protein transport	1/60	65/23328	0.1543	0.1207	1
BP	GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	1/60	66/23328	0.1565	0.1221	1
BP	GO:0042982	amyloid precursor protein metabolic process	1/60	66/23328	0.1565	0.1221	1
BP	GO:0070972	protein localization to endoplasmic reticulum	1/60	66/23328	0.1565	0.1221	1
BP	GO:0002293	alpha-beta T cell differentiation involved in immune response	1/60	67/23328	0.1587	0.1231	1
BP	GO:0006940	regulation of smooth muscle contraction	1/60	67/23328	0.1587	0.1231	1

BP	GO:0021695	cerebellar cortex development	1/60	67/23328	0.1587	0.1231	1
BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	1/60	67/23328	0.1587	0.1231	1
BP	GO:0051298	centrosome duplication	1/60	67/23328	0.1587	0.1231	1
BP	GO:0070613	regulation of protein processing	1/60	67/23328	0.1587	0.1231	1
BP	GO:0090307	mitotic spindle assembly	1/60	67/23328	0.1587	0.1231	1
BP	GO:0002287	alpha-beta T cell activation involved in immune response	1/60	68/23328	0.1609	0.1239	1
BP	GO:0007566	embryo implantation	1/60	68/23328	0.1609	0.1239	1
BP	GO:0015800	acidic amino acid transport	1/60	68/23328	0.1609	0.1239	1
BP	GO:0030837	negative regulation of actin filament polymerization	1/60	68/23328	0.1609	0.1239	1
BP	GO:0032507	maintenance of protein location in cell	1/60	68/23328	0.1609	0.1239	1
BP	GO:0046635	positive regulation of alpha-beta T cell activation	1/60	68/23328	0.1609	0.1239	1
BP	GO:0046637	regulation of alpha-beta T cell differentiation	1/60	68/23328	0.1609	0.1239	1
BP	GO:0050771	negative regulation of axonogenesis	1/60	68/23328	0.1609	0.1239	1
BP	GO:0071868	cellular response to monoamine stimulus	1/60	68/23328	0.1609	0.1239	1
BP	GO:0071870	cellular response to catecholamine stimulus	1/60	68/23328	0.1609	0.1239	1
BP	GO:0097194	execution phase of apoptosis	1/60	68/23328	0.1609	0.1239	1
BP	GO:0099601	regulation of neurotransmitter receptor activity	1/60	68/23328	0.1609	0.1239	1
BP	GO:1901264	carbohydrate derivative transport	1/60	68/23328	0.1609	0.1239	1
BP	GO:1902369	negative regulation of RNA catabolic process	1/60	68/23328	0.1609	0.1239	1
BP	GO:0000281	mitotic cytokinesis	1/60	69/23328	0.1630	0.1248	1
BP	GO:0006801	superoxide metabolic process	1/60	69/23328	0.1630	0.1248	1
BP	GO:0021536	diencephalon development	1/60	69/23328	0.1630	0.1248	1
BP	GO:0033627	cell adhesion mediated by integrin	1/60	69/23328	0.1630	0.1248	1
BP	GO:0061371	determination of heart left/right asymmetry	1/60	69/23328	0.1630	0.1248	1
BP	GO:0071867	response to monoamine	1/60	69/23328	0.1630	0.1248	1
BP	GO:0071869	response to catecholamine	1/60	69/23328	0.1630	0.1248	1
BP	GO:1904377	positive regulation of protein localization to cell periphery	1/60	69/23328	0.1630	0.1248	1

BP	GO:0003143	embryonic heart tube morphogenesis	1/60	70/23328	0.1652	0.1259	1
BP	GO:0006766	vitamin metabolic process	1/60	70/23328	0.1652	0.1259	1
BP	GO:0007405	neuroblast proliferation	1/60	70/23328	0.1652	0.1259	1
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	1/60	70/23328	0.1652	0.1259	1
BP	GO:0045669	positive regulation of osteoblast differentiation	1/60	70/23328	0.1652	0.1259	1
BP	GO:0150076	neuroinflammatory response	1/60	70/23328	0.1652	0.1259	1
BP	GO:1903317	regulation of protein maturation	1/60	70/23328	0.1652	0.1259	1
BP	GO:2000179	positive regulation of neural precursor cell proliferation	1/60	70/23328	0.1652	0.1259	1
BP	GO:0006635	fatty acid beta-oxidation	1/60	71/23328	0.1673	0.1271	1
BP	GO:0007492	endoderm development	1/60	71/23328	0.1673	0.1271	1
BP	GO:0043113	receptor clustering	1/60	71/23328	0.1673	0.1271	1
BP	GO:0043407	negative regulation of MAP kinase activity	1/60	71/23328	0.1673	0.1271	1
BP	GO:0060675	ureteric bud morphogenesis	1/60	71/23328	0.1673	0.1271	1
BP	GO:0061035	regulation of cartilage development	1/60	71/23328	0.1673	0.1271	1
BP	GO:1901796	regulation of signal transduction by p53 class mediator	1/60	71/23328	0.1673	0.1271	1
BP	GO:0010611	regulation of cardiac muscle hypertrophy	1/60	72/23328	0.1695	0.1285	1
BP	GO:0072171	mesonephric tubule morphogenesis	1/60	72/23328	0.1695	0.1285	1
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	1/60	72/23328	0.1695	0.1285	1
BP	GO:0002711	positive regulation of T cell mediated immunity	1/60	73/23328	0.1716	0.1298	1
BP	GO:0002886	regulation of myeloid leukocyte mediated immunity	1/60	73/23328	0.1716	0.1298	1
BP	GO:0042130	negative regulation of T cell proliferation	1/60	73/23328	0.1716	0.1298	1
BP	GO:0043627	response to estrogen	1/60	73/23328	0.1716	0.1298	1
BP	GO:0051155	positive regulation of striated muscle cell differentiation	1/60	73/23328	0.1716	0.1298	1
BP	GO:0002292	T cell differentiation involved in immune response	1/60	74/23328	0.1738	0.1310	1

BP	GO:0007029	endoplasmic reticulum organization	1/60	74/23328	0.1738	0.1310	1
BP	GO:0007422	peripheral nervous system development	1/60	74/23328	0.1738	0.1310	1
BP	GO:0043299	leukocyte degranulation	1/60	74/23328	0.1738	0.1310	1
BP	GO:2001021	negative regulation of response to DNA damage stimulus	1/60	74/23328	0.1738	0.1310	1
BP	GO:0014743	regulation of muscle hypertrophy	1/60	75/23328	0.1759	0.1319	1
BP	GO:0032642	regulation of chemokine production	1/60	75/23328	0.1759	0.1319	1
BP	GO:0034109	homotypic cell-cell adhesion	1/60	75/23328	0.1759	0.1319	1
BP	GO:0046626	regulation of insulin receptor signaling pathway	1/60	75/23328	0.1759	0.1319	1
BP	GO:0051145	smooth muscle cell differentiation	1/60	75/23328	0.1759	0.1319	1
BP	GO:0097755	positive regulation of blood vessel diameter	1/60	75/23328	0.1759	0.1319	1
BP	GO:0098661	inorganic anion transmembrane transport	1/60	75/23328	0.1759	0.1319	1
BP	GO:1903725	regulation of phospholipid metabolic process	1/60	75/23328	0.1759	0.1319	1
BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	1/60	76/23328	0.1780	0.1331	1
BP	GO:0045576	mast cell activation	1/60	76/23328	0.1780	0.1331	1
BP	GO:0050663	cytokine secretion	1/60	76/23328	0.1780	0.1331	1
BP	GO:0051865	protein autoubiquitination	1/60	76/23328	0.1780	0.1331	1
BP	GO:1901606	alpha-amino acid catabolic process	1/60	76/23328	0.1780	0.1331	1
BP	GO:0010822	positive regulation of mitochondrion organization	1/60	77/23328	0.1801	0.1343	1
BP	GO:0016575	histone deacetylation	1/60	77/23328	0.1801	0.1343	1
BP	GO:0030433	ubiquitin-dependent ERAD pathway	1/60	77/23328	0.1801	0.1343	1
BP	GO:0045843	negative regulation of striated muscle tissue development	1/60	77/23328	0.1801	0.1343	1
BP	GO:0071277	cellular response to calcium ion	1/60	77/23328	0.1801	0.1343	1
BP	GO:1901224	positive regulation of NIK/NF-kappaB signaling	1/60	77/23328	0.1801	0.1343	1
BP	GO:0003208	cardiac ventricle morphogenesis	1/60	78/23328	0.1823	0.1354	1

BP	GO:0032088	negative regulation of NF-kappaB transcription factor activity	1/60	78/23328	0.1823	0.1354	1
BP	GO:0050000	chromosome localization	1/60	78/23328	0.1823	0.1354	1
BP	GO:0051303	establishment of chromosome localization	1/60	78/23328	0.1823	0.1354	1
BP	GO:0061180	mammary gland epithelium development	1/60	78/23328	0.1823	0.1354	1
BP	GO:0032418	lysosome localization	1/60	79/23328	0.1844	0.1364	1
BP	GO:0032602	chemokine production	1/60	79/23328	0.1844	0.1364	1
BP	GO:0034644	cellular response to UV	1/60	79/23328	0.1844	0.1364	1
BP	GO:0045471	response to ethanol	1/60	79/23328	0.1844	0.1364	1
BP	GO:0051966	regulation of synaptic transmission, glutamatergic	1/60	79/23328	0.1844	0.1364	1
BP	GO:0055021	regulation of cardiac muscle tissue growth	1/60	79/23328	0.1844	0.1364	1
BP	GO:0032729	positive regulation of interferon-gamma production	1/60	80/23328	0.1865	0.1375	1
BP	GO:0050688	regulation of defense response to virus	1/60	80/23328	0.1865	0.1375	1
BP	GO:0072078	nephron tubule morphogenesis	1/60	80/23328	0.1865	0.1375	1
BP	GO:1901862	negative regulation of muscle tissue development	1/60	80/23328	0.1865	0.1375	1
BP	GO:1901880	negative regulation of protein depolymerization	1/60	80/23328	0.1865	0.1375	1
BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	1/60	80/23328	0.1865	0.1375	1
BP	GO:0045682	regulation of epidermis development	1/60	81/23328	0.1886	0.1390	1
BP	GO:0019915	lipid storage	1/60	82/23328	0.1907	0.1401	1
BP	GO:0030193	regulation of blood coagulation	1/60	82/23328	0.1907	0.1401	1
BP	GO:0050805	negative regulation of synaptic transmission	1/60	82/23328	0.1907	0.1401	1
BP	GO:0051262	protein tetramerization	1/60	82/23328	0.1907	0.1401	1
BP	GO:0072088	nephron epithelium morphogenesis	1/60	82/23328	0.1907	0.1401	1
BP	GO:0002532	production of molecular mediator involved in inflammatory response	1/60	83/23328	0.1928	0.1410	1
BP	GO:0030168	platelet activation	1/60	83/23328	0.1928	0.1410	1
BP	GO:0032272	negative regulation of protein polymerization	1/60	83/23328	0.1928	0.1410	1

BP	GO:0044106	cellular amine metabolic process	1/60	83/23328	0.1928	0.1410	1
BP	GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	1/60	83/23328	0.1928	0.1410	1
BP	GO:0072384	organelle transport along microtubule	1/60	83/23328	0.1928	0.1410	1
BP	GO:1900046	regulation of hemostasis	1/60	83/23328	0.1928	0.1410	1
BP	GO:1903901	negative regulation of viral life cycle	1/60	83/23328	0.1928	0.1410	1
BP	GO:0003151	outflow tract morphogenesis	1/60	84/23328	0.1948	0.1422	1
BP	GO:0014032	neural crest cell development	1/60	84/23328	0.1948	0.1422	1
BP	GO:0030148	sphingolipid biosynthetic process	1/60	84/23328	0.1948	0.1422	1
BP	GO:0050766	positive regulation of phagocytosis	1/60	84/23328	0.1948	0.1422	1
BP	GO:0072028	nephron morphogenesis	1/60	84/23328	0.1948	0.1422	1
BP	GO:0006835	dicarboxylic acid transport	1/60	85/23328	0.1969	0.1433	1
BP	GO:0030203	glycosaminoglycan metabolic process	1/60	85/23328	0.1969	0.1433	1
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	1/60	85/23328	0.1969	0.1433	1
BP	GO:0006970	response to osmotic stress	1/60	86/23328	0.1990	0.1441	1
BP	GO:0035050	embryonic heart tube development	1/60	86/23328	0.1990	0.1441	1
BP	GO:0048708	astrocyte differentiation	1/60	86/23328	0.1990	0.1441	1
BP	GO:0050818	regulation of coagulation	1/60	86/23328	0.1990	0.1441	1
BP	GO:0061333	renal tubule morphogenesis	1/60	86/23328	0.1990	0.1441	1
BP	GO:0097581	lamellipodium organization	1/60	86/23328	0.1990	0.1441	1
BP	GO:1905897	regulation of response to endoplasmic reticulum stress	1/60	86/23328	0.1990	0.1441	1
BP	GO:0060420	regulation of heart growth	1/60	87/23328	0.2011	0.1456	1
BP	GO:0006112	energy reserve metabolic process	1/60	88/23328	0.2031	0.1465	1
BP	GO:0010827	regulation of glucose transmembrane transport	1/60	88/23328	0.2031	0.1465	1
BP	GO:0035914	skeletal muscle cell differentiation	1/60	88/23328	0.2031	0.1465	1
BP	GO:0050672	negative regulation of lymphocyte proliferation	1/60	88/23328	0.2031	0.1465	1
BP	GO:0060079	excitatory postsynaptic potential	1/60	88/23328	0.2031	0.1465	1

BP	GO:0062207	regulation of pattern recognition receptor signaling pathway	1/60	88/23328	0.2031	0.1465	1
BP	GO:1903312	negative regulation of mRNA metabolic process	1/60	88/23328	0.2031	0.1465	1
BP	GO:0014031	mesenchymal cell development	1/60	89/23328	0.2052	0.1476	1
BP	GO:0032945	negative regulation of mononuclear cell proliferation	1/60	89/23328	0.2052	0.1476	1
BP	GO:0042770	signal transduction in response to DNA damage	1/60	89/23328	0.2052	0.1476	1
BP	GO:0051149	positive regulation of muscle cell differentiation	1/60	89/23328	0.2052	0.1476	1
BP	GO:0051702	interaction with symbiont	1/60	89/23328	0.2052	0.1476	1
BP	GO:0006672	ceramide metabolic process	1/60	90/23328	0.2072	0.1485	1
BP	GO:0009063	cellular amino acid catabolic process	1/60	90/23328	0.2072	0.1485	1
BP	GO:0019226	transmission of nerve impulse	1/60	90/23328	0.2072	0.1485	1
BP	GO:0043242	negative regulation of protein-containing complex disassembly	1/60	90/23328	0.2072	0.1485	1
BP	GO:0046888	negative regulation of hormone secretion	1/60	90/23328	0.2072	0.1485	1
BP	GO:0048864	stem cell development	1/60	90/23328	0.2072	0.1485	1
BP	GO:1900076	regulation of cellular response to insulin stimulus	1/60	90/23328	0.2072	0.1485	1
BP	GO:0001938	positive regulation of endothelial cell proliferation	1/60	91/23328	0.2093	0.1495	1
BP	GO:0002088	lens development in camera-type eye	1/60	91/23328	0.2093	0.1495	1
BP	GO:0014033	neural crest cell differentiation	1/60	91/23328	0.2093	0.1495	1
BP	GO:0040014	regulation of multicellular organism growth	1/60	91/23328	0.2093	0.1495	1
BP	GO:0042632	cholesterol homeostasis	1/60	91/23328	0.2093	0.1495	1
BP	GO:0072091	regulation of stem cell proliferation	1/60	91/23328	0.2093	0.1495	1
BP	GO:0000045	autophagosome assembly	1/60	92/23328	0.2113	0.1504	1
BP	GO:0002275	myeloid cell activation involved in immune response	1/60	92/23328	0.2113	0.1504	1
BP	GO:0002832	negative regulation of response to biotic stimulus	1/60	92/23328	0.2113	0.1504	1
BP	GO:0035773	insulin secretion involved in cellular response to glucose stimulus	1/60	92/23328	0.2113	0.1504	1

BP	GO:0045685	regulation of glial cell differentiation	1/60	92/23328	0.2113	0.1504	1
BP	GO:0055092	sterol homeostasis	1/60	92/23328	0.2113	0.1504	1
BP	GO:0002028	regulation of sodium ion transport	1/60	93/23328	0.2134	0.1516	1
BP	GO:0007215	glutamate receptor signaling pathway	1/60	93/23328	0.2134	0.1516	1
BP	GO:0009308	amine metabolic process	1/60	93/23328	0.2134	0.1516	1
BP	GO:0033077	T cell differentiation in thymus	1/60	93/23328	0.2134	0.1516	1
BP	GO:0010717	regulation of epithelial to mesenchymal transition	1/60	94/23328	0.2154	0.1526	1
BP	GO:0061640	cytoskeleton-dependent cytokinesis	1/60	94/23328	0.2154	0.1526	1
BP	GO:0070664	negative regulation of leukocyte proliferation	1/60	94/23328	0.2154	0.1526	1
BP	GO:1901879	regulation of protein depolymerization	1/60	94/23328	0.2154	0.1526	1
BP	GO:1903313	positive regulation of mRNA metabolic process	1/60	94/23328	0.2154	0.1526	1
BP	GO:0002251	organ or tissue specific immune response	1/60	95/23328	0.2174	0.1539	1
BP	GO:0055013	cardiac muscle cell development	1/60	95/23328	0.2174	0.1539	1
BP	GO:0002690	positive regulation of leukocyte chemotaxis	1/60	96/23328	0.2194	0.1551	1
BP	GO:0030838	positive regulation of actin filament polymerization	1/60	96/23328	0.2194	0.1551	1
BP	GO:0045638	negative regulation of myeloid cell differentiation	1/60	96/23328	0.2194	0.1551	1
BP	GO:0002027	regulation of heart rate	1/60	97/23328	0.2215	0.1562	1
BP	GO:0010660	regulation of muscle cell apoptotic process	1/60	97/23328	0.2215	0.1562	1
BP	GO:0045069	regulation of viral genome replication	1/60	97/23328	0.2215	0.1562	1
BP	GO:1905037	autophagosome organization	1/60	97/23328	0.2215	0.1562	1
BP	GO:0030279	negative regulation of ossification	1/60	98/23328	0.2235	0.1572	1
BP	GO:0045833	negative regulation of lipid metabolic process	1/60	98/23328	0.2235	0.1572	1
BP	GO:0071482	cellular response to light stimulus	1/60	98/23328	0.2235	0.1572	1
BP	GO:0072080	nephron tubule development	1/60	98/23328	0.2235	0.1572	1

BP	GO:0099565	chemical synaptic transmission, postsynaptic	1/60	98/23328	0.2235	0.1572	1
BP	GO:0006805	xenobiotic metabolic process	1/60	99/23328	0.2255	0.1583	1
BP	GO:0036503	ERAD pathway	1/60	99/23328	0.2255	0.1583	1
BP	GO:0043502	regulation of muscle adaptation	1/60	99/23328	0.2255	0.1583	1
BP	GO:0045185	maintenance of protein location	1/60	99/23328	0.2255	0.1583	1
BP	GO:0006476	protein deacetylation	1/60	100/23328	0.2275	0.1593	1
BP	GO:0010771	negative regulation of cell morphogenesis involved in differentiation	1/60	100/23328	0.2275	0.1593	1
BP	GO:0042102	positive regulation of T cell proliferation	1/60	100/23328	0.2275	0.1593	1
BP	GO:0042116	macrophage activation	1/60	100/23328	0.2275	0.1593	1
BP	GO:0009062	fatty acid catabolic process	1/60	101/23328	0.2295	0.1600	1
BP	GO:0031058	positive regulation of histone modification	1/60	101/23328	0.2295	0.1600	1
BP	GO:0032092	positive regulation of protein binding	1/60	101/23328	0.2295	0.1600	1
BP	GO:0032755	positive regulation of interleukin-6 production	1/60	101/23328	0.2295	0.1600	1
BP	GO:0033555	multicellular organismal response to stress	1/60	101/23328	0.2295	0.1600	1
BP	GO:0055006	cardiac cell development	1/60	101/23328	0.2295	0.1600	1
BP	GO:0060993	kidney morphogenesis	1/60	101/23328	0.2295	0.1600	1
BP	GO:0001704	formation of primary germ layer	1/60	102/23328	0.2315	0.1610	1
BP	GO:0007006	mitochondrial membrane organization	1/60	102/23328	0.2315	0.1610	1
BP	GO:0010657	muscle cell apoptotic process	1/60	102/23328	0.2315	0.1610	1
BP	GO:0035418	protein localization to synapse	1/60	102/23328	0.2315	0.1610	1
BP	GO:0045582	positive regulation of T cell differentiation	1/60	102/23328	0.2315	0.1610	1
BP	GO:0003300	cardiac muscle hypertrophy	1/60	103/23328	0.2334	0.1621	1
BP	GO:0006821	chloride transport	1/60	103/23328	0.2334	0.1621	1
BP	GO:0055024	regulation of cardiac muscle tissue development	1/60	103/23328	0.2334	0.1621	1
BP	GO:0071466	cellular response to xenobiotic stimulus	1/60	103/23328	0.2334	0.1621	1
BP	GO:0001657	ureteric bud development	1/60	104/23328	0.2354	0.1627	1
BP	GO:0006413	translational initiation	1/60	104/23328	0.2354	0.1627	1
BP	GO:0043488	regulation of mRNA stability	1/60	104/23328	0.2354	0.1627	1
BP	GO:0061326	renal tubule development	1/60	104/23328	0.2354	0.1627	1

BP	GO:0072163	mesonephric epithelium development	1/60	104/23328	0.2354	0.1627	1
BP	GO:0072164	mesonephric tubule development	1/60	104/23328	0.2354	0.1627	1
BP	GO:1901222	regulation of NIK/NF-kappaB signaling	1/60	104/23328	0.2354	0.1627	1
BP	GO:1902106	negative regulation of leukocyte differentiation	1/60	104/23328	0.2354	0.1627	1
BP	GO:0000077	DNA damage checkpoint	1/60	105/23328	0.2374	0.1639	1
BP	GO:0002444	myeloid leukocyte mediated immunity	1/60	105/23328	0.2374	0.1639	1
BP	GO:0006022	aminoglycan metabolic process	1/60	106/23328	0.2394	0.1650	1
BP	GO:0021510	spinal cord development	1/60	106/23328	0.2394	0.1650	1
BP	GO:0110110	positive regulation of animal organ morphogenesis	1/60	106/23328	0.2394	0.1650	1
BP	GO:0001823	mesonephros development	1/60	107/23328	0.2413	0.1658	1
BP	GO:0014897	striated muscle hypertrophy	1/60	107/23328	0.2413	0.1658	1
BP	GO:0019395	fatty acid oxidation	1/60	107/23328	0.2413	0.1658	1
BP	GO:0050709	negative regulation of protein secretion	1/60	107/23328	0.2413	0.1658	1
BP	GO:0090174	organelle membrane fusion	1/60	107/23328	0.2413	0.1658	1
BP	GO:0000956	nuclear-transcribed mRNA catabolic process	1/60	108/23328	0.2433	0.1665	1
BP	GO:0002224	toll-like receptor signaling pathway	1/60	108/23328	0.2433	0.1665	1
BP	GO:0006641	triglyceride metabolic process	1/60	108/23328	0.2433	0.1665	1
BP	GO:0021987	cerebral cortex development	1/60	108/23328	0.2433	0.1665	1
BP	GO:0045446	endothelial cell differentiation	1/60	108/23328	0.2433	0.1665	1
BP	GO:0045639	positive regulation of myeloid cell differentiation	1/60	108/23328	0.2433	0.1665	1
BP	GO:0048704	embryonic skeletal system morphogenesis	1/60	108/23328	0.2433	0.1665	1
BP	GO:0055017	cardiac muscle tissue growth	1/60	108/23328	0.2433	0.1665	1
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	1/60	109/23328	0.2452	0.1671	1
BP	GO:0002062	chondrocyte differentiation	1/60	109/23328	0.2452	0.1671	1
BP	GO:0002702	positive regulation of production of molecular mediator of immune response	1/60	109/23328	0.2452	0.1671	1
BP	GO:0014896	muscle hypertrophy	1/60	109/23328	0.2452	0.1671	1
BP	GO:0021549	cerebellum development	1/60	109/23328	0.2452	0.1671	1

BP	GO:0035249	synaptic transmission, glutamatergic	1/60	109/23328	0.2452	0.1671	1
BP	GO:0051028	mRNA transport	1/60	109/23328	0.2452	0.1671	1
BP	GO:0051668	localization within membrane	1/60	109/23328	0.2452	0.1671	1
BP	GO:1900006	positive regulation of dendrite development	1/60	109/23328	0.2452	0.1671	1
BP	GO:1905477	positive regulation of protein localization to membrane	1/60	109/23328	0.2452	0.1671	1
BP	GO:0006275	regulation of DNA replication	1/60	110/23328	0.2472	0.1682	1
BP	GO:0038061	NIK/NF-kappaB signaling	1/60	110/23328	0.2472	0.1682	1
BP	GO:0035601	protein deacylation	1/60	111/23328	0.2491	0.1693	1
BP	GO:0072009	nephron epithelium development	1/60	111/23328	0.2491	0.1693	1
BP	GO:0098732	macromolecule deacylation	1/60	111/23328	0.2491	0.1693	1
BP	GO:0007009	plasma membrane organization	1/60	112/23328	0.2511	0.1705	1
BP	GO:0051225	spindle assembly	1/60	112/23328	0.2511	0.1705	1
BP	GO:0031570	DNA integrity checkpoint	1/60	113/23328	0.2530	0.1717	1
BP	GO:0001892	embryonic placenta development	1/60	114/23328	0.2549	0.1724	1
BP	GO:0006939	smooth muscle contraction	1/60	114/23328	0.2549	0.1724	1
BP	GO:0032649	regulation of interferon-gamma production	1/60	114/23328	0.2549	0.1724	1
BP	GO:0060078	regulation of postsynaptic membrane potential	1/60	114/23328	0.2549	0.1724	1
BP	GO:0071346	cellular response to interferon-gamma	1/60	114/23328	0.2549	0.1724	1
BP	GO:1903076	regulation of protein localization to plasma membrane	1/60	114/23328	0.2549	0.1724	1
BP	GO:0016579	protein deubiquitination	1/60	115/23328	0.2569	0.1734	1
BP	GO:0019079	viral genome replication	1/60	115/23328	0.2569	0.1734	1
BP	GO:0019751	polyol metabolic process	1/60	115/23328	0.2569	0.1734	1
BP	GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	1/60	115/23328	0.2569	0.1734	1
BP	GO:0002792	negative regulation of peptide secretion	1/60	116/23328	0.2588	0.1742	1
BP	GO:0007052	mitotic spindle organization	1/60	116/23328	0.2588	0.1742	1
BP	GO:0034968	histone lysine methylation	1/60	116/23328	0.2588	0.1742	1
BP	GO:0042472	inner ear morphogenesis	1/60	116/23328	0.2588	0.1742	1
BP	GO:0043487	regulation of RNA stability	1/60	116/23328	0.2588	0.1742	1

BP	GO:0051952	regulation of amine transport	1/60	116/23328	0.2588	0.1742	1
BP	GO:0006612	protein targeting to membrane	1/60	117/23328	0.2607	0.1751	1
BP	GO:0045621	positive regulation of lymphocyte differentiation	1/60	117/23328	0.2607	0.1751	1
BP	GO:1905269	positive regulation of chromatin organization	1/60	117/23328	0.2607	0.1751	1
BP	GO:0014020	primary neural tube formation	1/60	118/23328	0.2626	0.1758	1
BP	GO:0018107	peptidyl-threonine phosphorylation	1/60	118/23328	0.2626	0.1758	1
BP	GO:0021782	glial cell development	1/60	118/23328	0.2626	0.1758	1
BP	GO:0046632	alpha-beta T cell differentiation	1/60	118/23328	0.2626	0.1758	1
BP	GO:0060419	heart growth	1/60	118/23328	0.2626	0.1758	1
BP	GO:2000177	regulation of neural precursor cell proliferation	1/60	118/23328	0.2626	0.1758	1
BP	GO:0000187	activation of MAPK activity	1/60	119/23328	0.2645	0.1768	1
BP	GO:0060759	regulation of response to cytokine stimulus	1/60	119/23328	0.2645	0.1768	1
BP	GO:2000278	regulation of DNA biosynthetic process	1/60	119/23328	0.2645	0.1768	1
BP	GO:0015837	amine transport	1/60	121/23328	0.2683	0.1788	1
BP	GO:0022037	metencephalon development	1/60	121/23328	0.2683	0.1788	1
BP	GO:0046467	membrane lipid biosynthetic process	1/60	121/23328	0.2683	0.1788	1
BP	GO:0046620	regulation of organ growth	1/60	121/23328	0.2683	0.1788	1
BP	GO:0072329	monocarboxylic acid catabolic process	1/60	121/23328	0.2683	0.1788	1
BP	GO:1901136	carbohydrate derivative catabolic process	1/60	121/23328	0.2683	0.1788	1
BP	GO:0007098	centrosome cycle	1/60	122/23328	0.2702	0.1795	1
BP	GO:0031109	microtubule polymerization or depolymerization	1/60	122/23328	0.2702	0.1795	1
BP	GO:0045807	positive regulation of endocytosis	1/60	122/23328	0.2702	0.1795	1
BP	GO:0050868	negative regulation of T cell activation	1/60	122/23328	0.2702	0.1795	1
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	1/60	122/23328	0.2702	0.1795	1
BP	GO:1903828	negative regulation of cellular protein localization	1/60	122/23328	0.2702	0.1795	1

BP	GO:0008286	insulin receptor signaling pathway	1/60	123/23328	0.2721	0.1805	1
BP	GO:0048565	digestive tract development	1/60	123/23328	0.2721	0.1805	1
BP	GO:0051261	protein depolymerization	1/60	123/23328	0.2721	0.1805	1
BP	GO:0006997	nucleus organization	1/60	124/23328	0.2740	0.1816	1
BP	GO:0043500	muscle adaptation	1/60	124/23328	0.2740	0.1816	1
BP	GO:0010212	response to ionizing radiation	1/60	125/23328	0.2759	0.1826	1
BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	1/60	125/23328	0.2759	0.1826	1
BP	GO:1902414	protein localization to cell junction	1/60	125/23328	0.2759	0.1826	1
BP	GO:0051053	negative regulation of DNA metabolic process	1/60	126/23328	0.2777	0.1837	1
BP	GO:1901216	positive regulation of neuron death	1/60	126/23328	0.2777	0.1837	1
BP	GO:0008277	regulation of G protein-coupled receptor signaling pathway	1/60	127/23328	0.2796	0.1845	1
BP	GO:0014902	myotube differentiation	1/60	127/23328	0.2796	0.1845	1
BP	GO:0018210	peptidyl-threonine modification	1/60	127/23328	0.2796	0.1845	1
BP	GO:0051101	regulation of DNA binding	1/60	127/23328	0.2796	0.1845	1
BP	GO:0060996	dendritic spine development	1/60	127/23328	0.2796	0.1845	1
BP	GO:0010811	positive regulation of cell-substrate adhesion	1/60	128/23328	0.2815	0.1852	1
BP	GO:0032609	interferon-gamma production	1/60	128/23328	0.2815	0.1852	1
BP	GO:0043244	regulation of protein-containing complex disassembly	1/60	128/23328	0.2815	0.1852	1
BP	GO:0051592	response to calcium ion	1/60	128/23328	0.2815	0.1852	1
BP	GO:0061013	regulation of mRNA catabolic process	1/60	128/23328	0.2815	0.1852	1
BP	GO:0061387	regulation of extent of cell growth	1/60	128/23328	0.2815	0.1852	1
BP	GO:0032273	positive regulation of protein polymerization	1/60	129/23328	0.2833	0.1860	1
BP	GO:0046434	organophosphate catabolic process	1/60	129/23328	0.2833	0.1860	1
BP	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	1/60	129/23328	0.2833	0.1860	1
BP	GO:0042177	negative regulation of protein catabolic process	1/60	130/23328	0.2852	0.1871	1
BP	GO:0050852	T cell receptor signaling pathway	1/60	130/23328	0.2852	0.1871	1

BP	GO:0006665	sphingolipid metabolic process	1/60	131/23328	0.2870	0.1880	1
BP	GO:0007368	determination of left/right symmetry	1/60	131/23328	0.2870	0.1880	1
BP	GO:0018022	peptidyl-lysine methylation	1/60	131/23328	0.2870	0.1880	1
BP	GO:0010469	regulation of signaling receptor activity	1/60	132/23328	0.2889	0.1889	1
BP	GO:0031023	microtubule organizing center organization	1/60	132/23328	0.2889	0.1889	1
BP	GO:0099175	regulation of postsynapse organization	1/60	132/23328	0.2889	0.1889	1
BP	GO:0001841	neural tube formation	1/60	133/23328	0.2907	0.1899	1
BP	GO:0001936	regulation of endothelial cell proliferation	1/60	134/23328	0.2925	0.1908	1
BP	GO:0009791	post-embryonic development	1/60	134/23328	0.2925	0.1908	1
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	1/60	134/23328	0.2925	0.1908	1
BP	GO:0030177	positive regulation of Wnt signaling pathway	1/60	135/23328	0.2944	0.1916	1
BP	GO:0070646	protein modification by small protein removal	1/60	135/23328	0.2944	0.1916	1
BP	GO:1901655	cellular response to ketone	1/60	135/23328	0.2944	0.1916	1
BP	GO:0055123	digestive system development	1/60	136/23328	0.2962	0.1927	1
BP	GO:0007050	cell cycle arrest	1/60	137/23328	0.2980	0.1937	1
BP	GO:0034341	response to interferon-gamma	1/60	137/23328	0.2980	0.1937	1
BP	GO:0006639	acylglycerol metabolic process	1/60	138/23328	0.2998	0.1944	1
BP	GO:0042471	ear morphogenesis	1/60	138/23328	0.2998	0.1944	1
BP	GO:0048284	organelle fusion	1/60	138/23328	0.2998	0.1944	1
BP	GO:0048675	axon extension	1/60	138/23328	0.2998	0.1944	1
BP	GO:0050671	positive regulation of lymphocyte proliferation	1/60	138/23328	0.2998	0.1944	1
BP	GO:0055007	cardiac muscle cell differentiation	1/60	139/23328	0.3017	0.1955	1
BP	GO:0006638	neutral lipid metabolic process	1/60	140/23328	0.3035	0.1963	1
BP	GO:0009855	determination of bilateral symmetry	1/60	140/23328	0.3035	0.1963	1
BP	GO:0032946	positive regulation of mononuclear cell proliferation	1/60	140/23328	0.3035	0.1963	1
BP	GO:1904375	regulation of protein localization to cell periphery	1/60	140/23328	0.3035	0.1963	1
BP	GO:0009152	purine ribonucleotide biosynthetic process	1/60	141/23328	0.3053	0.1972	1
BP	GO:0009799	specification of symmetry	1/60	141/23328	0.3053	0.1972	1

BP	GO:0048706	embryonic skeletal system development	1/60	142/23328	0.3071	0.1980	1
BP	GO:1902850	microtubule cytoskeleton organization involved in mitosis	1/60	142/23328	0.3071	0.1980	1
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	1/60	144/23328	0.3106	0.1998	1
BP	GO:0015698	inorganic anion transport	1/60	144/23328	0.3106	0.1998	1
BP	GO:0016571	histone methylation	1/60	144/23328	0.3106	0.1998	1
BP	GO:0043624	cellular protein complex disassembly	1/60	144/23328	0.3106	0.1998	1
BP	GO:0071333	cellular response to glucose stimulus	1/60	144/23328	0.3106	0.1998	1
BP	GO:0072089	stem cell proliferation	1/60	144/23328	0.3106	0.1998	1
BP	GO:0072073	kidney epithelium development	1/60	145/23328	0.3124	0.2008	1
BP	GO:0035637	multicellular organismal signaling	1/60	146/23328	0.3142	0.2018	1
BP	GO:0071331	cellular response to hexose stimulus	1/60	146/23328	0.3142	0.2018	1
BP	GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1/60	147/23328	0.3160	0.2024	1
BP	GO:0003206	cardiac chamber morphogenesis	1/60	147/23328	0.3160	0.2024	1
BP	GO:0003231	cardiac ventricle development	1/60	147/23328	0.3160	0.2024	1
BP	GO:0045667	regulation of osteoblast differentiation	1/60	147/23328	0.3160	0.2024	1
BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	1/60	147/23328	0.3160	0.2024	1
BP	GO:0071326	cellular response to monosaccharide stimulus	1/60	147/23328	0.3160	0.2024	1
BP	GO:0001935	endothelial cell proliferation	1/60	149/23328	0.3195	0.2045	1
BP	GO:0009260	ribonucleotide biosynthetic process	1/60	150/23328	0.3213	0.2052	1
BP	GO:0061025	membrane fusion	1/60	150/23328	0.3213	0.2052	1
BP	GO:0000070	mitotic sister chromatid segregation	1/60	151/23328	0.3230	0.2062	1
BP	GO:0072006	nephron development	1/60	151/23328	0.3230	0.2062	1
BP	GO:0070665	positive regulation of leukocyte proliferation	1/60	152/23328	0.3248	0.2071	1

BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	1/60	152/23328	0.3248	0.2071	1
BP	GO:0055088	lipid homeostasis	1/60	153/23328	0.3265	0.2081	1
BP	GO:0008360	regulation of cell shape	1/60	154/23328	0.3283	0.2091	1
BP	GO:0001838	embryonic epithelial tube formation	1/60	155/23328	0.3300	0.2099	1
BP	GO:0007292	female gamete generation	1/60	155/23328	0.3300	0.2099	1
BP	GO:0071322	cellular response to carbohydrate stimulus	1/60	155/23328	0.3300	0.2099	1
BP	GO:0002687	positive regulation of leukocyte migration	1/60	156/23328	0.3318	0.2109	1
BP	GO:0006937	regulation of muscle contraction	1/60	156/23328	0.3318	0.2109	1
BP	GO:0021543	pallium development	1/60	157/23328	0.3335	0.2116	1
BP	GO:0046390	ribose phosphate biosynthetic process	1/60	157/23328	0.3335	0.2116	1
BP	GO:0050657	nucleic acid transport	1/60	157/23328	0.3335	0.2116	1
BP	GO:0050658	RNA transport	1/60	157/23328	0.3335	0.2116	1
BP	GO:1903900	regulation of viral life cycle	1/60	159/23328	0.3369	0.2136	1
BP	GO:0000910	cytokinesis	1/60	160/23328	0.3386	0.2143	1
BP	GO:0006164	purine nucleotide biosynthetic process	1/60	160/23328	0.3386	0.2143	1
BP	GO:0007088	regulation of mitotic nuclear division	1/60	160/23328	0.3386	0.2143	1
BP	GO:0051236	establishment of RNA localization	1/60	160/23328	0.3386	0.2143	1
BP	GO:0072175	epithelial tube formation	1/60	162/23328	0.3421	0.2162	1
BP	GO:0001678	cellular glucose homeostasis	1/60	163/23328	0.3438	0.2171	1
BP	GO:0031056	regulation of histone modification	1/60	163/23328	0.3438	0.2171	1
BP	GO:0019730	antimicrobial humoral response	1/60	165/23328	0.3472	0.2191	1
BP	GO:0072522	purine-containing compound biosynthetic process	1/60	165/23328	0.3472	0.2191	1
BP	GO:0030509	BMP signaling pathway	1/60	167/23328	0.3505	0.2209	1
BP	GO:0051100	negative regulation of binding	1/60	167/23328	0.3505	0.2209	1
BP	GO:0071897	DNA biosynthetic process	1/60	169/23328	0.3539	0.2229	1
BP	GO:1904064	positive regulation of cation transmembrane transport	1/60	170/23328	0.3556	0.2239	1
BP	GO:0030902	hindbrain development	1/60	171/23328	0.3572	0.2247	1
BP	GO:0051494	negative regulation of cytoskeleton organization	1/60	171/23328	0.3572	0.2247	1

BP	GO:0060041	retina development in camera-type eye	1/60	172/23328	0.3589	0.2257	1
BP	GO:0071230	cellular response to amino acid stimulus	1/60	173/23328	0.3606	0.2266	1
BP	GO:0006643	membrane lipid metabolic process	1/60	174/23328	0.3622	0.2274	1
BP	GO:1901654	response to ketone	1/60	174/23328	0.3622	0.2274	1
BP	GO:0009612	response to mechanical stimulus	1/60	176/23328	0.3655	0.2292	1
BP	GO:0010977	negative regulation of neuron projection development	1/60	176/23328	0.3655	0.2292	1
BP	GO:2001257	regulation of cation channel activity	1/60	176/23328	0.3655	0.2292	1
BP	GO:0016202	regulation of striated muscle tissue development	1/60	177/23328	0.3672	0.2299	1
BP	GO:0035051	cardiocyte differentiation	1/60	177/23328	0.3672	0.2299	1
BP	GO:0035148	tube formation	1/60	177/23328	0.3672	0.2299	1
BP	GO:0050821	protein stabilization	1/60	178/23328	0.3688	0.2307	1
BP	GO:0071772	response to BMP	1/60	178/23328	0.3688	0.2307	1
BP	GO:0071773	cellular response to BMP stimulus	1/60	178/23328	0.3688	0.2307	1
BP	GO:0007051	spindle organization	1/60	179/23328	0.3705	0.2316	1
BP	GO:0000075	cell cycle checkpoint	1/60	180/23328	0.3721	0.2323	1
BP	GO:1901861	regulation of muscle tissue development	1/60	180/23328	0.3721	0.2323	1
BP	GO:1902107	positive regulation of leukocyte differentiation	1/60	180/23328	0.3721	0.2323	1
BP	GO:0000819	sister chromatid segregation	1/60	181/23328	0.3737	0.2330	1
BP	GO:0001659	temperature homeostasis	1/60	181/23328	0.3737	0.2330	1
BP	GO:0045088	regulation of innate immune response	1/60	181/23328	0.3737	0.2330	1
BP	GO:0006403	RNA localization	1/60	182/23328	0.3753	0.2338	1
BP	GO:0048813	dendrite morphogenesis	1/60	182/23328	0.3753	0.2338	1
BP	GO:0006479	protein methylation	1/60	183/23328	0.3770	0.2344	1
BP	GO:0008016	regulation of heart contraction	1/60	183/23328	0.3770	0.2344	1
BP	GO:0008213	protein alkylation	1/60	183/23328	0.3770	0.2344	1
BP	GO:0016331	morphogenesis of embryonic epithelium	1/60	183/23328	0.3770	0.2344	1
BP	GO:0030534	adult behavior	1/60	184/23328	0.3786	0.2352	1
BP	GO:2001235	positive regulation of apoptotic signaling pathway	1/60	184/23328	0.3786	0.2352	1

BP	GO:0002705	positive regulation of leukocyte mediated immunity	1/60	185/23328	0.3802	0.2359	1
BP	GO:0048754	branching morphogenesis of an epithelial tube	1/60	185/23328	0.3802	0.2359	1
BP	GO:0071229	cellular response to acid chemical	1/60	185/23328	0.3802	0.2359	1
BP	GO:0034767	positive regulation of ion transmembrane transport	1/60	187/23328	0.3834	0.2378	1
BP	GO:0001764	neuron migration	1/60	189/23328	0.3866	0.2396	1
BP	GO:0055002	striated muscle cell development	1/60	190/23328	0.3882	0.2404	1
BP	GO:0120032	regulation of plasma membrane bounded cell projection assembly	1/60	190/23328	0.3882	0.2404	1
BP	GO:0051783	regulation of nuclear division	1/60	191/23328	0.3898	0.2412	1
BP	GO:0061351	neural precursor cell proliferation	1/60	191/23328	0.3898	0.2412	1
BP	GO:0060491	regulation of cell projection assembly	1/60	192/23328	0.3913	0.2419	1
BP	GO:2001252	positive regulation of chromosome organization	1/60	192/23328	0.3913	0.2419	1
BP	GO:0006486	protein glycosylation	1/60	193/23328	0.3929	0.2425	1
BP	GO:0015931	nucleobase-containing compound transport	1/60	193/23328	0.3929	0.2425	1
BP	GO:0043413	macromolecule glycosylation	1/60	193/23328	0.3929	0.2425	1
BP	GO:1903305	regulation of regulated secretory pathway	1/60	193/23328	0.3929	0.2425	1
BP	GO:0003205	cardiac chamber development	1/60	194/23328	0.3945	0.2433	1
BP	GO:0021915	neural tube development	1/60	194/23328	0.3945	0.2433	1
BP	GO:0007519	skeletal muscle tissue development	1/60	196/23328	0.3976	0.2451	1
BP	GO:0050773	regulation of dendrite development	1/60	197/23328	0.3992	0.2459	1
BP	GO:0030307	positive regulation of cell growth	1/60	198/23328	0.4008	0.2468	1
BP	GO:0001906	cell killing	1/60	200/23328	0.4039	0.2482	1
BP	GO:0006839	mitochondrial transport	1/60	200/23328	0.4039	0.2482	1
BP	GO:0051099	positive regulation of binding	1/60	200/23328	0.4039	0.2482	1
BP	GO:0099173	postsynapse organization	1/60	200/23328	0.4039	0.2482	1
BP	GO:1902905	positive regulation of supramolecular fiber organization	1/60	200/23328	0.4039	0.2482	1

BP	GO:0009566	fertilization	1/60	201/23328	0.4054	0.2489	1
BP	GO:0070507	regulation of microtubule cytoskeleton organization	1/60	201/23328	0.4054	0.2489	1
BP	GO:0048736	appendage development	1/60	202/23328	0.4069	0.2496	1
BP	GO:0060173	limb development	1/60	202/23328	0.4069	0.2496	1
BP	GO:0001649	osteoblast differentiation	1/60	205/23328	0.4116	0.2520	1
BP	GO:0045216	cell-cell junction organization	1/60	205/23328	0.4116	0.2520	1
BP	GO:0048469	cell maturation	1/60	205/23328	0.4116	0.2520	1
BP	GO:0055001	muscle cell development	1/60	205/23328	0.4116	0.2520	1
BP	GO:0060538	skeletal muscle organ development	1/60	206/23328	0.4131	0.2527	1
BP	GO:1902115	regulation of organelle assembly	1/60	206/23328	0.4131	0.2527	1
BP	GO:0031345	negative regulation of cell projection organization	1/60	207/23328	0.4146	0.2534	1
BP	GO:0035265	organ growth	1/60	207/23328	0.4146	0.2534	1
BP	GO:0050770	regulation of axonogenesis	1/60	208/23328	0.4161	0.2541	1
BP	GO:0070085	glycosylation	1/60	208/23328	0.4161	0.2541	1
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	1/60	209/23328	0.4176	0.2549	1
BP	GO:1902275	regulation of chromatin organization	1/60	210/23328	0.4191	0.2556	1
BP	GO:2000027	regulation of animal organ morphogenesis	1/60	210/23328	0.4191	0.2556	1
BP	GO:0097305	response to alcohol	1/60	212/23328	0.4222	0.2574	1
BP	GO:0051651	maintenance of location in cell	1/60	213/23328	0.4237	0.2582	1
BP	GO:0010810	regulation of cell-substrate adhesion	1/60	214/23328	0.4252	0.2590	1
BP	GO:0006402	mRNA catabolic process	1/60	217/23328	0.4296	0.2615	1
BP	GO:0051054	positive regulation of DNA metabolic process	1/60	217/23328	0.4296	0.2615	1
BP	GO:0050871	positive regulation of B cell activation	1/60	220/23328	0.4341	0.2641	1
BP	GO:0060047	heart contraction	1/60	221/23328	0.4355	0.2648	1
BP	GO:0030324	lung development	1/60	222/23328	0.4370	0.2653	1
BP	GO:0043547	positive regulation of GTPase activity	1/60	222/23328	0.4370	0.2653	1
BP	GO:0060348	bone development	1/60	222/23328	0.4370	0.2653	1
BP	GO:2001020	regulation of response to DNA damage stimulus	1/60	222/23328	0.4370	0.2653	1

BP	GO:0051259	protein complex oligomerization	1/60	223/23328	0.4384	0.2660	1
BP	GO:0030323	respiratory tube development	1/60	225/23328	0.4414	0.2676	1
BP	GO:0051495	positive regulation of cytoskeleton organization	1/60	225/23328	0.4414	0.2676	1
BP	GO:0043406	positive regulation of MAP kinase activity	1/60	226/23328	0.4428	0.2683	1
BP	GO:0016197	endosomal transport	1/60	228/23328	0.4457	0.2700	1
BP	GO:0016485	protein processing	1/60	229/23328	0.4471	0.2707	1
BP	GO:0003015	heart process	1/60	231/23328	0.4500	0.2722	1
BP	GO:0043393	regulation of protein binding	1/60	231/23328	0.4500	0.2722	1
BP	GO:0032872	regulation of stress-activated MAPK cascade	1/60	232/23328	0.4514	0.2730	1
BP	GO:0090150	establishment of protein localization to membrane	1/60	233/23328	0.4529	0.2737	1
BP	GO:0006470	protein dephosphorylation	1/60	235/23328	0.4557	0.2751	1
BP	GO:0031334	positive regulation of protein-containing complex assembly	1/60	235/23328	0.4557	0.2751	1
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	1/60	235/23328	0.4557	0.2751	1
BP	GO:0045930	negative regulation of mitotic cell cycle	1/60	236/23328	0.4571	0.2758	1
BP	GO:0000209	protein polyubiquitination	1/60	237/23328	0.4585	0.2764	1
BP	GO:0048863	stem cell differentiation	1/60	237/23328	0.4585	0.2764	1
BP	GO:0006898	receptor-mediated endocytosis	1/60	240/23328	0.4627	0.2788	1
BP	GO:0034764	positive regulation of transmembrane transport	1/60	243/23328	0.4669	0.2812	1
BP	GO:0007568	aging	1/60	251/23328	0.4779	0.2877	1
BP	GO:0048705	skeletal system morphogenesis	1/60	253/23328	0.4806	0.2892	1
BP	GO:0006401	RNA catabolic process	1/60	254/23328	0.4820	0.2897	1
BP	GO:0017157	regulation of exocytosis	1/60	254/23328	0.4820	0.2897	1
BP	GO:0060541	respiratory system development	1/60	254/23328	0.4820	0.2897	1
BP	GO:0007626	locomotory behavior	1/60	258/23328	0.4873	0.2925	1
BP	GO:0032886	regulation of microtubule-based process	1/60	258/23328	0.4873	0.2925	1
BP	GO:0048738	cardiac muscle tissue development	1/60	258/23328	0.4873	0.2925	1
BP	GO:0032412	regulation of ion transmembrane transporter activity	1/60	259/23328	0.4887	0.2932	1
BP	GO:0045055	regulated exocytosis	1/60	261/23328	0.4913	0.2947	1

BP	GO:0098813	nuclear chromosome segregation	1/60	262/23328	0.4926	0.2953	1
BP	GO:1903311	regulation of mRNA metabolic process	1/60	266/23328	0.4979	0.2984	1
BP	GO:0140014	mitotic nuclear division	1/60	268/23328	0.5005	0.2998	1
BP	GO:0022898	regulation of transmembrane transporter activity	1/60	270/23328	0.5031	0.3012	1
BP	GO:0009101	glycoprotein biosynthetic process	1/60	273/23328	0.5070	0.3034	1
BP	GO:0003007	heart morphogenesis	1/60	277/23328	0.5121	0.3062	1
BP	GO:0050807	regulation of synapse organization	1/60	277/23328	0.5121	0.3062	1
BP	GO:0032409	regulation of transporter activity	1/60	280/23328	0.5159	0.3084	1
BP	GO:0070588	calcium ion transmembrane transport	1/60	282/23328	0.5184	0.3097	1
BP	GO:0031647	regulation of protein stability	1/60	287/23328	0.5246	0.3133	1
BP	GO:0050803	regulation of synapse structure or activity	1/60	289/23328	0.5271	0.3147	1
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	1/60	291/23328	0.5296	0.3160	1
BP	GO:0045165	cell fate commitment	1/60	292/23328	0.5308	0.3166	1
BP	GO:0051604	protein maturation	1/60	294/23328	0.5332	0.3179	1
BP	GO:0043414	macromolecule methylation	1/60	297/23328	0.5369	0.3200	1
BP	GO:0006936	muscle contraction	1/60	298/23328	0.5381	0.3205	1
BP	GO:0050851	antigen receptor-mediated signaling pathway	1/60	299/23328	0.5393	0.3211	1
BP	GO:0043087	regulation of GTPase activity	1/60	303/23328	0.5441	0.3238	1
BP	GO:0030111	regulation of Wnt signaling pathway	1/60	304/23328	0.5453	0.3244	1
BP	GO:1990830	cellular response to leukemia inhibitory factor	1/60	311/23328	0.5535	0.3292	1
BP	GO:0045927	positive regulation of growth	1/60	312/23328	0.5547	0.3296	1
BP	GO:1990823	response to leukemia inhibitory factor	1/60	312/23328	0.5547	0.3296	1
BP	GO:0007548	sex differentiation	1/60	315/23328	0.5581	0.3315	1
BP	GO:0001822	kidney development	1/60	318/23328	0.5616	0.3334	1
BP	GO:0007059	chromosome segregation	1/60	324/23328	0.5684	0.3373	1
BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	1/60	330/23328	0.5751	0.3410	1
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	1/60	330/23328	0.5751	0.3410	1

BP	GO:0002757	immune response-activating signal transduction	1/60	331/23328	0.5762	0.3415	1
BP	GO:0072001	renal system development	1/60	333/23328	0.5784	0.3427	1
BP	GO:0043270	positive regulation of ion transport	1/60	334/23328	0.5795	0.3432	1
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	1/60	342/23328	0.5882	0.3482	1
BP	GO:0002764	immune response-regulating signaling pathway	1/60	345/23328	0.5914	0.3499	1
BP	GO:0010769	regulation of cell morphogenesis involved in differentiation	1/60	351/23328	0.5978	0.3534	1
BP	GO:0031589	cell-substrate adhesion	1/60	351/23328	0.5978	0.3534	1
BP	GO:0034470	ncRNA processing	1/60	355/23328	0.6020	0.3557	1
BP	GO:0033044	regulation of chromosome organization	1/60	369/23328	0.6163	0.3640	1
BP	GO:0016311	dephosphorylation	1/60	374/23328	0.6213	0.3668	1
BP	GO:0051480	regulation of cytosolic calcium ion concentration	1/60	375/23328	0.6223	0.3673	1
BP	GO:0001655	urogenital system development	1/60	376/23328	0.6233	0.3677	1
BP	GO:0006887	exocytosis	1/60	389/23328	0.6359	0.3750	1
BP	GO:0006959	humoral immune response	1/60	406/23328	0.6517	0.3842	1
BP	GO:0002253	activation of immune response	1/60	416/23328	0.6607	0.3893	1
BP	GO:0000280	nuclear division	1/60	418/23328	0.6625	0.3902	1
BP	GO:0007264	small GTPase mediated signal transduction	1/60	437/23328	0.6789	0.3997	1
BP	GO:0042742	defense response to bacterium	1/60	464/23328	0.7009	0.4125	1
BP	GO:0048285	organelle fission	1/60	472/23328	0.7071	0.4159	1
BP	GO:0006874	cellular calcium ion homeostasis	1/60	476/23328	0.7102	0.4176	1
BP	GO:0050808	synapse organization	1/60	479/23328	0.7125	0.4187	1
BP	GO:0007409	axonogenesis	1/60	482/23328	0.7147	0.4199	1
BP	GO:0055074	calcium ion homeostasis	1/60	493/23328	0.7229	0.4245	1
CC	GO:0005845	mRNA cap binding complex	1/61	10/23271	0.0259	0.0959	1
CC	GO:0034518	RNA cap binding complex	1/61	10/23271	0.0259	0.0959	1
CC	GO:0046581	intercellular canaliculus	1/61	10/23271	0.0259	0.0959	1
CC	GO:0070578	RISC-loading complex	1/61	11/23271	0.0285	0.0961	1
CC	GO:0034045	phagophore assembly site membrane	1/61	12/23271	0.0310	0.0961	1

CC	GO:0034663	endoplasmic reticulum chaperone complex	1/61	12/23271	0.0310	0.0961	1
CC	GO:0043020	NADPH oxidase complex	1/61	12/23271	0.0310	0.0961	1
CC	GO:0048188	Set1C/COMPASS complex	1/61	12/23271	0.0310	0.0961	1
CC	GO:0071437	invadopodium	1/61	14/23271	0.0361	0.1062	1
CC	GO:0030014	CCR4-NOT complex	1/61	16/23271	0.0411	0.1158	1
CC	GO:0044233	mitochondria-associated endoplasmic reticulum membrane	1/61	16/23271	0.0411	0.1158	1
CC	GO:0034361	very-low-density lipoprotein particle	1/61	19/23271	0.0487	0.1286	1
CC	GO:0034385	triglyceride-rich plasma lipoprotein particle	1/61	19/23271	0.0487	0.1286	1
CC	GO:0090543	Flemming body	1/61	19/23271	0.0487	0.1286	1
CC	GO:0097449	astrocyte projection	1/61	20/23271	0.0512	0.1286	1
CC	GO:0005640	nuclear outer membrane	1/61	21/23271	0.0537	0.1286	1
CC	GO:0031528	microvillus membrane	1/61	21/23271	0.0537	0.1286	1
CC	GO:0045120	pronucleus	1/61	23/23271	0.0586	0.1296	1
CC	GO:0000178	exosome (RNase complex)	1/61	24/23271	0.0611	0.1296	1
CC	GO:0005782	peroxisomal matrix	1/61	24/23271	0.0611	0.1296	1
CC	GO:0030057	desmosome	1/61	24/23271	0.0611	0.1296	1
CC	GO:0031907	microbody lumen	1/61	24/23271	0.0611	0.1296	1
CC	GO:1905354	exoribonuclease complex	1/61	24/23271	0.0611	0.1296	1
CC	GO:0002080	acrosomal membrane	1/61	25/23271	0.0635	0.1327	1
CC	GO:0044232	organelle membrane contact site	1/61	28/23271	0.0709	0.1457	1
CC	GO:1902555	endoribonuclease complex	1/61	30/23271	0.0758	0.1509	1
CC	GO:0008180	COP9 signalosome	1/61	34/23271	0.0854	0.1537	1
CC	GO:0034358	plasma lipoprotein particle	1/61	34/23271	0.0854	0.1537	1
CC	GO:0097225	sperm midpiece	1/61	34/23271	0.0854	0.1537	1
CC	GO:1990777	lipoprotein particle	1/61	34/23271	0.0854	0.1537	1
CC	GO:0031463	Cul3-RING ubiquitin ligase complex	1/61	35/23271	0.0878	0.1537	1
CC	GO:0097386	glial cell projection	1/61	35/23271	0.0878	0.1537	1
CC	GO:0005790	smooth endoplasmic reticulum	1/61	36/23271	0.0902	0.1537	1
CC	GO:1905348	endonuclease complex	1/61	36/23271	0.0902	0.1537	1
CC	GO:0032994	protein-lipid complex	1/61	37/23271	0.0926	0.1557	1
CC	GO:0016235	aggresome	1/61	38/23271	0.0950	0.1577	1
CC	GO:0005637	nuclear inner membrane	1/61	45/23271	0.1115	0.1754	1
CC	GO:0034707	chloride channel complex	1/61	46/23271	0.1138	0.1754	1
CC	GO:0005771	multivesicular body	1/61	51/23271	0.1254	0.1847	1

CC	GO:0031312	extrinsic component of organelle membrane	1/61	56/23271	0.1368	0.1991	1
CC	GO:0001917	photoreceptor inner segment	1/61	60/23271	0.1459	0.2076	1
CC	GO:0014704	intercalated disc	1/61	62/23271	0.1504	0.2116	1
CC	GO:0000502	proteasome complex	1/61	64/23271	0.1548	0.2155	1
CC	GO:0016328	lateral plasma membrane	1/61	66/23271	0.1593	0.2194	1
CC	GO:0005905	clathrin-coated pit	1/61	69/23271	0.1659	0.2243	1
CC	GO:0010494	cytoplasmic stress granule	1/61	70/23271	0.1681	0.2243	1
CC	GO:1905369	endopeptidase complex	1/61	70/23271	0.1681	0.2243	1
CC	GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	1/61	72/23271	0.1724	0.2278	1
CC	GO:0005844	polysome	1/61	74/23271	0.1768	0.2312	1
CC	GO:0016605	PML body	1/61	75/23271	0.1789	0.2317	1
CC	GO:0016234	inclusion body	1/61	76/23271	0.1811	0.2322	1
CC	GO:0031526	brush border membrane	1/61	78/23271	0.1854	0.2353	1
CC	GO:0035097	histone methyltransferase complex	1/61	80/23271	0.1897	0.2384	1
CC	GO:1902554	serine/threonine protein kinase complex	1/61	83/23271	0.1961	0.2441	1
CC	GO:0005788	endoplasmic reticulum lumen	1/61	85/23271	0.2003	0.2446	1
CC	GO:0044291	cell-cell contact zone	1/61	85/23271	0.2003	0.2446	1
CC	GO:0030667	secretory granule membrane	1/61	88/23271	0.2066	0.2500	1
CC	GO:0030864	cortical actin cytoskeleton	1/61	89/23271	0.2087	0.2502	1
CC	GO:0005791	rough endoplasmic reticulum	1/61	93/23271	0.2170	0.2577	1
CC	GO:0032432	actin filament bundle	1/61	95/23271	0.2211	0.2579	1
CC	GO:1905368	peptidase complex	1/61	95/23271	0.2211	0.2579	1
CC	GO:0098839	postsynaptic density membrane	1/61	97/23271	0.2252	0.2603	1
CC	GO:1902911	protein kinase complex	1/61	99/23271	0.2293	0.2627	1
CC	GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	1/61	104/23271	0.2393	0.2717	1
CC	GO:0034708	methyltransferase complex	1/61	105/23271	0.2414	0.2717	1
CC	GO:0045335	phagocytic vesicle	1/61	111/23271	0.2533	0.2827	1
CC	GO:0022626	cytosolic ribosome	1/61	115/23271	0.2611	0.2862	1
CC	GO:0030672	synaptic vesicle membrane	1/61	116/23271	0.2630	0.2862	1
CC	GO:0099501	exocytic vesicle membrane	1/61	116/23271	0.2630	0.2862	1
CC	GO:0005814	centriole	1/61	119/23271	0.2689	0.2901	1
CC	GO:0030863	cortical cytoskeleton	1/61	123/23271	0.2765	0.2959	1
CC	GO:0005765	lysosomal membrane	1/61	130/23271	0.2898	0.2978	1
CC	GO:0098852	lytic vacuole membrane	1/61	130/23271	0.2898	0.2978	1
CC	GO:0001669	acrosomal vesicle	1/61	134/23271	0.2972	0.3011	1

CC	GO:0072686	mitotic spindle	1/61	135/23271	0.2991	0.3011	1
CC	GO:0099634	postsynaptic specialization membrane	1/61	136/23271	0.3009	0.3011	1
CC	GO:0005912	adherens junction	1/61	138/23271	0.3046	0.3011	1
CC	GO:0005903	brush border	1/61	140/23271	0.3083	0.3019	1
CC	GO:0036126	sperm flagellum	1/61	141/23271	0.3101	0.3019	1
CC	GO:0030658	transport vesicle membrane	1/61	147/23271	0.3209	0.3055	1
CC	GO:0031256	leading edge membrane	1/61	150/23271	0.3263	0.3084	1
CC	GO:0030176	integral component of endoplasmic reticulum membrane	1/61	153/23271	0.3316	0.3105	1
CC	GO:0097729	9+2 motile cilium	1/61	154/23271	0.3334	0.3105	1
CC	GO:0090575	RNA polymerase II transcription regulator complex	1/61	159/23271	0.3421	0.3142	1
CC	GO:0031227	intrinsic component of endoplasmic reticulum membrane	1/61	161/23271	0.3456	0.3151	1
CC	GO:0031461	cullin-RING ubiquitin ligase complex	1/61	163/23271	0.3491	0.3154	1
CC	GO:0042383	sarcolemma	1/61	164/23271	0.3508	0.3154	1
CC	GO:0009898	cytoplasmic side of plasma membrane	1/61	169/23271	0.3593	0.3208	1
CC	GO:0005774	vacuolar membrane	1/61	183/23271	0.3826	0.3393	1
CC	GO:0098562	cytoplasmic side of membrane	1/61	186/23271	0.3875	0.3404	1
CC	GO:0098802	plasma membrane signaling receptor complex	1/61	187/23271	0.3891	0.3404	1
CC	GO:0019897	extrinsic component of plasma membrane	1/61	189/23271	0.3923	0.3409	1
CC	GO:0043197	dendritic spine	1/61	195/23271	0.4019	0.3469	1
CC	GO:0044309	neuron spine	1/61	200/23271	0.4097	0.3490	1
CC	GO:0098862	cluster of actin-based cell projections	1/61	200/23271	0.4097	0.3490	1
CC	GO:0005770	late endosome	1/61	219/23271	0.4387	0.3713	1
CC	GO:0099699	integral component of synaptic membrane	1/61	226/23271	0.4490	0.3775	1
CC	GO:0005840	ribosome	1/61	234/23271	0.4606	0.3847	1
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	1/61	241/23271	0.4705	0.3905	1
CC	GO:0099240	intrinsic component of synaptic membrane	1/61	244/23271	0.4747	0.3913	1
CC	GO:0031965	nuclear membrane	1/61	246/23271	0.4775	0.3913	1

CC	GO:0005759	mitochondrial matrix	1/61	273/23271	0.5136	0.4182	1
CC	GO:0000151	ubiquitin ligase complex	1/61	285/23271	0.5289	0.4280	1
CC	GO:0034702	ion channel complex	1/61	296/23271	0.5425	0.4345	1
CC	GO:0005819	spindle	1/61	297/23271	0.5437	0.4345	1
CC	GO:0005938	cell cortex	1/61	307/23271	0.5557	0.4414	1
CC	GO:1902495	transmembrane transporter complex	1/61	312/23271	0.5615	0.4433	1
CC	GO:1990351	transporter complex	1/61	319/23271	0.5696	0.4452	1
CC	GO:0016607	nuclear speck	1/61	320/23271	0.5708	0.4452	1
CC	GO:0045211	postsynaptic membrane	1/61	330/23271	0.5820	0.4512	1
CC	GO:0030659	cytoplasmic vesicle membrane	1/61	337/23271	0.5898	0.4545	1
CC	GO:0012506	vesicle membrane	1/61	363/23271	0.6172	0.4729	1
CC	GO:0031301	integral component of organelle membrane	1/61	368/23271	0.6223	0.4739	1
CC	GO:0031300	intrinsic component of organelle membrane	1/61	403/23271	0.6560	0.4967	1
CC	GO:0019866	organelle inner membrane	1/61	489/23271	0.7267	0.5470	1
MF	GO:0005381	iron ion transmembrane transporter activity	1/58	10/22669	0.0253	0.0704	1
MF	GO:0008526	phosphatidylinositol transfer activity	1/58	10/22669	0.0253	0.0704	1
MF	GO:0016175	superoxide-generating NAD(P)H oxidase activity	1/58	10/22669	0.0253	0.0704	1
MF	GO:0050544	arachidonic acid binding	1/58	10/22669	0.0253	0.0704	1
MF	GO:0061578	Lys63-specific deubiquitinase activity	1/58	10/22669	0.0253	0.0704	1
MF	GO:0102391	decanoate-CoA ligase activity	1/58	10/22669	0.0253	0.0704	1
MF	GO:0005247	voltage-gated chloride channel activity	1/58	11/22669	0.0278	0.0704	1
MF	GO:0008330	protein tyrosine/threonine phosphatase activity	1/58	11/22669	0.0278	0.0704	1
MF	GO:0017128	phospholipid scramblase activity	1/58	11/22669	0.0278	0.0704	1
MF	GO:0019107	myristoyltransferase activity	1/58	11/22669	0.0278	0.0704	1
MF	GO:0047676	arachidonate-CoA ligase activity	1/58	11/22669	0.0278	0.0704	1
MF	GO:0050542	icosanoid binding	1/58	11/22669	0.0278	0.0704	1
MF	GO:0050543	icosatetraenoic acid binding	1/58	11/22669	0.0278	0.0704	1
MF	GO:0001224	RNA polymerase II transcription cofactor binding	1/58	12/22669	0.0303	0.0748	1
MF	GO:0005536	glucose binding	1/58	12/22669	0.0303	0.0748	1

MF	GO:0008525	phosphatidylcholine transporter activity	1/58	13/22669	0.0328	0.0770	1
MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	1/58	13/22669	0.0328	0.0770	1
MF	GO:0042301	phosphate ion binding	1/58	13/22669	0.0328	0.0770	1
MF	GO:0004303	estradiol 17-beta-dehydrogenase activity	1/58	14/22669	0.0352	0.0771	1
MF	GO:0004467	long-chain fatty acid-CoA ligase activity	1/58	14/22669	0.0352	0.0771	1
MF	GO:0015562	efflux transmembrane transporter activity	1/58	14/22669	0.0352	0.0771	1
MF	GO:0016595	glutamate binding	1/58	14/22669	0.0352	0.0771	1
MF	GO:0033549	MAP kinase phosphatase activity	1/58	14/22669	0.0352	0.0771	1
MF	GO:0070700	BMP receptor binding	1/58	14/22669	0.0352	0.0771	1
MF	GO:0005229	intracellular calcium activated chloride channel activity	1/58	15/22669	0.0377	0.0790	1
MF	GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	1/58	15/22669	0.0377	0.0790	1
MF	GO:0045236	CXCR chemokine receptor binding	1/58	15/22669	0.0377	0.0790	1
MF	GO:0061778	intracellular chloride channel activity	1/58	15/22669	0.0377	0.0790	1
MF	GO:0008308	voltage-gated anion channel activity	1/58	16/22669	0.0402	0.0798	1
MF	GO:0030228	lipoprotein particle receptor activity	1/58	16/22669	0.0402	0.0798	1
MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	1/58	16/22669	0.0402	0.0798	1
MF	GO:0016290	palmitoyl-CoA hydrolase activity	1/58	17/22669	0.0426	0.0830	1
MF	GO:0071617	lysophospholipid acyltransferase activity	1/58	17/22669	0.0426	0.0830	1
MF	GO:0008199	ferric iron binding	1/58	18/22669	0.0451	0.0851	1
MF	GO:0034185	apolipoprotein binding	1/58	18/22669	0.0451	0.0851	1
MF	GO:0072349	modified amino acid transmembrane transporter activity	1/58	18/22669	0.0451	0.0851	1
MF	GO:0031434	mitogen-activated protein kinase kinase binding	1/58	19/22669	0.0475	0.0872	1

MF	GO:0055106	ubiquitin-protein transferase regulator activity	1/58	20/22669	0.0500	0.0900	1
MF	GO:0120020	cholesterol transfer activity	1/58	20/22669	0.0500	0.0900	1
MF	GO:0120015	sterol transfer activity	1/58	21/22669	0.0524	0.0920	1
MF	GO:0005540	hyaluronic acid binding	1/58	22/22669	0.0548	0.0920	1
MF	GO:0016408	C-acyltransferase activity	1/58	22/22669	0.0548	0.0920	1
MF	GO:0120014	phospholipid transfer activity	1/58	22/22669	0.0548	0.0920	1
MF	GO:0051787	misfolded protein binding	1/58	23/22669	0.0572	0.0920	1
MF	GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	1/58	24/22669	0.0597	0.0920	1
MF	GO:0070696	transmembrane receptor protein serine/threonine kinase binding	1/58	24/22669	0.0597	0.0920	1
MF	GO:0140303	intramembrane lipid transporter activity	1/58	24/22669	0.0597	0.0920	1
MF	GO:0005160	transforming growth factor beta receptor binding	1/58	25/22669	0.0621	0.0920	1
MF	GO:0005212	structural constituent of eye lens	1/58	25/22669	0.0621	0.0920	1
MF	GO:0005227	calcium activated cation channel activity	1/58	25/22669	0.0621	0.0920	1
MF	GO:0016866	intramolecular transferase activity	1/58	25/22669	0.0621	0.0920	1
MF	GO:0019957	C-C chemokine binding	1/58	25/22669	0.0621	0.0920	1
MF	GO:0048027	mRNA 5'-UTR binding	1/58	25/22669	0.0621	0.0920	1
MF	GO:0001618	virus receptor activity	1/58	26/22669	0.0645	0.0920	1
MF	GO:0047617	acyl-CoA hydrolase activity	1/58	26/22669	0.0645	0.0920	1
MF	GO:0140272	exogenous protein binding	1/58	26/22669	0.0645	0.0920	1
MF	GO:1904680	peptide transmembrane transporter activity	1/58	27/22669	0.0669	0.0947	1
MF	GO:0001223	transcription coactivator binding	1/58	28/22669	0.0693	0.0953	1
MF	GO:0016289	CoA hydrolase activity	1/58	28/22669	0.0693	0.0953	1
MF	GO:0035925	mRNA 3'-UTR AU-rich region binding	1/58	28/22669	0.0693	0.0953	1
MF	GO:0017091	AU-rich element binding	1/58	29/22669	0.0716	0.0965	1
MF	GO:0030291	protein serine/threonine kinase inhibitor activity	1/58	29/22669	0.0716	0.0965	1
MF	GO:0045499	chemorepellent activity	1/58	29/22669	0.0716	0.0965	1
MF	GO:0015248	sterol transporter activity	1/58	30/22669	0.0740	0.0990	1
MF	GO:0071813	lipoprotein particle binding	1/58	31/22669	0.0764	0.1008	1
MF	GO:0071814	protein-lipid complex binding	1/58	31/22669	0.0764	0.1008	1

MF	GO:0033612	receptor serine/threonine kinase binding	1/58	32/22669	0.0788	0.1025	1
MF	GO:0035035	histone acetyltransferase binding	1/58	32/22669	0.0788	0.1025	1
MF	GO:0019956	chemokine binding	1/58	33/22669	0.0811	0.1035	1
MF	GO:0051059	NF-kappaB binding	1/58	33/22669	0.0811	0.1035	1
MF	GO:0008198	ferrous iron binding	1/58	35/22669	0.0858	0.1081	1
MF	GO:0005154	epidermal growth factor receptor binding	1/58	36/22669	0.0882	0.1089	1
MF	GO:0015175	neutral amino acid transmembrane transporter activity	1/58	36/22669	0.0882	0.1089	1
MF	GO:0031369	translation initiation factor binding	1/58	37/22669	0.0905	0.1104	1
MF	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	1/58	38/22669	0.0928	0.1104	1
MF	GO:0033764	steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	1/58	38/22669	0.0928	0.1104	1
MF	GO:0046915	transition metal ion transmembrane transporter activity	1/58	38/22669	0.0928	0.1104	1
MF	GO:1901682	sulfur compound transmembrane transporter activity	1/58	38/22669	0.0928	0.1104	1
MF	GO:0035255	ionotropic glutamate receptor binding	1/58	39/22669	0.0952	0.1124	1
MF	GO:0042805	actinin binding	1/58	40/22669	0.0975	0.1124	1
MF	GO:0043531	ADP binding	1/58	40/22669	0.0975	0.1124	1
MF	GO:0051539	4 iron, 4 sulfur cluster binding	1/58	40/22669	0.0975	0.1124	1
MF	GO:0001965	G-protein alpha-subunit binding	1/58	41/22669	0.0998	0.1137	1
MF	GO:0120013	lipid transfer activity	1/58	41/22669	0.0998	0.1137	1
MF	GO:0022839	ion gated channel activity	1/58	42/22669	0.1021	0.1150	1
MF	GO:0051019	mitogen-activated protein kinase binding	1/58	42/22669	0.1021	0.1150	1
MF	GO:0018024	histone-lysine N-methyltransferase activity	1/58	43/22669	0.1044	0.1155	1
MF	GO:0004177	aminopeptidase activity	1/58	44/22669	0.1067	0.1155	1
MF	GO:0008009	chemokine activity	1/58	44/22669	0.1067	0.1155	1
MF	GO:0042169	SH2 domain binding	1/58	44/22669	0.1067	0.1155	1

MF	GO:0042887	amide transmembrane transporter activity	1/58	44/22669	0.1067	0.1155	1
MF	GO:0016229	steroid dehydrogenase activity	1/58	45/22669	0.1090	0.1173	1
MF	GO:0008374	O-acyltransferase activity	1/58	46/22669	0.1113	0.1184	1
MF	GO:0015485	cholesterol binding	1/58	46/22669	0.1113	0.1184	1
MF	GO:0050661	NADP binding	1/58	48/22669	0.1158	0.1219	1
MF	GO:0051879	Hsp90 protein binding	1/58	48/22669	0.1158	0.1219	1
MF	GO:0001102	RNA polymerase II activating transcription factor binding	1/58	49/22669	0.1181	0.1236	1
MF	GO:0001046	core promoter sequence-specific DNA binding	1/58	50/22669	0.1203	0.1240	1
MF	GO:0016790	thiolester hydrolase activity	1/58	50/22669	0.1203	0.1240	1
MF	GO:0004601	peroxidase activity	1/58	53/22669	0.1271	0.1282	1
MF	GO:0004879	nuclear receptor activity	1/58	53/22669	0.1271	0.1282	1
MF	GO:0017046	peptide hormone binding	1/58	53/22669	0.1271	0.1282	1
MF	GO:0098531	ligand-activated transcription factor activity	1/58	53/22669	0.1271	0.1282	1
MF	GO:0003707	steroid hormone receptor activity	1/58	54/22669	0.1293	0.1298	1
MF	GO:0032934	sterol binding	1/58	55/22669	0.1316	0.1313	1
MF	GO:0016836	hydro-lyase activity	1/58	56/22669	0.1338	0.1329	1
MF	GO:0016278	lysine N-methyltransferase activity	1/58	57/22669	0.1360	0.1330	1
MF	GO:0016279	protein-lysine N-methyltransferase activity	1/58	57/22669	0.1360	0.1330	1
MF	GO:0042054	histone methyltransferase activity	1/58	57/22669	0.1360	0.1330	1
MF	GO:0001540	amyloid-beta binding	1/58	58/22669	0.1382	0.1338	1
MF	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	1/58	58/22669	0.1382	0.1338	1
MF	GO:0001221	transcription cofactor binding	1/58	59/22669	0.1404	0.1353	1
MF	GO:0005507	copper ion binding	1/58	61/22669	0.1449	0.1375	1
MF	GO:0051287	NAD binding	1/58	61/22669	0.1449	0.1375	1
MF	GO:0043022	ribosome binding	1/58	62/22669	0.1470	0.1382	1
MF	GO:0070063	RNA polymerase binding	1/58	62/22669	0.1470	0.1382	1
MF	GO:0000049	tRNA binding	1/58	64/22669	0.1514	0.1409	1
MF	GO:0051536	iron-sulfur cluster binding	1/58	66/22669	0.1558	0.1435	1
MF	GO:0051540	metal cluster binding	1/58	66/22669	0.1558	0.1435	1
MF	GO:0004722	protein serine/threonine phosphatase activity	1/58	67/22669	0.1579	0.1435	1
MF	GO:0016835	carbon-oxygen lyase activity	1/58	67/22669	0.1579	0.1435	1

MF	GO:0035254	glutamate receptor binding	1/58	67/22669	0.1579	0.1435	1
MF	GO:0016597	amino acid binding	1/58	70/22669	0.1644	0.1487	1
MF	GO:0002039	p53 binding	1/58	71/22669	0.1665	0.1492	1
MF	GO:0005518	collagen binding	1/58	71/22669	0.1665	0.1492	1
MF	GO:0005254	chloride channel activity	1/58	73/22669	0.1708	0.1516	1
MF	GO:0038024	cargo receptor activity	1/58	76/22669	0.1772	0.1566	1
MF	GO:0042379	chemokine receptor binding	1/58	78/22669	0.1814	0.1596	1
MF	GO:0048029	monosaccharide binding	1/58	82/22669	0.1898	0.1657	1
MF	GO:0005253	anion channel activity	1/58	83/22669	0.1919	0.1657	1
MF	GO:0008081	phosphoric diester hydrolase activity	1/58	83/22669	0.1919	0.1657	1
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	1/58	83/22669	0.1919	0.1657	1
MF	GO:0016209	antioxidant activity	1/58	84/22669	0.1939	0.1668	1
MF	GO:0043178	alcohol binding	1/58	85/22669	0.1960	0.1678	1
MF	GO:0008276	protein methyltransferase activity	1/58	88/22669	0.2022	0.1716	1
MF	GO:0042562	hormone binding	1/58	88/22669	0.2022	0.1716	1
MF	GO:0048306	calcium-dependent protein binding	1/58	89/22669	0.2042	0.1726	1
MF	GO:0008238	exopeptidase activity	1/58	91/22669	0.2083	0.1752	1
MF	GO:0004620	phospholipase activity	1/58	93/22669	0.2124	0.1779	1
MF	GO:0031490	chromatin DNA binding	1/58	94/22669	0.2144	0.1788	1
MF	GO:0003730	mRNA 3'-UTR binding	1/58	98/22669	0.2224	0.1816	1
MF	GO:0004725	protein tyrosine phosphatase activity	1/58	98/22669	0.2224	0.1816	1
MF	GO:0004896	cytokine receptor activity	1/58	98/22669	0.2224	0.1816	1
MF	GO:0004843	thiol-dependent ubiquitin-specific protease activity	1/58	99/22669	0.2244	0.1824	1
MF	GO:0101005	ubiquitinyl hydrolase activity	1/58	100/22669	0.2264	0.1833	1
MF	GO:0042626	ATPase-coupled transmembrane transporter activity	1/58	101/22669	0.2284	0.1841	1
MF	GO:0015108	chloride transmembrane transporter activity	1/58	102/22669	0.2304	0.1849	1
MF	GO:0051219	phosphoprotein binding	1/58	104/22669	0.2344	0.1865	1
MF	GO:0008242	omega peptidase activity	1/58	107/22669	0.2402	0.1904	1
MF	GO:0015399	primary active transmembrane transporter activity	1/58	108/22669	0.2422	0.1912	1
MF	GO:0005496	steroid binding	1/58	119/22669	0.2634	0.2071	1
MF	GO:0140375	immune receptor activity	1/58	123/22669	0.2709	0.2113	1

MF	GO:0045182	translation regulator activity	1/58	127/22669	0.2784	0.2154	1
MF	GO:0016298	lipase activity	1/58	128/22669	0.2802	0.2159	1
MF	GO:0047485	protein N-terminus binding	1/58	129/22669	0.2821	0.2165	1
MF	GO:0005179	hormone activity	1/58	130/22669	0.2839	0.2170	1
MF	GO:0015103	inorganic anion transmembrane transporter activity	1/58	136/22669	0.2949	0.2246	1
MF	GO:0043021	ribonucleoprotein complex binding	1/58	146/22669	0.3129	0.2354	1
MF	GO:0019838	growth factor binding	1/58	147/22669	0.3146	0.2358	1
MF	GO:0035257	nuclear hormone receptor binding	1/58	152/22669	0.3234	0.2405	1
MF	GO:0072509	divalent inorganic cation transmembrane transporter activity	1/58	163/22669	0.3423	0.2536	1
MF	GO:0004721	phosphoprotein phosphatase activity	1/58	171/22669	0.3558	0.2626	1
MF	GO:0003714	transcription corepressor activity	1/58	176/22669	0.3640	0.2677	1
MF	GO:0051427	hormone receptor binding	1/58	181/22669	0.3722	0.2726	1
MF	GO:0004252	serine-type endopeptidase activity	1/58	186/22669	0.3803	0.2775	1
MF	GO:0005244	voltage-gated ion channel activity	1/58	190/22669	0.3866	0.2800	1
MF	GO:0022832	voltage-gated channel activity	1/58	190/22669	0.3866	0.2800	1
MF	GO:0008236	serine-type peptidase activity	1/58	207/22669	0.4130	0.2980	1
MF	GO:0051015	actin filament binding	1/58	210/22669	0.4175	0.3001	1
MF	GO:0017171	serine hydrolase activity	1/58	212/22669	0.4205	0.3011	1
MF	GO:0005539	glycosaminoglycan binding	1/58	213/22669	0.4220	0.3011	1
MF	GO:0015291	secondary active transmembrane transporter activity	1/58	231/22669	0.4483	0.3187	1
MF	GO:0005096	GTPase activator activity	1/58	238/22669	0.4582	0.3245	1
MF	GO:0030695	GTPase regulator activity	1/58	258/22669	0.4856	0.3426	1
MF	GO:0008017	microtubule binding	1/58	260/22669	0.4882	0.3433	1
MF	GO:0016791	phosphatase activity	1/58	271/22669	0.5026	0.3521	1
MF	GO:0030246	carbohydrate binding	1/58	274/22669	0.5065	0.3535	1
MF	GO:0060589	nucleoside-triphosphatase regulator activity	1/58	298/22669	0.5363	0.3729	1
MF	GO:0001664	G protein-coupled receptor binding	1/58	310/22669	0.5505	0.3815	1
MF	GO:0022836	gated channel activity	1/58	323/22669	0.5654	0.3904	1

MF	GO:0005261	cation channel activity	1/58	327/22669	0.5699	0.3921	1
MF	GO:0015631	tubulin binding	1/58	366/22669	0.6114	0.4191	1
MF	GO:0004842	ubiquitin-protein transferase activity	1/58	418/22669	0.6607	0.4513	1
MF	GO:0005216	ion channel activity	1/58	421/22669	0.6633	0.4515	1
MF	GO:0046873	metal ion transmembrane transporter activity	1/58	426/22669	0.6677	0.4529	1
MF	GO:0003779	actin binding	1/58	434/22669	0.6746	0.4549	1
MF	GO:0019787	ubiquitin-like protein transferase activity	1/58	435/22669	0.6754	0.4549	1
MF	GO:0004175	endopeptidase activity	1/58	453/22669	0.6903	0.4628	1
MF	GO:0008047	enzyme activator activity	1/58	460/22669	0.6959	0.4628	1
MF	GO:0015267	channel activity	1/58	461/22669	0.6967	0.4628	1
MF	GO:0022803	passive transmembrane transporter activity	1/58	461/22669	0.6967	0.4628	1

Table S8 Significant Enrichment Results of GO Analysis of IRGs

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	qvalue	Count
BP	GO:0019221	cytokine-mediated signaling pathway	63/292	369/23328	5.30E-53	9.79E-50	63
BP	GO:0032103	positive regulation of response to external stimulus	62/292	418/23328	2.96E-48	2.73E-45	62
BP	GO:0060326	cell chemotaxis	54/292	303/23328	2.37E-46	1.46E-43	54
BP	GO:0001819	positive regulation of cytokine production	60/292	449/23328	6.23E-44	2.88E-41	60
BP	GO:0050727	regulation of inflammatory response	53/292	372/23328	3.27E-40	1.21E-37	53
BP	GO:0050900	leukocyte migration	51/292	360/23328	1.47E-38	4.53E-36	51
BP	GO:0055074	calcium ion homeostasis	56/292	493/23328	4.55E-37	1.18E-34	56

BP	GO:0050920	regulation of chemotaxis	42/292	224/23328	5.12E-37	1.18E-34	42
BP	GO:0030595	leukocyte chemotaxis	41/292	219/23328	4.07E-36	8.34E-34	41
BP	GO:0006874	cellular calcium ion homeostasis	53/292	476/23328	1.28E-34	2.37E-32	53
BP	GO:0051480	regulation of cytosolic calcium ion concentration	48/292	375/23328	3.50E-34	5.87E-32	48
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	45/292	330/23328	2.78E-33	4.28E-31	45
BP	GO:0018108	peptidyl-tyrosine phosphorylation	44/292	322/23328	1.38E-32	1.95E-30	44
BP	GO:0018212	peptidyl-tyrosine modification	44/292	325/23328	2.06E-32	2.72E-30	44
BP	GO:0097529	myeloid leukocyte migration	37/292	219/23328	6.20E-31	7.63E-29	37
BP	GO:0031349	positive regulation of defense response	39/292	278/23328	2.22E-29	2.56E-27	39
BP	GO:0032944	regulation of mononuclear cell proliferation	36/292	234/23328	1.27E-28	1.38E-26	36
BP	GO:0002697	regulation of immune effector process	45/292	440/23328	8.23E-28	8.44E-26	45
BP	GO:0050921	positive regulation of chemotaxis	30/292	149/23328	1.28E-27	1.20E-25	30
BP	GO:0050670	regulation of lymphocyte proliferation	35/292	231/23328	1.30E-27	1.20E-25	35
BP	GO:0070663	regulation of leukocyte proliferation	36/292	251/23328	1.62E-27	1.42E-25	36

BP	GO:1901342	regulation of vasculature development	41/292	356/23328	2.10E-27	1.76E-25	41
BP	GO:0045860	positive regulation of protein kinase activity	44/292	440/23328	8.57E-27	6.66E-25	44
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	36/292	263/23328	8.67E-27	6.66E-25	36
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	32/292	195/23328	1.92E-26	1.42E-24	32
BP	GO:0032102	negative regulation of response to external stimulus	41/292	384/23328	4.16E-26	2.95E-24	41
BP	GO:0032943	mononuclear cell proliferation	38/292	320/23328	6.22E-26	4.10E-24	38
BP	GO:0045765	regulation of angiogenesis	38/292	320/23328	6.22E-26	4.10E-24	38
BP	GO:0002237	response to molecule of bacterial origin	41/292	389/23328	6.90E-26	4.39E-24	41
BP	GO:0070661	leukocyte proliferation	39/292	344/23328	7.73E-26	4.75E-24	39
BP	GO:0071621	granulocyte chemotaxis	27/292	126/23328	9.86E-26	5.87E-24	27
BP	GO:0019932	second-messenger-mediated signaling	43/292	445/23328	1.37E-25	7.89E-24	43
BP	GO:0002274	myeloid leukocyte activation	33/292	231/23328	3.11E-25	1.74E-23	33
BP	GO:0046651	lymphocyte proliferation	37/292	317/23328	5.33E-25	2.89E-23	37
BP	GO:0050673	epithelial cell proliferation	42/292	438/23328	7.10E-25	3.75E-23	42

BP	GO:0050867	positive regulation of cell activation	44/292	496/23328	1.19E-24	6.11E-23	44
BP	GO:0097530	granulocyte migration	28/292	155/23328	1.84E-24	9.20E-23	28
BP	GO:0030593	neutrophil chemotaxis	24/292	99/23328	2.21E-24	1.07E-22	24
BP	GO:0002696	positive regulation of leukocyte activation	43/292	479/23328	2.63E-24	1.25E-22	43
BP	GO:0032496	response to lipopolysaccharide	38/292	368/23328	1.02E-23	4.71E-22	38
BP	GO:0022407	regulation of cell-cell adhesion	40/292	427/23328	2.45E-23	1.10E-21	40
BP	GO:1990266	neutrophil migration	25/292	124/23328	3.34E-23	1.47E-21	25
BP	GO:0032946	positive regulation of mononuclear cell proliferation	26/292	140/23328	4.10E-23	1.76E-21	26
BP	GO:0050678	regulation of epithelial cell proliferation	37/292	372/23328	1.53E-22	6.41E-21	37
BP	GO:0001667	ameboidal-type cell migration	39/292	427/23328	2.27E-22	9.30E-21	39
BP	GO:0070665	positive regulation of leukocyte proliferation	26/292	152/23328	3.75E-22	1.50E-20	26
BP	GO:0045785	positive regulation of cell adhesion	39/292	435/23328	4.44E-22	1.74E-20	39
BP	GO:0050671	positive regulation of lymphocyte proliferation	25/292	138/23328	5.50E-22	2.11E-20	25
BP	GO:0002687	positive regulation of leukocyte migration	26/292	156/23328	7.50E-22	2.82E-20	26

BP	GO:0002700	regulation of production of molecular mediator of immune response	26/292	159/23328	1.24E-21	4.59E-20	26
BP	GO:0070371	ERK1 and ERK2 cascade	34/292	325/23328	1.74E-21	6.30E-20	34
BP	GO:0009615	response to virus	32/292	286/23328	3.63E-21	1.29E-19	32
BP	GO:0050729	positive regulation of inflammatory response	25/292	152/23328	6.61E-21	2.30E-19	25
BP	GO:0046879	hormone secretion	35/292	364/23328	6.97E-21	2.38E-19	35
BP	GO:0070997	neuron death	37/292	416/23328	7.26E-21	2.39E-19	37
BP	GO:0048659	smooth muscle cell proliferation	26/292	170/23328	7.27E-21	2.39E-19	26
BP	GO:0002367	cytokine production involved in immune response	22/292	107/23328	9.41E-21	3.05E-19	22
BP	GO:0009914	hormone transport	35/292	372/23328	1.42E-20	4.52E-19	35
BP	GO:0070098	chemokine-mediated signaling pathway	18/292	60/23328	1.94E-20	6.06E-19	18
BP	GO:0097696	receptor signaling pathway via STAT	27/292	196/23328	2.13E-20	6.54E-19	27
BP	GO:0002685	regulation of leukocyte migration	28/292	217/23328	2.50E-20	7.55E-19	28
BP	GO:0032609	interferon-gamma production	23/292	128/23328	3.11E-20	9.26E-19	23
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	32/292	308/23328	3.49E-20	1.02E-18	32

BP	GO:0009611	response to wounding	39/292	492/23328	3.60E-20	1.04E-18	39
BP	GO:0032649	regulation of interferon-gamma production	22/292	114/23328	4.09E-20	1.16E-18	22
BP	GO:0022409	positive regulation of cell-cell adhesion	30/292	265/23328	4.74E-20	1.32E-18	30
BP	GO:0007259	receptor signaling pathway via JAK-STAT	26/292	191/23328	1.50E-19	4.13E-18	26
BP	GO:0002688	regulation of leukocyte chemotaxis	22/292	121/23328	1.60E-19	4.35E-18	22
BP	GO:0002819	regulation of adaptive immune response	27/292	213/23328	1.95E-19	5.13E-18	27
BP	GO:0042098	T cell proliferation	27/292	213/23328	1.95E-19	5.13E-18	27
BP	GO:1901214	regulation of neuron death	34/292	377/23328	1.98E-19	5.14E-18	34
BP	GO:0046883	regulation of hormone secretion	31/292	303/23328	2.19E-19	5.60E-18	31
BP	GO:0033002	muscle cell proliferation	28/292	236/23328	2.47E-19	6.25E-18	28
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	27/292	216/23328	2.82E-19	7.03E-18	27
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	31/292	309/23328	3.88E-19	9.54E-18	31
BP	GO:0002690	positive regulation of leukocyte chemotaxis	20/292	96/23328	4.27E-19	1.02E-17	20
BP	GO:1990868	response to chemokine	18/292	70/23328	4.35E-19	1.02E-17	18

BP	GO:1990869	cellular response to chemokine	18/292	70/23328	4.35E-19	1.02E-17	18
BP	GO:0001763	morphogenesis of a branching structure	28/292	241/23328	4.36E-19	1.02E-17	28
BP	GO:0002440	production of molecular mediator of immune response	33/292	361/23328	4.59E-19	1.06E-17	33
BP	GO:1903532	positive regulation of secretion by cell	34/292	388/23328	4.88E-19	1.11E-17	34
BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	36/292	445/23328	5.76E-19	1.29E-17	36
BP	GO:0061138	morphogenesis of a branching epithelium	27/292	222/23328	5.80E-19	1.29E-17	27
BP	GO:0002831	regulation of response to biotic stimulus	30/292	291/23328	6.90E-19	1.52E-17	30
BP	GO:0048660	regulation of smooth muscle cell proliferation	24/292	165/23328	8.05E-19	1.75E-17	24
BP	GO:0060560	developmental growth involved in morphogenesis	29/292	275/23328	1.46E-18	3.13E-17	29
BP	GO:2000027	regulation of animal organ morphogenesis	26/292	210/23328	1.69E-18	3.59E-17	26
BP	GO:0051047	positive regulation of secretion	35/292	440/23328	3.13E-18	6.56E-17	35
BP	GO:0042129	regulation of T cell proliferation	24/292	175/23328	3.28E-18	6.81E-17	24
BP	GO:0001818	negative regulation of cytokine production	28/292	260/23328	3.35E-18	6.86E-17	28
BP	GO:0110110	positive regulation of animal organ morphogenesis	20/292	106/23328	3.43E-18	6.96E-17	20

BP	GO:0051607	defense response to virus	27/292	239/23328	3.98E-18	7.97E-17	27
BP	GO:1904894	positive regulation of receptor signaling pathway via STAT	20/292	107/23328	4.18E-18	8.29E-17	20
BP	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	25/292	197/23328	4.32E-18	8.47E-17	25
BP	GO:0032147	activation of protein kinase activity	27/292	242/23328	5.49E-18	1.07E-16	27
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	26/292	221/23328	6.15E-18	1.18E-16	26
BP	GO:1903706	regulation of hemopoiesis	34/292	424/23328	7.65E-18	1.45E-16	34
BP	GO:1903708	positive regulation of hemopoiesis	26/292	224/23328	8.62E-18	1.62E-16	26
BP	GO:0007159	leukocyte cell-cell adhesion	31/292	345/23328	9.40E-18	1.75E-16	31
BP	GO:0071219	cellular response to molecule of bacterial origin	29/292	295/23328	9.97E-18	1.83E-16	29
BP	GO:0071216	cellular response to biotic stimulus	30/292	320/23328	1.00E-17	1.83E-16	30
BP	GO:0050863	regulation of T cell activation	30/292	321/23328	1.09E-17	1.98E-16	30
BP	GO:0002699	positive regulation of immune effector process	28/292	273/23328	1.22E-17	2.19E-16	28
BP	GO:0002718	regulation of cytokine production involved in immune response	18/292	85/23328	1.91E-17	3.39E-16	18
BP	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	17/292	73/23328	2.68E-17	4.72E-16	17

BP	GO:0019722	calcium-mediated signaling	25/292	214/23328	3.23E-17	5.62E-16	25
BP	GO:1904892	regulation of receptor signaling pathway via STAT	23/292	173/23328	3.41E-17	5.89E-16	23
BP	GO:0022612	gland morphogenesis	22/292	154/23328	3.53E-17	6.04E-16	22
BP	GO:0046427	positive regulation of receptor signaling pathway via JAK-STAT	19/292	103/23328	3.78E-17	6.38E-16	19
BP	GO:0071222	cellular response to lipopolysaccharide	28/292	285/23328	3.81E-17	6.38E-16	28
BP	GO:0071674	mononuclear cell migration	18/292	89/23328	4.59E-17	7.63E-16	18
BP	GO:0048762	mesenchymal cell differentiation	25/292	225/23328	1.08E-16	1.77E-15	25
BP	GO:0002702	positive regulation of production of molecular mediator of immune response	19/292	109/23328	1.15E-16	1.88E-15	19
BP	GO:0002526	acute inflammatory response	19/292	110/23328	1.38E-16	2.23E-15	19
BP	GO:0050919	negative chemotaxis	14/292	44/23328	1.39E-16	2.24E-15	14
BP	GO:0040013	negative regulation of locomotion	29/292	326/23328	1.48E-16	2.33E-15	29
BP	GO:0051271	negative regulation of cellular component movement	29/292	326/23328	1.48E-16	2.33E-15	29
BP	GO:0050679	positive regulation of epithelial cell proliferation	24/292	208/23328	1.89E-16	2.95E-15	24
BP	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	20/292	129/23328	1.93E-16	3.00E-15	20

BP	GO:0046425	regulation of receptor signaling pathway via JAK-STAT	22/292	168/23328	2.35E-16	3.61E-15	22
BP	GO:0051251	positive regulation of lymphocyte activation	32/292	416/23328	2.50E-16	3.81E-15	32
BP	GO:0042116	macrophage activation	18/292	100/23328	4.11E-16	6.21E-15	18
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	16/292	71/23328	4.15E-16	6.23E-15	16
BP	GO:0043523	regulation of neuron apoptotic process	26/292	270/23328	8.67E-16	1.29E-14	26
BP	GO:0042060	wound healing	29/292	349/23328	9.01E-16	1.33E-14	29
BP	GO:0007260	tyrosine phosphorylation of STAT protein	16/292	75/23328	1.06E-15	1.55E-14	16
BP	GO:0048638	regulation of developmental growth	31/292	409/23328	1.13E-15	1.65E-14	31
BP	GO:0001659	temperature homeostasis	22/292	181/23328	1.17E-15	1.68E-14	22
BP	GO:0043406	positive regulation of MAP kinase activity	24/292	226/23328	1.27E-15	1.81E-14	24
BP	GO:1901215	negative regulation of neuron death	25/292	251/23328	1.44E-15	2.04E-14	25
BP	GO:0031348	negative regulation of defense response	24/292	228/23328	1.55E-15	2.18E-14	24
BP	GO:0051897	positive regulation of protein kinase B signaling	18/292	109/23328	2.02E-15	2.82E-14	18
BP	GO:0019730	antimicrobial humoral response	21/292	165/23328	2.06E-15	2.86E-14	21

BP	GO:0060485	mesenchyme development	26/292	281/23328	2.28E-15	3.13E-14	26
BP	GO:0019233	sensory perception of pain	20/292	146/23328	2.30E-15	3.13E-14	20
BP	GO:0043270	positive regulation of ion transport	28/292	334/23328	2.31E-15	3.13E-14	28
BP	GO:0045766	positive regulation of angiogenesis	22/292	188/23328	2.62E-15	3.53E-14	22
BP	GO:0032635	interleukin-6 production	21/292	167/23328	2.64E-15	3.53E-14	21
BP	GO:0032729	positive regulation of interferon-gamma production	16/292	80/23328	3.16E-15	4.20E-14	16
BP	GO:0002703	regulation of leukocyte mediated immunity	25/292	261/23328	3.59E-15	4.73E-14	25
BP	GO:0010959	regulation of metal ion transport	31/292	427/23328	3.72E-15	4.86E-14	31
BP	GO:0071347	cellular response to interleukin-1	16/292	81/23328	3.90E-15	5.06E-14	16
BP	GO:1901652	response to peptide	30/292	400/23328	4.46E-15	5.75E-14	30
BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	18/292	114/23328	4.59E-15	5.88E-14	18
BP	GO:0002683	negative regulation of immune system process	32/292	462/23328	4.89E-15	6.22E-14	32
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	26/292	291/23328	5.28E-15	6.67E-14	26
BP	GO:0001936	regulation of endothelial cell proliferation	19/292	134/23328	6.10E-15	7.65E-14	19

BP	GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	17/292	99/23328	6.26E-15	7.81E-14	17
BP	GO:0002821	positive regulation of adaptive immune response	20/292	154/23328	6.57E-15	8.14E-14	20
BP	GO:0001558	regulation of cell growth	31/292	438/23328	7.45E-15	9.17E-14	31
BP	GO:0150076	neuroinflammatory response	15/292	70/23328	7.88E-15	9.63E-14	15
BP	GO:0050728	negative regulation of inflammatory response	20/292	156/23328	8.47E-15	1.03E-13	20
BP	GO:0051402	neuron apoptotic process	26/292	298/23328	9.31E-15	1.12E-13	26
BP	GO:0051048	negative regulation of secretion	23/292	223/23328	9.58E-15	1.15E-13	23
BP	GO:0050870	positive regulation of T cell activation	22/292	200/23328	9.67E-15	1.15E-13	22
BP	GO:1901343	negative regulation of vasculature development	19/292	139/23328	1.22E-14	1.44E-13	19
BP	GO:0072676	lymphocyte migration	17/292	103/23328	1.25E-14	1.47E-13	17
BP	GO:0060562	epithelial tube morphogenesis	29/292	387/23328	1.34E-14	1.56E-13	29
BP	GO:0042088	T-helper 1 type immune response	13/292	47/23328	1.36E-14	1.58E-13	13
BP	GO:0050886	endocrine process	17/292	104/23328	1.47E-14	1.70E-13	17
BP	GO:0001503	ossification	29/292	394/23328	2.12E-14	2.43E-13	29

BP	GO:0030217	T cell differentiation	25/292	282/23328	2.15E-14	2.45E-13	25
BP	GO:1904018	positive regulation of vasculature development	22/292	208/23328	2.20E-14	2.49E-13	22
BP	GO:0042063	gliogenesis	27/292	338/23328	2.43E-14	2.73E-13	27
BP	GO:0097191	extrinsic apoptotic signaling pathway	23/292	233/23328	2.47E-14	2.77E-13	23
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	17/292	108/23328	2.83E-14	3.14E-13	17
BP	GO:0031640	killing of cells of other organism	14/292	62/23328	2.88E-14	3.17E-13	14
BP	GO:0032613	interleukin-10 production	14/292	62/23328	2.88E-14	3.17E-13	14
BP	GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	19/292	147/23328	3.46E-14	3.78E-13	19
BP	GO:0061387	regulation of extent of cell growth	18/292	128/23328	3.71E-14	4.03E-13	18
BP	GO:0014065	phosphatidylinositol 3-kinase signaling	18/292	129/23328	4.26E-14	4.60E-13	18
BP	GO:0001935	endothelial cell proliferation	19/292	149/23328	4.45E-14	4.78E-13	19
BP	GO:0002791	regulation of peptide secretion	29/292	406/23328	4.58E-14	4.88E-13	29
BP	GO:0072593	reactive oxygen species metabolic process	25/292	292/23328	4.79E-14	5.08E-13	25
BP	GO:1903531	negative regulation of secretion by cell	21/292	193/23328	4.95E-14	5.22E-13	21

BP	GO:0048732	gland development	31/292	471/23328	5.32E-14	5.57E-13	31
BP	GO:0030098	lymphocyte differentiation	29/292	409/23328	5.52E-14	5.76E-13	29
BP	GO:0010631	epithelial cell migration	25/292	295/23328	6.04E-14	6.27E-13	25
BP	GO:0030516	regulation of axon extension	17/292	113/23328	6.13E-14	6.32E-13	17
BP	GO:0070555	response to interleukin-1	16/292	96/23328	6.49E-14	6.65E-13	16
BP	GO:0043491	protein kinase B signaling	21/292	196/23328	6.74E-14	6.87E-13	21
BP	GO:0090132	epithelium migration	25/292	297/23328	7.05E-14	7.15E-13	25
BP	GO:0048247	lymphocyte chemotaxis	13/292	53/23328	7.63E-14	7.69E-13	13
BP	GO:0051090	regulation of DNA-binding transcription factor activity	29/292	415/23328	8.00E-14	8.03E-13	29
BP	GO:0090130	tissue migration	25/292	299/23328	8.21E-14	8.19E-13	25
BP	GO:0043405	regulation of MAP kinase activity	25/292	301/23328	9.55E-14	9.48E-13	25
BP	GO:0003018	vascular process in circulatory system	22/292	224/23328	1.02E-13	1.01E-12	22
BP	GO:0042102	positive regulation of T cell proliferation	16/292	100/23328	1.26E-13	1.24E-12	16
BP	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	13/292	55/23328	1.29E-13	1.25E-12	13

BP	GO:0050922	negative regulation of chemotaxis	13/292	55/23328	1.29E-13	1.25E-12	13
BP	GO:0048841	regulation of axon extension involved in axon guidance	11/292	33/23328	1.48E-13	1.43E-12	11
BP	GO:0061900	glial cell activation	13/292	56/23328	1.66E-13	1.59E-12	13
BP	GO:1902105	regulation of leukocyte differentiation	25/292	309/23328	1.73E-13	1.65E-12	25
BP	GO:2000377	regulation of reactive oxygen species metabolic process	21/292	207/23328	1.99E-13	1.90E-12	21
BP	GO:0002548	monocyte chemotaxis	13/292	57/23328	2.12E-13	2.01E-12	13
BP	GO:0031644	regulation of nervous system process	20/292	185/23328	2.28E-13	2.13E-12	20
BP	GO:0048754	branching morphogenesis of an epithelial tube	20/292	185/23328	2.28E-13	2.13E-12	20
BP	GO:0071526	semaphorin-plexin signaling pathway	12/292	45/23328	2.35E-13	2.19E-12	12
BP	GO:0008217	regulation of blood pressure	21/292	209/23328	2.41E-13	2.24E-12	21
BP	GO:0032653	regulation of interleukin-10 production	13/292	58/23328	2.70E-13	2.50E-12	13
BP	GO:0010632	regulation of epithelial cell migration	22/292	235/23328	2.73E-13	2.51E-12	22
BP	GO:0009306	protein secretion	30/292	470/23328	3.07E-13	2.81E-12	30
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	16/292	106/23328	3.23E-13	2.92E-12	16

BP	GO:0035592	establishment of protein localization to extracellular region	30/292	471/23328	3.25E-13	2.92E-12	30
BP	GO:0046631	alpha-beta T cell activation	19/292	166/23328	3.26E-13	2.92E-12	19
BP	GO:0051896	regulation of protein kinase B signaling	19/292	166/23328	3.26E-13	2.92E-12	19
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	21/292	215/23328	4.21E-13	3.75E-12	21
BP	GO:2001233	regulation of apoptotic signaling pathway	28/292	413/23328	4.61E-13	4.09E-12	28
BP	GO:0071692	protein localization to extracellular region	30/292	478/23328	4.74E-13	4.19E-12	30
BP	GO:0032637	interleukin-8 production	14/292	75/23328	4.80E-13	4.22E-12	14
BP	GO:0048843	negative regulation of axon extension involved in axon guidance	10/292	27/23328	5.66E-13	4.95E-12	10
BP	GO:0007409	axonogenesis	30/292	482/23328	5.87E-13	5.11E-12	30
BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	21/292	219/23328	6.04E-13	5.24E-12	21
BP	GO:0048846	axon extension involved in axon guidance	11/292	37/23328	6.27E-13	5.38E-12	11
BP	GO:1902284	neuron projection extension involved in neuron projection guidance	11/292	37/23328	6.27E-13	5.38E-12	11
BP	GO:1901653	cellular response to peptide	24/292	299/23328	6.38E-13	5.45E-12	24
BP	GO:1902668	negative regulation of axon guidance	10/292	28/23328	8.71E-13	7.40E-12	10

BP	GO:0019216	regulation of lipid metabolic process	26/292	363/23328	9.38E-13	7.94E-12	26
BP	GO:0001906	cell killing	20/292	200/23328	9.94E-13	8.38E-12	20
BP	GO:0007411	axon guidance	22/292	251/23328	1.04E-12	8.72E-12	22
BP	GO:0097485	neuron projection guidance	22/292	252/23328	1.13E-12	9.41E-12	22
BP	GO:0032675	regulation of interleukin-6 production	18/292	156/23328	1.21E-12	1.00E-11	18
BP	GO:1902107	positive regulation of leukocyte differentiation	19/292	180/23328	1.41E-12	1.17E-11	19
BP	GO:0048675	axon extension	17/292	138/23328	1.76E-12	1.44E-11	17
BP	GO:0071887	leukocyte apoptotic process	17/292	138/23328	1.76E-12	1.44E-11	17
BP	GO:0002825	regulation of T-helper 1 type immune response	10/292	30/23328	1.95E-12	1.59E-11	10
BP	GO:0050770	regulation of axonogenesis	20/292	208/23328	2.07E-12	1.68E-11	20
BP	GO:0002369	T cell cytokine production	11/292	41/23328	2.22E-12	1.79E-11	11
BP	GO:0032755	positive regulation of interleukin-6 production	15/292	101/23328	2.30E-12	1.85E-11	15
BP	GO:0032680	regulation of tumor necrosis factor production	16/292	120/23328	2.33E-12	1.87E-11	16
BP	GO:1903034	regulation of response to wounding	19/292	186/23328	2.55E-12	2.03E-11	19

BP	GO:0048015	phosphatidylinositol-mediated signaling	18/292	164/23328	2.86E-12	2.27E-11	18
BP	GO:0045926	negative regulation of growth	22/292	264/23328	2.87E-12	2.27E-11	22
BP	GO:0032677	regulation of interleukin-8 production	13/292	69/23328	2.93E-12	2.31E-11	13
BP	GO:0016525	negative regulation of angiogenesis	16/292	122/23328	3.02E-12	2.36E-11	16
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	16/292	122/23328	3.02E-12	2.36E-11	16
BP	GO:0034612	response to tumor necrosis factor	19/292	188/23328	3.08E-12	2.40E-11	19
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	18/292	165/23328	3.17E-12	2.46E-11	18
BP	GO:0002673	regulation of acute inflammatory response	12/292	55/23328	3.21E-12	2.48E-11	12
BP	GO:0048588	developmental cell growth	22/292	267/23328	3.59E-12	2.76E-11	22
BP	GO:0030278	regulation of ossification	21/292	241/23328	3.87E-12	2.96E-11	21
BP	GO:0048017	inositol lipid-mediated signaling	18/292	167/23328	3.90E-12	2.97E-11	18
BP	GO:0044060	regulation of endocrine process	12/292	56/23328	4.04E-12	3.06E-11	12
BP	GO:0032640	tumor necrosis factor production	16/292	126/23328	5.00E-12	3.77E-11	16
BP	GO:2000181	negative regulation of blood vessel morphogenesis	16/292	126/23328	5.00E-12	3.77E-11	16

BP	GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	21/292	246/23328	5.74E-12	4.31E-11	21
BP	GO:0002221	pattern recognition receptor signaling pathway	17/292	149/23328	6.20E-12	4.63E-11	17
BP	GO:0001755	neural crest cell migration	12/292	58/23328	6.30E-12	4.69E-11	12
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	16/292	128/23328	6.39E-12	4.74E-11	16
BP	GO:0051924	regulation of calcium ion transport	22/292	275/23328	6.45E-12	4.76E-11	22
BP	GO:0002706	regulation of lymphocyte mediated immunity	19/292	196/23328	6.48E-12	4.76E-11	19
BP	GO:0046888	negative regulation of hormone secretion	14/292	90/23328	6.55E-12	4.78E-11	14
BP	GO:0048864	stem cell development	14/292	90/23328	6.55E-12	4.78E-11	14
BP	GO:1903522	regulation of blood circulation	21/292	248/23328	6.70E-12	4.87E-11	21
BP	GO:0050708	regulation of protein secretion	25/292	365/23328	6.97E-12	5.02E-11	25
BP	GO:0051961	negative regulation of nervous system development	25/292	365/23328	6.97E-12	5.02E-11	25
BP	GO:0035743	CD4-positive, alpha-beta T cell cytokine production	9/292	24/23328	7.40E-12	5.31E-11	9
BP	GO:0060443	mammary gland morphogenesis	12/292	59/23328	7.82E-12	5.60E-11	12
BP	GO:0007631	feeding behavior	16/292	130/23328	8.14E-12	5.79E-11	16

BP	GO:0002449	lymphocyte mediated immunity	27/292	432/23328	8.16E-12	5.79E-11	27
BP	GO:2000106	regulation of leukocyte apoptotic process	15/292	110/23328	8.20E-12	5.79E-11	15
BP	GO:0050768	negative regulation of neurogenesis	24/292	337/23328	8.23E-12	5.79E-11	24
BP	GO:0030308	negative regulation of cell growth	19/292	199/23328	8.48E-12	5.95E-11	19
BP	GO:1902667	regulation of axon guidance	11/292	46/23328	8.86E-12	6.19E-11	11
BP	GO:0002833	positive regulation of response to biotic stimulus	17/292	154/23328	1.06E-11	7.39E-11	17
BP	GO:0030517	negative regulation of axon extension	11/292	47/23328	1.14E-11	7.93E-11	11
BP	GO:0032615	interleukin-12 production	12/292	61/23328	1.19E-11	8.23E-11	12
BP	GO:0002285	lymphocyte activation involved in immune response	19/292	203/23328	1.20E-11	8.29E-11	19
BP	GO:0002366	leukocyte activation involved in immune response	22/292	285/23328	1.31E-11	8.96E-11	22
BP	GO:0071900	regulation of protein serine/threonine kinase activity	27/292	442/23328	1.38E-11	9.43E-11	27
BP	GO:0061180	mammary gland epithelium development	13/292	78/23328	1.51E-11	1.03E-10	13
BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	21/292	260/23328	1.65E-11	1.12E-10	21
BP	GO:0043524	negative regulation of neuron apoptotic process	18/292	182/23328	1.68E-11	1.14E-10	18

BP	GO:0002263	cell activation involved in immune response	22/292	289/23328	1.72E-11	1.16E-10	22
BP	GO:0032760	positive regulation of tumor necrosis factor production	12/292	63/23328	1.78E-11	1.20E-10	12
BP	GO:0034341	response to interferon-gamma	16/292	137/23328	1.83E-11	1.23E-10	16
BP	GO:0002675	positive regulation of acute inflammatory response	10/292	37/23328	2.09E-11	1.39E-10	10
BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	12/292	64/23328	2.17E-11	1.44E-10	12
BP	GO:0002705	positive regulation of leukocyte mediated immunity	18/292	185/23328	2.21E-11	1.46E-10	18
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	18/292	185/23328	2.21E-11	1.46E-10	18
BP	GO:0048863	stem cell differentiation	20/292	237/23328	2.29E-11	1.51E-10	20
BP	GO:0010721	negative regulation of cell development	25/292	387/23328	2.47E-11	1.62E-10	25
BP	GO:0008361	regulation of cell size	19/292	213/23328	2.80E-11	1.83E-10	19
BP	GO:0048872	homeostasis of number of cells	23/292	330/23328	3.52E-11	2.28E-10	23
BP	GO:0034764	positive regulation of transmembrane transport	20/292	243/23328	3.61E-11	2.34E-10	20
BP	GO:0032757	positive regulation of interleukin-8 production	11/292	52/23328	3.75E-11	2.42E-10	11
BP	GO:0045834	positive regulation of lipid metabolic process	17/292	167/23328	3.92E-11	2.52E-10	17

BP	GO:0014032	neural crest cell development	13/292	84/23328	4.01E-11	2.57E-10	13
BP	GO:0050771	negative regulation of axonogenesis	12/292	68/23328	4.60E-11	2.94E-10	12
BP	GO:0071356	cellular response to tumor necrosis factor	17/292	169/23328	4.74E-11	3.02E-10	17
BP	GO:0061041	regulation of wound healing	16/292	146/23328	4.86E-11	3.08E-10	16
BP	GO:0042092	type 2 immune response	10/292	40/23328	4.93E-11	3.11E-10	10
BP	GO:0002507	tolerance induction	9/292	29/23328	5.36E-11	3.38E-10	9
BP	GO:0048146	positive regulation of fibroblast proliferation	12/292	69/23328	5.51E-11	3.46E-10	12
BP	GO:0010001	glial cell differentiation	20/292	249/23328	5.61E-11	3.51E-10	20
BP	GO:0006953	acute-phase response	10/292	41/23328	6.44E-11	4.00E-10	10
BP	GO:0060603	mammary gland duct morphogenesis	10/292	41/23328	6.44E-11	4.00E-10	10
BP	GO:1990138	neuron projection extension	18/292	198/23328	6.88E-11	4.26E-10	18
BP	GO:0002720	positive regulation of cytokine production involved in immune response	11/292	55/23328	7.19E-11	4.44E-10	11
BP	GO:0001660	fever generation	7/292	13/23328	7.21E-11	4.44E-10	7
BP	GO:0010634	positive regulation of epithelial cell migration	16/292	150/23328	7.33E-11	4.48E-10	16

BP	GO:0031099	regeneration	16/292	150/23328	7.33E-11	4.48E-10	16
BP	GO:0045639	positive regulation of myeloid cell differentiation	14/292	108/23328	8.28E-11	5.04E-10	14
BP	GO:0033138	positive regulation of peptidyl-serine phosphorylation	15/292	129/23328	8.44E-11	5.12E-10	15
BP	GO:0014031	mesenchymal cell development	13/292	89/23328	8.53E-11	5.16E-10	13
BP	GO:0035296	regulation of tube diameter	17/292	176/23328	9.04E-11	5.43E-10	17
BP	GO:0097746	regulation of blood vessel diameter	17/292	176/23328	9.04E-11	5.43E-10	17
BP	GO:1901623	regulation of lymphocyte chemotaxis	8/292	21/23328	9.68E-11	5.80E-10	8
BP	GO:0035150	regulation of tube size	17/292	177/23328	9.89E-11	5.90E-10	17
BP	GO:0030099	myeloid cell differentiation	25/292	414/23328	1.04E-10	6.20E-10	25
BP	GO:0048640	negative regulation of developmental growth	15/292	131/23328	1.05E-10	6.25E-10	15
BP	GO:0014015	positive regulation of gliogenesis	13/292	91/23328	1.14E-10	6.70E-10	13
BP	GO:0014033	neural crest cell differentiation	13/292	91/23328	1.14E-10	6.70E-10	13
BP	GO:0002456	T cell mediated immunity	15/292	132/23328	1.17E-10	6.90E-10	15
BP	GO:0032655	regulation of interleukin-12 production	11/292	58/23328	1.32E-10	7.75E-10	11

BP	GO:0045088	regulation of innate immune response	17/292	181/23328	1.41E-10	8.21E-10	17
BP	GO:0006816	calcium ion transport	25/292	420/23328	1.41E-10	8.21E-10	25
BP	GO:0031649	heat generation	8/292	22/23328	1.50E-10	8.73E-10	8
BP	GO:0032642	regulation of chemokine production	12/292	75/23328	1.53E-10	8.84E-10	12
BP	GO:0050764	regulation of phagocytosis	14/292	113/23328	1.54E-10	8.86E-10	14
BP	GO:0050918	positive chemotaxis	10/292	45/23328	1.75E-10	1.01E-09	10
BP	GO:1990845	adaptive thermogenesis	16/292	159/23328	1.77E-10	1.01E-09	16
BP	GO:0006809	nitric oxide biosynthetic process	12/292	77/23328	2.10E-10	1.20E-09	12
BP	GO:0002827	positive regulation of T-helper 1 type immune response	8/292	23/23328	2.28E-10	1.30E-09	8
BP	GO:0060986	endocrine hormone secretion	11/292	61/23328	2.35E-10	1.33E-09	11
BP	GO:0070838	divalent metal ion transport	26/292	467/23328	2.53E-10	1.43E-09	26
BP	GO:0046632	alpha-beta T cell differentiation	14/292	118/23328	2.76E-10	1.56E-09	14
BP	GO:0033135	regulation of peptidyl-serine phosphorylation	16/292	164/23328	2.81E-10	1.58E-09	16
BP	GO:0046887	positive regulation of hormone secretion	16/292	164/23328	2.81E-10	1.58E-09	16

BP	GO:0032602	chemokine production	12/292	79/23328	2.87E-10	1.60E-09	12
BP	GO:0051781	positive regulation of cell division	12/292	79/23328	2.87E-10	1.60E-09	12
BP	GO:0072511	divalent inorganic cation transport	26/292	470/23328	2.91E-10	1.62E-09	26
BP	GO:0030728	ovulation	8/292	24/23328	3.38E-10	1.88E-09	8
BP	GO:0001774	microglial cell activation	10/292	48/23328	3.48E-10	1.91E-09	10
BP	GO:0002269	leukocyte activation involved in inflammatory response	10/292	48/23328	3.48E-10	1.91E-09	10
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	10/292	48/23328	3.48E-10	1.91E-09	10
BP	GO:0006959	humoral immune response	24/292	406/23328	3.85E-10	2.11E-09	24
BP	GO:0046209	nitric oxide metabolic process	12/292	81/23328	3.87E-10	2.11E-09	12
BP	GO:0002573	myeloid leukocyte differentiation	18/292	220/23328	3.89E-10	2.12E-09	18
BP	GO:0048608	reproductive structure development	26/292	477/23328	3.99E-10	2.16E-09	26
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	15/292	144/23328	4.07E-10	2.20E-09	15
BP	GO:1904407	positive regulation of nitric oxide metabolic process	10/292	49/23328	4.32E-10	2.33E-09	10
BP	GO:0019933	cAMP-mediated signaling	17/292	195/23328	4.52E-10	2.43E-09	17

BP	GO:0001655	urogenital system development	23/292	376/23328	4.66E-10	2.50E-09	23
BP	GO:0061458	reproductive system development	26/292	481/23328	4.77E-10	2.55E-09	26
BP	GO:0019935	cyclic-nucleotide-mediated signaling	18/292	223/23328	4.84E-10	2.58E-09	18
BP	GO:0045927	positive regulation of growth	21/292	312/23328	4.87E-10	2.59E-09	21
BP	GO:0048771	tissue remodeling	17/292	196/23328	4.90E-10	2.60E-09	17
BP	GO:0045637	regulation of myeloid cell differentiation	18/292	224/23328	5.21E-10	2.75E-09	18
BP	GO:0032535	regulation of cellular component size	24/292	413/23328	5.42E-10	2.86E-09	24
BP	GO:1903409	reactive oxygen species biosynthetic process	14/292	125/23328	6.00E-10	3.16E-09	14
BP	GO:2000273	positive regulation of signaling receptor activity	9/292	37/23328	6.10E-10	3.20E-09	9
BP	GO:0032722	positive regulation of chemokine production	10/292	51/23328	6.58E-10	3.44E-09	10
BP	GO:0060688	regulation of morphogenesis of a branching structure	11/292	67/23328	6.76E-10	3.52E-09	11
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	12/292	85/23328	6.89E-10	3.58E-09	12
BP	GO:0031620	regulation of fever generation	6/292	10/23328	7.36E-10	3.81E-09	6
BP	GO:0140131	positive regulation of lymphocyte chemotaxis	7/292	17/23328	7.83E-10	4.05E-09	7

BP	GO:0014002	astrocyte development	9/292	38/23328	7.91E-10	4.06E-09	9
BP	GO:0032733	positive regulation of interleukin-10 production	9/292	38/23328	7.91E-10	4.06E-09	9
BP	GO:2001057	reactive nitrogen species metabolic process	12/292	86/23328	7.91E-10	4.06E-09	12
BP	GO:2001234	negative regulation of apoptotic signaling pathway	18/292	231/23328	8.56E-10	4.38E-09	18
BP	GO:0045428	regulation of nitric oxide biosynthetic process	11/292	69/23328	9.38E-10	4.78E-09	11
BP	GO:0002224	toll-like receptor signaling pathway	13/292	108/23328	1.01E-09	5.14E-09	13
BP	GO:0062012	regulation of small molecule metabolic process	22/292	358/23328	1.04E-09	5.25E-09	22
BP	GO:0048144	fibroblast proliferation	13/292	109/23328	1.13E-09	5.74E-09	13
BP	GO:0032612	interleukin-1 production	13/292	110/23328	1.27E-09	6.41E-09	13
BP	GO:0002437	inflammatory response to antigenic stimulus	11/292	71/23328	1.29E-09	6.48E-09	11
BP	GO:0050866	negative regulation of cell activation	17/292	210/23328	1.42E-09	7.12E-09	17
BP	GO:0042692	muscle cell differentiation	23/292	399/23328	1.47E-09	7.35E-09	23
BP	GO:0050777	negative regulation of immune response	15/292	158/23328	1.50E-09	7.48E-09	15
BP	GO:0001938	positive regulation of endothelial cell proliferation	12/292	91/23328	1.54E-09	7.64E-09	12

BP	GO:0032611	interleukin-1 beta production	12/292	91/23328	1.54E-09	7.64E-09	12
BP	GO:1903524	positive regulation of blood circulation	12/292	91/23328	1.54E-09	7.64E-09	12
BP	GO:0043542	endothelial cell migration	17/292	212/23328	1.64E-09	8.10E-09	17
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	22/292	368/23328	1.73E-09	8.50E-09	22
BP	GO:0071675	regulation of mononuclear cell migration	10/292	56/23328	1.73E-09	8.51E-09	10
BP	GO:0014909	smooth muscle cell migration	12/292	92/23328	1.76E-09	8.60E-09	12
BP	GO:0003014	renal system process	13/292	113/23328	1.78E-09	8.70E-09	13
BP	GO:0048143	astrocyte activation	7/292	19/23328	1.99E-09	9.66E-09	7
BP	GO:0071346	cellular response to interferon-gamma	13/292	114/23328	1.99E-09	9.66E-09	13
BP	GO:0002292	T cell differentiation involved in immune response	11/292	74/23328	2.03E-09	9.83E-09	11
BP	GO:0007422	peripheral nervous system development	11/292	74/23328	2.03E-09	9.83E-09	11
BP	GO:0001776	leukocyte homeostasis	13/292	115/23328	2.22E-09	1.07E-08	13
BP	GO:0002695	negative regulation of leukocyte activation	16/292	189/23328	2.28E-09	1.10E-08	16
BP	GO:0061448	connective tissue development	19/292	276/23328	2.30E-09	1.10E-08	19

BP	GO:0048639	positive regulation of developmental growth	17/292	217/23328	2.34E-09	1.12E-08	17
BP	GO:0051145	smooth muscle cell differentiation	11/292	75/23328	2.36E-09	1.12E-08	11
BP	GO:0030879	mammary gland development	15/292	164/23328	2.52E-09	1.19E-08	15
BP	GO:0010863	positive regulation of phospholipase C activity	8/292	30/23328	2.52E-09	1.19E-08	8
BP	GO:0061082	myeloid leukocyte cytokine production	8/292	30/23328	2.52E-09	1.19E-08	8
BP	GO:0030336	negative regulation of cell migration	19/292	278/23328	2.60E-09	1.22E-08	19
BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	14/292	140/23328	2.70E-09	1.27E-08	14
BP	GO:0002286	T cell activation involved in immune response	13/292	117/23328	2.75E-09	1.29E-08	13
BP	GO:2000243	positive regulation of reproductive process	12/292	96/23328	2.89E-09	1.35E-08	12
BP	GO:0060193	positive regulation of lipase activity	10/292	59/23328	2.96E-09	1.38E-08	10
BP	GO:0010594	regulation of endothelial cell migration	15/292	166/23328	2.98E-09	1.39E-08	15
BP	GO:1901224	positive regulation of NIK/NF-kappaB signaling	11/292	77/23328	3.15E-09	1.46E-08	11
BP	GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	8/292	31/23328	3.36E-09	1.56E-08	8
BP	GO:0000187	activation of MAPK activity	13/292	119/23328	3.39E-09	1.56E-08	13

BP	GO:0060759	regulation of response to cytokine stimulus	13/292	119/23328	3.39E-09	1.56E-08	13
BP	GO:0072678	T cell migration	10/292	60/23328	3.51E-09	1.62E-08	10
BP	GO:0032652	regulation of interleukin-1 production	12/292	98/23328	3.68E-09	1.69E-08	12
BP	GO:0106106	cold-induced thermogenesis	14/292	144/23328	3.90E-09	1.78E-08	14
BP	GO:0120161	regulation of cold-induced thermogenesis	14/292	144/23328	3.90E-09	1.78E-08	14
BP	GO:0030072	peptide hormone secretion	19/292	285/23328	3.91E-09	1.78E-08	19
BP	GO:0002637	regulation of immunoglobulin production	11/292	79/23328	4.16E-09	1.89E-08	11
BP	GO:0010771	negative regulation of cell morphogenesis involved in differentiation	12/292	100/23328	4.65E-09	2.11E-08	12
BP	GO:0032651	regulation of interleukin-1 beta production	11/292	80/23328	4.77E-09	2.16E-08	11
BP	GO:0010518	positive regulation of phospholipase activity	9/292	46/23328	4.90E-09	2.21E-08	9
BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	14/292	147/23328	5.10E-09	2.30E-08	14
BP	GO:0051216	cartilage development	16/292	200/23328	5.17E-09	2.32E-08	16
BP	GO:0007162	negative regulation of cell adhesion	19/292	290/23328	5.20E-09	2.33E-08	19
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	12/292	101/23328	5.22E-09	2.33E-08	12

BP	GO:0045665	negative regulation of neuron differentiation	18/292	259/23328	5.29E-09	2.36E-08	18
BP	GO:2000146	negative regulation of cell motility	19/292	291/23328	5.50E-09	2.45E-08	19
BP	GO:0003073	regulation of systemic arterial blood pressure	13/292	124/23328	5.63E-09	2.50E-08	13
BP	GO:1903428	positive regulation of reactive oxygen species biosynthetic process	10/292	63/23328	5.76E-09	2.55E-08	10
BP	GO:1901186	positive regulation of ERBB signaling pathway	8/292	33/23328	5.79E-09	2.56E-08	8
BP	GO:0042310	vasoconstriction	12/292	103/23328	6.55E-09	2.89E-08	12
BP	GO:0010977	negative regulation of neuron projection development	15/292	176/23328	6.65E-09	2.92E-08	15
BP	GO:1901222	regulation of NIK/NF-kappaB signaling	12/292	104/23328	7.32E-09	3.21E-08	12
BP	GO:1900274	regulation of phospholipase C activity	8/292	34/23328	7.50E-09	3.28E-08	8
BP	GO:0042093	T-helper cell differentiation	10/292	65/23328	7.90E-09	3.44E-08	10
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	10/292	65/23328	7.90E-09	3.44E-08	10
BP	GO:0050766	positive regulation of phagocytosis	11/292	84/23328	8.09E-09	3.51E-08	11
BP	GO:0014812	muscle cell migration	12/292	106/23328	9.12E-09	3.95E-08	12
BP	GO:0007218	neuropeptide signaling pathway	11/292	85/23328	9.19E-09	3.96E-08	11

BP	GO:0014910	regulation of smooth muscle cell migration	11/292	85/23328	9.19E-09	3.96E-08	11
BP	GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	10/292	66/23328	9.20E-09	3.96E-08	10
BP	GO:0014013	regulation of gliogenesis	14/292	154/23328	9.33E-09	4.00E-08	14
BP	GO:0048145	regulation of fibroblast proliferation	12/292	107/23328	1.02E-08	4.34E-08	12
BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	12/292	107/23328	1.02E-08	4.34E-08	12
BP	GO:0043434	response to peptide hormone	20/292	336/23328	1.04E-08	4.43E-08	20
BP	GO:0048708	astrocyte differentiation	11/292	86/23328	1.04E-08	4.43E-08	11
BP	GO:0002293	alpha-beta T cell differentiation involved in immune response	10/292	67/23328	1.07E-08	4.54E-08	10
BP	GO:0002287	alpha-beta T cell activation involved in immune response	10/292	68/23328	1.24E-08	5.25E-08	10
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	12/292	109/23328	1.26E-08	5.29E-08	12
BP	GO:0097756	negative regulation of blood vessel diameter	12/292	109/23328	1.26E-08	5.29E-08	12
BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	9/292	51/23328	1.28E-08	5.37E-08	9
BP	GO:0060760	positive regulation of response to cytokine stimulus	9/292	51/23328	1.28E-08	5.37E-08	9
BP	GO:0036314	response to sterol	7/292	24/23328	1.29E-08	5.41E-08	7

BP	GO:0044070	regulation of anion transport	13/292	133/23328	1.33E-08	5.53E-08	13
BP	GO:0050672	negative regulation of lymphocyte proliferation	11/292	88/23328	1.33E-08	5.56E-08	11
BP	GO:0038061	NIK/NF-kappaB signaling	12/292	110/23328	1.39E-08	5.78E-08	12
BP	GO:0045089	positive regulation of innate immune response	12/292	110/23328	1.39E-08	5.78E-08	12
BP	GO:0009266	response to temperature stimulus	14/292	159/23328	1.41E-08	5.81E-08	14
BP	GO:0045580	regulation of T cell differentiation	14/292	159/23328	1.41E-08	5.81E-08	14
BP	GO:0032945	negative regulation of mononuclear cell proliferation	11/292	89/23328	1.51E-08	6.20E-08	11
BP	GO:0034767	positive regulation of ion transmembrane transport	15/292	187/23328	1.51E-08	6.22E-08	15
BP	GO:0002639	positive regulation of immunoglobulin production	9/292	52/23328	1.53E-08	6.27E-08	9
BP	GO:0140353	lipid export from cell	9/292	52/23328	1.53E-08	6.27E-08	9
BP	GO:2000107	negative regulation of leukocyte apoptotic process	10/292	70/23328	1.66E-08	6.75E-08	10
BP	GO:0010819	regulation of T cell chemotaxis	6/292	15/23328	1.66E-08	6.75E-08	6
BP	GO:0031650	regulation of heat generation	6/292	15/23328	1.66E-08	6.75E-08	6
BP	GO:0050930	induction of positive chemotaxis	6/292	15/23328	1.66E-08	6.75E-08	6

BP	GO:0034114	regulation of heterotypic cell-cell adhesion	7/292	25/23328	1.78E-08	7.19E-08	7
BP	GO:0051783	regulation of nuclear division	15/292	191/23328	2.01E-08	8.11E-08	15
BP	GO:0061351	neural precursor cell proliferation	15/292	191/23328	2.01E-08	8.11E-08	15
BP	GO:0010769	regulation of cell morphogenesis involved in differentiation	20/292	351/23328	2.16E-08	8.70E-08	20
BP	GO:0051147	regulation of muscle cell differentiation	14/292	165/23328	2.26E-08	9.07E-08	14
BP	GO:0071375	cellular response to peptide hormone stimulus	17/292	253/23328	2.34E-08	9.35E-08	17
BP	GO:0050927	positive regulation of positive chemotaxis	7/292	26/23328	2.40E-08	9.57E-08	7
BP	GO:0032735	positive regulation of interleukin-12 production	8/292	39/23328	2.41E-08	9.57E-08	8
BP	GO:2000403	positive regulation of lymphocyte migration	8/292	39/23328	2.41E-08	9.57E-08	8
BP	GO:0010712	regulation of collagen metabolic process	9/292	55/23328	2.56E-08	1.02E-07	9
BP	GO:0002830	positive regulation of type 2 immune response	6/292	16/23328	2.63E-08	1.04E-07	6
BP	GO:2000241	regulation of reproductive process	15/292	195/23328	2.66E-08	1.05E-07	15
BP	GO:0070664	negative regulation of leukocyte proliferation	11/292	94/23328	2.69E-08	1.06E-07	11
BP	GO:0051341	regulation of oxidoreductase activity	11/292	95/23328	3.01E-08	1.18E-07	11

BP	GO:0051930	regulation of sensory perception of pain	9/292	56/23328	3.02E-08	1.19E-07	9
BP	GO:1904019	epithelial cell apoptotic process	12/292	118/23328	3.09E-08	1.21E-07	12
BP	GO:0050926	regulation of positive chemotaxis	7/292	27/23328	3.21E-08	1.26E-07	7
BP	GO:1904062	regulation of cation transmembrane transport	20/292	361/23328	3.45E-08	1.34E-07	20
BP	GO:0043030	regulation of macrophage activation	9/292	57/23328	3.55E-08	1.38E-07	9
BP	GO:0051931	regulation of sensory perception	9/292	57/23328	3.55E-08	1.38E-07	9
BP	GO:0098801	regulation of renal system process	8/292	41/23328	3.66E-08	1.42E-07	8
BP	GO:0002793	positive regulation of peptide secretion	16/292	230/23328	3.76E-08	1.45E-07	16
BP	GO:0010517	regulation of phospholipase activity	9/292	58/23328	4.15E-08	1.60E-07	9
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	11/292	99/23328	4.65E-08	1.79E-07	11
BP	GO:0072001	renal system development	19/292	333/23328	4.81E-08	1.85E-07	19
BP	GO:0060191	regulation of lipase activity	10/292	79/23328	5.45E-08	2.09E-07	10
BP	GO:0003012	muscle system process	21/292	408/23328	5.48E-08	2.10E-07	21
BP	GO:0060444	branching involved in mammary gland duct morphogenesis	7/292	29/23328	5.52E-08	2.11E-07	7

BP	GO:2000401	regulation of lymphocyte migration	9/292	60/23328	5.64E-08	2.15E-07	9
BP	GO:0010976	positive regulation of neuron projection development	20/292	372/23328	5.64E-08	2.15E-07	20
BP	GO:0031345	negative regulation of cell projection organization	15/292	207/23328	5.89E-08	2.23E-07	15
BP	GO:0043087	regulation of GTPase activity	18/292	303/23328	5.95E-08	2.25E-07	18
BP	GO:0050688	regulation of defense response to virus	10/292	80/23328	6.16E-08	2.33E-07	10
BP	GO:0034765	regulation of ion transmembrane transport	23/292	489/23328	6.51E-08	2.46E-07	23
BP	GO:0032768	regulation of monooxygenase activity	8/292	44/23328	6.56E-08	2.47E-07	8
BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	8/292	44/23328	6.56E-08	2.47E-07	8
BP	GO:0051785	positive regulation of nuclear division	10/292	81/23328	6.95E-08	2.61E-07	10
BP	GO:0035744	T-helper 1 cell cytokine production	5/292	10/23328	7.11E-08	2.66E-07	5
BP	GO:0002724	regulation of T cell cytokine production	7/292	30/23328	7.13E-08	2.66E-07	7
BP	GO:0014911	positive regulation of smooth muscle cell migration	9/292	62/23328	7.57E-08	2.82E-07	9
BP	GO:0045778	positive regulation of ossification	11/292	104/23328	7.79E-08	2.90E-07	11
BP	GO:0001961	positive regulation of cytokine-mediated signaling pathway	8/292	45/23328	7.90E-08	2.93E-07	8

BP	GO:0045923	positive regulation of fatty acid metabolic process	8/292	45/23328	7.90E-08	2.93E-07	8
BP	GO:0042113	B cell activation	21/292	417/23328	7.92E-08	2.93E-07	21
BP	GO:0008016	regulation of heart contraction	14/292	183/23328	8.34E-08	3.08E-07	14
BP	GO:0046634	regulation of alpha-beta T cell activation	11/292	105/23328	8.60E-08	3.17E-07	11
BP	GO:0002643	regulation of tolerance induction	6/292	19/23328	8.64E-08	3.17E-07	6
BP	GO:0002726	positive regulation of T cell cytokine production	6/292	19/23328	8.64E-08	3.17E-07	6
BP	GO:0046890	regulation of lipid biosynthetic process	14/292	184/23328	8.93E-08	3.27E-07	14
BP	GO:0007517	muscle organ development	21/292	420/23328	8.94E-08	3.27E-07	21
BP	GO:0002828	regulation of type 2 immune response	7/292	31/23328	9.11E-08	3.30E-07	7
BP	GO:0042634	regulation of hair cycle	7/292	31/23328	9.11E-08	3.30E-07	7
BP	GO:0045662	negative regulation of myoblast differentiation	7/292	31/23328	9.11E-08	3.30E-07	7
BP	GO:0048535	lymph node development	7/292	31/23328	9.11E-08	3.30E-07	7
BP	GO:0032368	regulation of lipid transport	12/292	130/23328	9.15E-08	3.31E-07	12
BP	GO:0060402	calcium ion transport into cytosol	13/292	157/23328	9.65E-08	3.48E-07	13

BP	GO:0062013	positive regulation of small molecule metabolic process	13/292	157/23328	9.65E-08	3.48E-07	13
BP	GO:0050707	regulation of cytokine secretion	9/292	64/23328	1.01E-07	3.62E-07	9
BP	GO:0010469	regulation of signaling receptor activity	12/292	132/23328	1.08E-07	3.89E-07	12
BP	GO:0048246	macrophage chemotaxis	8/292	47/23328	1.13E-07	4.03E-07	8
BP	GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	8/292	47/23328	1.13E-07	4.03E-07	8
BP	GO:0045840	positive regulation of mitotic nuclear division	9/292	65/23328	1.15E-07	4.12E-07	9
BP	GO:0042303	molting cycle	12/292	133/23328	1.18E-07	4.19E-07	12
BP	GO:0042633	hair cycle	12/292	133/23328	1.18E-07	4.19E-07	12
BP	GO:0010818	T cell chemotaxis	6/292	20/23328	1.22E-07	4.33E-07	6
BP	GO:0048245	eosinophil chemotaxis	6/292	20/23328	1.22E-07	4.33E-07	6
BP	GO:0001822	kidney development	18/292	318/23328	1.23E-07	4.35E-07	18
BP	GO:0050878	regulation of body fluid levels	19/292	354/23328	1.25E-07	4.42E-07	19
BP	GO:0051209	release of sequestered calcium ion into cytosol	11/292	109/23328	1.27E-07	4.46E-07	11
BP	GO:0045444	fat cell differentiation	16/292	252/23328	1.33E-07	4.67E-07	16

BP	GO:0022602	ovulation cycle process	8/292	48/23328	1.34E-07	4.69E-07	8
BP	GO:0032965	regulation of collagen biosynthetic process	8/292	48/23328	1.34E-07	4.69E-07	8
BP	GO:0051235	maintenance of location	18/292	320/23328	1.35E-07	4.72E-07	18
BP	GO:0034103	regulation of tissue remodeling	10/292	87/23328	1.39E-07	4.83E-07	10
BP	GO:0060047	heart contraction	15/292	221/23328	1.39E-07	4.84E-07	15
BP	GO:0051283	negative regulation of sequestering of calcium ion	11/292	110/23328	1.39E-07	4.84E-07	11
BP	GO:0042119	neutrophil activation	7/292	33/23328	1.45E-07	5.02E-07	7
BP	GO:0043547	positive regulation of GTPase activity	15/292	222/23328	1.47E-07	5.10E-07	15
BP	GO:0045787	positive regulation of cell cycle	19/292	358/23328	1.49E-07	5.16E-07	19
BP	GO:0051928	positive regulation of calcium ion transport	12/292	136/23328	1.51E-07	5.18E-07	12
BP	GO:0097553	calcium ion transmembrane import into cytosol	12/292	136/23328	1.51E-07	5.18E-07	12
BP	GO:0022408	negative regulation of cell-cell adhesion	14/292	192/23328	1.51E-07	5.19E-07	14
BP	GO:0045619	regulation of lymphocyte differentiation	14/292	192/23328	1.51E-07	5.19E-07	14
BP	GO:0019218	regulation of steroid metabolic process	11/292	111/23328	1.53E-07	5.24E-07	11

BP	GO:0010827	regulation of glucose transmembrane transport	10/292	88/23328	1.55E-07	5.28E-07	10
BP	GO:0051282	regulation of sequestering of calcium ion	11/292	112/23328	1.68E-07	5.72E-07	11
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	9/292	68/23328	1.72E-07	5.86E-07	9
BP	GO:1905952	regulation of lipid localization	13/292	165/23328	1.73E-07	5.87E-07	13
BP	GO:0010714	positive regulation of collagen metabolic process	7/292	34/23328	1.80E-07	6.12E-07	7
BP	GO:0001942	hair follicle development	11/292	113/23328	1.84E-07	6.21E-07	11
BP	GO:0051208	sequestering of calcium ion	11/292	113/23328	1.84E-07	6.21E-07	11
BP	GO:0006939	smooth muscle contraction	11/292	114/23328	2.01E-07	6.77E-07	11
BP	GO:1905330	regulation of morphogenesis of an epithelium	11/292	114/23328	2.01E-07	6.77E-07	11
BP	GO:0032890	regulation of organic acid transport	10/292	91/23328	2.13E-07	7.16E-07	10
BP	GO:0030888	regulation of B cell proliferation	9/292	70/23328	2.22E-07	7.46E-07	9
BP	GO:0018105	peptidyl-serine phosphorylation	18/292	331/23328	2.23E-07	7.46E-07	18
BP	GO:0050832	defense response to fungus	7/292	35/23328	2.23E-07	7.46E-07	7
BP	GO:0051797	regulation of hair follicle development	6/292	22/23328	2.30E-07	7.67E-07	6

BP	GO:0060602	branch elongation of an epithelium	6/292	22/23328	2.30E-07	7.67E-07	6
BP	GO:0022404	molting cycle process	11/292	116/23328	2.40E-07	7.96E-07	11
BP	GO:0022405	hair cycle process	11/292	116/23328	2.40E-07	7.96E-07	11
BP	GO:0098773	skin epidermis development	11/292	116/23328	2.40E-07	7.96E-07	11
BP	GO:1904064	positive regulation of cation transmembrane transport	13/292	170/23328	2.44E-07	8.08E-07	13
BP	GO:0003015	heart process	15/292	231/23328	2.47E-07	8.14E-07	15
BP	GO:0009620	response to fungus	8/292	52/23328	2.56E-07	8.39E-07	8
BP	GO:0032481	positive regulation of type I interferon production	8/292	52/23328	2.56E-07	8.39E-07	8
BP	GO:0032731	positive regulation of interleukin-1 beta production	8/292	52/23328	2.56E-07	8.39E-07	8
BP	GO:0007611	learning or memory	17/292	299/23328	2.60E-07	8.53E-07	17
BP	GO:0010573	vascular endothelial growth factor production	7/292	36/23328	2.74E-07	8.95E-07	7
BP	GO:1902624	positive regulation of neutrophil migration	7/292	36/23328	2.74E-07	8.95E-07	7
BP	GO:0050890	cognition	18/292	336/23328	2.78E-07	9.07E-07	18
BP	GO:0021782	glial cell development	11/292	118/23328	2.86E-07	9.31E-07	11

BP	GO:1904035	regulation of epithelial cell apoptotic process	10/292	94/23328	2.90E-07	9.42E-07	10
BP	GO:0002714	positive regulation of B cell mediated immunity	8/292	53/23328	2.98E-07	9.61E-07	8
BP	GO:0002891	positive regulation of immunoglobulin mediated immune response	8/292	53/23328	2.98E-07	9.61E-07	8
BP	GO:0010596	negative regulation of endothelial cell migration	8/292	53/23328	2.98E-07	9.61E-07	8
BP	GO:0051955	regulation of amino acid transport	8/292	53/23328	2.98E-07	9.61E-07	8
BP	GO:0072073	kidney epithelium development	12/292	145/23328	3.04E-07	9.78E-07	12
BP	GO:0090276	regulation of peptide hormone secretion	15/292	235/23328	3.07E-07	9.88E-07	15
BP	GO:0002719	negative regulation of cytokine production involved in immune response	6/292	23/23328	3.08E-07	9.90E-07	6
BP	GO:0042130	negative regulation of T cell proliferation	9/292	73/23328	3.21E-07	1.03E-06	9
BP	GO:0034113	heterotypic cell-cell adhesion	8/292	54/23328	3.46E-07	1.10E-06	8
BP	GO:0045687	positive regulation of glial cell differentiation	8/292	54/23328	3.46E-07	1.10E-06	8
BP	GO:1904705	regulation of vascular associated smooth muscle cell proliferation	8/292	54/23328	3.46E-07	1.10E-06	8
BP	GO:1990874	vascular associated smooth muscle cell proliferation	8/292	54/23328	3.46E-07	1.10E-06	8
BP	GO:0002517	T cell tolerance induction	5/292	13/23328	3.52E-07	1.11E-06	5

BP	GO:0031652	positive regulation of heat generation	5/292	13/23328	3.52E-07	1.11E-06	5
BP	GO:0045741	positive regulation of epidermal growth factor-activated receptor activity	5/292	13/23328	3.52E-07	1.11E-06	5
BP	GO:0035265	organ growth	14/292	207/23328	3.81E-07	1.20E-06	14
BP	GO:0060401	cytosolic calcium ion transport	13/292	177/23328	3.89E-07	1.23E-06	13
BP	GO:0120162	positive regulation of cold-induced thermogenesis	10/292	97/23328	3.90E-07	1.23E-06	10
BP	GO:0042593	glucose homeostasis	16/292	273/23328	3.92E-07	1.23E-06	16
BP	GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	8/292	55/23328	4.00E-07	1.25E-06	8
BP	GO:2000351	regulation of endothelial cell apoptotic process	8/292	55/23328	4.00E-07	1.25E-06	8
BP	GO:0001666	response to hypoxia	14/292	208/23328	4.04E-07	1.26E-06	14
BP	GO:0070498	interleukin-1-mediated signaling pathway	6/292	24/23328	4.07E-07	1.27E-06	6
BP	GO:0072677	eosinophil migration	6/292	24/23328	4.07E-07	1.27E-06	6
BP	GO:0046660	female sex differentiation	12/292	149/23328	4.08E-07	1.27E-06	12
BP	GO:0002764	immune response-regulating signaling pathway	18/292	345/23328	4.10E-07	1.27E-06	18
BP	GO:0033500	carbohydrate homeostasis	16/292	274/23328	4.12E-07	1.28E-06	16

BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	14/292	209/23328	4.28E-07	1.32E-06	14
BP	GO:0060395	SMAD protein signal transduction	10/292	98/23328	4.30E-07	1.33E-06	10
BP	GO:0002040	sprouting angiogenesis	11/292	123/23328	4.36E-07	1.35E-06	11
BP	GO:0050663	cytokine secretion	9/292	76/23328	4.56E-07	1.41E-06	9
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	8/292	56/23328	4.62E-07	1.42E-06	8
BP	GO:0042742	defense response to bacterium	21/292	464/23328	4.64E-07	1.43E-06	21
BP	GO:0033028	myeloid cell apoptotic process	7/292	39/23328	4.89E-07	1.50E-06	7
BP	GO:0036230	granulocyte activation	7/292	39/23328	4.89E-07	1.50E-06	7
BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	11/292	125/23328	5.13E-07	1.57E-06	11
BP	GO:0046889	positive regulation of lipid biosynthetic process	10/292	100/23328	5.19E-07	1.58E-06	10
BP	GO:0032964	collagen biosynthetic process	8/292	57/23328	5.32E-07	1.62E-06	8
BP	GO:0071622	regulation of granulocyte chemotaxis	8/292	57/23328	5.32E-07	1.62E-06	8
BP	GO:0007548	sex differentiation	17/292	315/23328	5.41E-07	1.64E-06	17
BP	GO:0010820	positive regulation of T cell chemotaxis	5/292	14/23328	5.42E-07	1.64E-06	5

BP	GO:0035815	positive regulation of renal sodium excretion	5/292	14/23328	5.42E-07	1.64E-06	5
BP	GO:0007586	digestion	11/292	126/23328	5.56E-07	1.68E-06	11
BP	GO:1901216	positive regulation of neuron death	11/292	126/23328	5.56E-07	1.68E-06	11
BP	GO:0019229	regulation of vasoconstriction	9/292	78/23328	5.71E-07	1.71E-06	9
BP	GO:0070228	regulation of lymphocyte apoptotic process	9/292	78/23328	5.71E-07	1.71E-06	9
BP	GO:1903036	positive regulation of response to wounding	9/292	78/23328	5.71E-07	1.71E-06	9
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	15/292	247/23328	5.81E-07	1.74E-06	15
BP	GO:0046006	regulation of activated T cell proliferation	7/292	40/23328	5.86E-07	1.75E-06	7
BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	8/292	58/23328	6.10E-07	1.82E-06	8
BP	GO:0072577	endothelial cell apoptotic process	8/292	58/23328	6.10E-07	1.82E-06	8
BP	GO:0045666	positive regulation of neuron differentiation	21/292	472/23328	6.13E-07	1.82E-06	21
BP	GO:0070227	lymphocyte apoptotic process	10/292	102/23328	6.25E-07	1.86E-06	10
BP	GO:0018209	peptidyl-serine modification	18/292	357/23328	6.73E-07	2.00E-06	18
BP	GO:0007620	copulation	6/292	26/23328	6.81E-07	2.01E-06	6

BP	GO:0031100	animal organ regeneration	6/292	26/23328	6.81E-07	2.01E-06	6
BP	GO:0042104	positive regulation of activated T cell proliferation	6/292	26/23328	6.81E-07	2.01E-06	6
BP	GO:0045723	positive regulation of fatty acid biosynthetic process	6/292	26/23328	6.81E-07	2.01E-06	6
BP	GO:0010522	regulation of calcium ion transport into cytosol	10/292	103/23328	6.85E-07	2.02E-06	10
BP	GO:0038034	signal transduction in absence of ligand	9/292	80/23328	7.11E-07	2.08E-06	9
BP	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	9/292	80/23328	7.11E-07	2.08E-06	9
BP	GO:0048545	response to steroid hormone	14/292	218/23328	7.11E-07	2.08E-06	14
BP	GO:0031346	positive regulation of cell projection organization	21/292	478/23328	7.51E-07	2.20E-06	21
BP	GO:0051250	negative regulation of lymphocyte activation	12/292	158/23328	7.66E-07	2.24E-06	12
BP	GO:0070231	T cell apoptotic process	8/292	60/23328	7.97E-07	2.32E-06	8
BP	GO:1905517	macrophage migration	8/292	60/23328	7.97E-07	2.32E-06	8
BP	GO:0035745	T-helper 2 cell cytokine production	5/292	15/23328	8.05E-07	2.34E-06	5
BP	GO:1905954	positive regulation of lipid localization	10/292	105/23328	8.19E-07	2.38E-06	10
BP	GO:0002761	regulation of myeloid leukocyte differentiation	11/292	131/23328	8.22E-07	2.38E-06	11

BP	GO:0090068	positive regulation of cell cycle process	15/292	254/23328	8.26E-07	2.39E-06	15
BP	GO:0010742	macrophage derived foam cell differentiation	6/292	27/23328	8.67E-07	2.49E-06	6
BP	GO:0048305	immunoglobulin secretion	6/292	27/23328	8.67E-07	2.49E-06	6
BP	GO:0071677	positive regulation of mononuclear cell migration	6/292	27/23328	8.67E-07	2.49E-06	6
BP	GO:0090023	positive regulation of neutrophil chemotaxis	6/292	27/23328	8.67E-07	2.49E-06	6
BP	GO:0007088	regulation of mitotic nuclear division	12/292	160/23328	8.76E-07	2.51E-06	12
BP	GO:0051302	regulation of cell division	12/292	160/23328	8.76E-07	2.51E-06	12
BP	GO:0032370	positive regulation of lipid transport	9/292	82/23328	8.79E-07	2.51E-06	9
BP	GO:0032732	positive regulation of interleukin-1 production	8/292	61/23328	9.07E-07	2.59E-06	8
BP	GO:0042698	ovulation cycle	8/292	61/23328	9.07E-07	2.59E-06	8
BP	GO:0051403	stress-activated MAPK cascade	15/292	257/23328	9.58E-07	2.73E-06	15
BP	GO:0032620	interleukin-17 production	7/292	43/23328	9.82E-07	2.79E-06	7
BP	GO:0070232	regulation of T cell apoptotic process	7/292	43/23328	9.82E-07	2.79E-06	7
BP	GO:0002698	negative regulation of immune effector process	11/292	134/23328	1.03E-06	2.92E-06	11

BP	GO:0051384	response to glucocorticoid	9/292	84/23328	1.08E-06	3.06E-06	9
BP	GO:0060445	branching involved in salivary gland morphogenesis	6/292	28/23328	1.09E-06	3.08E-06	6
BP	GO:0090077	foam cell differentiation	6/292	28/23328	1.09E-06	3.08E-06	6
BP	GO:0043114	regulation of vascular permeability	7/292	44/23328	1.15E-06	3.24E-06	7
BP	GO:0045823	positive regulation of heart contraction	7/292	44/23328	1.15E-06	3.24E-06	7
BP	GO:0050691	regulation of defense response to virus by host	7/292	44/23328	1.15E-06	3.24E-06	7
BP	GO:0042359	vitamin D metabolic process	5/292	16/23328	1.16E-06	3.24E-06	5
BP	GO:0043084	penile erection	5/292	16/23328	1.16E-06	3.24E-06	5
BP	GO:0045661	regulation of myoblast differentiation	8/292	63/23328	1.17E-06	3.26E-06	8
BP	GO:0002377	immunoglobulin production	15/292	262/23328	1.22E-06	3.40E-06	15
BP	GO:0006936	muscle contraction	16/292	298/23328	1.25E-06	3.49E-06	16
BP	GO:0030073	insulin secretion	14/292	229/23328	1.28E-06	3.56E-06	14
BP	GO:0044403	symbiotic process	18/292	374/23328	1.31E-06	3.64E-06	18
BP	GO:0030890	positive regulation of B cell proliferation	7/292	45/23328	1.35E-06	3.75E-06	7

BP	GO:0031295	T cell costimulation	6/292	29/23328	1.36E-06	3.76E-06	6
BP	GO:0043032	positive regulation of macrophage activation	6/292	29/23328	1.36E-06	3.76E-06	6
BP	GO:0071624	positive regulation of granulocyte chemotaxis	6/292	29/23328	1.36E-06	3.76E-06	6
BP	GO:0030316	osteoclast differentiation	10/292	111/23328	1.37E-06	3.77E-06	10
BP	GO:0032963	collagen metabolic process	10/292	111/23328	1.37E-06	3.77E-06	10
BP	GO:1904659	glucose transmembrane transport	10/292	111/23328	1.37E-06	3.77E-06	10
BP	GO:0048511	rhythmic process	16/292	301/23328	1.43E-06	3.92E-06	16
BP	GO:0008645	hexose transmembrane transport	10/292	112/23328	1.49E-06	4.08E-06	10
BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	8/292	65/23328	1.49E-06	4.08E-06	8
BP	GO:0032874	positive regulation of stress-activated MAPK cascade	12/292	169/23328	1.56E-06	4.28E-06	12
BP	GO:2000404	regulation of T cell migration	7/292	46/23328	1.58E-06	4.31E-06	7
BP	GO:0002312	B cell activation involved in immune response	9/292	88/23328	1.60E-06	4.35E-06	9
BP	GO:0031960	response to corticosteroid	9/292	88/23328	1.60E-06	4.35E-06	9
BP	GO:0062207	regulation of pattern recognition receptor signaling pathway	9/292	88/23328	1.60E-06	4.35E-06	9

BP	GO:1900182	positive regulation of protein localization to nucleus	9/292	88/23328	1.60E-06	4.35E-06	9
BP	GO:0036293	response to decreased oxygen levels	14/292	234/23328	1.65E-06	4.47E-06	14
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	14/292	234/23328	1.65E-06	4.47E-06	14
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	17/292	342/23328	1.68E-06	4.52E-06	17
BP	GO:0032623	interleukin-2 production	8/292	66/23328	1.68E-06	4.52E-06	8
BP	GO:0001759	organ induction	6/292	30/23328	1.68E-06	4.54E-06	6
BP	GO:0015749	monosaccharide transmembrane transport	10/292	114/23328	1.75E-06	4.71E-06	10
BP	GO:0045931	positive regulation of mitotic cell cycle	12/292	171/23328	1.77E-06	4.75E-06	12
BP	GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	12/292	171/23328	1.77E-06	4.75E-06	12
BP	GO:0008406	gonad development	14/292	236/23328	1.83E-06	4.89E-06	14
BP	GO:0001990	regulation of systemic arterial blood pressure by hormone	7/292	47/23328	1.84E-06	4.89E-06	7
BP	GO:0010718	positive regulation of epithelial to mesenchymal transition	7/292	47/23328	1.84E-06	4.89E-06	7
BP	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	7/292	47/23328	1.84E-06	4.89E-06	7
BP	GO:0008585	female gonad development	10/292	115/23328	1.90E-06	5.04E-06	10

BP	GO:0034219	carbohydrate transmembrane transport	10/292	115/23328	1.90E-06	5.04E-06	10
BP	GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	10/292	115/23328	1.90E-06	5.04E-06	10
BP	GO:0031098	stress-activated protein kinase signaling cascade	15/292	272/23328	1.94E-06	5.15E-06	15
BP	GO:0052548	regulation of endopeptidase activity	17/292	346/23328	1.96E-06	5.19E-06	17
BP	GO:0071695	anatomical structure maturation	15/292	273/23328	2.03E-06	5.37E-06	15
BP	GO:0001649	osteoblast differentiation	13/292	205/23328	2.05E-06	5.40E-06	13
BP	GO:0002792	negative regulation of peptide secretion	10/292	116/23328	2.05E-06	5.40E-06	10
BP	GO:0051952	regulation of amine transport	10/292	116/23328	2.05E-06	5.40E-06	10
BP	GO:0031294	lymphocyte costimulation	6/292	31/23328	2.07E-06	5.42E-06	6
BP	GO:0032967	positive regulation of collagen biosynthetic process	6/292	31/23328	2.07E-06	5.42E-06	6
BP	GO:0044062	regulation of excretion	6/292	31/23328	2.07E-06	5.42E-06	6
BP	GO:0072089	stem cell proliferation	11/292	144/23328	2.10E-06	5.49E-06	11
BP	GO:0002712	regulation of B cell mediated immunity	8/292	68/23328	2.11E-06	5.51E-06	8
BP	GO:0002889	regulation of immunoglobulin mediated immune response	8/292	68/23328	2.11E-06	5.51E-06	8

BP	GO:0051222	positive regulation of protein transport	17/292	348/23328	2.12E-06	5.51E-06	17
BP	GO:0043271	negative regulation of ion transport	12/292	174/23328	2.13E-06	5.51E-06	12
BP	GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	7/292	48/23328	2.13E-06	5.51E-06	7
BP	GO:0050798	activated T cell proliferation	7/292	48/23328	2.13E-06	5.51E-06	7
BP	GO:1902622	regulation of neutrophil migration	7/292	48/23328	2.13E-06	5.51E-06	7
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	9/292	91/23328	2.13E-06	5.51E-06	9
BP	GO:0045621	positive regulation of lymphocyte differentiation	10/292	117/23328	2.22E-06	5.74E-06	10
BP	GO:0045137	development of primary sexual characteristics	14/292	240/23328	2.23E-06	5.74E-06	14
BP	GO:0032740	positive regulation of interleukin-17 production	5/292	18/23328	2.23E-06	5.74E-06	5
BP	GO:0045685	regulation of glial cell differentiation	9/292	92/23328	2.34E-06	6.01E-06	9
BP	GO:0042058	regulation of epidermal growth factor receptor signaling pathway	8/292	69/23328	2.36E-06	6.07E-06	8
BP	GO:0008544	epidermis development	16/292	313/23328	2.37E-06	6.08E-06	16
BP	GO:0007369	gastrulation	12/292	176/23328	2.40E-06	6.14E-06	12
BP	GO:0046545	development of primary female sexual characteristics	10/292	118/23328	2.40E-06	6.14E-06	10

BP	GO:0071560	cellular response to transforming growth factor beta stimulus	13/292	208/23328	2.41E-06	6.15E-06	13
BP	GO:0002438	acute inflammatory response to antigenic stimulus	6/292	32/23328	2.52E-06	6.41E-06	6
BP	GO:0010574	regulation of vascular endothelial growth factor production	6/292	32/23328	2.52E-06	6.41E-06	6
BP	GO:0051150	regulation of smooth muscle cell differentiation	6/292	32/23328	2.52E-06	6.41E-06	6
BP	GO:0045445	myoblast differentiation	9/292	93/23328	2.56E-06	6.49E-06	9
BP	GO:0071774	response to fibroblast growth factor	9/292	93/23328	2.56E-06	6.49E-06	9
BP	GO:0042476	odontogenesis	10/292	119/23328	2.59E-06	6.56E-06	10
BP	GO:0043534	blood vessel endothelial cell migration	10/292	119/23328	2.59E-06	6.56E-06	10
BP	GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response	8/292	70/23328	2.64E-06	6.67E-06	8
BP	GO:0090257	regulation of muscle system process	14/292	244/23328	2.70E-06	6.82E-06	14
BP	GO:0050680	negative regulation of epithelial cell proliferation	11/292	148/23328	2.74E-06	6.91E-06	11
BP	GO:0043535	regulation of blood vessel endothelial cell migration	9/292	94/23328	2.80E-06	7.04E-06	9
BP	GO:0090287	regulation of cellular response to growth factor stimulus	15/292	281/23328	2.90E-06	7.29E-06	15
BP	GO:0043112	receptor metabolic process	13/292	212/23328	2.97E-06	7.45E-06	13

BP	GO:0071559	response to transforming growth factor beta	13/292	212/23328	2.97E-06	7.45E-06	13
BP	GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	5/292	19/23328	2.99E-06	7.49E-06	5
BP	GO:0015837	amine transport	10/292	121/23328	3.01E-06	7.54E-06	10
BP	GO:0045672	positive regulation of osteoclast differentiation	6/292	33/23328	3.05E-06	7.59E-06	6
BP	GO:0050999	regulation of nitric-oxide synthase activity	6/292	33/23328	3.05E-06	7.59E-06	6
BP	GO:0010633	negative regulation of epithelial cell migration	8/292	72/23328	3.27E-06	8.15E-06	8
BP	GO:0002709	regulation of T cell mediated immunity	9/292	97/23328	3.64E-06	9.03E-06	9
BP	GO:0002021	response to dietary excess	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:0033032	regulation of myeloid cell apoptotic process	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:0090022	regulation of neutrophil chemotaxis	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:1904646	cellular response to amyloid-beta	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:2000108	positive regulation of leukocyte apoptotic process	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:2000406	positive regulation of T cell migration	6/292	34/23328	3.66E-06	9.03E-06	6
BP	GO:0048483	autonomic nervous system development	7/292	52/23328	3.70E-06	9.10E-06	7

BP	GO:0051353	positive regulation of oxidoreductase activity	7/292	52/23328	3.70E-06	9.10E-06	7
BP	GO:1904036	negative regulation of epithelial cell apoptotic process	7/292	52/23328	3.70E-06	9.10E-06	7
BP	GO:0051153	regulation of striated muscle cell differentiation	10/292	124/23328	3.76E-06	9.23E-06	10
BP	GO:1904951	positive regulation of establishment of protein localization	17/292	364/23328	3.88E-06	9.50E-06	17
BP	GO:0032495	response to muramyl dipeptide	5/292	20/23328	3.95E-06	9.61E-06	5
BP	GO:0033033	negative regulation of myeloid cell apoptotic process	5/292	20/23328	3.95E-06	9.61E-06	5
BP	GO:0045649	regulation of macrophage differentiation	5/292	20/23328	3.95E-06	9.61E-06	5
BP	GO:0060252	positive regulation of glial cell proliferation	5/292	20/23328	3.95E-06	9.61E-06	5
BP	GO:0070723	response to cholesterol	5/292	20/23328	3.95E-06	9.61E-06	5
BP	GO:1901184	regulation of ERBB signaling pathway	8/292	74/23328	4.03E-06	9.80E-06	8
BP	GO:0043903	regulation of symbiotic process	13/292	218/23328	4.04E-06	9.80E-06	13
BP	GO:0044058	regulation of digestive system process	7/292	53/23328	4.22E-06	1.02E-05	7
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	7/292	53/23328	4.22E-06	1.02E-05	7
BP	GO:0001889	liver development	10/292	126/23328	4.35E-06	1.05E-05	10

BP	GO:0031341	regulation of cell killing	10/292	126/23328	4.35E-06	1.05E-05	10
BP	GO:0032660	regulation of interleukin-17 production	6/292	35/23328	4.37E-06	1.05E-05	6
BP	GO:0060142	regulation of syncytium formation by plasma membrane fusion	6/292	35/23328	4.37E-06	1.05E-05	6
BP	GO:0097755	positive regulation of blood vessel diameter	8/292	75/23328	4.47E-06	1.07E-05	8
BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	16/292	330/23328	4.66E-06	1.12E-05	16
BP	GO:0014009	glial cell proliferation	7/292	54/23328	4.80E-06	1.15E-05	7
BP	GO:0035272	exocrine system development	7/292	54/23328	4.80E-06	1.15E-05	7
BP	GO:0002757	immune response-activating signal transduction	16/292	331/23328	4.85E-06	1.16E-05	16
BP	GO:0030324	lung development	13/292	222/23328	4.93E-06	1.18E-05	13
BP	GO:0043117	positive regulation of vascular permeability	5/292	21/23328	5.13E-06	1.22E-05	5
BP	GO:0070230	positive regulation of lymphocyte apoptotic process	5/292	21/23328	5.13E-06	1.22E-05	5
BP	GO:0002701	negative regulation of production of molecular mediator of immune response	6/292	36/23328	5.19E-06	1.23E-05	6
BP	GO:0003401	axis elongation	6/292	36/23328	5.19E-06	1.23E-05	6
BP	GO:0042832	defense response to protozoan	6/292	36/23328	5.19E-06	1.23E-05	6

BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	6/292	36/23328	5.19E-06	1.23E-05	6
BP	GO:0061008	hepaticobiliary system development	10/292	129/23328	5.37E-06	1.27E-05	10
BP	GO:0045582	positive regulation of T cell differentiation	9/292	102/23328	5.52E-06	1.31E-05	9
BP	GO:0030323	respiratory tube development	13/292	225/23328	5.70E-06	1.35E-05	13
BP	GO:0002253	activation of immune response	18/292	416/23328	5.81E-06	1.37E-05	18
BP	GO:0007173	epidermal growth factor receptor signaling pathway	9/292	103/23328	5.99E-06	1.41E-05	9
BP	GO:0010595	positive regulation of endothelial cell migration	9/292	103/23328	5.99E-06	1.41E-05	9
BP	GO:0007435	salivary gland morphogenesis	6/292	37/23328	6.13E-06	1.44E-05	6
BP	GO:0001657	ureteric bud development	9/292	104/23328	6.48E-06	1.52E-05	9
BP	GO:0072163	mesonephric epithelium development	9/292	104/23328	6.48E-06	1.52E-05	9
BP	GO:0072164	mesonephric tubule development	9/292	104/23328	6.48E-06	1.52E-05	9
BP	GO:0044851	hair cycle phase	5/292	22/23328	6.57E-06	1.53E-05	5
BP	GO:0006865	amino acid transport	11/292	162/23328	6.57E-06	1.53E-05	11
BP	GO:0051279	regulation of release of sequestered calcium ion into cytosol	8/292	79/23328	6.62E-06	1.54E-05	8

BP	GO:0009896	positive regulation of catabolic process	19/292	463/23328	6.81E-06	1.59E-05	19
BP	GO:0052547	regulation of peptidase activity	18/292	421/23328	6.84E-06	1.59E-05	18
BP	GO:0006109	regulation of carbohydrate metabolic process	12/292	195/23328	6.90E-06	1.60E-05	12
BP	GO:0033003	regulation of mast cell activation	7/292	57/23328	6.94E-06	1.61E-05	7
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	7/292	57/23328	6.94E-06	1.61E-05	7
BP	GO:0045058	T cell selection	7/292	57/23328	6.94E-06	1.61E-05	7
BP	GO:0030198	extracellular matrix organization	15/292	302/23328	6.95E-06	1.61E-05	15
BP	GO:1903169	regulation of calcium ion transmembrane transport	11/292	163/23328	6.97E-06	1.61E-05	11
BP	GO:0002861	regulation of inflammatory response to antigenic stimulus	6/292	38/23328	7.20E-06	1.66E-05	6
BP	GO:0090322	regulation of superoxide metabolic process	6/292	38/23328	7.20E-06	1.66E-05	6
BP	GO:0043062	extracellular structure organization	15/292	303/23328	7.23E-06	1.66E-05	15
BP	GO:0051224	negative regulation of protein transport	11/292	164/23328	7.39E-06	1.69E-05	11
BP	GO:0002664	regulation of T cell tolerance induction	4/292	11/23328	7.41E-06	1.69E-05	4
BP	GO:0002676	regulation of chronic inflammatory response	4/292	11/23328	7.41E-06	1.69E-05	4

BP	GO:0034115	negative regulation of heterotypic cell-cell adhesion	4/292	11/23328	7.41E-06	1.69E-05	4
BP	GO:0060693	regulation of branching involved in salivary gland morphogenesis	4/292	11/23328	7.41E-06	1.69E-05	4
BP	GO:0070587	regulation of cell-cell adhesion involved in gastrulation	4/292	11/23328	7.41E-06	1.69E-05	4
BP	GO:0045995	regulation of embryonic development	10/292	134/23328	7.53E-06	1.72E-05	10
BP	GO:0010761	fibroblast migration	7/292	58/23328	7.80E-06	1.78E-05	7
BP	GO:0048016	inositol phosphate-mediated signaling	7/292	58/23328	7.80E-06	1.78E-05	7
BP	GO:0032872	regulation of stress-activated MAPK cascade	13/292	232/23328	7.94E-06	1.80E-05	13
BP	GO:0030307	positive regulation of cell growth	12/292	198/23328	8.06E-06	1.83E-05	12
BP	GO:0001823	mesonephros development	9/292	107/23328	8.19E-06	1.85E-05	9
BP	GO:0050709	negative regulation of protein secretion	9/292	107/23328	8.19E-06	1.85E-05	9
BP	GO:0010743	regulation of macrophage derived foam cell differentiation	5/292	23/23328	8.30E-06	1.87E-05	5
BP	GO:0032727	positive regulation of interferon-alpha production	5/292	23/23328	8.30E-06	1.87E-05	5
BP	GO:0032930	positive regulation of superoxide anion generation	5/292	23/23328	8.30E-06	1.87E-05	5
BP	GO:0051969	regulation of transmission of nerve impulse	5/292	23/23328	8.30E-06	1.87E-05	5

BP	GO:0042554	superoxide anion generation	6/292	39/23328	8.42E-06	1.89E-05	6
BP	GO:0050715	positive regulation of cytokine secretion	6/292	39/23328	8.42E-06	1.89E-05	6
BP	GO:0060537	muscle tissue development	19/292	470/23328	8.42E-06	1.89E-05	19
BP	GO:0050714	positive regulation of protein secretion	12/292	199/23328	8.48E-06	1.90E-05	12
BP	GO:0050864	regulation of B cell activation	14/292	270/23328	8.66E-06	1.94E-05	14
BP	GO:0032479	regulation of type I interferon production	8/292	82/23328	8.75E-06	1.96E-05	8
BP	GO:0043255	regulation of carbohydrate biosynthetic process	9/292	108/23328	8.83E-06	1.97E-05	9
BP	GO:0032868	response to insulin	13/292	235/23328	9.12E-06	2.03E-05	13
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	13/292	235/23328	9.12E-06	2.03E-05	13
BP	GO:0008202	steroid metabolic process	15/292	309/23328	9.13E-06	2.03E-05	15
BP	GO:0016032	viral process	15/292	309/23328	9.13E-06	2.03E-05	15
BP	GO:0051098	regulation of binding	17/292	390/23328	9.60E-06	2.13E-05	17
BP	GO:0001562	response to protozoan	6/292	40/23328	9.81E-06	2.16E-05	6
BP	GO:0043551	regulation of phosphatidylinositol 3-kinase activity	6/292	40/23328	9.81E-06	2.16E-05	6

BP	GO:1904645	response to amyloid-beta	6/292	40/23328	9.81E-06	2.16E-05	6
BP	GO:0010524	positive regulation of calcium ion transport into cytosol	7/292	60/23328	9.81E-06	2.16E-05	7
BP	GO:0090303	positive regulation of wound healing	7/292	60/23328	9.81E-06	2.16E-05	7
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	11/292	169/23328	9.83E-06	2.16E-05	11
BP	GO:1904950	negative regulation of establishment of protein localization	11/292	169/23328	9.83E-06	2.16E-05	11
BP	GO:0000302	response to reactive oxygen species	12/292	202/23328	9.87E-06	2.17E-05	12
BP	GO:0022600	digestive system process	9/292	110/23328	1.03E-05	2.25E-05	9
BP	GO:0010565	regulation of cellular ketone metabolic process	10/292	139/23328	1.04E-05	2.28E-05	10
BP	GO:1900180	regulation of protein localization to nucleus	10/292	139/23328	1.04E-05	2.28E-05	10
BP	GO:0001878	response to yeast	4/292	12/23328	1.10E-05	2.40E-05	4
BP	GO:0051798	positive regulation of hair follicle development	4/292	12/23328	1.10E-05	2.40E-05	4
BP	GO:0070586	cell-cell adhesion involved in gastrulation	4/292	12/23328	1.10E-05	2.40E-05	4
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	9/292	111/23328	1.10E-05	2.41E-05	9
BP	GO:0007431	salivary gland development	6/292	41/23328	1.14E-05	2.47E-05	6

BP	GO:0010470	regulation of gastrulation	6/292	41/23328	1.14E-05	2.47E-05	6
BP	GO:0030225	macrophage differentiation	6/292	41/23328	1.14E-05	2.47E-05	6
BP	GO:0038127	ERBB signaling pathway	9/292	112/23328	1.19E-05	2.58E-05	9
BP	GO:0051148	negative regulation of muscle cell differentiation	7/292	62/23328	1.22E-05	2.65E-05	7
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	7/292	62/23328	1.22E-05	2.65E-05	7
BP	GO:0032606	type I interferon production	8/292	86/23328	1.25E-05	2.70E-05	8
BP	GO:0030522	intracellular receptor signaling pathway	12/292	207/23328	1.26E-05	2.73E-05	12
BP	GO:0035813	regulation of renal sodium excretion	5/292	25/23328	1.28E-05	2.77E-05	5
BP	GO:1901739	regulation of myoblast fusion	5/292	25/23328	1.28E-05	2.77E-05	5
BP	GO:0006909	phagocytosis	16/292	358/23328	1.29E-05	2.78E-05	16
BP	GO:0010092	specification of animal organ identity	6/292	42/23328	1.31E-05	2.82E-05	6
BP	GO:0010762	regulation of fibroblast migration	6/292	42/23328	1.31E-05	2.82E-05	6
BP	GO:0046633	alpha-beta T cell proliferation	6/292	42/23328	1.31E-05	2.82E-05	6
BP	GO:0010830	regulation of myotube differentiation	7/292	63/23328	1.36E-05	2.92E-05	7

BP	GO:0042100	B cell proliferation	9/292	114/23328	1.37E-05	2.94E-05	9
BP	GO:0070588	calcium ion transmembrane transport	14/292	282/23328	1.41E-05	3.02E-05	14
BP	GO:0001837	epithelial to mesenchymal transition	10/292	144/23328	1.42E-05	3.03E-05	10
BP	GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	6/292	43/23328	1.51E-05	3.22E-05	6
BP	GO:0042304	regulation of fatty acid biosynthetic process	6/292	43/23328	1.51E-05	3.22E-05	6
BP	GO:0014706	striated muscle tissue development	18/292	447/23328	1.54E-05	3.27E-05	18
BP	GO:0042482	positive regulation of odontogenesis	4/292	13/23328	1.57E-05	3.32E-05	4
BP	GO:0042635	positive regulation of hair cycle	4/292	13/23328	1.57E-05	3.32E-05	4
BP	GO:0010575	positive regulation of vascular endothelial growth factor production	5/292	26/23328	1.57E-05	3.32E-05	5
BP	GO:0032800	receptor biosynthetic process	5/292	26/23328	1.57E-05	3.32E-05	5
BP	GO:0032928	regulation of superoxide anion generation	5/292	26/23328	1.57E-05	3.32E-05	5
BP	GO:0034104	negative regulation of tissue remodeling	5/292	26/23328	1.57E-05	3.32E-05	5
BP	GO:0035929	steroid hormone secretion	5/292	26/23328	1.57E-05	3.32E-05	5
BP	GO:0051149	positive regulation of muscle cell differentiation	8/292	89/23328	1.61E-05	3.39E-05	8

BP	GO:0034121	regulation of toll-like receptor signaling pathway	7/292	65/23328	1.68E-05	3.53E-05	7
BP	GO:0051651	maintenance of location in cell	12/292	213/23328	1.68E-05	3.53E-05	12
BP	GO:0003231	cardiac ventricle development	10/292	147/23328	1.70E-05	3.57E-05	10
BP	GO:0045667	regulation of osteoblast differentiation	10/292	147/23328	1.70E-05	3.57E-05	10
BP	GO:0070482	response to oxygen levels	14/292	287/23328	1.72E-05	3.61E-05	14
BP	GO:1903523	negative regulation of blood circulation	6/292	44/23328	1.73E-05	3.62E-05	6
BP	GO:0021700	developmental maturation	15/292	327/23328	1.78E-05	3.73E-05	15
BP	GO:2000177	regulation of neural precursor cell proliferation	9/292	118/23328	1.81E-05	3.78E-05	9
BP	GO:0032970	regulation of actin filament-based process	17/292	410/23328	1.83E-05	3.82E-05	17
BP	GO:0048839	inner ear development	12/292	215/23328	1.84E-05	3.84E-05	12
BP	GO:0042632	cholesterol homeostasis	8/292	91/23328	1.89E-05	3.94E-05	8
BP	GO:0072091	regulation of stem cell proliferation	8/292	91/23328	1.89E-05	3.94E-05	8
BP	GO:0014821	phasic smooth muscle contraction	5/292	27/23328	1.91E-05	3.95E-05	5
BP	GO:0014829	vascular associated smooth muscle contraction	5/292	27/23328	1.91E-05	3.95E-05	5

BP	GO:0032770	positive regulation of monooxygenase activity	5/292	27/23328	1.91E-05	3.95E-05	5
BP	GO:0035812	renal sodium excretion	5/292	27/23328	1.91E-05	3.95E-05	5
BP	GO:0060713	labyrinthine layer morphogenesis	5/292	27/23328	1.91E-05	3.95E-05	5
BP	GO:0007613	memory	10/292	149/23328	1.91E-05	3.95E-05	10
BP	GO:0001937	negative regulation of endothelial cell proliferation	6/292	45/23328	1.97E-05	4.06E-05	6
BP	GO:0003156	regulation of animal organ formation	6/292	45/23328	1.97E-05	4.06E-05	6
BP	GO:0031128	developmental induction	6/292	45/23328	1.97E-05	4.06E-05	6
BP	GO:0061756	leukocyte adhesion to vascular endothelial cell	6/292	45/23328	1.97E-05	4.06E-05	6
BP	GO:0090184	positive regulation of kidney development	6/292	45/23328	1.97E-05	4.06E-05	6
BP	GO:0055092	sterol homeostasis	8/292	92/23328	2.05E-05	4.21E-05	8
BP	GO:0030282	bone mineralization	9/292	120/23328	2.07E-05	4.25E-05	9
BP	GO:0060541	respiratory system development	13/292	254/23328	2.08E-05	4.26E-05	13
BP	GO:0045165	cell fate commitment	14/292	292/23328	2.08E-05	4.26E-05	14
BP	GO:0008643	carbohydrate transport	10/292	151/23328	2.15E-05	4.39E-05	10

BP	GO:0045651	positive regulation of macrophage differentiation	4/292	14/23328	2.18E-05	4.45E-05	4
BP	GO:1905063	regulation of vascular associated smooth muscle cell differentiation	4/292	14/23328	2.18E-05	4.45E-05	4
BP	GO:2001235	positive regulation of apoptotic signaling pathway	11/292	184/23328	2.18E-05	4.45E-05	11
BP	GO:0061098	positive regulation of protein tyrosine kinase activity	6/292	46/23328	2.25E-05	4.57E-05	6
BP	GO:0046324	regulation of glucose import	7/292	68/23328	2.26E-05	4.59E-05	7
BP	GO:0046635	positive regulation of alpha-beta T cell activation	7/292	68/23328	2.26E-05	4.59E-05	7
BP	GO:0046637	regulation of alpha-beta T cell differentiation	7/292	68/23328	2.26E-05	4.59E-05	7
BP	GO:0032647	regulation of interferon-alpha production	5/292	28/23328	2.30E-05	4.65E-05	5
BP	GO:0048820	hair follicle maturation	5/292	28/23328	2.30E-05	4.65E-05	5
BP	GO:0090025	regulation of monocyte chemotaxis	5/292	28/23328	2.30E-05	4.65E-05	5
BP	GO:2000178	negative regulation of neural precursor cell proliferation	5/292	28/23328	2.30E-05	4.65E-05	5
BP	GO:0002064	epithelial cell development	13/292	257/23328	2.35E-05	4.75E-05	13
BP	GO:0003158	endothelium development	9/292	122/23328	2.37E-05	4.76E-05	9
BP	GO:0050868	negative regulation of T cell activation	9/292	122/23328	2.37E-05	4.76E-05	9

BP	GO:0009408	response to heat	8/292	94/23328	2.40E-05	4.83E-05	8
BP	GO:0006801	superoxide metabolic process	7/292	69/23328	2.49E-05	4.99E-05	7
BP	GO:0033627	cell adhesion mediated by integrin	7/292	69/23328	2.49E-05	4.99E-05	7
BP	GO:0009991	response to extracellular stimulus	16/292	378/23328	2.51E-05	5.03E-05	16
BP	GO:0043902	positive regulation of multi-organism process	6/292	47/23328	2.55E-05	5.10E-05	6
BP	GO:0007405	neuroblast proliferation	7/292	70/23328	2.74E-05	5.47E-05	7
BP	GO:0001516	prostaglandin biosynthetic process	5/292	29/23328	2.76E-05	5.49E-05	5
BP	GO:0007176	regulation of epidermal growth factor-activated receptor activity	5/292	29/23328	2.76E-05	5.49E-05	5
BP	GO:0035094	response to nicotine	5/292	29/23328	2.76E-05	5.49E-05	5
BP	GO:0046457	prostanoid biosynthetic process	5/292	29/23328	2.76E-05	5.49E-05	5
BP	GO:0044848	biological phase	6/292	48/23328	2.88E-05	5.73E-05	6
BP	GO:0001933	negative regulation of protein phosphorylation	17/292	425/23328	2.88E-05	5.73E-05	17
BP	GO:0050796	regulation of insulin secretion	11/292	190/23328	2.94E-05	5.82E-05	11
BP	GO:0010935	regulation of macrophage cytokine production	4/292	15/23328	2.94E-05	5.82E-05	4

BP	GO:0070234	positive regulation of T cell apoptotic process	4/292	15/23328	2.94E-05	5.82E-05	4
BP	GO:1903799	negative regulation of production of miRNAs involved in gene silencing by miRNA	4/292	15/23328	2.94E-05	5.82E-05	4
BP	GO:0061035	regulation of cartilage development	7/292	71/23328	3.00E-05	5.94E-05	7
BP	GO:0001570	vasculogenesis	8/292	97/23328	3.02E-05	5.94E-05	8
BP	GO:0002027	regulation of heart rate	8/292	97/23328	3.02E-05	5.94E-05	8
BP	GO:0019217	regulation of fatty acid metabolic process	8/292	97/23328	3.02E-05	5.94E-05	8
BP	GO:0042326	negative regulation of phosphorylation	18/292	471/23328	3.06E-05	6.03E-05	18
BP	GO:0045862	positive regulation of proteolysis	15/292	344/23328	3.20E-05	6.29E-05	15
BP	GO:0043550	regulation of lipid kinase activity	6/292	49/23328	3.25E-05	6.38E-05	6
BP	GO:0030279	negative regulation of ossification	8/292	98/23328	3.25E-05	6.38E-05	8
BP	GO:0032607	interferon-alpha production	5/292	30/23328	3.27E-05	6.39E-05	5
BP	GO:0035767	endothelial cell chemotaxis	5/292	30/23328	3.27E-05	6.39E-05	5
BP	GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	5/292	30/23328	3.27E-05	6.39E-05	5
BP	GO:0072539	T-helper 17 cell differentiation	5/292	30/23328	3.27E-05	6.39E-05	5

BP	GO:0045123	cellular extravasation	7/292	72/23328	3.29E-05	6.42E-05	7
BP	GO:0010906	regulation of glucose metabolic process	9/292	128/23328	3.46E-05	6.75E-05	9
BP	GO:0051155	positive regulation of striated muscle cell differentiation	7/292	73/23328	3.60E-05	7.01E-05	7
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	6/292	50/23328	3.66E-05	7.11E-05	6
BP	GO:0002230	positive regulation of defense response to virus by host	5/292	31/23328	3.86E-05	7.48E-05	5
BP	GO:0042481	regulation of odontogenesis	5/292	31/23328	3.86E-05	7.48E-05	5
BP	GO:0072574	hepatocyte proliferation	5/292	31/23328	3.86E-05	7.48E-05	5
BP	GO:0072575	epithelial cell proliferation involved in liver morphogenesis	5/292	31/23328	3.86E-05	7.48E-05	5
BP	GO:0002467	germinal center formation	4/292	16/23328	3.89E-05	7.51E-05	4
BP	GO:0051151	negative regulation of smooth muscle cell differentiation	4/292	16/23328	3.89E-05	7.51E-05	4
BP	GO:0072330	monocarboxylic acid biosynthetic process	11/292	196/23328	3.91E-05	7.54E-05	11
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	10/292	162/23328	3.93E-05	7.56E-05	10
BP	GO:0031214	biomineral tissue development	10/292	162/23328	3.93E-05	7.56E-05	10
BP	GO:0110148	biomineralization	10/292	162/23328	3.93E-05	7.56E-05	10

BP	GO:0033555	multicellular organismal response to stress	8/292	101/23328	4.04E-05	7.77E-05	8
BP	GO:0042306	regulation of protein import into nucleus	7/292	75/23328	4.30E-05	8.23E-05	7
BP	GO:0048645	animal organ formation	7/292	75/23328	4.30E-05	8.23E-05	7
BP	GO:0051057	positive regulation of small GTPase mediated signal transduction	7/292	75/23328	4.30E-05	8.23E-05	7
BP	GO:1903670	regulation of sprouting angiogenesis	7/292	75/23328	4.30E-05	8.23E-05	7
BP	GO:0031331	positive regulation of cellular catabolic process	16/292	396/23328	4.39E-05	8.40E-05	16
BP	GO:0031645	negative regulation of nervous system process	5/292	32/23328	4.53E-05	8.62E-05	5
BP	GO:0045830	positive regulation of isotype switching	5/292	32/23328	4.53E-05	8.62E-05	5
BP	GO:0060561	apoptotic process involved in morphogenesis	5/292	32/23328	4.53E-05	8.62E-05	5
BP	GO:0060669	embryonic placenta morphogenesis	5/292	32/23328	4.53E-05	8.62E-05	5
BP	GO:2000352	negative regulation of endothelial cell apoptotic process	5/292	32/23328	4.53E-05	8.62E-05	5
BP	GO:0001974	blood vessel remodeling	6/292	52/23328	4.59E-05	8.70E-05	6
BP	GO:0042307	positive regulation of protein import into nucleus	6/292	52/23328	4.59E-05	8.70E-05	6
BP	GO:0043268	positive regulation of potassium ion transport	6/292	52/23328	4.59E-05	8.70E-05	6

BP	GO:0006606	protein import into nucleus	10/292	165/23328	4.59E-05	8.70E-05	10
BP	GO:0050772	positive regulation of axonogenesis	8/292	103/23328	4.65E-05	8.81E-05	8
BP	GO:0008543	fibroblast growth factor receptor signaling pathway	7/292	76/23328	4.68E-05	8.84E-05	7
BP	GO:0045576	mast cell activation	7/292	76/23328	4.68E-05	8.84E-05	7
BP	GO:0045670	regulation of osteoclast differentiation	7/292	76/23328	4.68E-05	8.84E-05	7
BP	GO:0043588	skin development	13/292	275/23328	4.74E-05	8.94E-05	13
BP	GO:0032869	cellular response to insulin stimulus	11/292	201/23328	4.91E-05	9.25E-05	11
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	9/292	134/23328	4.97E-05	9.34E-05	9
BP	GO:0048525	negative regulation of viral process	8/292	104/23328	4.99E-05	9.37E-05	8
BP	GO:0010934	macrophage cytokine production	4/292	17/23328	5.03E-05	9.43E-05	4
BP	GO:0032570	response to progesterone	4/292	17/23328	5.03E-05	9.43E-05	4
BP	GO:0035729	cellular response to hepatocyte growth factor stimulus	4/292	17/23328	5.03E-05	9.43E-05	4
BP	GO:0043507	positive regulation of JUN kinase activity	7/292	77/23328	5.10E-05	9.54E-05	7
BP	GO:0006111	regulation of gluconeogenesis	6/292	53/23328	5.12E-05	9.56E-05	6

BP	GO:0030850	prostate gland development	6/292	53/23328	5.12E-05	9.56E-05	6
BP	GO:0072576	liver morphogenesis	5/292	33/23328	5.29E-05	9.85E-05	5
BP	GO:1901099	negative regulation of signal transduction in absence of ligand	5/292	33/23328	5.29E-05	9.85E-05	5
BP	GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	5/292	33/23328	5.29E-05	9.85E-05	5
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	8/292	105/23328	5.34E-05	9.94E-05	8
BP	GO:0006898	receptor-mediated endocytosis	12/292	240/23328	5.41E-05	0.00010057	12
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	7/292	78/23328	5.54E-05	0.00010275	7
BP	GO:0050810	regulation of steroid biosynthetic process	7/292	78/23328	5.54E-05	0.00010275	7
BP	GO:0032956	regulation of actin cytoskeleton organization	15/292	361/23328	5.55E-05	0.00010275	15
BP	GO:0051170	import into nucleus	10/292	169/23328	5.62E-05	0.00010404	10
BP	GO:0055025	positive regulation of cardiac muscle tissue development	6/292	54/23328	5.70E-05	0.00010534	6
BP	GO:0002260	lymphocyte homeostasis	7/292	79/23328	6.01E-05	0.0001111	7
BP	GO:0006869	lipid transport	15/292	364/23328	6.09E-05	0.00011233	15
BP	GO:0032728	positive regulation of interferon-beta production	5/292	34/23328	6.14E-05	0.00011277	5

BP	GO:0043537	negative regulation of blood vessel endothelial cell migration	5/292	34/23328	6.14E-05	0.00011277	5
BP	GO:0062149	detection of stimulus involved in sensory perception of pain	5/292	34/23328	6.14E-05	0.00011277	5
BP	GO:0090218	positive regulation of lipid kinase activity	5/292	34/23328	6.14E-05	0.00011277	5
BP	GO:0010952	positive regulation of peptidase activity	10/292	171/23328	6.21E-05	0.00011396	10
BP	GO:0002534	cytokine production involved in inflammatory response	6/292	55/23328	6.33E-05	0.00011584	6
BP	GO:0032608	interferon-beta production	6/292	55/23328	6.33E-05	0.00011584	6
BP	GO:0032892	positive regulation of organic acid transport	6/292	55/23328	6.33E-05	0.00011584	6
BP	GO:0036315	cellular response to sterol	4/292	18/23328	6.41E-05	0.00011706	4
BP	GO:0042026	protein refolding	4/292	18/23328	6.41E-05	0.00011706	4
BP	GO:0006979	response to oxidative stress	16/292	409/23328	6.43E-05	0.00011739	16
BP	GO:0045446	endothelial cell differentiation	8/292	108/23328	6.53E-05	0.00011896	8
BP	GO:0055017	cardiac muscle tissue growth	8/292	108/23328	6.53E-05	0.00011896	8
BP	GO:0043583	ear development	12/292	246/23328	6.86E-05	0.00012482	12
BP	GO:0046330	positive regulation of JNK cascade	9/292	140/23328	6.98E-05	0.00012695	9

BP	GO:0007618	mating	6/292	56/23328	7.01E-05	0.00012726	6
BP	GO:0045777	positive regulation of blood pressure	6/292	56/23328	7.01E-05	0.00012726	6
BP	GO:0021675	nerve development	7/292	81/23328	7.06E-05	0.00012731	7
BP	GO:0043525	positive regulation of neuron apoptotic process	7/292	81/23328	7.06E-05	0.00012731	7
BP	GO:0045682	regulation of epidermis development	7/292	81/23328	7.06E-05	0.00012731	7
BP	GO:1904589	regulation of protein import	7/292	81/23328	7.06E-05	0.00012731	7
BP	GO:0001773	myeloid dendritic cell activation	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:0010758	regulation of macrophage chemotaxis	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:0014047	glutamate secretion	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:0072538	T-helper 17 type immune response	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:1990089	response to nerve growth factor	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:1990090	cellular response to nerve growth factor stimulus	5/292	35/23328	7.09E-05	0.00012731	5
BP	GO:0010876	lipid localization	16/292	413/23328	7.21E-05	0.00012939	16
BP	GO:0001909	leukocyte mediated cytotoxicity	9/292	141/23328	7.38E-05	0.00013232	9

BP	GO:0007612	learning	10/292	175/23328	7.53E-05	0.00013496	10
BP	GO:0042180	cellular ketone metabolic process	11/292	211/23328	7.61E-05	0.00013619	11
BP	GO:0003170	heart valve development	6/292	57/23328	7.76E-05	0.0001387	6
BP	GO:0002544	chronic inflammatory response	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0002922	positive regulation of humoral immune response	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0010623	programmed cell death involved in cell development	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0034138	toll-like receptor 3 signaling pathway	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0035728	response to hepatocyte growth factor	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0048484	enteric nervous system development	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0060965	negative regulation of gene silencing by miRNA	4/292	19/23328	8.04E-05	0.00014273	4
BP	GO:0006775	fat-soluble vitamin metabolic process	5/292	36/23328	8.14E-05	0.00014396	5
BP	GO:0033005	positive regulation of mast cell activation	5/292	36/23328	8.14E-05	0.00014396	5
BP	GO:0035886	vascular associated smooth muscle cell differentiation	5/292	36/23328	8.14E-05	0.00014396	5
BP	GO:1904707	positive regulation of vascular associated smooth muscle cell proliferation	5/292	36/23328	8.14E-05	0.00014396	5

BP	GO:1905209	positive regulation of cardiocyte differentiation	5/292	36/23328	8.14E-05	0.00014396	5
BP	GO:0002532	production of molecular mediator involved in inflammatory response	7/292	83/23328	8.26E-05	0.00014523	7
BP	GO:0045844	positive regulation of striated muscle tissue development	7/292	83/23328	8.26E-05	0.00014523	7
BP	GO:0046323	glucose import	7/292	83/23328	8.26E-05	0.00014523	7
BP	GO:0048636	positive regulation of muscle organ development	7/292	83/23328	8.26E-05	0.00014523	7
BP	GO:1904427	positive regulation of calcium ion transmembrane transport	7/292	83/23328	8.26E-05	0.00014523	7
BP	GO:0000280	nuclear division	16/292	418/23328	8.29E-05	0.00014577	16
BP	GO:0030038	contractile actin filament bundle assembly	8/292	112/23328	8.45E-05	0.00014807	8
BP	GO:0043149	stress fiber assembly	8/292	112/23328	8.45E-05	0.00014807	8
BP	GO:0060606	tube closure	8/292	112/23328	8.45E-05	0.00014807	8
BP	GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	6/292	58/23328	8.56E-05	0.00014934	6
BP	GO:0002208	somatic diversification of immunoglobulins involved in immune response	6/292	58/23328	8.56E-05	0.00014934	6
BP	GO:0032663	regulation of interleukin-2 production	6/292	58/23328	8.56E-05	0.00014934	6
BP	GO:0045190	isotype switching	6/292	58/23328	8.56E-05	0.00014934	6

BP	GO:1904591	positive regulation of protein import	6/292	58/23328	8.56E-05	0.00014934	6
BP	GO:0046942	carboxylic acid transport	14/292	333/23328	8.65E-05	0.00015069	14
BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	7/292	84/23328	8.91E-05	0.00015498	7
BP	GO:1901863	positive regulation of muscle tissue development	7/292	84/23328	8.91E-05	0.00015498	7
BP	GO:0034504	protein localization to nucleus	13/292	293/23328	9.02E-05	0.00015676	13
BP	GO:0007588	excretion	6/292	59/23328	9.43E-05	0.00016374	6
BP	GO:0045598	regulation of fat cell differentiation	9/292	146/23328	9.65E-05	0.00016738	9
BP	GO:0051054	positive regulation of DNA metabolic process	11/292	217/23328	9.77E-05	0.00016928	11
BP	GO:0015849	organic acid transport	14/292	337/23328	9.81E-05	0.00016981	14
BP	GO:0032310	prostaglandin secretion	4/292	20/23328	9.95E-05	0.0001717	4
BP	GO:0032695	negative regulation of interleukin-12 production	4/292	20/23328	9.95E-05	0.0001717	4
BP	GO:0044321	response to leptin	4/292	20/23328	9.95E-05	0.0001717	4
BP	GO:0048634	regulation of muscle organ development	10/292	181/23328	9.97E-05	0.00017196	10
BP	GO:0003206	cardiac chamber morphogenesis	9/292	147/23328	0.00010017	0.00017505	9

BP	GO:0035270	endocrine system development	9/292	147/23328	0.0001017	0.00017505	9
BP	GO:0031646	positive regulation of nervous system process	7/292	86/23328	0.00010349	0.00017781	7
BP	GO:0060411	cardiac septum morphogenesis	7/292	86/23328	0.00010349	0.00017781	7
BP	GO:0090183	regulation of kidney development	6/292	60/23328	0.00010371	0.00017786	6
BP	GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	6/292	60/23328	0.00010371	0.00017786	6
BP	GO:0045622	regulation of T-helper cell differentiation	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:0045684	positive regulation of epidermis development	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:0046640	regulation of alpha-beta T cell proliferation	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:0048265	response to pain	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:0097028	dendritic cell differentiation	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:2000249	regulation of actin cytoskeleton reorganization	5/292	38/23328	0.00010625	0.0001812	5
BP	GO:0048738	cardiac muscle tissue development	12/292	258/23328	0.00010778	0.00018365	12
BP	GO:0016331	morphogenesis of embryonic epithelium	10/292	183/23328	0.0001092	0.00018589	10
BP	GO:0050871	positive regulation of B cell activation	11/292	220/23328	0.00011034	0.00018766	11

BP	GO:0031641	regulation of myelination	6/292	61/23328	0.00011383	0.00019324	6
BP	GO:0045776	negative regulation of blood pressure	6/292	61/23328	0.00011383	0.00019324	6
BP	GO:0032414	positive regulation of ion transmembrane transporter activity	8/292	117/23328	0.00011484	0.00019477	8
BP	GO:0042311	vasodilation	5/292	39/23328	0.00012064	0.00020422	5
BP	GO:0060251	regulation of glial cell proliferation	5/292	39/23328	0.00012064	0.00020422	5
BP	GO:0001976	nervous system process involved in regulation of systemic arterial blood pressure	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0002863	positive regulation of inflammatory response to antigenic stimulus	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0007202	activation of phospholipase C activity	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0032693	negative regulation of interleukin-10 production	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0051023	regulation of immunoglobulin secretion	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0051956	negative regulation of amino acid transport	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0060149	negative regulation of posttranscriptional gene silencing	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0060967	negative regulation of gene silencing by RNA	4/292	21/23328	0.00012167	0.00020428	4
BP	GO:0090026	positive regulation of monocyte chemotaxis	4/292	21/23328	0.00012167	0.00020428	4

BP	GO:0060419	heart growth	8/292	118/23328	0.00012187	0.00020444	8
BP	GO:0031102	neuron projection regeneration	6/292	62/23328	0.00012472	0.00020884	6
BP	GO:0046850	regulation of bone remodeling	6/292	62/23328	0.00012472	0.00020884	6
BP	GO:0050830	defense response to Gram-positive bacterium	9/292	151/23328	0.00012483	0.00020884	9
BP	GO:0002262	myeloid cell homeostasis	10/292	187/23328	0.00013047	0.00021808	10
BP	GO:1901617	organic hydroxy compound biosynthetic process	11/292	225/23328	0.00013451	0.00022461	11
BP	GO:0016447	somatic recombination of immunoglobulin gene segments	6/292	63/23328	0.00013641	0.0002276	6
BP	GO:0016064	immunoglobulin mediated immune response	12/292	265/23328	0.00013854	0.00023093	12
BP	GO:0030900	forebrain development	15/292	393/23328	0.00014226	0.00023693	15
BP	GO:0008360	regulation of cell shape	9/292	154/23328	0.00014494	0.00024107	9
BP	GO:0042542	response to hydrogen peroxide	8/292	121/23328	0.00014514	0.00024107	8
BP	GO:0050829	defense response to Gram-negative bacterium	8/292	121/23328	0.00014514	0.00024107	8
BP	GO:0032148	activation of protein kinase B activity	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:0042107	cytokine metabolic process	4/292	22/23328	0.00014724	0.00024281	4

BP	GO:0045624	positive regulation of T-helper cell differentiation	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:0046641	positive regulation of alpha-beta T cell proliferation	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:0060749	mammary gland alveolus development	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:0061377	mammary gland lobule development	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:1901741	positive regulation of myoblast fusion	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	4/292	22/23328	0.00014724	0.00024281	4
BP	GO:0048644	muscle organ morphogenesis	7/292	91/23328	0.00014783	0.00024335	7
BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	7/292	91/23328	0.00014783	0.00024335	7
BP	GO:0007292	female gamete generation	9/292	155/23328	0.00015222	0.00025034	9
BP	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	5/292	41/23328	0.00015384	0.00025258	5
BP	GO:0140014	mitotic nuclear division	12/292	268/23328	0.00015385	0.00025258	12
BP	GO:0019724	B cell mediated immunity	12/292	269/23328	0.00015927	0.00026124	12
BP	GO:0006937	regulation of muscle contraction	9/292	156/23328	0.00015979	0.00026163	9
BP	GO:0030856	regulation of epithelial cell differentiation	9/292	156/23328	0.00015979	0.00026163	9

BP	GO:0019318	hexose metabolic process	11/292	231/23328	0.00016932	0.00027662	11
BP	GO:0043393	regulation of protein binding	11/292	231/23328	0.00016932	0.00027662	11
BP	GO:0043506	regulation of JUN kinase activity	7/292	93/23328	0.0001694	0.00027662	7
BP	GO:0032411	positive regulation of transporter activity	8/292	124/23328	0.00017196	0.00028056	8
BP	GO:0045191	regulation of isotype switching	5/292	42/23328	0.00017286	0.00028178	5
BP	GO:0003205	cardiac chamber development	10/292	194/23328	0.00017613	0.00028669	10
BP	GO:0051043	regulation of membrane protein ectodomain proteolysis	4/292	23/23328	0.00017649	0.00028669	4
BP	GO:2000345	regulation of hepatocyte proliferation	4/292	23/23328	0.00017649	0.00028669	4
BP	GO:2000831	regulation of steroid hormone secretion	4/292	23/23328	0.00017649	0.00028669	4
BP	GO:0010717	regulation of epithelial to mesenchymal transition	7/292	94/23328	0.0001811	0.00029391	7
BP	GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	8/292	125/23328	0.00018176	0.00029472	8
BP	GO:0000768	syncytium formation by plasma membrane fusion	6/292	67/23328	0.00019216	0.0003105	6
BP	GO:0006940	regulation of smooth muscle contraction	6/292	67/23328	0.00019216	0.0003105	6
BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	6/292	67/23328	0.00019216	0.0003105	6

BP	GO:0140253	cell-cell fusion	6/292	67/23328	0.00019216	0.0003105	6
BP	GO:0010950	positive regulation of endopeptidase activity	9/292	160/23328	0.00019333	0.00031203	9
BP	GO:1902742	apoptotic process involved in development	5/292	43/23328	0.00019362	0.00031203	5
BP	GO:1903053	regulation of extracellular matrix organization	5/292	43/23328	0.00019362	0.00031203	5
BP	GO:0051146	striated muscle cell differentiation	13/292	317/23328	0.00019653	0.00031618	13
BP	GO:1903829	positive regulation of cellular protein localization	13/292	317/23328	0.00019653	0.00031618	13
BP	GO:0016051	carbohydrate biosynthetic process	10/292	197/23328	0.00019946	0.00032061	10
BP	GO:0031016	pancreas development	7/292	96/23328	0.00020645	0.00033155	7
BP	GO:0015800	acidic amino acid transport	6/292	68/23328	0.00020857	0.00033438	6
BP	GO:0046579	positive regulation of Ras protein signal transduction	6/292	68/23328	0.00020857	0.00033438	6
BP	GO:0015732	prostaglandin transport	4/292	24/23328	0.00020972	0.00033534	4
BP	GO:0031643	positive regulation of myelination	4/292	24/23328	0.00020972	0.00033534	4
BP	GO:0062009	secondary palate development	4/292	24/23328	0.00020972	0.00033534	4
BP	GO:0072175	epithelial tube formation	9/292	162/23328	0.00021217	0.00033897	9

BP	GO:0003279	cardiac septum development	8/292	128/23328	0.00021393	0.00034149	8
BP	GO:0032924	activin receptor signaling pathway	5/292	44/23328	0.00021622	0.00034485	5
BP	GO:0002634	regulation of germinal center formation	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0019732	antifungal humoral response	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0032224	positive regulation of synaptic transmission, cholinergic	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0046543	development of secondary female sexual characteristics	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0046884	follicle-stimulating hormone secretion	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0090269	fibroblast growth factor production	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0090270	regulation of fibroblast growth factor production	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:2000489	regulation of hepatic stellate cell activation	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:2000551	regulation of T-helper 2 cell cytokine production	3/292	10/23328	0.00021825	0.00034539	3
BP	GO:0007254	JNK cascade	10/292	200/23328	0.00022533	0.00035629	10
BP	GO:0006949	syncytium formation	6/292	69/23328	0.00022606	0.00035715	6
BP	GO:0032409	regulation of transporter activity	12/292	280/23328	0.0002305	0.00036384	12

BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	9/292	164/23328	0.00023252	0.00036672	9
BP	GO:0050792	regulation of viral process	10/292	201/23328	0.00023455	0.00036961	10
BP	GO:0001569	branching involved in blood vessel morphogenesis	5/292	45/23328	0.00024078	0.00037846	5
BP	GO:0034340	response to type I interferon	5/292	45/23328	0.00024078	0.00037846	5
BP	GO:2000826	regulation of heart morphogenesis	5/292	45/23328	0.00024078	0.00037846	5
BP	GO:0006006	glucose metabolic process	10/292	202/23328	0.00024409	0.00038334	10
BP	GO:0016445	somatic diversification of immunoglobulins	6/292	70/23328	0.00024469	0.00038394	6
BP	GO:0010759	positive regulation of macrophage chemotaxis	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:0014048	regulation of glutamate secretion	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:0051883	killing of cells in other organism involved in symbiotic interaction	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:1904738	vascular associated smooth muscle cell migration	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:1904752	regulation of vascular associated smooth muscle cell migration	4/292	25/23328	0.00024722	0.00038594	4
BP	GO:0070167	regulation of biomineral tissue development	7/292	99/23328	0.00024978	0.00038929	7

BP	GO:0110149	regulation of biomineralization	7/292	99/23328	0.00024978	0.00038929	7
BP	GO:0034763	negative regulation of transmembrane transport	8/292	132/23328	0.00026396	0.00041104	8
BP	GO:0001885	endothelial cell development	6/292	71/23328	0.0002645	0.00041153	6
BP	GO:0042552	myelination	9/292	167/23328	0.00026606	0.00041361	9
BP	GO:0006636	unsaturated fatty acid biosynthetic process	5/292	46/23328	0.00026741	0.0004155	5
BP	GO:1905521	regulation of macrophage migration	5/292	46/23328	0.00026741	0.0004155	5
BP	GO:0060993	kidney morphogenesis	7/292	101/23328	0.00028253	0.0004381	7
BP	GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	6/292	72/23328	0.00028556	0.00044168	6
BP	GO:0016444	somatic cell DNA recombination	6/292	72/23328	0.00028556	0.00044168	6
BP	GO:0061045	negative regulation of wound healing	6/292	72/23328	0.00028556	0.00044168	6
BP	GO:0010829	negative regulation of glucose transmembrane transport	4/292	26/23328	0.0002893	0.00044598	4
BP	GO:0044342	type B pancreatic cell proliferation	4/292	26/23328	0.0002893	0.00044598	4
BP	GO:0070233	negative regulation of T cell apoptotic process	4/292	26/23328	0.0002893	0.00044598	4
BP	GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	4/292	26/23328	0.0002893	0.00044598	4

BP	GO:0003179	heart valve morphogenesis	5/292	47/23328	0.00029621	0.00045511	5
BP	GO:0045911	positive regulation of DNA recombination	5/292	47/23328	0.00029621	0.00045511	5
BP	GO:0060135	maternal process involved in female pregnancy	5/292	47/23328	0.00029621	0.00045511	5
BP	GO:0120163	negative regulation of cold-induced thermogenesis	5/292	47/23328	0.00029621	0.00045511	5
BP	GO:0038180	nerve growth factor signaling pathway	3/292	11/23328	0.00029731	0.00045529	3
BP	GO:0042368	vitamin D biosynthetic process	3/292	11/23328	0.00029731	0.00045529	3
BP	GO:1902023	L-arginine transport	3/292	11/23328	0.00029731	0.00045529	3
BP	GO:2001280	positive regulation of unsaturated fatty acid biosynthetic process	3/292	11/23328	0.00029731	0.00045529	3
BP	GO:0007272	ensheathment of neurons	9/292	170/23328	0.00030352	0.00046401	9
BP	GO:0008366	axon ensheathment	9/292	170/23328	0.00030352	0.00046401	9
BP	GO:0002711	positive regulation of T cell mediated immunity	6/292	73/23328	0.0003079	0.00046994	6
BP	GO:1903793	positive regulation of anion transport	6/292	73/23328	0.0003079	0.00046994	6
BP	GO:0055024	regulation of cardiac muscle tissue development	7/292	103/23328	0.00031864	0.00048593	7
BP	GO:0045907	positive regulation of vasoconstriction	5/292	48/23328	0.0003273	0.00049749	5

BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	5/292	48/23328	0.0003273	0.00049749	5
BP	GO:0050850	positive regulation of calcium-mediated signaling	5/292	48/23328	0.0003273	0.00049749	5
BP	GO:1903727	positive regulation of phospholipid metabolic process	5/292	48/23328	0.0003273	0.00049749	5
BP	GO:0048285	organelle fission	16/292	472/23328	0.00032829	0.00049859	16
BP	GO:0046824	positive regulation of nucleocytoplasmic transport	6/292	74/23328	0.00033159	0.00050319	6
BP	GO:0006925	inflammatory cell apoptotic process	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:0016048	detection of temperature stimulus	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:0030212	hyaluronan metabolic process	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:0035809	regulation of urine volume	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:0150077	regulation of neuroinflammatory response	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	4/292	27/23328	0.00033629	0.00050781	4
BP	GO:0044262	cellular carbohydrate metabolic process	12/292	292/23328	0.00033752	0.0005092	12
BP	GO:0046849	bone remodeling	7/292	104/23328	0.00033804	0.0005092	7
BP	GO:0061326	renal tubule development	7/292	104/23328	0.00033804	0.0005092	7

BP	GO:1903725	regulation of phospholipid metabolic process	6/292		75/23328	0.00035669	0.00053686	6
BP	GO:0021537	telencephalon development	11/292		252/23328	0.00035748	0.00053761	11
BP	GO:0097305	response to alcohol	10/292		212/23328	0.00035874	0.00053906	10
BP	GO:0001890	placenta development	9/292		174/23328	0.00036014	0.00053909	9
BP	GO:0006692	prostanoid metabolic process	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:0006693	prostaglandin metabolic process	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:0032941	secretion by tissue	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:0033173	calcineurin-NFAT signaling cascade	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:1903018	regulation of glycoprotein metabolic process	5/292		49/23328	0.0003608	0.00053909	5
BP	GO:0031532	actin cytoskeleton reorganization	7/292		106/23328	0.00037966	0.00056681	7
BP	GO:0006094	gluconeogenesis	6/292		76/23328	0.00038325	0.00057124	6
BP	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	6/292		76/23328	0.00038325	0.00057124	6
BP	GO:0002693	positive regulation of cellular extravasation	4/292		28/23328	0.0003885	0.00057747	4

BP	GO:0010460	positive regulation of heart rate	4/292	28/23328	0.0003885	0.00057747	4
BP	GO:0009612	response to mechanical stimulus	9/292	176/23328	0.00039157	0.00057747	9
BP	GO:0001787	natural killer cell proliferation	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0002016	regulation of blood volume by renin-angiotensin	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0014824	artery smooth muscle contraction	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0031392	regulation of prostaglandin biosynthetic process	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0032754	positive regulation of interleukin-5 production	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0035733	hepatic stellate cell activation	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0070278	extracellular matrix constituent secretion	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0071639	positive regulation of monocyte chemotactic protein-1 production	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0097421	liver regeneration	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0150079	negative regulation of neuroinflammatory response	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:1902093	positive regulation of flagellated sperm motility	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:1902287	semaphorin-plexin signaling pathway involved in axon guidance	3/292	12/23328	0.00039275	0.00057747	3

BP	GO:2000155	positive regulation of cilium-dependent cell motility	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	3/292	12/23328	0.00039275	0.00057747	3
BP	GO:0007520	myoblast fusion	5/292	50/23328	0.00039683	0.00058208	5
BP	GO:0032309	icosanoid secretion	5/292	50/23328	0.00039683	0.00058208	5
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	5/292	50/23328	0.00039683	0.00058208	5
BP	GO:0016202	regulation of striated muscle tissue development	9/292	177/23328	0.00040811	0.00059767	9
BP	GO:0035148	tube formation	9/292	177/23328	0.00040811	0.00059767	9
BP	GO:0045453	bone resorption	6/292	77/23328	0.00041133	0.00060144	6
BP	GO:0061097	regulation of protein tyrosine kinase activity	6/292	77/23328	0.00041133	0.00060144	6
BP	GO:0046394	carboxylic acid biosynthetic process	12/292	299/23328	0.0004175	0.00060997	12
BP	GO:0008306	associative learning	7/292	108/23328	0.00042529	0.00062038	7
BP	GO:0043266	regulation of potassium ion transport	7/292	108/23328	0.00042529	0.00062038	7
BP	GO:0016053	organic acid biosynthetic process	12/292	300/23328	0.00043014	0.00062695	12
BP	GO:0017038	protein import	10/292	217/23328	0.00043107	0.00062782	10

BP	GO:2001056	positive regulation of cysteine-type endopeptidase activity	8/292	142/23328	0.00043195	0.0006286	8
BP	GO:0072132	mesenchyme morphogenesis	5/292	51/23328	0.0004355	0.00063327	5
BP	GO:0003208	cardiac ventricle morphogenesis	6/292	78/23328	0.00044099	0.00064074	6
BP	GO:0003085	negative regulation of systemic arterial blood pressure	4/292	29/23328	0.00044625	0.00064736	4
BP	GO:0003148	outflow tract septum morphogenesis	4/292	29/23328	0.00044625	0.00064736	4
BP	GO:0002062	chondrocyte differentiation	7/292	109/23328	0.0004497	0.00065185	7
BP	GO:0032412	regulation of ion transmembrane transporter activity	11/292	259/23328	0.00045027	0.00065218	11
BP	GO:0007219	Notch signaling pathway	9/292	180/23328	0.00046121	0.00066698	9
BP	GO:1901861	regulation of muscle tissue development	9/292	180/23328	0.00046121	0.00066698	9
BP	GO:0019319	hexose biosynthetic process	6/292	79/23328	0.00047229	0.00068246	6
BP	GO:0010828	positive regulation of glucose transmembrane transport	5/292	52/23328	0.00047696	0.00068759	5
BP	GO:0045124	regulation of bone resorption	5/292	52/23328	0.00047696	0.00068759	5
BP	GO:1900015	regulation of cytokine production involved in inflammatory response	5/292	52/23328	0.00047696	0.00068759	5
BP	GO:0001894	tissue homeostasis	11/292	261/23328	0.00048022	0.00069121	11

BP	GO:0005996	monosaccharide metabolic process	11/292	261/23328	0.00048022	0.00069121	11
BP	GO:0006633	fatty acid biosynthetic process	8/292	145/23328	0.00049654	0.00071414	8
BP	GO:0010951	negative regulation of endopeptidase activity	9/292	182/23328	0.00049968	0.00071583	9
BP	GO:0001843	neural tube closure	7/292	111/23328	0.00050185	0.00071583	7
BP	GO:0072009	nephron epithelium development	7/292	111/23328	0.00050185	0.00071583	7
BP	GO:0002200	somatic diversification of immune receptors	6/292	80/23328	0.0005053	0.00071583	6
BP	GO:0001542	ovulation from ovarian follicle	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0001781	neutrophil apoptotic process	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0002430	complement receptor mediated signaling pathway	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0002551	mast cell chemotaxis	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0003353	positive regulation of cilium movement	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0010739	positive regulation of protein kinase A signaling	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0010744	positive regulation of macrophage derived foam cell differentiation	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0015809	arginine transport	3/292	13/23328	0.00050586	0.00071583	3

BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0045136	development of secondary sexual characteristics	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0048711	positive regulation of astrocyte differentiation	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0060340	positive regulation of type I interferon-mediated signaling pathway	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0060670	branching involved in labyrinthine layer morphogenesis	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0072216	positive regulation of metanephros development	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:2000833	positive regulation of steroid hormone secretion	3/292	13/23328	0.00050586	0.00071583	3
BP	GO:0045861	negative regulation of proteolysis	13/292	350/23328	0.00050642	0.00071608	13
BP	GO:0002335	mature B cell differentiation	4/292	30/23328	0.00050986	0.00071874	4
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	4/292	30/23328	0.00050986	0.00071874	4
BP	GO:0051085	chaperone cofactor-dependent protein refolding	4/292	30/23328	0.00050986	0.00071874	4
BP	GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	4/292	30/23328	0.00050986	0.00071874	4

BP	GO:0032648	regulation of interferon-beta production	5/292	53/23328	0.00052131	0.00073375	5
BP	GO:0097720	calcineurin-mediated signaling	5/292	53/23328	0.00052131	0.00073375	5
BP	GO:0007589	body fluid secretion	7/292	112/23328	0.00052967	0.00074496	7
BP	GO:0046456	icosanoid biosynthetic process	5/292	54/23328	0.00056869	0.00079862	5
BP	GO:2001222	regulation of neuron migration	5/292	54/23328	0.00056869	0.00079862	5
BP	GO:0019915	lipid storage	6/292	82/23328	0.00057668	0.00080738	6
BP	GO:0030193	regulation of blood coagulation	6/292	82/23328	0.00057668	0.00080738	6
BP	GO:0030500	regulation of bone mineralization	6/292	82/23328	0.00057668	0.00080738	6
BP	GO:0072088	nephron epithelium morphogenesis	6/292	82/23328	0.00057668	0.00080738	6
BP	GO:0045932	negative regulation of muscle contraction	4/292	31/23328	0.00057967	0.00080912	4
BP	GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	4/292	31/23328	0.00057967	0.00080912	4
BP	GO:1905314	semi-lunar valve development	4/292	31/23328	0.00057967	0.00080912	4
BP	GO:1905523	positive regulation of macrophage migration	4/292	31/23328	0.00057967	0.00080912	4
BP	GO:0046328	regulation of JNK cascade	9/292	186/23328	0.00058452	0.00081527	9

BP	GO:1901615	organic hydroxy compound metabolic process	16/292	498/23328	0.00058756	0.00081889	16
BP	GO:0042391	regulation of membrane potential	15/292	450/23328	0.00059609	0.00083014	15
BP	GO:1900046	regulation of hemostasis	6/292	83/23328	0.00061518	0.00085544	6
BP	GO:1903901	negative regulation of viral life cycle	6/292	83/23328	0.00061518	0.00085544	6
BP	GO:0002042	cell migration involved in sprouting angiogenesis	5/292	55/23328	0.00061923	0.00085913	5
BP	GO:0033619	membrane protein proteolysis	5/292	55/23328	0.00061923	0.00085913	5
BP	GO:0045773	positive regulation of axon extension	5/292	55/23328	0.00061923	0.00085913	5
BP	GO:0034614	cellular response to reactive oxygen species	8/292	150/23328	0.00062143	0.00086153	8
BP	GO:0022898	regulation of transmembrane transporter activity	11/292	270/23328	0.00063643	0.00087447	11
BP	GO:0002756	MyD88-independent toll-like receptor signaling pathway	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0014820	tonic smooth muscle contraction	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0032276	regulation of gonadotropin secretion	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0032494	response to peptidoglycan	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0032604	granulocyte macrophage colony-stimulating factor production	3/292	14/23328	0.00063787	0.00087447	3

BP	GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0034116	positive regulation of heterotypic cell-cell adhesion	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0042035	regulation of cytokine biosynthetic process	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0042362	fat-soluble vitamin biosynthetic process	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0061469	regulation of type B pancreatic cell proliferation	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0097531	mast cell migration	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:2000347	positive regulation of hepatocyte proliferation	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:2001279	regulation of unsaturated fatty acid biosynthetic process	3/292	14/23328	0.00063787	0.00087447	3
BP	GO:0001764	neuron migration	9/292	189/23328	0.00065561	0.00089751	9
BP	GO:0072028	nephron morphogenesis	6/292	84/23328	0.00065565	0.00089751	6
BP	GO:0035924	cellular response to vascular endothelial growth factor stimulus	5/292	56/23328	0.00067306	0.00091795	5
BP	GO:0045599	negative regulation of fat cell differentiation	5/292	56/23328	0.00067306	0.00091795	5
BP	GO:0071715	icosanoid transport	5/292	56/23328	0.00067306	0.00091795	5

BP	GO:0098586	cellular response to virus	5/292	56/23328	0.00067306	0.00091795	5
BP	GO:1901571	fatty acid derivative transport	5/292	56/23328	0.00067306	0.00091795	5
BP	GO:0006835	dicarboxylic acid transport	6/292	85/23328	0.00069814	0.00095075	6
BP	GO:0046364	monosaccharide biosynthetic process	6/292	85/23328	0.00069814	0.00095075	6
BP	GO:0055088	lipid homeostasis	8/292	153/23328	0.00070778	0.00096315	8
BP	GO:0014020	primary neural tube formation	7/292	118/23328	0.00072345	0.00098376	7
BP	GO:0046622	positive regulation of organ growth	5/292	57/23328	0.00073032	0.00099164	5
BP	GO:0055078	sodium ion homeostasis	5/292	57/23328	0.00073032	0.00099164	5
BP	GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	4/292	33/23328	0.0007392	0.00099928	4
BP	GO:0022617	extracellular matrix disassembly	4/292	33/23328	0.0007392	0.00099928	4
BP	GO:0032891	negative regulation of organic acid transport	4/292	33/23328	0.0007392	0.00099928	4
BP	GO:0033598	mammary gland epithelial cell proliferation	4/292	33/23328	0.0007392	0.00099928	4
BP	GO:0060740	prostate gland epithelium morphogenesis	4/292	33/23328	0.0007392	0.00099928	4
BP	GO:0060969	negative regulation of gene silencing	4/292	33/23328	0.0007392	0.00099928	4

BP	GO:0003281	ventricular septum development	6/292	86/23328	0.00074274	0.0010026	6
BP	GO:0050818	regulation of coagulation	6/292	86/23328	0.00074274	0.0010026	6
BP	GO:0034599	cellular response to oxidative stress	11/292	276/23328	0.00076247	0.00102847	11
BP	GO:0001838	embryonic epithelial tube formation	8/292	155/23328	0.00077053	0.00103859	8
BP	GO:0003007	heart morphogenesis	11/292	277/23328	0.00078536	0.00105326	11
BP	GO:0006924	activation-induced cell death of T cells	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0010715	regulation of extracellular matrix disassembly	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0023035	CD40 signaling pathway	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0030656	regulation of vitamin metabolic process	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0032222	regulation of synaptic transmission, cholinergic	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0032308	positive regulation of prostaglandin secretion	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0042089	cytokine biosynthetic process	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0042976	activation of Janus kinase activity	3/292	15/23328	0.00078998	0.00105326	3

BP	GO:0043031	negative regulation of macrophage activation	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0045760	positive regulation of action potential	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0046541	saliva secretion	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0061042	vascular wound healing	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0090594	inflammatory response to wounding	3/292	15/23328	0.00078998	0.00105326	3
BP	GO:0043330	response to exogenous dsRNA	5/292	58/23328	0.00079114	0.0010533	5
BP	GO:0045071	negative regulation of viral genome replication	5/292	58/23328	0.00079114	0.0010533	5
BP	GO:0015711	organic anion transport	15/292	463/23328	0.00079632	0.00105942	15
BP	GO:0010506	regulation of autophagy	11/292	278/23328	0.00080883	0.00107529	11
BP	GO:0003209	cardiac atrium morphogenesis	4/292	34/23328	0.00082958	0.00109892	4
BP	GO:0032689	negative regulation of interferon-gamma production	4/292	34/23328	0.00082958	0.00109892	4
BP	GO:0048710	regulation of astrocyte differentiation	4/292	34/23328	0.00082958	0.00109892	4
BP	GO:0060512	prostate gland morphogenesis	4/292	34/23328	0.00082958	0.00109892	4
BP	GO:0071634	regulation of transforming growth factor beta production	4/292	34/23328	0.00082958	0.00109892	4

BP	GO:0042475	odontogenesis of dentin-containing tooth	6/292	88/23328	0.00083852	0.00110997	6
BP	GO:0042445	hormone metabolic process	9/292	196/23328	0.00084923	0.00112334	9
BP	GO:0001654	eye development	14/292	418/23328	0.00086034	0.00113722	14
BP	GO:0045807	positive regulation of endocytosis	7/292	122/23328	0.00088112	0.00116385	7
BP	GO:0042490	mechanoreceptor differentiation	6/292	89/23328	0.00088985	0.0011737	6
BP	GO:0070301	cellular response to hydrogen peroxide	6/292	89/23328	0.00088985	0.0011737	6
BP	GO:0060711	labyrinthine layer development	5/292	60/23328	0.00092402	0.00121638	5
BP	GO:0098900	regulation of action potential	5/292	60/23328	0.00092402	0.00121638	5
BP	GO:0008286	insulin receptor signaling pathway	7/292	123/23328	0.00092448	0.00121638	7
BP	GO:0006458	'de novo' protein folding	4/292	35/23328	0.00092748	0.00121638	4
BP	GO:0045987	positive regulation of smooth muscle contraction	4/292	35/23328	0.00092748	0.00121638	4
BP	GO:0051084	'de novo' posttranslational protein folding	4/292	35/23328	0.00092748	0.00121638	4
BP	GO:0055090	acylglycerol homeostasis	4/292	35/23328	0.00092748	0.00121638	4
BP	GO:0070328	triglyceride homeostasis	4/292	35/23328	0.00092748	0.00121638	4

BP	GO:0150063	visual system development	14/292	422/23328	0.00094249	0.00123483	14
BP	GO:1900076	regulation of cellular response to insulin stimulus	6/292	90/23328	0.00094356	0.00123483	6
BP	GO:1903035	negative regulation of response to wounding	6/292	90/23328	0.00094356	0.00123483	6
BP	GO:0015802	basic amino acid transport	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0030238	male sex determination	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0051044	positive regulation of membrane protein ectodomain proteolysis	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0051709	regulation of killing of cells of other organism	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0070572	positive regulation of neuron projection regeneration	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0072537	fibroblast activation	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:1902337	regulation of apoptotic process involved in morphogenesis	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:2000647	negative regulation of stem cell proliferation	3/292	16/23328	0.00096331	0.00125357	3
BP	GO:0046777	protein autophosphorylation	10/292	241/23328	0.00096824	0.0012591	10
BP	GO:0051099	positive regulation of binding	9/292	200/23328	0.00097926	0.00127253	9
BP	GO:0009755	hormone-mediated signaling pathway	8/292	161/23328	0.00098608	0.00128049	8

BP	GO:0048286	lung alveolus development	5/292	61/23328	0.00099636	0.00129293	5
BP	GO:0048880	sensory system development	14/292	426/23328	0.00103115	0.00133608	14
BP	GO:0031069	hair follicle morphogenesis	4/292	36/23328	0.00103323	0.00133608	4
BP	GO:0034142	toll-like receptor 4 signaling pathway	4/292	36/23328	0.00103323	0.00133608	4
BP	GO:0061384	heart trabecula morphogenesis	4/292	36/23328	0.00103323	0.00133608	4
BP	GO:0071604	transforming growth factor beta production	4/292	36/23328	0.00103323	0.00133608	4
BP	GO:0062197	cellular response to chemical stress	12/292	332/23328	0.00104354	0.00134847	12
BP	GO:0002832	negative regulation of response to biotic stimulus	6/292	92/23328	0.00105843	0.00136579	6
BP	GO:0043900	regulation of multi-organism process	6/292	92/23328	0.00105843	0.00136579	6
BP	GO:0046822	regulation of nucleocytoplasmic transport	7/292	126/23328	0.00106471	0.00137294	7
BP	GO:0051926	negative regulation of calcium ion transport	5/292	62/23328	0.00107282	0.00138146	5
BP	GO:1905207	regulation of cardiocyte differentiation	5/292	62/23328	0.00107282	0.00138146	5
BP	GO:0009743	response to carbohydrate	9/292	203/23328	0.00108701	0.00139876	9
BP	GO:0014902	myotube differentiation	7/292	127/23328	0.0011115	0.00143377	7

BP	GO:0033077	T cell differentiation in thymus	6/292	93/23328	0.00111974	0.00143887	6
BP	GO:0010466	negative regulation of peptidase activity	10/292	246/23328	0.00113051	0.0014517	10
BP	GO:0002053	positive regulation of mesenchymal cell proliferation	4/292	37/23328	0.00114718	0.00147003	4
BP	GO:0002691	regulation of cellular extravasation	4/292	37/23328	0.00114718	0.00147003	4
BP	GO:0002920	regulation of humoral immune response	4/292	37/23328	0.00114718	0.00147003	4
BP	GO:0060038	cardiac muscle cell proliferation	5/292	63/23328	0.00115355	0.00147182	5
BP	GO:0002024	diet induced thermogenesis	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0002431	Fc receptor mediated stimulatory signaling pathway	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0003198	epithelial to mesenchymal transition involved in endocardial cushion formation	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0006968	cellular defense response	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0032306	regulation of prostaglandin secretion	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0042756	drinking behavior	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0044320	cellular response to leptin stimulus	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0045064	T-helper 2 cell differentiation	3/292	17/23328	0.00115895	0.00147182	3

BP	GO:0070886	positive regulation of calcineurin-NFAT signaling cascade	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0071360	cellular response to exogenous dsRNA	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0106058	positive regulation of calcineurin-mediated signaling	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:1904748	regulation of apoptotic process involved in development	3/292	17/23328	0.00115895	0.00147182	3
BP	GO:0045216	cell-cell junction organization	9/292	205/23328	0.00116403	0.00147727	9
BP	GO:0007596	blood coagulation	8/292	166/23328	0.00120041	0.00152238	8
BP	GO:0015850	organic hydroxy compound transport	10/292	249/23328	0.0012381	0.00156447	10
BP	GO:0001658	branching involved in ureteric bud morphogenesis	5/292	64/23328	0.00123868	0.00156447	5
BP	GO:0008347	glial cell migration	5/292	64/23328	0.00123868	0.00156447	5
BP	GO:0030858	positive regulation of epithelial cell differentiation	5/292	64/23328	0.00123868	0.00156447	5
BP	GO:0035904	aorta development	5/292	64/23328	0.00123868	0.00156447	5
BP	GO:0043331	response to dsRNA	5/292	64/23328	0.00123868	0.00156447	5
BP	GO:0031032	actomyosin structure organization	9/292	207/23328	0.00124541	0.00157189	9
BP	GO:0030509	BMP signaling pathway	8/292	167/23328	0.00124742	0.00157335	8

BP	GO:0031343	positive regulation of cell killing	6/292	95/23328	0.0012505	0.00157509	6
BP	GO:0051492	regulation of stress fiber assembly	6/292	95/23328	0.0012505	0.00157509	6
BP	GO:0010831	positive regulation of myotube differentiation	4/292	38/23328	0.00126964	0.00159375	4
BP	GO:0045940	positive regulation of steroid metabolic process	4/292	38/23328	0.00126964	0.00159375	4
BP	GO:0051953	negative regulation of amine transport	4/292	38/23328	0.00126964	0.00159375	4
BP	GO:0062208	positive regulation of pattern recognition receptor signaling pathway	4/292	38/23328	0.00126964	0.00159375	4
BP	GO:0110111	negative regulation of animal organ morphogenesis	4/292	38/23328	0.00126964	0.00159375	4
BP	GO:0007599	hemostasis	8/292	168/23328	0.00129588	0.00162559	8
BP	GO:0097193	intrinsic apoptotic signaling pathway	11/292	295/23328	0.00130563	0.0016367	11
BP	GO:0060021	roof of mouth development	6/292	96/23328	0.0013201	0.00165373	6
BP	GO:0050817	coagulation	8/292	169/23328	0.00134584	0.00168368	8
BP	GO:0051017	actin filament bundle assembly	8/292	169/23328	0.00134584	0.00168368	8
BP	GO:0002883	regulation of hypersensitivity	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0003214	cardiac left ventricle morphogenesis	3/292	18/23328	0.00137792	0.00170646	3

BP	GO:0010832	negative regulation of myotube differentiation	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0030540	female genitalia development	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0032674	regulation of interleukin-5 production	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0042487	regulation of odontogenesis of dentin-containing tooth	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0042659	regulation of cell fate specification	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0045342	MHC class II biosynthetic process	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0045779	negative regulation of bone resorption	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0060572	morphogenesis of an epithelial bud	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0060841	venous blood vessel development	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:1901317	regulation of flagellated sperm motility	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:1904706	negative regulation of vascular associated smooth muscle cell proliferation	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:2000846	regulation of corticosteroid hormone secretion	3/292	18/23328	0.00137792	0.00170646	3
BP	GO:0003230	cardiac atrium development	4/292	39/23328	0.00140095	0.00173034	4

BP	GO:0021983	pituitary gland development	4/292	39/23328	0.00140095	0.00173034	4
BP	GO:0032781	positive regulation of ATPase activity	4/292	39/23328	0.00140095	0.00173034	4
BP	GO:0090049	regulation of cell migration involved in sprouting angiogenesis	4/292	39/23328	0.00140095	0.00173034	4
BP	GO:0046661	male sex differentiation	8/292	171/23328	0.00145033	0.00179013	8
BP	GO:0001841	neural tube formation	7/292	133/23328	0.00145709	0.00179727	7
BP	GO:0072080	nephron tubule development	6/292	98/23328	0.00146815	0.0018097	6
BP	GO:0031667	response to nutrient levels	12/292	346/23328	0.00148125	0.00182463	12
BP	GO:0061572	actin filament bundle organization	8/292	172/23328	0.00150494	0.00185258	8
BP	GO:0060425	lung morphogenesis	5/292	67/23328	0.001522	0.00187108	5
BP	GO:1901570	fatty acid derivative biosynthetic process	5/292	67/23328	0.001522	0.00187108	5
BP	GO:0042176	regulation of protein catabolic process	13/292	395/23328	0.00152474	0.0018732	13
BP	GO:0032633	interleukin-4 production	4/292	40/23328	0.00154145	0.00188745	4
BP	GO:0038179	neurotrophin signaling pathway	4/292	40/23328	0.00154145	0.00188745	4
BP	GO:0060337	type I interferon signaling pathway	4/292	40/23328	0.00154145	0.00188745	4

BP	GO:0071357	cellular response to type I interferon	4/292	40/23328	0.00154145	0.00188745	4
BP	GO:1902692	regulation of neuroblast proliferation	4/292	40/23328	0.00154145	0.00188745	4
BP	GO:1901654	response to ketone	8/292	174/23328	0.00161905	0.00196555	8
BP	GO:0002524	hypersensitivity	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0032274	gonadotropin secretion	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0032634	interleukin-5 production	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0035930	corticosteroid hormone secretion	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0035994	response to muscle stretch	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0045721	negative regulation of gluconeogenesis	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0051546	keratinocyte migration	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0060712	spongiotrophoblast layer development	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0071605	monocyte chemotactic protein-1 production	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0071637	regulation of monocyte chemotactic protein-1 production	3/292	19/23328	0.00162121	0.00196555	3

BP	GO:1900451	positive regulation of glutamate receptor signaling pathway	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:1904754	positive regulation of vascular associated smooth muscle cell migration	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:2000251	positive regulation of actin cytoskeleton reorganization	3/292	19/23328	0.00162121	0.00196555	3
BP	GO:0022029	telencephalon cell migration	5/292	68/23328	0.00162624	0.00197035	5
BP	GO:0055123	digestive system development	7/292	136/23328	0.00165629	0.00200544	7
BP	GO:0010737	protein kinase A signaling	4/292	41/23328	0.00169146	0.00204266	4
BP	GO:0048730	epidermis morphogenesis	4/292	41/23328	0.00169146	0.00204266	4
BP	GO:1900744	regulation of p38MAPK cascade	4/292	41/23328	0.00169146	0.00204266	4
BP	GO:1905332	positive regulation of morphogenesis of an epithelium	4/292	41/23328	0.00169146	0.00204266	4
BP	GO:0042493	response to drug	10/292	260/23328	0.00170639	0.00205934	10
BP	GO:0032092	positive regulation of protein binding	6/292	101/23328	0.00171353	0.00206661	6
BP	GO:0021536	diencephalon development	5/292	69/23328	0.00173563	0.0020919	5
BP	GO:0001541	ovarian follicle development	5/292	70/23328	0.00185032	0.00222117	5
BP	GO:0006766	vitamin metabolic process	5/292	70/23328	0.00185032	0.00222117	5

BP	GO:0045669	positive regulation of osteoblast differentiation	5/292	70/23328	0.00185032	0.00222117	5
BP	GO:0055008	cardiac muscle tissue morphogenesis	5/292	70/23328	0.00185032	0.00222117	5
BP	GO:0006509	membrane protein ectodomain proteolysis	4/292	42/23328	0.00185131	0.00222117	4
BP	GO:0030501	positive regulation of bone mineralization	4/292	42/23328	0.00185131	0.00222117	4
BP	GO:0055023	positive regulation of cardiac muscle tissue growth	4/292	42/23328	0.00185131	0.00222117	4
BP	GO:0071772	response to BMP	8/292	178/23328	0.00186779	0.00223802	8
BP	GO:0071773	cellular response to BMP stimulus	8/292	178/23328	0.00186779	0.00223802	8
BP	GO:0008584	male gonad development	7/292	139/23328	0.00187605	0.00224647	7
BP	GO:0010763	positive regulation of fibroblast migration	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0010875	positive regulation of cholesterol efflux	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0010888	negative regulation of lipid storage	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0021534	cell proliferation in hindbrain	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0043011	myeloid dendritic cell differentiation	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0045986	negative regulation of smooth muscle contraction	3/292	20/23328	0.00188975	0.00225119	3

BP	GO:0046851	negative regulation of bone remodeling	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0050965	detection of temperature stimulus involved in sensory perception of pain	3/292	20/23328	0.00188975	0.00225119	3
BP	GO:0019058	viral life cycle	9/292	221/23328	0.00195243	0.00232435	9
BP	GO:0046546	development of primary male sexual characteristics	7/292	140/23328	0.00195412	0.00232486	7
BP	GO:0007492	endoderm development	5/292	71/23328	0.00197046	0.00233978	5
BP	GO:0021885	forebrain cell migration	5/292	71/23328	0.00197046	0.00233978	5
BP	GO:0060675	ureteric bud morphogenesis	5/292	71/23328	0.00197046	0.00233978	5
BP	GO:0030100	regulation of endocytosis	9/292	222/23328	0.00201316	0.00238741	9
BP	GO:0045732	positive regulation of protein catabolic process	9/292	222/23328	0.00201316	0.00238741	9
BP	GO:0046326	positive regulation of glucose import	4/292	43/23328	0.00202133	0.00239403	4
BP	GO:1903792	negative regulation of anion transport	4/292	43/23328	0.00202133	0.00239403	4
BP	GO:0002444	myeloid leukocyte mediated immunity	6/292	105/23328	0.00208767	0.00247101	6
BP	GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	5/292	72/23328	0.0020962	0.00247792	5
BP	GO:0072171	mesonephric tubule morphogenesis	5/292	72/23328	0.0020962	0.00247792	5

BP	GO:0002363	alpha-beta T cell lineage commitment	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0003177	pulmonary valve development	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0007190	activation of adenylate cyclase activity	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0009110	vitamin biosynthetic process	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0010869	regulation of receptor biosynthetic process	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0032305	positive regulation of icosanoid secretion	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0033630	positive regulation of cell adhesion mediated by integrin	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0034694	response to prostaglandin	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0045063	T-helper 1 cell differentiation	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0046325	negative regulation of glucose import	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0046697	decidualization	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0048486	parasympathetic nervous system development	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0050966	detection of mechanical stimulus involved in sensory perception of pain	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0060055	angiogenesis involved in wound healing	3/292	21/23328	0.00218444	0.00255603	3

BP	GO:0060456	positive regulation of digestive system process	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	3/292	21/23328	0.00218444	0.00255603	3
BP	GO:0010559	regulation of glycoprotein biosynthetic process	4/292	44/23328	0.00220184	0.00256826	4
BP	GO:0033628	regulation of cell adhesion mediated by integrin	4/292	44/23328	0.00220184	0.00256826	4
BP	GO:0045747	positive regulation of Notch signaling pathway	4/292	44/23328	0.00220184	0.00256826	4
BP	GO:0071385	cellular response to glucocorticoid stimulus	4/292	44/23328	0.00220184	0.00256826	4
BP	GO:1903672	positive regulation of sprouting angiogenesis	4/292	44/23328	0.00220184	0.00256826	4
BP	GO:0002886	regulation of myeloid leukocyte mediated immunity	5/292	73/23328	0.00222769	0.00259676	5
BP	GO:0090316	positive regulation of intracellular protein transport	7/292	144/23328	0.00229184	0.00266986	7
BP	GO:0110020	regulation of actomyosin structure organization	6/292	107/23328	0.00229638	0.00267345	6
BP	GO:0009749	response to glucose	8/292	185/23328	0.00237478	0.00276299	8
BP	GO:0010464	regulation of mesenchymal cell proliferation	4/292	45/23328	0.00239317	0.00277912	4
BP	GO:0060421	positive regulation of heart growth	4/292	45/23328	0.00239317	0.00277912	4
BP	GO:1901031	regulation of response to reactive oxygen species	4/292	45/23328	0.00239317	0.00277912	4

BP	GO:0060840	artery development	6/292	108/23328	0.00240644	0.00279278	6
BP	GO:0110053	regulation of actin filament organization	10/292	273/23328	0.00243484	0.00282396	10
BP	GO:0032616	interleukin-13 production	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:0045683	negative regulation of epidermis development	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:0048532	anatomical structure arrangement	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:0051873	killing by host of symbiont cells	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:0072215	regulation of metanephros development	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:1903055	positive regulation of extracellular matrix organization	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:2000010	positive regulation of protein localization to cell surface	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:2001026	regulation of endothelial cell chemotaxis	3/292	22/23328	0.0025061	0.00289206	3
BP	GO:0046626	regulation of insulin receptor signaling pathway	5/292	75/23328	0.00250854	0.00289308	5
BP	GO:0031952	regulation of protein autophosphorylation	4/292	46/23328	0.00259562	0.0029879	4
BP	GO:0043616	keratinocyte proliferation	4/292	46/23328	0.00259562	0.0029879	4
BP	GO:0071384	cellular response to corticosteroid stimulus	4/292	46/23328	0.00259562	0.0029879	4

BP	GO:0009746	response to hexose	8/292	188/23328	0.00262256	0.00301515	8
BP	GO:0010770	positive regulation of cell morphogenesis involved in differentiation	8/292	188/23328	0.00262256	0.00301515	8
BP	GO:0032231	regulation of actin filament bundle assembly	6/292	110/23328	0.00263842	0.0030315	6
BP	GO:0033157	regulation of intracellular protein transport	9/292	232/23328	0.00270729	0.00310869	9
BP	GO:0034284	response to monosaccharide	8/292	189/23328	0.0027095	0.00310896	8
BP	GO:0060249	anatomical structure homeostasis	13/292	422/23328	0.0027109	0.00310896	13
BP	GO:0043029	T cell homeostasis	4/292	47/23328	0.00280952	0.00321807	4
BP	GO:0060964	regulation of gene silencing by miRNA	4/292	47/23328	0.00280952	0.00321807	4
BP	GO:0002313	mature B cell differentiation involved in immune response	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0003176	aortic valve development	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0003283	atrial septum development	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0010560	positive regulation of glycoprotein biosynthetic process	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0048485	sympathetic nervous system development	3/292	23/23328	0.00285554	0.00324459	3

BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0050961	detection of temperature stimulus involved in sensory perception	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0071359	cellular response to dsRNA	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0072202	cell differentiation involved in metanephros development	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0101023	vascular endothelial cell proliferation	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:1905562	regulation of vascular endothelial cell proliferation	3/292	23/23328	0.00285554	0.00324459	3
BP	GO:0072594	establishment of protein localization to organelle	13/292	426/23328	0.00293803	0.00333627	13
BP	GO:0014855	striated muscle cell proliferation	5/292	78/23328	0.0029768	0.00337822	5
BP	GO:0072006	nephron development	7/292	151/23328	0.00298927	0.00339029	7
BP	GO:0010883	regulation of lipid storage	4/292	48/23328	0.00303518	0.00343812	4
BP	GO:0038066	p38MAPK cascade	4/292	48/23328	0.00303518	0.00343812	4
BP	GO:0050808	synapse organization	14/292	479/23328	0.00303813	0.00343935	14
BP	GO:0051052	regulation of DNA metabolic process	12/292	379/23328	0.00313181	0.00354324	12

BP	GO:0055021	regulation of cardiac muscle tissue growth	5/292	79/23328	0.00314602	0.00355713	5
BP	GO:0001892	embryonic placenta development	6/292	114/23328	0.00315224	0.00356198	6
BP	GO:0021915	neural tube development	8/292	194/23328	0.0031785	0.00358946	8
BP	GO:0002523	leukocyte migration involved in inflammatory response	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0002864	regulation of acute inflammatory response to antigenic stimulus	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0003181	atrioventricular valve morphogenesis	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0003272	endocardial cushion formation	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0007205	protein kinase C-activating G protein-coupled receptor signaling pathway	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0048670	regulation of collateral sprouting	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0050687	negative regulation of defense response to virus	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0072207	metanephric epithelium development	3/292	24/23328	0.00323351	0.00363379	3
BP	GO:0035196	production of miRNAs involved in gene silencing by miRNA	4/292	49/23328	0.0032729	0.00366688	4
BP	GO:0042755	eating behavior	4/292	49/23328	0.0032729	0.00366688	4
BP	GO:0061028	establishment of endothelial barrier	4/292	49/23328	0.0032729	0.00366688	4

BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	4/292	49/23328	0.0032729	0.00366688	4
BP	GO:1905953	negative regulation of lipid localization	4/292	49/23328	0.0032729	0.00366688	4
BP	GO:0072078	nephron tubule morphogenesis	5/292	80/23328	0.00332207	0.00371972	5
BP	GO:0042472	inner ear morphogenesis	6/292	116/23328	0.00343549	0.00384438	6
BP	GO:0032715	negative regulation of interleukin-6 production	4/292	50/23328	0.00352299	0.00393038	4
BP	GO:0060147	regulation of posttranscriptional gene silencing	4/292	50/23328	0.00352299	0.00393038	4
BP	GO:0060966	regulation of gene silencing by RNA	4/292	50/23328	0.00352299	0.00393038	4
BP	GO:0070169	positive regulation of biomineral tissue development	4/292	50/23328	0.00352299	0.00393038	4
BP	GO:0110151	positive regulation of biomineralization	4/292	50/23328	0.00352299	0.00393038	4
BP	GO:0032703	negative regulation of interleukin-2 production	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:0032753	positive regulation of interleukin-4 production	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:0046426	negative regulation of receptor signaling pathway via JAK-STAT	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:0060295	regulation of cilium movement involved in cell motility	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:0061213	positive regulation of mesonephros development	3/292	25/23328	0.00364073	0.0040349	3

BP	GO:1901032	negative regulation of response to reactive oxygen species	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:1902019	regulation of cilium-dependent cell motility	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:1902993	positive regulation of amyloid precursor protein catabolic process	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:1903020	positive regulation of glycoprotein metabolic process	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:1903206	negative regulation of hydrogen peroxide-induced cell death	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:2000193	positive regulation of fatty acid transport	3/292	25/23328	0.00364073	0.0040349	3
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	5/292	82/23328	0.00369525	0.00409041	5
BP	GO:0050805	negative regulation of synaptic transmission	5/292	82/23328	0.00369525	0.00409041	5
BP	GO:0031050	dsRNA processing	4/292	51/23328	0.00378576	0.00417806	4
BP	GO:0043303	mast cell degranulation	4/292	51/23328	0.00378576	0.00417806	4
BP	GO:0060043	regulation of cardiac muscle cell proliferation	4/292	51/23328	0.00378576	0.00417806	4
BP	GO:0060412	ventricular septum morphogenesis	4/292	51/23328	0.00378576	0.00417806	4
BP	GO:0070918	production of small RNA involved in gene silencing by RNA	4/292	51/23328	0.00378576	0.00417806	4
BP	GO:0034250	positive regulation of cellular amide metabolic process	7/292	158/23328	0.00383865	0.00423138	7

BP	GO:0055067	monovalent inorganic cation homeostasis	7/292	158/23328	0.00383865	0.00423138	7
BP	GO:0030168	platelet activation	5/292	83/23328	0.00389269	0.00428583	5
BP	GO:0060415	muscle tissue morphogenesis	5/292	83/23328	0.00389269	0.00428583	5
BP	GO:1903900	regulation of viral life cycle	7/292	159/23328	0.00397355	0.00437224	7
BP	GO:0002279	mast cell activation involved in immune response	4/292	52/23328	0.00406149	0.00444989	4
BP	GO:0002448	mast cell mediated immunity	4/292	52/23328	0.00406149	0.00444989	4
BP	GO:0045933	positive regulation of muscle contraction	4/292	52/23328	0.00406149	0.00444989	4
BP	GO:0060612	adipose tissue development	4/292	52/23328	0.00406149	0.00444989	4
BP	GO:0001780	neutrophil homeostasis	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0003084	positive regulation of systemic arterial blood pressure	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0032303	regulation of icosanoid secretion	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0034123	positive regulation of toll-like receptor signaling pathway	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0060065	uterus development	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0060338	regulation of type I interferon-mediated signaling pathway	3/292	26/23328	0.00407788	0.00444989	3

BP	GO:0071549	cellular response to dexamethasone stimulus	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0090189	regulation of branching involved in ureteric bud morphogenesis	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0090280	positive regulation of calcium ion import	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:1904893	negative regulation of receptor signaling pathway via STAT	3/292	26/23328	0.00407788	0.00444989	3
BP	GO:0003151	outflow tract morphogenesis	5/292	84/23328	0.00409757	0.00446873	5
BP	GO:0046620	regulation of organ growth	6/292	121/23328	0.00422621	0.00460631	6
BP	GO:0006694	steroid biosynthetic process	7/292	161/23328	0.0042541	0.00463396	7
BP	GO:0001960	negative regulation of cytokine-mediated signaling pathway	4/292	53/23328	0.00435048	0.00472501	4
BP	GO:0032371	regulation of sterol transport	4/292	53/23328	0.00435048	0.00472501	4
BP	GO:0032374	regulation of cholesterol transport	4/292	53/23328	0.00435048	0.00472501	4
BP	GO:0032720	negative regulation of tumor necrosis factor production	4/292	53/23328	0.00435048	0.00472501	4
BP	GO:0061383	trabecula morphogenesis	4/292	53/23328	0.00435048	0.00472501	4
BP	GO:0048469	cell maturation	8/292	205/23328	0.0044316	0.00481028	8
BP	GO:0061333	renal tubule morphogenesis	5/292	86/23328	0.00453024	0.00490514	5

BP	GO:0003171	atrioventricular valve development	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:0003338	metanephros morphogenesis	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:0032925	regulation of activin receptor signaling pathway	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response to virus	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:0042753	positive regulation of circadian rhythm	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:0060045	positive regulation of cardiac muscle cell proliferation	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:1900017	positive regulation of cytokine production involved in inflammatory response	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:1900120	regulation of receptor binding	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:2000727	positive regulation of cardiac muscle cell differentiation	3/292	27/23328	0.00454558	0.00490514	3
BP	GO:1902115	regulation of organelle assembly	8/292	206/23328	0.004562	0.00491999	8
BP	GO:0048565	digestive tract development	6/292	123/23328	0.00457743	0.00493374	6
BP	GO:0051954	positive regulation of amine transport	4/292	54/23328	0.00465303	0.00500353	4
BP	GO:0061077	chaperone-mediated protein folding	4/292	54/23328	0.00465303	0.00500353	4
BP	GO:1902930	regulation of alcohol biosynthetic process	4/292	54/23328	0.00465303	0.00500353	4

BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	4/292	54/23328	0.00465303	0.00500353	4
BP	GO:0045786	negative regulation of cell cycle	13/292	451/23328	0.00473528	0.00508902	13
BP	GO:0060420	regulation of heart growth	5/292	87/23328	0.00475833	0.00511081	5
BP	GO:0045912	negative regulation of carbohydrate metabolic process	4/292	55/23328	0.0049694	0.00533298	4
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	8/292	209/23328	0.00497095	0.00533298	8
BP	GO:0008593	regulation of Notch signaling pathway	5/292	88/23328	0.00499446	0.00535509	5
BP	GO:0007271	synaptic transmission, cholinergic	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:0010738	regulation of protein kinase A signaling	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:0045061	thymic T cell selection	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:0045648	positive regulation of erythrocyte differentiation	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:0061217	regulation of mesonephros development	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:1900745	positive regulation of p38MAPK cascade	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:1903671	negative regulation of sprouting angiogenesis	3/292	28/23328	0.00504443	0.00538674	3
BP	GO:0001656	metanephros development	5/292	89/23328	0.00523879	0.00558783	5

BP	GO:0051702	interaction with symbiont	5/292	89/23328	0.00523879	0.00558783	5
BP	GO:0051346	negative regulation of hydrolase activity	12/292	405/23328	0.00528658	0.00563555	12
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	4/292	56/23328	0.00529989	0.00564322	4
BP	GO:0050873	brown fat cell differentiation	4/292	56/23328	0.00529989	0.00564322	4
BP	GO:0051101	regulation of DNA binding	6/292	127/23328	0.00534372	0.0056866	6
BP	GO:0019226	transmission of nerve impulse	5/292	90/23328	0.00549145	0.00584044	5
BP	GO:0010893	positive regulation of steroid biosynthetic process	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:0045109	intermediate filament organization	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:0045589	regulation of regulatory T cell differentiation	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:0060571	morphogenesis of an epithelial fold	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:0071548	response to dexamethasone	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:1900078	positive regulation of cellular response to insulin stimulus	3/292	29/23328	0.00557498	0.00590885	3
BP	GO:0006631	fatty acid metabolic process	12/292	408/23328	0.00559694	0.00592872	12
BP	GO:0002067	glandular epithelial cell differentiation	4/292	57/23328	0.00564476	0.00596568	4

BP	GO:0007585	respiratory gaseous exchange by respiratory system	4/292	57/23328	0.00564476	0.00596568	4
BP	GO:0010463	mesenchymal cell proliferation	4/292	57/23328	0.00564476	0.00596568	4
BP	GO:0060761	negative regulation of response to cytokine stimulus	4/292	57/23328	0.00564476	0.00596568	4
BP	GO:0006913	nucleocytoplasmic transport	10/292	308/23328	0.00568112	0.00599724	10
BP	GO:0051169	nuclear transport	10/292	308/23328	0.00568112	0.00599724	10
BP	GO:0007160	cell-matrix adhesion	8/292	214/23328	0.00571425	0.00602876	8
BP	GO:0040014	regulation of multicellular organism growth	5/292	91/23328	0.00575259	0.00606574	5
BP	GO:1901888	regulation of cell junction assembly	8/292	215/23328	0.00587256	0.0061887	8
BP	GO:0050852	T cell receptor signaling pathway	6/292	130/23328	0.00597717	0.00629535	6
BP	GO:0035456	response to interferon-beta	4/292	58/23328	0.00600429	0.0063131	4
BP	GO:0042267	natural killer cell mediated cytotoxicity	4/292	58/23328	0.00600429	0.0063131	4
BP	GO:0051445	regulation of meiotic cell cycle	4/292	58/23328	0.00600429	0.0063131	4
BP	GO:0009895	negative regulation of catabolic process	10/292	311/23328	0.00606891	0.00637378	10
BP	GO:0090596	sensory organ morphogenesis	10/292	311/23328	0.00606891	0.00637378	10

BP	GO:0002360	T cell lineage commitment	3/292	30/23328	0.00613778	0.00642782	3
BP	GO:0010874	regulation of cholesterol efflux	3/292	30/23328	0.00613778	0.00642782	3
BP	GO:0050951	sensory perception of temperature stimulus	3/292	30/23328	0.00613778	0.00642782	3
BP	GO:0051957	positive regulation of amino acid transport	3/292	30/23328	0.00613778	0.00642782	3
BP	GO:0060317	cardiac epithelial to mesenchymal transition	3/292	30/23328	0.00613778	0.00642782	3
BP	GO:0007623	circadian rhythm	8/292	217/23328	0.00619917	0.00648194	8
BP	GO:0031668	cellular response to extracellular stimulus	8/292	217/23328	0.00619917	0.00648194	8
BP	GO:0031623	receptor internalization	6/292	131/23328	0.00619999	0.00648194	6
BP	GO:0002028	regulation of sodium ion transport	5/292	93/23328	0.00630093	0.00658374	5
BP	GO:0043462	regulation of ATPase activity	4/292	59/23328	0.00637874	0.00666126	4
BP	GO:0009582	detection of abiotic stimulus	6/292	132/23328	0.0064288	0.00670975	6
BP	GO:0002315	marginal zone B cell differentiation	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0002645	positive regulation of tolerance induction	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0003149	membranous septum morphogenesis	2/292	10/23328	0.00657565	0.0067711	2

BP	GO:0006591	ornithine metabolic process	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0010692	regulation of alkaline phosphatase activity	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0010745	negative regulation of macrophage derived foam cell differentiation	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0021612	facial nerve structural organization	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0021826	substrate-independent telencephalic tangential migration	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0021843	substrate-independent telencephalic tangential interneuron migration	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0032927	positive regulation of activin receptor signaling pathway	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0033029	regulation of neutrophil apoptotic process	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0035907	dorsal aorta development	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0039532	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0051001	negative regulation of nitric-oxide synthase activity	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0060484	lung-associated mesenchyme development	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0060513	prostatic bud formation	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0060710	chorio-allantoic fusion	2/292	10/23328	0.00657565	0.0067711	2

BP	GO:0060907	positive regulation of macrophage cytokine production	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0070391	response to lipoteichoic acid	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0070673	response to interleukin-18	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0070857	regulation of bile acid biosynthetic process	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0071223	cellular response to lipoteichoic acid	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0090091	positive regulation of extracellular matrix disassembly	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0090186	regulation of pancreatic juice secretion	2/292	10/23328	0.00657565	0.0067711	2
BP	GO:0015908	fatty acid transport	5/292	94/23328	0.00658842	0.00678046	5
BP	GO:0009581	detection of external stimulus	6/292	133/23328	0.00666369	0.0068541	6
BP	GO:0007530	sex determination	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:0032373	positive regulation of sterol transport	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:0032376	positive regulation of cholesterol transport	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:0050901	leukocyte tethering or rolling	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:0061036	positive regulation of cartilage development	3/292	31/23328	0.00673329	0.00689494	3

BP	GO:0061037	negative regulation of cartilage development	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:1901889	negative regulation of cell junction assembly	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:1902932	positive regulation of alcohol biosynthetic process	3/292	31/23328	0.00673329	0.00689494	3
BP	GO:0048260	positive regulation of receptor-mediated endocytosis	4/292	60/23328	0.00676836	0.00692701	4
BP	GO:2001257	regulation of cation channel activity	7/292	176/23328	0.00686128	0.00701822	7
BP	GO:0007229	integrin-mediated signaling pathway	5/292	95/23328	0.00688497	0.00703465	5
BP	GO:0021954	central nervous system neuron development	5/292	95/23328	0.00688497	0.00703465	5
BP	GO:0035051	cardiocyte differentiation	7/292	177/23328	0.00706956	0.00721926	7
BP	GO:0030177	positive regulation of Wnt signaling pathway	6/292	135/23328	0.00715204	0.00729945	6
BP	GO:0002228	natural killer cell mediated immunity	4/292	61/23328	0.00717341	0.00731721	4
BP	GO:1902903	regulation of supramolecular fiber organization	11/292	370/23328	0.00725156	0.00739284	11
BP	GO:0001893	maternal placenta development	3/292	32/23328	0.00736197	0.00748472	3
BP	GO:0008206	bile acid metabolic process	3/292	32/23328	0.00736197	0.00748472	3
BP	GO:0032673	regulation of interleukin-4 production	3/292	32/23328	0.00736197	0.00748472	3

BP	GO:0048668	collateral sprouting	3/292	32/23328	0.00736197	0.00748472	3
BP	GO:0060977	coronary vasculature morphogenesis	3/292	32/23328	0.00736197	0.00748472	3
BP	GO:0051056	regulation of small GTPase mediated signal transduction	9/292	271/23328	0.00738549	0.0075045	9
BP	GO:0045069	regulation of viral genome replication	5/292	97/23328	0.00750584	0.0076226	5
BP	GO:0007389	pattern specification process	13/292	478/23328	0.00757673	0.00769035	13
BP	GO:0031018	endocrine pancreas development	4/292	62/23328	0.00759414	0.00770379	4
BP	GO:0051495	positive regulation of cytoskeleton organization	8/292	225/23328	0.00764529	0.00775142	8
BP	GO:0034329	cell junction assembly	12/292	426/23328	0.00777595	0.00787956	12
BP	GO:0006066	alcohol metabolic process	10/292	323/23328	0.0078304	0.00793038	10
BP	GO:0042471	ear morphogenesis	6/292	138/23328	0.00793238	0.00800669	6
BP	GO:0046165	alcohol biosynthetic process	6/292	138/23328	0.00793238	0.00800669	6
BP	GO:0002118	aggressive behavior	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0002468	dendritic cell antigen processing and presentation	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0002579	positive regulation of antigen processing and presentation	2/292	11/23328	0.00797084	0.00800669	2

BP	GO:0021559	trigeminal nerve development	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0031943	regulation of glucocorticoid metabolic process	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0060020	Bergmann glial cell differentiation	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0060174	limb bud formation	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0060405	regulation of penile erection	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0060600	dichotomous subdivision of an epithelial terminal unit	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0090037	positive regulation of protein kinase C signaling	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0097084	vascular associated smooth muscle cell development	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:2000322	regulation of glucocorticoid receptor signaling pathway	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:2000849	regulation of glucocorticoid secretion	2/292	11/23328	0.00797084	0.00800669	2
BP	GO:0045066	regulatory T cell differentiation	3/292	33/23328	0.00802425	0.0080472	3
BP	GO:0051354	negative regulation of oxidoreductase activity	3/292	33/23328	0.00802425	0.0080472	3
BP	GO:1903205	regulation of hydrogen peroxide-induced cell death	3/292	33/23328	0.00802425	0.0080472	3
BP	GO:0030101	natural killer cell activation	5/292	99/23328	0.00816469	0.00817915	5

BP	GO:0043502	regulation of muscle adaptation	5/292	99/23328	0.00816469	0.00817915	5
BP	GO:0006879	cellular iron ion homeostasis	4/292	64/23328	0.0084836	0.00848021	4
BP	GO:0045668	negative regulation of osteoblast differentiation	4/292	64/23328	0.0084836	0.00848021	4
BP	GO:0090278	negative regulation of peptide hormone secretion	4/292	64/23328	0.0084836	0.00848021	4
BP	GO:1903510	mucopolysaccharide metabolic process	4/292	64/23328	0.0084836	0.00848021	4
BP	GO:0050795	regulation of behavior	5/292	100/23328	0.0085087	0.0085007	5
BP	GO:0030534	adult behavior	7/292	184/23328	0.00866128	0.00864377	7
BP	GO:0032388	positive regulation of intracellular transport	7/292	184/23328	0.00866128	0.00864377	7
BP	GO:0003203	endocardial cushion morphogenesis	3/292	34/23328	0.00872051	0.00868878	3
BP	GO:0003352	regulation of cilium movement	3/292	34/23328	0.00872051	0.00868878	3
BP	GO:0098868	bone growth	3/292	34/23328	0.00872051	0.00868878	3
BP	GO:0015807	L-amino acid transport	4/292	65/23328	0.0089528	0.00891542	4
BP	GO:0071496	cellular response to external stimulus	9/292	280/23328	0.00904172	0.00899911	9
BP	GO:0001704	formation of primary germ layer	5/292	102/23328	0.00922657	0.00917319	5

BP	GO:0050848	regulation of calcium-mediated signaling	5/292	102/23328	0.00922657	0.00917319	5
BP	GO:0022411	cellular component disassembly	11/292	383/23328	0.00925742	0.00919891	11
BP	GO:0007015	actin filament organization	12/292	437/23328	0.00940448	0.00928155	12
BP	GO:0001707	mesoderm formation	4/292	66/23328	0.0094386	0.00928155	4
BP	GO:0010837	regulation of keratinocyte proliferation	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0034110	regulation of homotypic cell-cell adhesion	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0043243	positive regulation of protein-containing complex disassembly	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0050869	negative regulation of B cell activation	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0055083	monovalent inorganic anion homeostasis	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:1903203	regulation of oxidative stress-induced neuron death	3/292	35/23328	0.0094511	0.00928155	3
BP	GO:0003337	mesenchymal to epithelial transition involved in metanephros morphogenesis	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0010459	negative regulation of heart rate	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0016264	gap junction assembly	2/292	12/23328	0.00948645	0.00928155	2

BP	GO:0021561	facial nerve development	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0021610	facial nerve morphogenesis	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0035933	glucocorticoid secretion	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0045625	regulation of T-helper 1 cell differentiation	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0051024	positive regulation of immunoglobulin secretion	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0051132	NK T cell activation	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0060068	vagina development	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0060430	lung saccule development	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0060872	semicircular canal development	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0070943	neutrophil-mediated killing of symbiont cell	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0097709	connective tissue replacement	2/292	12/23328	0.00948645	0.00928155	2

BP	GO:1902947	regulation of tau-protein kinase activity	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	2/292	12/23328	0.00948645	0.00928155	2
BP	GO:0003300	cardiac muscle hypertrophy	5/292	103/23328	0.0096007	0.00938835	5
BP	GO:0010508	positive regulation of autophagy	6/292	144/23328	0.00967392	0.00945495	6
BP	GO:0034766	negative regulation of ion transmembrane transport	5/292	104/23328	0.00998514	0.00975395	5
BP	GO:0008045	motor neuron axon guidance	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:0010453	regulation of cell fate commitment	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:0036475	neuron death in response to oxidative stress	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:0070306	lens fiber cell differentiation	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:0097242	amyloid-beta clearance	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:2000191	regulation of fatty acid transport	3/292	36/23328	0.01021636	0.00994822	3
BP	GO:0016239	positive regulation of macroautophagy	4/292	69/23328	0.01099788	0.01065318	4
BP	GO:0034394	protein localization to cell surface	4/292	69/23328	0.01099788	0.01065318	4

BP	GO:0048678	response to axon injury	4/292	69/23328	0.01099788	0.01065318	4
BP	GO:0001782	B cell homeostasis	3/292	37/23328	0.01101659	0.01065318	3
BP	GO:0036474	cell death in response to hydrogen peroxide	3/292	37/23328	0.01101659	0.01065318	3
BP	GO:0040020	regulation of meiotic nuclear division	3/292	37/23328	0.01101659	0.01065318	3
BP	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	3/292	37/23328	0.01101659	0.01065318	3
BP	GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	3/292	37/23328	0.01101659	0.01065318	3
BP	GO:0046578	regulation of Ras protein signal transduction	8/292	240/23328	0.01102278	0.01065318	8
BP	GO:0001553	luteinization	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0007320	insemination	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0021604	cranial nerve structural organization	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0031953	negative regulation of protein autophosphorylation	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0035810	positive regulation of urine volume	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0045628	regulation of T-helper 2 cell differentiation	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0045906	negative regulation of vasoconstriction	2/292	13/23328	0.01111929	0.01065318	2

BP	GO:0048012	hepatocyte growth factor receptor signaling pathway	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0048304	positive regulation of isotype switching to IgG isotypes	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0051549	positive regulation of keratinocyte migration	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0055062	phosphate ion homeostasis	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0060601	lateral sprouting from an epithelium	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0070091	glucagon secretion	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0070092	regulation of glucagon secretion	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0070471	uterine smooth muscle contraction	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0071679	commissural neuron axon guidance	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0072505	divalent inorganic anion homeostasis	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0072506	trivalent inorganic anion homeostasis	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0072540	T-helper 17 cell lineage commitment	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:1904251	regulation of bile acid metabolic process	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:2000674	regulation of type B pancreatic cell apoptotic process	2/292	13/23328	0.01111929	0.01065318	2

BP	GO:2001223	negative regulation of neuron migration	2/292	13/23328	0.01111929	0.01065318	2
BP	GO:0000018	regulation of DNA recombination	5/292	107/23328	0.01120158	0.01072088	5
BP	GO:0014897	striated muscle hypertrophy	5/292	107/23328	0.01120158	0.01072088	5
BP	GO:0032922	circadian regulation of gene expression	4/292	70/23328	0.01155227	0.01104507	4
BP	GO:0048332	mesoderm morphogenesis	4/292	70/23328	0.01155227	0.01104507	4
BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	6/292	150/23328	0.01167222	0.01115397	6
BP	GO:0010543	regulation of platelet activation	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0032228	regulation of synaptic transmission, GABAergic	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0043304	regulation of mast cell degranulation	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0046627	negative regulation of insulin receptor signaling pathway	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0051968	positive regulation of synaptic transmission, glutamatergic	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0072210	metanephric nephron development	3/292	38/23328	0.01185204	0.01129072	3
BP	GO:0014896	muscle hypertrophy	5/292	109/23328	0.01206642	0.01148902	5
BP	GO:0055081	anion homeostasis	4/292	71/23328	0.01212432	0.0115382	4

BP	GO:0044706	multi-multicellular organism process	7/292	197/23328	0.01229324	0.01169291	7
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	6/292	152/23328	0.01239852	0.01178699	6
BP	GO:0006091	generation of precursor metabolites and energy	11/292	400/23328	0.012498	0.01187544	11
BP	GO:0008344	adult locomotory behavior	5/292	110/23328	0.01251537	0.01187971	5
BP	GO:0048709	oligodendrocyte differentiation	5/292	110/23328	0.01251537	0.01187971	5
BP	GO:0010611	regulation of cardiac muscle hypertrophy	4/292	72/23328	0.01271421	0.01203931	4
BP	GO:0007257	activation of JUN kinase activity	3/292	39/23328	0.01272296	0.01203931	3
BP	GO:0010613	positive regulation of cardiac muscle hypertrophy	3/292	39/23328	0.01272296	0.01203931	3
BP	GO:0033006	regulation of mast cell activation involved in immune response	3/292	39/23328	0.01272296	0.01203931	3
BP	GO:0035850	epithelial cell differentiation involved in kidney development	3/292	39/23328	0.01272296	0.01203931	3
BP	GO:0050892	intestinal absorption	3/292	39/23328	0.01272296	0.01203931	3
BP	GO:0030183	B cell differentiation	6/292	153/23328	0.01277334	0.01203931	6
BP	GO:0001865	NK T cell differentiation	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0002885	positive regulation of hypersensitivity	2/292	14/23328	0.01286619	0.01203931	2

BP	GO:0021984	adenohypophysis development	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0030213	hyaluronan biosynthetic process	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0030432	peristalsis	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0032769	negative regulation of monooxygenase activity	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0042921	glucocorticoid receptor signaling pathway	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0045060	negative thymic T cell selection	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0045835	negative regulation of meiotic nuclear division	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0046642	negative regulation of alpha-beta T cell proliferation	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0048537	mucosa-associated lymphoid tissue development	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0048541	Peyer's patch development	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0048672	positive regulation of collateral sprouting	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0051152	positive regulation of smooth muscle cell differentiation	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0051284	positive regulation of sequestering of calcium ion	2/292	14/23328	0.01286619	0.01203931	2

BP	GO:0060736	prostate gland growth	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0070942	neutrophil mediated cytotoxicity	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0071397	cellular response to cholesterol	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0072683	T cell extravasation	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0099550	trans-synaptic signaling, modulating synaptic transmission	2/292	14/23328	0.01286619	0.01203931	2
BP	GO:0050851	antigen receptor-mediated signaling pathway	9/292	299/23328	0.01344621	0.01257567	9
BP	GO:0031589	cell-substrate adhesion	10/292	351/23328	0.01346213	0.01258418	10
BP	GO:0009409	response to cold	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0014742	positive regulation of muscle hypertrophy	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0030431	sleep	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0034105	positive regulation of tissue remodeling	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0043368	positive T cell selection	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0060259	regulation of feeding behavior	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0070570	regulation of neuron projection regeneration	3/292	40/23328	0.01362957	0.01267648	3

BP	GO:0070884	regulation of calcineurin-NFAT signaling cascade	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0071542	dopaminergic neuron differentiation	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0097009	energy homeostasis	3/292	40/23328	0.01362957	0.01267648	3
BP	GO:0043299	leukocyte degranulation	4/292	74/23328	0.01394824	0.01296634	4
BP	GO:0007498	mesoderm development	5/292	114/23328	0.01442417	0.01340201	5
BP	GO:0050806	positive regulation of synaptic transmission	10/292	355/23328	0.0144658	0.01343392	10
BP	GO:0106056	regulation of calcineurin-mediated signaling	3/292	41/23328	0.01457205	0.01349716	3
BP	GO:1902991	regulation of amyloid precursor protein catabolic process	3/292	41/23328	0.01457205	0.01349716	3
BP	GO:0010507	negative regulation of autophagy	4/292	75/23328	0.01459273	0.01349716	4
BP	GO:0014743	regulation of muscle hypertrophy	4/292	75/23328	0.01459273	0.01349716	4
BP	GO:0002862	negative regulation of inflammatory response to antigenic stimulus	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:0010523	negative regulation of calcium ion transport into cytosol	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:0010839	negative regulation of keratinocyte proliferation	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:0010958	regulation of amino acid import across plasma membrane	2/292	15/23328	0.01472407	0.01349716	2

BP	GO:0010960	magnesium ion homeostasis	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0014049	positive regulation of glutamate secretion	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0021781	glial cell fate commitment	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0030157	pancreatic juice secretion	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0031958	corticosteroid receptor signaling pathway	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0042416	dopamine biosynthetic process	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0043383	negative T cell selection	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0048680	positive regulation of axon regeneration	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0051547	regulation of keratinocyte migration	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0051712	positive regulation of killing of cells of other organism	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0072283	metanephric renal vesicle morphogenesis	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:0099527	postsynapse to nucleus signaling pathway	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:1900121	negative regulation of receptor binding	2/292		15/23328	0.01472407	0.01349716	2
BP	GO:1903543	positive regulation of exosomal secretion	2/292		15/23328	0.01472407	0.01349716	2

BP	GO:1903587	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:1903789	regulation of amino acid transmembrane transport	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:1904862	inhibitory synapse assembly	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:2001241	positive regulation of extrinsic apoptotic signaling pathway in absence of ligand	2/292	15/23328	0.01472407	0.01349716	2
BP	GO:0018958	phenol-containing compound metabolic process	5/292	115/23328	0.0149302	0.01367253	5
BP	GO:0019079	viral genome replication	5/292	115/23328	0.0149302	0.01367253	5
BP	GO:0055001	muscle cell development	7/292	205/23328	0.01501151	0.01374017	7
BP	GO:0071383	cellular response to steroid hormone stimulus	6/292	159/23328	0.01519048	0.01389709	6
BP	GO:0022412	cellular process involved in reproduction in multicellular organism	12/292	468/23328	0.01544084	0.01411867	12
BP	GO:0019882	antigen processing and presentation	5/292	116/23328	0.01544798	0.01411867	5
BP	GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/292	42/23328	0.01555057	0.01417032	3
BP	GO:0010765	positive regulation of sodium ion transport	3/292	42/23328	0.01555057	0.01417032	3
BP	GO:0048873	homeostasis of number of cells within a tissue	3/292	42/23328	0.01555057	0.01417032	3
BP	GO:0051154	negative regulation of striated muscle cell differentiation	3/292	42/23328	0.01555057	0.01417032	3

BP	GO:1900077	negative regulation of cellular response to insulin stimulus	3/292		42/23328	0.01555057	0.01417032	3
BP	GO:2000008	regulation of protein localization to cell surface	3/292		42/23328	0.01555057	0.01417032	3
BP	GO:1903201	regulation of oxidative stress-induced cell death	4/292		77/23328	0.01593749	0.01450856	4
BP	GO:2000573	positive regulation of DNA biosynthetic process	4/292		77/23328	0.01593749	0.01450856	4
BP	GO:0038083	peptidyl-tyrosine autophosphorylation	3/292		43/23328	0.01656527	0.0149865	3
BP	GO:0040018	positive regulation of multicellular organism growth	3/292		43/23328	0.01656527	0.0149865	3
BP	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	3/292		43/23328	0.01656527	0.0149865	3
BP	GO:1901381	positive regulation of potassium ion transmembrane transport	3/292		43/23328	0.01656527	0.0149865	3
BP	GO:0002295	T-helper cell lineage commitment	2/292		16/23328	0.0166899	0.0149865	2
BP	GO:0002407	dendritic cell chemotaxis	2/292		16/23328	0.0166899	0.0149865	2
BP	GO:0002866	positive regulation of acute inflammatory response to antigenic stimulus	2/292		16/23328	0.0166899	0.0149865	2
BP	GO:0003222	ventricular trabecula myocardium morphogenesis	2/292		16/23328	0.0166899	0.0149865	2
BP	GO:0007250	activation of NF-kappaB-inducing kinase activity	2/292		16/23328	0.0166899	0.0149865	2
BP	GO:0042492	gamma-delta T cell differentiation	2/292		16/23328	0.0166899	0.0149865	2

BP	GO:0042640	anagen	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0048302	regulation of isotype switching to IgG isotypes	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0050862	positive regulation of T cell receptor signaling pathway	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0051386	regulation of neurotrophin TRK receptor signaling pathway	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0055057	neuroblast division	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0060979	vasculogenesis involved in coronary vascular morphogenesis	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0061548	ganglion development	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0070486	leukocyte aggregation	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0071379	cellular response to prostaglandin stimulus	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0072567	chemokine (C-X-C motif) ligand 2 production	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0097050	type B pancreatic cell apoptotic process	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:1901550	regulation of endothelial cell development	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:1903140	regulation of establishment of endothelial barrier	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:1903541	regulation of exosomal secretion	2/292	16/23328	0.0166899	0.0149865	2

BP	GO:1903978	regulation of microglial cell activation	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:1905564	positive regulation of vascular endothelial cell proliferation	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:2000194	regulation of female gonad development	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	2/292	16/23328	0.0166899	0.0149865	2
BP	GO:0001678	cellular glucose homeostasis	6/292	163/23328	0.01696783	0.01522866	6
BP	GO:2000278	regulation of DNA biosynthetic process	5/292	119/23328	0.01707291	0.01531551	5
BP	GO:0032418	lysosome localization	4/292	79/23328	0.01735764	0.01554826	4
BP	GO:0048635	negative regulation of muscle organ development	4/292	79/23328	0.01735764	0.01554826	4
BP	GO:1902117	positive regulation of organelle assembly	4/292	79/23328	0.01735764	0.01554826	4
BP	GO:0042269	regulation of natural killer cell mediated cytotoxicity	3/292	44/23328	0.01761625	0.01577225	3
BP	GO:0033559	unsaturated fatty acid metabolic process	5/292	120/23328	0.01763876	0.01578475	5
BP	GO:0060968	regulation of gene silencing	4/292	80/23328	0.01809635	0.01617855	4
BP	GO:2001259	positive regulation of cation channel activity	4/292	80/23328	0.01809635	0.01617855	4
BP	GO:0090199	regulation of release of cytochrome c from mitochondria	3/292	45/23328	0.01870361	0.01654009	3

BP	GO:0043010	camera-type eye development	10/292	370/23328	0.01873288	0.01654009	10
BP	GO:0006914	autophagy	11/292	425/23328	0.01874716	0.01654009	11
BP	GO:0061919	process utilizing autophagic mechanism	11/292	425/23328	0.01874716	0.01654009	11
BP	GO:0002689	negative regulation of leukocyte chemotaxis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0003159	morphogenesis of an endothelium	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0003184	pulmonary valve morphogenesis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0010713	negative regulation of collagen metabolic process	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0019048	modulation by virus of host process	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0030730	sequestering of triglyceride	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0032225	regulation of synaptic transmission, dopaminergic	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0032230	positive regulation of synaptic transmission, GABAergic	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0032966	negative regulation of collagen biosynthetic process	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0040015	negative regulation of multicellular organism growth	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0045346	regulation of MHC class II biosynthetic process	2/292	17/23328	0.01876069	0.01654009	2

BP	GO:0048291	isotype switching to IgG isotypes	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0048853	forebrain morphogenesis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0060413	atrial septum morphogenesis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0060644	mammary gland epithelial cell differentiation	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0060850	regulation of transcription involved in cell fate commitment	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0060973	cell migration involved in heart development	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0061154	endothelial tube morphogenesis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0070243	regulation of thymocyte apoptotic process	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0070293	renal absorption	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:0071636	positive regulation of transforming growth factor beta production	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:1900119	positive regulation of execution phase of apoptosis	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:1905331	negative regulation of morphogenesis of an epithelium	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:2000252	negative regulation of feeding behavior	2/292	17/23328	0.01876069	0.01654009	2
BP	GO:2001028	positive regulation of endothelial cell chemotaxis	2/292	17/23328	0.01876069	0.01654009	2

BP	GO:0060113	inner ear receptor cell differentiation	4/292	82/23328	0.01963173	0.01729977	4
BP	GO:0002715	regulation of natural killer cell mediated immunity	3/292	46/23328	0.01982742	0.01744722	3
BP	GO:0033344	cholesterol efflux	3/292	46/23328	0.01982742	0.01744722	3
BP	GO:0045740	positive regulation of DNA replication	3/292	46/23328	0.01982742	0.01744722	3
BP	GO:0043500	muscle adaptation	5/292	124/23328	0.02002588	0.01760506	5
BP	GO:0090277	positive regulation of peptide hormone secretion	5/292	124/23328	0.02002588	0.01760506	5
BP	GO:0001991	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0002076	osteoblast development	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0002836	positive regulation of response to tumor cell	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0002839	positive regulation of immune response to tumor cell	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0007350	blastoderm segmentation	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0009299	mRNA transcription	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0014041	regulation of neuron maturation	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0016540	protein autoprocessing	2/292	18/23328	0.02093354	0.0182293	2

BP	GO:0021783	preganglionic parasympathetic fiber development	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0034695	response to prostaglandin E	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0038093	Fc receptor signaling pathway	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0042711	maternal behavior	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0050710	negative regulation of cytokine secretion	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0051000	positive regulation of nitric-oxide synthase activity	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0051580	regulation of neurotransmitter uptake	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0071801	regulation of podosome assembly	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0072077	renal vesicle morphogenesis	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:1900424	regulation of defense response to bacterium	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:1901673	regulation of mitotic spindle assembly	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:1903019	negative regulation of glycoprotein metabolic process	2/292	18/23328	0.02093354	0.0182293	2
BP	GO:0015672	monovalent inorganic cation transport	12/292	489/23328	0.02095514	0.01823347	12
BP	GO:0002820	negative regulation of adaptive immune response	3/292	47/23328	0.02098773	0.01823347	3

BP	GO:0003197	endocardial cushion development	3/292	47/23328	0.02098773	0.01823347	3
BP	GO:0032814	regulation of natural killer cell activation	3/292	47/23328	0.02098773	0.01823347	3
BP	GO:0050974	detection of mechanical stimulus involved in sensory perception	3/292	47/23328	0.02098773	0.01823347	3
BP	GO:0051817	modulation of process of other organism involved in symbiotic interaction	4/292	84/23328	0.0212452	0.01844846	4
BP	GO:0043409	negative regulation of MAPK cascade	6/292	173/23328	0.02202594	0.01911743	6
BP	GO:0030203	glycosaminoglycan metabolic process	4/292	85/23328	0.0220815	0.01914764	4
BP	GO:0030301	cholesterol transport	4/292	85/23328	0.0220815	0.01914764	4
BP	GO:0030195	negative regulation of blood coagulation	3/292	48/23328	0.02218457	0.01921895	3
BP	GO:0090279	regulation of calcium ion import	3/292	48/23328	0.02218457	0.01921895	3
BP	GO:0007264	small GTPase mediated signal transduction	11/292	437/23328	0.02246169	0.01944989	11
BP	GO:0015718	monocarboxylic acid transport	6/292	174/23328	0.02258193	0.01954484	6
BP	GO:0045727	positive regulation of translation	5/292	128/23328	0.02261535	0.01956459	5
BP	GO:0043254	regulation of protein-containing complex assembly	11/292	438/23328	0.02279393	0.01970984	11
BP	GO:0015918	sterol transport	4/292	86/23328	0.02293766	0.01982426	4

BP	GO:0048562	embryonic organ morphogenesis	9/292	328/23328	0.02298784	0.01982426	9
BP	GO:0035107	appendage morphogenesis	6/292	175/23328	0.02314729	0.01982426	6
BP	GO:0035108	limb morphogenesis	6/292	175/23328	0.02314729	0.01982426	6
BP	GO:0002710	negative regulation of T cell mediated immunity	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0003180	aortic valve morphogenesis	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0003215	cardiac right ventricle morphogenesis	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0006027	glycosaminoglycan catabolic process	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0007252	I-kappaB phosphorylation	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0020027	hemoglobin metabolic process	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0021924	cell proliferation in external granule layer	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0021930	cerebellar granule cell precursor proliferation	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0032656	regulation of interleukin-13 production	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0032700	negative regulation of interleukin-17 production	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pathway	2/292	19/23328	0.02320557	0.01982426	2

BP	GO:0035988	chondrocyte proliferation	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0039531	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0040037	negative regulation of fibroblast growth factor receptor signaling pathway	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0042730	fibrinolysis	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0043116	negative regulation of vascular permeability	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0045837	negative regulation of membrane potential	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0060081	membrane hyperpolarization	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0060231	mesenchymal to epithelial transition	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0060707	trophoblast giant cell differentiation	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0060746	parental behavior	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:1905276	regulation of epithelial tube formation	2/292	19/23328	0.02320557	0.01982426	2
BP	GO:0006690	icosanoid metabolic process	5/292	129/23328	0.0232955	0.01989144	5
BP	GO:0032386	regulation of intracellular transport	9/292	329/23328	0.02338555	0.01995952	9
BP	GO:1900047	negative regulation of hemostasis	3/292	49/23328	0.02341794	0.0199687	3

BP	GO:2000725	regulation of cardiac muscle cell differentiation	3/292	49/23328	0.02341794	0.0199687	3
BP	GO:0042752	regulation of circadian rhythm	5/292	130/23328	0.02398771	0.0204451	5
BP	GO:0008038	neuron recognition	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0010677	negative regulation of cellular carbohydrate metabolic process	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0021988	olfactory lobe development	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0045646	regulation of erythrocyte differentiation	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0050819	negative regulation of coagulation	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0061005	cell differentiation involved in kidney development	3/292	50/23328	0.02468783	0.02095419	3
BP	GO:0007368	determination of left/right symmetry	5/292	131/23328	0.02469357	0.02095419	5
BP	GO:0034620	cellular response to unfolded protein	4/292	88/23328	0.02470993	0.02095419	4
BP	GO:0045913	positive regulation of carbohydrate metabolic process	4/292	88/23328	0.02470993	0.02095419	4
BP	GO:0046683	response to organophosphorus	4/292	88/23328	0.02470993	0.02095419	4
BP	GO:1904063	negative regulation of cation transmembrane transport	4/292	88/23328	0.02470993	0.02095419	4
BP	GO:0001946	lymphangiogenesis	2/292	20/23328	0.0255574	0.02153846	2

BP	GO:0002577	regulation of antigen processing and presentation	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0002755	MyD88-dependent toll-like receptor signaling pathway	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0006699	bile acid biosynthetic process	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0008209	androgen metabolic process	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0030889	negative regulation of B cell proliferation	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0034143	regulation of toll-like receptor 4 signaling pathway	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0046629	gamma-delta T cell activation	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0051447	negative regulation of meiotic cell cycle	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0071157	negative regulation of cell cycle arrest	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0072087	renal vesicle development	2/292	20/23328	0.025574	0.02153846	2
BP	GO:0072243	metanephric nephron epithelium development	2/292	20/23328	0.025574	0.02153846	2
BP	GO:1904385	cellular response to angiotensin	2/292	20/23328	0.025574	0.02153846	2
BP	GO:1990182	exosomal secretion	2/292	20/23328	0.025574	0.02153846	2

BP	GO:0030901	midbrain development	3/292	51/23328	0.02599421	0.02185247	3
BP	GO:0042987	amyloid precursor protein catabolic process	3/292	51/23328	0.02599421	0.02185247	3
BP	GO:0046189	phenol-containing compound biosynthetic process	3/292	51/23328	0.02599421	0.02185247	3
BP	GO:0048806	genitalia development	3/292	51/23328	0.02599421	0.02185247	3
BP	GO:0009791	post-embryonic development	5/292	134/23328	0.02689079	0.02259589	5
BP	GO:0002888	positive regulation of myeloid leukocyte mediated immunity	3/292	52/23328	0.02733703	0.0229291	3
BP	GO:0045104	intermediate filament cytoskeleton organization	3/292	52/23328	0.02733703	0.0229291	3
BP	GO:0060632	regulation of microtubule-based movement	3/292	52/23328	0.02733703	0.0229291	3
BP	GO:1903202	negative regulation of oxidative stress-induced cell death	3/292	52/23328	0.02733703	0.0229291	3
BP	GO:0002088	lens development in camera-type eye	4/292	91/23328	0.02751951	0.02306119	4
BP	GO:1900407	regulation of cellular response to oxidative stress	4/292	91/23328	0.02751951	0.02306119	4
BP	GO:1901655	cellular response to ketone	5/292	135/23328	0.02764997	0.02315999	5
BP	GO:0002043	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0003417	growth plate cartilage development	2/292	21/23328	0.02803606	0.02333509	2

BP	GO:0006071	glycerol metabolic process	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0010039	response to iron ion	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0036336	dendritic cell migration	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0045821	positive regulation of glycolytic process	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0046716	muscle cell cellular homeostasis	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0060333	interferon-gamma-mediated signaling pathway	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0060457	negative regulation of digestive system process	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0072170	metanephric tubule development	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0090036	regulation of protein kinase C signaling	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0097734	extracellular exosome biogenesis	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:1902004	positive regulation of amyloid-beta formation	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:2001224	positive regulation of neuron migration	2/292	21/23328	0.02803606	0.02333509	2
BP	GO:0002275	myeloid cell activation involved in immune response	4/292	92/23328	0.02849665	0.02369708	4
BP	GO:0055072	iron ion homeostasis	4/292	92/23328	0.02849665	0.02369708	4

BP	GO:0031103	axon regeneration	3/292	53/23328	0.02871622	0.02382599	3
BP	GO:0045103	intermediate filament-based process	3/292	53/23328	0.02871622	0.02382599	3
BP	GO:0046676	negative regulation of insulin secretion	3/292	53/23328	0.02871622	0.02382599	3
BP	GO:0055010	ventricular cardiac muscle tissue morphogenesis	3/292	53/23328	0.02871622	0.02382599	3
BP	GO:1900408	negative regulation of cellular response to oxidative stress	3/292	53/23328	0.02871622	0.02382599	3
BP	GO:0021953	central nervous system neuron differentiation	7/292	235/23328	0.02901536	0.02405255	7
BP	GO:0031334	positive regulation of protein-containing complex assembly	7/292	235/23328	0.02901536	0.02405255	7
BP	GO:0007050	cell cycle arrest	5/292	137/23328	0.0292089	0.02420211	5
BP	GO:0001508	action potential	5/292	138/23328	0.03000877	0.02484256	5
BP	GO:0097306	cellular response to alcohol	5/292	138/23328	0.03000877	0.02484256	5
BP	GO:0032355	response to estradiol	3/292	54/23328	0.03013171	0.02488851	3
BP	GO:0042743	hydrogen peroxide metabolic process	3/292	54/23328	0.03013171	0.02488851	3
BP	GO:0043300	regulation of leukocyte degranulation	3/292	54/23328	0.03013171	0.02488851	3
BP	GO:0048546	digestive tract morphogenesis	3/292	54/23328	0.03013171	0.02488851	3

BP	GO:0070542	response to fatty acid	3/292	54/23328	0.03013171	0.02488851	3
BP	GO:0003323	type B pancreatic cell development	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0010666	positive regulation of cardiac muscle cell apoptotic process	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0048339	paraxial mesoderm development	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0070242	thymocyte apoptotic process	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0071800	podosome assembly	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:0072273	metanephric nephron morphogenesis	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:1901223	negative regulation of NIK/NF-kappaB signaling	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:1903975	regulation of glial cell migration	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:1990776	response to angiotensin	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:2000353	positive regulation of endothelial cell apoptotic process	2/292	22/23328	0.03058905	0.02514247	2
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	4/292	95/23328	0.03155081	0.02592144	4
BP	GO:0006826	iron ion transport	3/292	55/23328	0.03158338	0.02592511	3

BP	GO:0051496	positive regulation of stress fiber assembly	3/292		55/23328	0.03158338	0.02592511	3
BP	GO:0009855	determination of bilateral symmetry	5/292		140/23328	0.0316496	0.02596792	5
BP	GO:0006813	potassium ion transport	7/292		240/23328	0.03199517	0.02623978	7
BP	GO:0009799	specification of symmetry	5/292		141/23328	0.03249069	0.02663432	5
BP	GO:0007265	Ras protein signal transduction	9/292		350/23328	0.03291176	0.02696752	9
BP	GO:0002704	negative regulation of leukocyte mediated immunity	3/292		56/23328	0.03307112	0.02703807	3
BP	GO:0017145	stem cell division	3/292		56/23328	0.03307112	0.02703807	3
BP	GO:0051932	synaptic transmission, GABAergic	3/292		56/23328	0.03307112	0.02703807	3
BP	GO:1900449	regulation of glutamate receptor signaling pathway	3/292		56/23328	0.03307112	0.02703807	3
BP	GO:1902883	negative regulation of response to oxidative stress	3/292		56/23328	0.03307112	0.02703807	3
BP	GO:0002834	regulation of response to tumor cell	2/292		23/23328	0.03323034	0.02707228	2
BP	GO:0002837	regulation of immune response to tumor cell	2/292		23/23328	0.03323034	0.02707228	2
BP	GO:0010663	positive regulation of striated muscle cell apoptotic process	2/292		23/23328	0.03323034	0.02707228	2
BP	GO:0032098	regulation of appetite	2/292		23/23328	0.03323034	0.02707228	2

BP	GO:0036303	lymph vessel morphogenesis	2/292	23/23328	0.03323034	0.02707228	2
BP	GO:0048333	mesodermal cell differentiation	2/292	23/23328	0.03323034	0.02707228	2
BP	GO:0071276	cellular response to cadmium ion	2/292	23/23328	0.03323034	0.02707228	2
BP	GO:0140112	extracellular vesicle biogenesis	2/292	23/23328	0.03323034	0.02707228	2
BP	GO:0050906	detection of stimulus involved in sensory perception	5/292	142/23328	0.03334561	0.0271542	5
BP	GO:0007416	synapse assembly	6/292	191/23328	0.03351469	0.02727985	6
BP	GO:0006885	regulation of pH	4/292	97/23328	0.03368969	0.0274102	4
BP	GO:0051591	response to cAMP	3/292	57/23328	0.03459481	0.02813421	3
BP	GO:0036473	cell death in response to oxidative stress	4/292	98/23328	0.03479008	0.02828055	4
BP	GO:0021761	limbic system development	4/292	99/23328	0.03591115	0.02907569	4
BP	GO:0062014	negative regulation of small molecule metabolic process	4/292	99/23328	0.03591115	0.02907569	4
BP	GO:0019400	alditol metabolic process	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0021889	olfactory bulb interneuron differentiation	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0031639	plasminogen activation	2/292	24/23328	0.03595733	0.02907569	2

BP	GO:0031954	positive regulation of protein autophosphorylation	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0033008	positive regulation of mast cell activation involved in immune response	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0043306	positive regulation of mast cell degranulation	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0046628	positive regulation of insulin receptor signaling pathway	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0050765	negative regulation of phagocytosis	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0090335	regulation of brown fat cell differentiation	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:1903204	negative regulation of oxidative stress-induced neuron death	2/292	24/23328	0.03595733	0.02907569	2
BP	GO:0035690	cellular response to drug	3/292	58/23328	0.03615429	0.02922216	3
BP	GO:0051606	detection of stimulus	7/292	247/23328	0.03650132	0.02948973	7
BP	GO:0035637	multicellular organismal signaling	5/292	146/23328	0.03690466	0.02980254	5
BP	GO:1902882	regulation of response to oxidative stress	4/292	100/23328	0.03705292	0.02990918	4
BP	GO:0015980	energy derivation by oxidation of organic compounds	7/292	248/23328	0.03717751	0.02999663	7
BP	GO:0001836	release of cytochrome c from mitochondria	3/292	59/23328	0.03774941	0.03040489	3
BP	GO:0002011	morphogenesis of an epithelial sheet	3/292	59/23328	0.03774941	0.03040489	3

BP	GO:0042551	neuron maturation	3/292	59/23328	0.03774941	0.03040489	3
BP	GO:0071156	regulation of cell cycle arrest	3/292	59/23328	0.03774941	0.03040489	3
BP	GO:0007043	cell-cell junction assembly	5/292	147/23328	0.03782948	0.03045609	5
BP	GO:0030258	lipid modification	7/292	250/23328	0.03855453	0.03102627	7
BP	GO:0002418	immune response to tumor cell	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0003094	glomerular filtration	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0008211	glucocorticoid metabolic process	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0044003	modulation by symbiont of host process	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0046685	response to arsenic-containing substance	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0048266	behavioral response to pain	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0050995	negative regulation of lipid catabolic process	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0090169	regulation of spindle assembly	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	2/292	25/23328	0.03876746	0.03107566	2
BP	GO:0060324	face development	3/292	60/23328	0.03937999	0.03155295	3

BP	GO:1902905	positive regulation of supramolecular fiber organization	6/292	200/23328	0.04048716	0.03242598	6
BP	GO:0090263	positive regulation of canonical Wnt signaling pathway	4/292	103/23328	0.04060258	0.03250432	4
BP	GO:0045824	negative regulation of innate immune response	3/292	61/23328	0.04104585	0.03281646	3
BP	GO:0060119	inner ear receptor cell development	3/292	61/23328	0.04104585	0.03281646	3
BP	GO:0061912	selective autophagy	3/292	61/23328	0.04104585	0.03281646	3
BP	GO:0006817	phosphate ion transport	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0009713	catechol-containing compound biosynthetic process	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0030325	adrenal gland development	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0042423	catecholamine biosynthetic process	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0070168	negative regulation of biomineral tissue development	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0090200	positive regulation of release of cytochrome c from mitochondria	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0097205	renal filtration	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0110150	negative regulation of biomineralization	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:2000637	positive regulation of gene silencing by miRNA	2/292	26/23328	0.04165826	0.0331575	2

BP	GO:2000738	positive regulation of stem cell differentiation	2/292	26/23328	0.04165826	0.0331575	2
BP	GO:0051588	regulation of neurotransmitter transport	5/292	151/23328	0.04167007	0.0331575	5
BP	GO:0014074	response to purine-containing compound	4/292	104/23328	0.04182728	0.03322529	4
BP	GO:0015844	monoamine transport	4/292	104/23328	0.04182728	0.03322529	4
BP	GO:0019731	antibacterial humoral response	4/292	104/23328	0.04182728	0.03322529	4
BP	GO:0046916	cellular transition metal ion homeostasis	4/292	104/23328	0.04182728	0.03322529	4
BP	GO:0048736	appendage development	6/292	202/23328	0.04215213	0.03345453	6
BP	GO:0060173	limb development	6/292	202/23328	0.04215213	0.03345453	6
BP	GO:0003229	ventricular cardiac muscle tissue development	3/292	62/23328	0.04274679	0.03386821	3
BP	GO:0050854	regulation of antigen receptor-mediated signaling pathway	3/292	62/23328	0.04274679	0.03386821	3
BP	GO:0050982	detection of mechanical stimulus	3/292	62/23328	0.04274679	0.03386821	3
BP	GO:0060350	endochondral bone morphogenesis	3/292	62/23328	0.04274679	0.03386821	3
BP	GO:0045921	positive regulation of exocytosis	4/292	105/23328	0.04307272	0.0341118	4
BP	GO:0006022	aminoglycan metabolic process	4/292	106/23328	0.04433888	0.03509949	4

BP	GO:0007626	locomotory behavior	7/292	258/23328	0.04439554	0.03512927	7
BP	GO:0001947	heart looping	3/292	63/23328	0.04448258	0.03513186	3
BP	GO:0050994	regulation of lipid catabolic process	3/292	63/23328	0.04448258	0.03513186	3
BP	GO:0002068	glandular epithelial cell development	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0045730	respiratory burst	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0051767	nitric-oxide synthase biosynthetic process	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic process	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0060148	positive regulation of posttranscriptional gene silencing	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0071425	hematopoietic stem cell proliferation	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:0090103	cochlea morphogenesis	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:1901018	positive regulation of potassium ion transmembrane transporter activity	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:1905939	regulation of gonad development	2/292	27/23328	0.04462728	0.03513186	2
BP	GO:1901568	fatty acid derivative metabolic process	5/292	154/23328	0.04469973	0.03517388	5

BP	GO:0060538	skeletal muscle organ development	6/292	206/23328	0.04560997	0.03587199	6
BP	GO:0019395	fatty acid oxidation	4/292	107/23328	0.04562577	0.03587199	4
BP	GO:0043388	positive regulation of DNA binding	3/292	64/23328	0.04625303	0.03630328	3
BP	GO:0046173	polyol biosynthetic process	3/292	64/23328	0.04625303	0.03630328	3
BP	GO:0048008	platelet-derived growth factor receptor signaling pathway	3/292	64/23328	0.04625303	0.03630328	3
BP	GO:0051784	negative regulation of nuclear division	3/292	64/23328	0.04625303	0.03630328	3
BP	GO:0006644	phospholipid metabolic process	9/292	374/23328	0.04675526	0.03668187	9
BP	GO:0032091	negative regulation of protein binding	4/292	108/23328	0.04693336	0.03680595	4
BP	GO:0002347	response to tumor cell	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0006026	aminoglycan catabolic process	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0030878	thyroid gland development	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0035987	endodermal cell differentiation	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0051446	positive regulation of meiotic cell cycle	2/292	28/23328	0.04767211	0.03722708	2

BP	GO:0060039	pericardium development	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0060390	regulation of SMAD protein signal transduction	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:1904861	excitatory synapse assembly	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:2000310	regulation of NMDA receptor activity	2/292	28/23328	0.04767211	0.03722708	2
BP	GO:0032233	positive regulation of actin filament bundle assembly	3/292	65/23328	0.04805788	0.03749659	3
BP	GO:0042246	tissue regeneration	3/292	65/23328	0.04805788	0.03749659	3
BP	GO:0035249	synaptic transmission, glutamatergic	4/292	109/23328	0.04826162	0.03763964	4
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	4/292	110/23328	0.04961054	0.03865899	4
BP	GO:0035967	cellular response to topologically incorrect protein	4/292	110/23328	0.04961054	0.03865899	4
BP	GO:0042982	amyloid precursor protein metabolic process	3/292	66/23328	0.04989689	0.03886572	3
BP	GO:0003002	regionalization	9/292	379/23328	0.05006266	0.03897839	9
BP	GO:0002029	desensitization of G protein-coupled receptor signaling pathway	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0002717	positive regulation of natural killer cell mediated immunity	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0003416	endochondral bone growth	2/292	29/23328	0.05079042	0.03936232	2

BP	GO:0010800	positive regulation of peptidyl-threonine phosphorylation	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0021952	central nervous system projection neuron axonogenesis	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0022401	negative adaptation of signaling pathway	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0030318	melanocyte differentiation	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0042403	thyroid hormone metabolic process	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0045822	negative regulation of heart contraction	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0061311	cell surface receptor signaling pathway involved in heart development	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0071353	cellular response to interleukin-4	2/292	29/23328	0.05079042	0.03936232	2
BP	GO:0016241	regulation of macroautophagy	4/292	111/23328	0.05098007	0.03949271	4
BP	GO:0010676	positive regulation of cellular carbohydrate metabolic process	3/292	67/23328	0.05176981	0.04007086	3
BP	GO:2000242	negative regulation of reproductive process	3/292	67/23328	0.05176981	0.04007086	3
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	4/292	112/23328	0.05237019	0.04051856	4
BP	GO:0010810	regulation of cell-substrate adhesion	6/292	214/23328	0.05304244	0.04102149	6
BP	GO:0097194	execution phase of apoptosis	3/292	68/23328	0.05367637	0.04147698	3

BP	GO:0099601	regulation of neurotransmitter receptor activity	3/292	68/23328	0.05367637	0.04147698	3
BP	GO:0001945	lymph vessel development	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0003309	type B pancreatic cell differentiation	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0006929	substrate-dependent cell migration	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0021602	cranial nerve morphogenesis	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0032816	positive regulation of natural killer cell activation	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0048521	negative regulation of behavior	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0048714	positive regulation of oligodendrocyte differentiation	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0050996	positive regulation of lipid catabolic process	2/292	30/23328	0.05397989	0.04155491	2
BP	GO:0006941	striated muscle contraction	5/292	163/23328	0.05456166	0.04198525	5
BP	GO:0035264	multicellular organism growth	6/292	216/23328	0.05500908	0.04231189	6
BP	GO:0034440	lipid oxidation	4/292	114/23328	0.05521199	0.04245027	4
BP	GO:0009880	embryonic pattern specification	3/292	69/23328	0.05561631	0.04270775	3

BP	GO:0048168	regulation of neuronal synaptic plasticity	3/292	69/23328	0.05561631	0.04270775	3
BP	GO:0061371	determination of heart left/right asymmetry	3/292	69/23328	0.05561631	0.04270775	3
BP	GO:0019751	polyol metabolic process	4/292	115/23328	0.05666359	0.04347577	4
BP	GO:0048259	regulation of receptor-mediated endocytosis	4/292	115/23328	0.05666359	0.04347577	4
BP	GO:0006887	exocytosis	9/292	389/23328	0.05713206	0.04371676	9
BP	GO:0001963	synaptic transmission, dopaminergic	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0002026	regulation of the force of heart contraction	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0002063	chondrocyte development	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0002092	positive regulation of receptor internalization	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0023058	adaptation of signaling pathway	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0044319	wound healing, spreading of cells	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0048011	neurotrophin TRK receptor signaling pathway	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0070670	response to interleukin-4	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0090505	epiboly involved in wound healing	2/292	31/23328	0.05723828	0.04371676	2

BP	GO:1900117	regulation of execution phase of apoptosis	2/292	31/23328	0.05723828	0.04371676	2
BP	GO:0003143	embryonic heart tube morphogenesis	3/292	70/23328	0.05758932	0.04396668	3
BP	GO:0007565	female pregnancy	5/292	166/23328	0.05810739	0.04432869	5
BP	GO:0009636	response to toxic substance	4/292	116/23328	0.05813558	0.04432869	4
BP	GO:0043487	regulation of RNA stability	4/292	116/23328	0.05813558	0.04432869	4
BP	GO:0051100	negative regulation of binding	5/292	167/23328	0.059318	0.04519295	5
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	5/292	167/23328	0.059318	0.04519295	5
BP	GO:0043407	negative regulation of MAP kinase activity	3/292	71/23328	0.05959513	0.04535415	3
BP	GO:0006986	response to unfolded protein	4/292	117/23328	0.05962789	0.04535415	4
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	4/292	117/23328	0.05962789	0.04535415	4
BP	GO:1901890	positive regulation of cell junction assembly	4/292	117/23328	0.05962789	0.04535415	4
BP	GO:0002902	regulation of B cell apoptotic process	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0032692	negative regulation of interleukin-1 production	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0032743	positive regulation of interleukin-2 production	2/292	32/23328	0.06056337	0.04583895	2

BP	GO:0032958	inositol phosphate biosynthetic process	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0035066	positive regulation of histone acetylation	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0042749	regulation of circadian sleep/wake cycle	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0050482	arachidonic acid secretion	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0071354	cellular response to interleukin-6	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0090504	epiboly	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:1903963	arachidonate transport	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	2/292	32/23328	0.06056337	0.04583895	2
BP	GO:0060348	bone development	6/292	222/23328	0.06117096	0.04627984	6
BP	GO:0048002	antigen processing and presentation of peptide antigen	3/292	72/23328	0.06163343	0.04661061	3
BP	GO:0071897	DNA biosynthetic process	5/292	169/23328	0.06178224	0.04670401	5
BP	GO:0016054	organic acid catabolic process	6/292	223/23328	0.06223622	0.04700868	6
BP	GO:0046395	carboxylic acid catabolic process	6/292	223/23328	0.06223622	0.04700868	6

BP	GO:0001952	regulation of cell-matrix adhesion	4/292	119/23328	0.06267326	0.04731942	4
BP	GO:0021879	forebrain neuron differentiation	3/292	73/23328	0.06370392	0.04805825	3
BP	GO:0043627	response to estrogen	3/292	73/23328	0.06370392	0.04805825	3
BP	GO:0000186	activation of MAPKK activity	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0021884	forebrain neuron development	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0032369	negative regulation of lipid transport	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0032467	positive regulation of cytokinesis	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0045616	regulation of keratinocyte differentiation	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0048240	sperm capacitation	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0048566	embryonic digestive tract development	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0060706	cell differentiation involved in embryonic placenta development	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0070266	necroptotic process	2/292	33/23328	0.06395299	0.04806928	2
BP	GO:0006090	pyruvate metabolic process	4/292	120/23328	0.06422618	0.04825497	4
BP	GO:0030833	regulation of actin filament polymerization	5/292	171/23328	0.06430372	0.04827392	5

BP	GO:0030902	hindbrain development	5/292	171/23328	0.06430372	0.04827392	5
BP	GO:0021766	hippocampus development	3/292	74/23328	0.06580627	0.04938181	3
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4/292	122/23328	0.06739209	0.05049939	4
BP	GO:0035883	enteroendocrine cell differentiation	2/292	34/23328	0.06740502	0.05049939	2
BP	GO:0043950	positive regulation of cAMP-mediated signaling	2/292	34/23328	0.06740502	0.05049939	2
BP	GO:0070741	response to interleukin-6	2/292	34/23328	0.06740502	0.05049939	2
BP	GO:0034109	homotypic cell-cell adhesion	3/292	75/23328	0.06794017	0.05087966	3
BP	GO:0016485	protein processing	6/292	229/23328	0.06885753	0.05154575	6
BP	GO:0000271	polysaccharide biosynthetic process	3/292	76/23328	0.07010528	0.05245851	3
BP	GO:0001702	gastrulation with mouth forming second	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0002446	neutrophil mediated immunity	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0003016	respiratory system process	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0006308	DNA catabolic process	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0034122	negative regulation of toll-like receptor signaling pathway	2/292	35/23328	0.07091738	0.05283053	2

BP	GO:0035025	positive regulation of Rho protein signal transduction	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0043302	positive regulation of leukocyte degranulation	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0046686	response to cadmium ion	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0060236	regulation of mitotic spindle organization	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:1902003	regulation of amyloid-beta formation	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:1903429	regulation of cell maturation	2/292	35/23328	0.07091738	0.05283053	2
BP	GO:0045843	negative regulation of striated muscle tissue development	3/292	77/23328	0.07230127	0.05381802	3
BP	GO:0071277	cellular response to calcium ion	3/292	77/23328	0.07230127	0.05381802	3
BP	GO:0035909	aorta morphogenesis	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0042745	circadian sleep/wake cycle	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0048169	regulation of long-term neuronal synaptic plasticity	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0048679	regulation of axon regeneration	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0071398	cellular response to fatty acid	2/292	36/23328	0.07448802	0.05518595	2

BP	GO:2000758	positive regulation of peptidyl-lysine acetylation	2/292	36/23328	0.07448802	0.05518595	2
BP	GO:0002066	columnar/cuboidal epithelial cell development	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0032088	negative regulation of NF-kappaB transcription factor activity	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0060563	neuroepithelial cell differentiation	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0060976	coronary vasculature development	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0070373	negative regulation of ERK1 and ERK2 cascade	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	3/292	78/23328	0.0745278	0.05518595	3
BP	GO:0006814	sodium ion transport	6/292	234/23328	0.07467581	0.05527337	6
BP	GO:0051258	protein polymerization	7/292	293/23328	0.07643742	0.05655459	7
BP	GO:0048663	neuron fate commitment	3/292	79/23328	0.07678451	0.05676588	3
BP	GO:0051966	regulation of synaptic transmission, glutamatergic	3/292	79/23328	0.07678451	0.05676588	3
BP	GO:0010811	positive regulation of cell-substrate adhesion	4/292	128/23328	0.07736425	0.05714868	4
BP	GO:0043244	regulation of protein-containing complex disassembly	4/292	128/23328	0.07736425	0.05714868	4
BP	GO:0002218	activation of innate immune response	2/292	37/23328	0.07811496	0.05763401	2

BP	GO:0014823	response to activity	2/292		37/23328	0.07811496	0.05763401	2
BP	GO:0021680	cerebellar Purkinje cell layer development	2/292		37/23328	0.07811496	0.05763401	2
BP	GO:0034637	cellular carbohydrate biosynthetic process	3/292		80/23328	0.07907107	0.05829282	3
BP	GO:1901862	negative regulation of muscle tissue development	3/292		80/23328	0.07907107	0.05829282	3
BP	GO:0001706	endoderm formation	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0010661	positive regulation of muscle cell apoptotic process	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0030851	granulocyte differentiation	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0038084	vascular endothelial growth factor signaling pathway	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0045601	regulation of endothelial cell differentiation	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0051452	intracellular pH reduction	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0060674	placenta blood vessel development	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:0070528	protein kinase C signaling	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:1903170	negative regulation of calcium ion transmembrane transport	2/292		38/23328	0.08179624	0.06003802	2
BP	GO:1904037	positive regulation of epithelial cell apoptotic process	2/292		38/23328	0.08179624	0.06003802	2

BP	GO:2000463	positive regulation of excitatory postsynaptic potential	2/292	38/23328	0.08179624	0.06003802	2
BP	GO:1903320	regulation of protein modification by small protein conjugation or removal	6/292	240/23328	0.0820166	0.06017583	6
BP	GO:0140013	meiotic nuclear division	5/292	184/23328	0.08207613	0.06019558	5
BP	GO:0007281	germ cell development	8/292	359/23328	0.08317439	0.06097682	8
BP	GO:0046486	glycerolipid metabolic process	8/292	360/23328	0.08419473	0.06170033	8
BP	GO:0030513	positive regulation of BMP signaling pathway	2/292	39/23328	0.08552993	0.06257939	2
BP	GO:0032885	regulation of polysaccharide biosynthetic process	2/292	39/23328	0.08552993	0.06257939	2
BP	GO:0050931	pigment cell differentiation	2/292	39/23328	0.08552993	0.06257939	2
BP	GO:0090224	regulation of spindle organization	2/292	39/23328	0.08552993	0.06257939	2
BP	GO:0021872	forebrain generation of neurons	3/292	83/23328	0.08610612	0.062976	3
BP	GO:0030041	actin filament polymerization	5/292	187/23328	0.08651306	0.06324856	5
BP	GO:0008064	regulation of actin polymerization or depolymerization	5/292	188/23328	0.08801952	0.06430759	5
BP	GO:0055076	transition metal ion homeostasis	4/292	134/23328	0.08803134	0.06430759	4
BP	GO:0006942	regulation of striated muscle contraction	3/292	84/23328	0.08850838	0.06463049	3

BP	GO:0001504	neurotransmitter uptake	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0007616	long-term memory	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0015804	neutral amino acid transport	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0040019	positive regulation of embryonic development	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0045981	positive regulation of nucleotide metabolic process	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0060325	face morphogenesis	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0085029	extracellular matrix assembly	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0086004	regulation of cardiac muscle cell contraction	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:1900544	positive regulation of purine nucleotide metabolic process	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:1903959	regulation of anion transmembrane transport	2/292	40/23328	0.08931416	0.06496181	2
BP	GO:0048167	regulation of synaptic plasticity	8/292	365/23328	0.08940679	0.06500357	8
BP	GO:0051701	interaction with host	4/292	135/23328	0.08987504	0.06531828	4
BP	GO:0051937	catecholamine transport	3/292	85/23328	0.09093863	0.06606524	3
BP	GO:0055002	striated muscle cell development	5/292	190/23328	0.09107337	0.06613709	5

BP	GO:0035195	gene silencing by miRNA	4/292	136/23328	0.09173724	0.06659298	4
BP	GO:0030832	regulation of actin filament length	5/292	191/23328	0.09262065	0.06720781	5
BP	GO:0002686	negative regulation of leukocyte migration	2/292	41/23328	0.09314709	0.06745718	2
BP	GO:0014037	Schwann cell differentiation	2/292	41/23328	0.09314709	0.06745718	2
BP	GO:0034205	amyloid-beta formation	2/292	41/23328	0.09314709	0.06745718	2
BP	GO:0045806	negative regulation of endocytosis	2/292	41/23328	0.09314709	0.06745718	2
BP	GO:0097300	programmed necrotic cell death	2/292	41/23328	0.09314709	0.06745718	2
BP	GO:0035050	embryonic heart tube development	3/292	86/23328	0.09339649	0.06755825	3
BP	GO:0120192	tight junction assembly	3/292	86/23328	0.09339649	0.06755825	3
BP	GO:1901379	regulation of potassium ion transmembrane transport	3/292	86/23328	0.09339649	0.06755825	3
BP	GO:0035821	modulation of process of other organism	4/292	137/23328	0.09361779	0.06769179	4
BP	GO:0031330	negative regulation of cellular catabolic process	6/292	250/23328	0.09511156	0.06874495	6
BP	GO:0009913	epidermal cell differentiation	5/292	193/23328	0.09575562	0.06918337	5
BP	GO:0007568	aging	6/292	251/23328	0.09647947	0.0696518	6

BP	GO:0098657	import into cell	6/292	251/23328	0.09647947	0.0696518	6
BP	GO:0001709	cell fate determination	2/292	42/23328	0.09702691	0.0699649	2
BP	GO:0021955	central nervous system neuron axonogenesis	2/292	42/23328	0.09702691	0.0699649	2
BP	GO:0042417	dopamine metabolic process	2/292	42/23328	0.09702691	0.0699649	2
BP	GO:0055007	cardiac muscle cell differentiation	4/292	139/23328	0.09743343	0.0702306	4
BP	GO:0006112	energy reserve metabolic process	3/292	88/23328	0.09839353	0.0708122	3
BP	GO:0060079	excitatory postsynaptic potential	3/292	88/23328	0.09839353	0.0708122	3
BP	GO:1901992	positive regulation of mitotic cell cycle phase transition	3/292	88/23328	0.09839353	0.0708122	3
BP	GO:1903321	negative regulation of protein modification by small protein conjugation or removal	3/292	88/23328	0.09839353	0.0708122	3
BP	GO:0046034	ATP metabolic process	6/292	253/23328	0.09924676	0.07139821	6
BP	GO:0007519	skeletal muscle tissue development	5/292	196/23328	0.10055823	0.07231348	5
BP	GO:0017157	regulation of exocytosis	6/292	254/23328	0.10064609	0.07231474	6
BP	GO:0001783	B cell apoptotic process	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0003298	physiological muscle hypertrophy	2/292	43/23328	0.10095187	0.07231474	2

BP	GO:0003301	physiological cardiac muscle hypertrophy	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0045851	pH reduction	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0046636	negative regulation of alpha-beta T cell activation	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0046854	phosphatidylinositol phosphorylation	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0060122	inner ear receptor cell stereocilium organization	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0061049	cell growth involved in cardiac muscle cell development	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0097484	dendrite extension	2/292	43/23328	0.10095187	0.07231474	2
BP	GO:0035966	response to topologically incorrect protein	4/292	141/23328	0.10132088	0.07252277	4
BP	GO:1902652	secondary alcohol metabolic process	4/292	141/23328	0.10132088	0.07252277	4
BP	GO:0035194	post-transcriptional gene silencing by RNA	4/292	142/23328	0.10329118	0.07384712	4
BP	GO:0046488	phosphatidylinositol metabolic process	4/292	142/23328	0.10329118	0.07384712	4
BP	GO:0048706	embryonic skeletal system development	4/292	142/23328	0.10329118	0.07384712	4
BP	GO:0070509	calcium ion import	3/292	90/23328	0.10349638	0.07396517	3
BP	GO:0006650	glycerophospholipid metabolic process	6/292	257/23328	0.10490636	0.07475114	6

BP	GO:0005978	glycogen biosynthetic process	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0006024	glycosaminoglycan biosynthetic process	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0009250	glucan biosynthetic process	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0016925	protein sumoylation	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0032350	regulation of hormone metabolic process	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0048854	brain morphogenesis	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0097237	cellular response to toxic substance	2/292	44/23328	0.10492023	0.07475114	2
BP	GO:0030010	establishment of cell polarity	4/292	143/23328	0.105279	0.07491996	4
BP	GO:0030326	embryonic limb morphogenesis	4/292	143/23328	0.105279	0.07491996	4
BP	GO:0035113	embryonic appendage morphogenesis	4/292	143/23328	0.105279	0.07491996	4
BP	GO:0120193	tight junction organization	3/292	91/23328	0.1060865	0.0754655	3
BP	GO:0032886	regulation of microtubule-based process	6/292	258/23328	0.10634709	0.07562172	6
BP	GO:0015698	inorganic anion transport	4/292	144/23328	0.10728419	0.07622933	4
BP	GO:0071333	cellular response to glucose stimulus	4/292	144/23328	0.10728419	0.07622933	4

BP	GO:0044282	small molecule catabolic process	7/292	320/23328	0.10848457	0.07705257	7
BP	GO:0006096	glycolytic process	3/292	92/23328	0.10870189	0.07714754	3
BP	GO:0090630	activation of GTPase activity	3/292	92/23328	0.10870189	0.07714754	3
BP	GO:0010907	positive regulation of glucose metabolic process	2/292	45/23328	0.10893031	0.07722055	2
BP	GO:0050856	regulation of T cell receptor signaling pathway	2/292	45/23328	0.10893031	0.07722055	2
BP	GO:0089718	amino acid import across plasma membrane	2/292	45/23328	0.10893031	0.07722055	2
BP	GO:1903364	positive regulation of cellular protein catabolic process	4/292	145/23328	0.10930661	0.07745755	4
BP	GO:1903046	meiotic cell cycle process	5/292	202/23328	0.11051755	0.07828559	5
BP	GO:0006757	ATP generation from ADP	3/292	93/23328	0.11134215	0.07866113	3
BP	GO:0007215	glutamate receptor signaling pathway	3/292	93/23328	0.11134215	0.07866113	3
BP	GO:0008589	regulation of smoothened signaling pathway	3/292	93/23328	0.11134215	0.07866113	3
BP	GO:0009308	amine metabolic process	3/292	93/23328	0.11134215	0.07866113	3
BP	GO:0009798	axis specification	3/292	93/23328	0.11134215	0.07866113	3
BP	GO:0016441	posttranscriptional gene silencing	4/292	146/23328	0.1113461	0.07866113	4

BP	GO:0071331	cellular response to hexose stimulus	4/292	146/23328	0.1113461	0.07866113	4
BP	GO:0002707	negative regulation of lymphocyte mediated immunity	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0003254	regulation of membrane depolarization	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0010799	regulation of peptidyl-threonine phosphorylation	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0032881	regulation of polysaccharide metabolic process	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0048536	spleen development	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0060323	head morphogenesis	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0090317	negative regulation of intracellular protein transport	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0098926	postsynaptic signal transduction	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:1901985	positive regulation of protein acetylation	2/292	46/23328	0.11298044	0.07954164	2
BP	GO:0071326	cellular response to monosaccharide stimulus	4/292	147/23328	0.11340251	0.07980835	4
BP	GO:0002251	organ or tissue specific immune response	3/292	95/23328	0.11669565	0.08138184	3
BP	GO:0021772	olfactory bulb development	2/292	47/23328	0.117069	0.08138184	2
BP	GO:0035458	cellular response to interferon-beta	2/292	47/23328	0.117069	0.08138184	2

BP	GO:0043277	apoptotic cell clearance	2/292	47/23328	0.117069	0.08138184	2
BP	GO:0045214	sarcomere organization	2/292	47/23328	0.117069	0.08138184	2
BP	GO:0031396	regulation of protein ubiquitination	5/292	206/23328	0.11741325	0.08138184	5
BP	GO:0034101	erythrocyte homeostasis	4/292	149/23328	0.11756546	0.08138184	4
BP	GO:0000050	urea cycle	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0000185	activation of MAPKKK activity	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0002176	male germ cell proliferation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0002423	natural killer cell mediated immune response to tumor cell	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0002855	regulation of natural killer cell mediated immune response to tumor cell	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0003307	regulation of Wnt signaling pathway involved in heart development	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0006000	fructose metabolic process	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0006527	arginine catabolic process	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0009650	UV protection	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0014883	transition between fast and slow fiber	1/292	10/23328	0.11837274	0.08138184	1

BP	GO:0030300	regulation of intestinal cholesterol absorption	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0030853	negative regulation of granulocyte differentiation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0032354	response to follicle-stimulating hormone	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0032621	interleukin-18 production	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0032650	regulation of interleukin-1 alpha production	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0033234	negative regulation of protein sumoylation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0033299	secretion of lysosomal enzymes	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0034145	positive regulation of toll-like receptor 4 signaling pathway	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0035811	negative regulation of urine volume	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0035871	protein K11-linked deubiquitination	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0043301	negative regulation of leukocyte degranulation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0046085	adenosine metabolic process	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0048671	negative regulation of collateral sprouting	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0048702	embryonic neurocranium morphogenesis	1/292	10/23328	0.11837274	0.08138184	1

BP	GO:0051006	positive regulation of lipoprotein lipase activity	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0051583	dopamine uptake involved in synaptic transmission	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0051917	regulation of fibrinolysis	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0051934	catecholamine uptake involved in synaptic transmission	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0051971	positive regulation of transmission of nerve impulse	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0061517	macrophage proliferation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0061626	pharyngeal arch artery morphogenesis	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0061684	chaperone-mediated autophagy	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0070244	negative regulation of thymocyte apoptotic process	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0071305	cellular response to vitamin D	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0071609	chemokine (C-C motif) ligand 5 production	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0071635	negative regulation of transforming growth factor beta production	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0072173	metanephric tubule morphogenesis	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0090009	primitive streak formation	1/292	10/23328	0.11837274	0.08138184	1

BP	GO:0090237	regulation of arachidonic acid secretion	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0090381	regulation of heart induction	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0098908	regulation of neuronal action potential	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0099541	trans-synaptic signaling by lipid	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0099542	trans-synaptic signaling by endocannabinoid	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0106049	regulation of cellular response to osmotic stress	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1900122	positive regulation of receptor binding	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1902033	regulation of hematopoietic stem cell proliferation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1902746	regulation of lens fiber cell differentiation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1902959	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1903223	positive regulation of oxidative stress-induced neuron death	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1905522	negative regulation of macrophage migration	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:1990535	neuron projection maintenance	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:2000109	regulation of macrophage apoptotic process	1/292	10/23328	0.11837274	0.08138184	1

BP	GO:2000318	positive regulation of T-helper 17 type immune response	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:2000391	positive regulation of neutrophil extravasation	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:2000774	positive regulation of cellular senescence	1/292	10/23328	0.11837274	0.08138184	1
BP	GO:0006469	negative regulation of protein kinase activity	5/292	207/23328	0.1191685	0.08189841	5
BP	GO:0030838	positive regulation of actin filament polymerization	3/292	96/23328	0.11940809	0.08193176	3
BP	GO:0045638	negative regulation of myeloid cell differentiation	3/292	96/23328	0.11940809	0.08193176	3
BP	GO:0060998	regulation of dendritic spine development	3/292	96/23328	0.11940809	0.08193176	3
BP	GO:1903578	regulation of ATP metabolic process	3/292	96/23328	0.11940809	0.08193176	3
BP	GO:0044270	cellular nitrogen compound catabolic process	8/292	391/23328	0.11943903	0.08193176	8
BP	GO:0006110	regulation of glycolytic process	2/292	48/23328	0.12119441	0.08298167	2
BP	GO:0019098	reproductive behavior	2/292	48/23328	0.12119441	0.08298167	2
BP	GO:0046596	regulation of viral entry into host cell	2/292	48/23328	0.12119441	0.08298167	2
BP	GO:1903115	regulation of actin filament-based movement	2/292	48/23328	0.12119441	0.08298167	2
BP	GO:1903580	positive regulation of ATP metabolic process	2/292	48/23328	0.12119441	0.08298167	2

BP	GO:0010660	regulation of muscle cell apoptotic process	3/292	97/23328	0.12214379	0.08360068	3
BP	GO:0009100	glycoprotein metabolic process	7/292	332/23328	0.12471916	0.08533173	7
BP	GO:0030510	regulation of BMP signaling pathway	3/292	98/23328	0.12490233	0.0853621	3
BP	GO:0045833	negative regulation of lipid metabolic process	3/292	98/23328	0.12490233	0.0853621	3
BP	GO:0099565	chemical synaptic transmission, postsynaptic	3/292	98/23328	0.12490233	0.0853621	3
BP	GO:0043090	amino acid import	2/292	49/23328	0.12535512	0.08551319	2
BP	GO:0048255	mRNA stabilization	2/292	49/23328	0.12535512	0.08551319	2
BP	GO:0090102	cochlea development	2/292	49/23328	0.12535512	0.08551319	2
BP	GO:0090207	regulation of triglyceride metabolic process	2/292	49/23328	0.12535512	0.08551319	2
BP	GO:0090342	regulation of cell aging	2/292	49/23328	0.12535512	0.08551319	2
BP	GO:0046700	heterocycle catabolic process	8/292	397/23328	0.12705155	0.08655343	8
BP	GO:0006805	xenobiotic metabolic process	3/292	99/23328	0.1276833	0.08655343	3
BP	GO:0046031	ADP metabolic process	3/292	99/23328	0.1276833	0.08655343	3
BP	GO:0001767	establishment of lymphocyte polarity	1/292	11/23328	0.12941293	0.08655343	1

BP	GO:0001768	establishment of T cell polarity	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0002923	regulation of humoral immune response mediated by circulating immunoglobulin	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0003139	secondary heart field specification	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0006568	tryptophan metabolic process	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0006586	indolalkylamine metabolic process	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0014010	Schwann cell proliferation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0015886	heme transport	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0019627	urea metabolic process	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0021940	positive regulation of cerebellar granule cell precursor proliferation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0031053	primary miRNA processing	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0031077	post-embryonic camera-type eye development	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0031642	negative regulation of myelination	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0033084	regulation of immature T cell proliferation in thymus	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0033625	positive regulation of integrin activation	1/292	11/23328	0.12941293	0.08655343	1

BP	GO:0035726	common myeloid progenitor cell proliferation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0036005	response to macrophage colony-stimulating factor	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0036006	cellular response to macrophage colony-stimulating factor stimulus	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0036093	germ cell proliferation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0045924	regulation of female receptivity	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0048563	post-embryonic animal organ morphogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0048617	embryonic foregut morphogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0048630	skeletal muscle tissue growth	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0048845	venous blood vessel morphogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0051458	corticotropin secretion	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0060056	mammary gland involution	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0061309	cardiac neural crest cell development involved in outflow tract morphogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0061365	positive regulation of triglyceride lipase activity	1/292	11/23328	0.12941293	0.08655343	1

BP	GO:0061709	reticulophagy	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0070493	thrombin-activated receptor signaling pathway	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0071600	otic vesicle morphogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0071864	positive regulation of cell proliferation in bone marrow	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0071888	macrophage apoptotic process	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0072172	mesonephric tubule formation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0072182	regulation of nephron tubule epithelial cell differentiation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0097278	complement-dependent cytotoxicity	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1901033	positive regulation of response to reactive oxygen species	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1901142	insulin metabolic process	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1902166	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1902231	positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1902548	negative regulation of cellular response to vascular endothelial growth factor stimulus	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1903911	positive regulation of receptor clustering	1/292	11/23328	0.12941293	0.08655343	1

BP	GO:1904058	positive regulation of sensory perception of pain	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1904729	regulation of intestinal lipid absorption	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:1905245	regulation of aspartic-type peptidase activity	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:2000121	regulation of removal of superoxide radicals	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:2000389	regulation of neutrophil extravasation	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:2000786	positive regulation of autophagosome assembly	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:2001204	regulation of osteoclast development	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:2001214	positive regulation of vasculogenesis	1/292	11/23328	0.12941293	0.08655343	1
BP	GO:0021545	cranial nerve development	2/292	50/23328	0.12954959	0.08658206	2
BP	GO:1902475	L-alpha-amino acid transmembrane transport	2/292	50/23328	0.12954959	0.08658206	2
BP	GO:0006457	protein folding	4/292	155/23328	0.13044361	0.08711646	4
BP	GO:0071322	cellular response to carbohydrate stimulus	4/292	155/23328	0.13044361	0.08711646	4
BP	GO:0032984	protein-containing complex disassembly	5/292	214/23328	0.13179686	0.08798839	5
BP	GO:0007224	smoothened signaling pathway	4/292	156/23328	0.13264499	0.08849057	4

BP	GO:0071248	cellular response to metal ion	4/292	156/23328	0.13264499	0.08849057	4
BP	GO:0071456	cellular response to hypoxia	3/292	101/23328	0.13331092	0.08890269	3
BP	GO:0008154	actin polymerization or depolymerization	5/292	215/23328	0.13364869	0.08908428	5
BP	GO:0032330	regulation of chondrocyte differentiation	2/292	51/23328	0.13377634	0.08908428	2
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	2/292	51/23328	0.13377634	0.08908428	2
BP	GO:0060428	lung epithelium development	2/292	51/23328	0.13377634	0.08908428	2
BP	GO:0021543	pallium development	4/292	157/23328	0.13486165	0.08970989	4
BP	GO:0045333	cellular respiration	4/292	157/23328	0.13486165	0.08970989	4
BP	GO:1903707	negative regulation of hemopoiesis	4/292	157/23328	0.13486165	0.08970989	4
BP	GO:0050807	regulation of synapse organization	6/292	277/23328	0.13562096	0.09018247	6
BP	GO:0010657	muscle cell apoptotic process	3/292	102/23328	0.13615675	0.09047354	3
BP	GO:1901989	positive regulation of cell cycle phase transition	3/292	102/23328	0.13615675	0.09047354	3
BP	GO:0042491	inner ear auditory receptor cell differentiation	2/292	52/23328	0.13803391	0.09132936	2
BP	GO:0030004	cellular monovalent inorganic cation homeostasis	3/292	103/23328	0.13902337	0.09132936	3

BP	GO:0048477	oogenesis	3/292	103/23328	0.13902337	0.09132936	3
BP	GO:0071466	cellular response to xenobiotic stimulus	3/292	103/23328	0.13902337	0.09132936	3
BP	GO:0003129	heart induction	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0006213	pyrimidine nucleoside metabolic process	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0007440	foregut morphogenesis	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0007501	mesodermal cell fate specification	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0010870	positive regulation of receptor biosynthetic process	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0010872	regulation of cholesterol esterification	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0014832	urinary bladder smooth muscle contraction	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0014842	regulation of skeletal muscle satellite cell proliferation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0014874	response to stimulus involved in regulation of muscle adaptation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0032275	luteinizing hormone secretion	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0032610	interleukin-1 alpha production	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0032825	positive regulation of natural killer cell differentiation	1/292	12/23328	0.14031534	0.09132936	1

BP	GO:0033004	negative regulation of mast cell activation	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0033080	immature T cell proliferation in thymus	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0033210	leptin-mediated signaling pathway	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0033632	regulation of cell-cell adhesion mediated by integrin	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0035437	maintenance of protein localization in endoplasmic reticulum	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0042789	mRNA transcription by RNA polymerase II	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0043455	regulation of secondary metabolic process	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0043922	negative regulation by host of viral transcription	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0045348	positive regulation of MHC class II biosynthetic process	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0045586	regulation of gamma-delta T cell differentiation	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0045899	positive regulation of RNA polymerase II transcription preinitiation complex assembly	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0046643	regulation of gamma-delta T cell activation	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0048021	regulation of melanin biosynthetic process	1/292		12/23328	0.14031534	0.09132936	1
BP	GO:0048241	epinephrine transport	1/292		12/23328	0.14031534	0.09132936	1

BP	GO:0048570	notochord morphogenesis	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060073	micturition	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060433	bronchus development	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060439	trachea morphogenesis	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060453	regulation of gastric acid secretion	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060525	prostate glandular acinus development	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060536	cartilage morphogenesis	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0060586	multicellular organismal iron ion homeostasis	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0070341	fat cell proliferation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0070344	regulation of fat cell proliferation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0070472	regulation of uterine smooth muscle contraction	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0070839	divalent metal ion export	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0071863	regulation of cell proliferation in bone marrow	1/292	12/23328	0.14031534	0.09132936	1

BP	GO:0071941	nitrogen cycle metabolic process	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0090209	negative regulation of triglyceride metabolic process	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0090343	positive regulation of cell aging	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0090557	establishment of endothelial intestinal barrier	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0098722	asymmetric stem cell division	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:0098792	xenophagy	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:1900272	negative regulation of long-term synaptic potentiation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:1900376	regulation of secondary metabolite biosynthetic process	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:1901298	regulation of hydrogen peroxide-mediated programmed cell death	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:1902510	regulation of apoptotic DNA fragmentation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:1903431	positive regulation of cell maturation	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:2000105	positive regulation of DNA-dependent DNA replication	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:2000253	positive regulation of feeding behavior	1/292	12/23328	0.14031534	0.09132936	1
BP	GO:2000303	regulation of ceramide biosynthetic process	1/292	12/23328	0.14031534	0.09132936	1

BP	GO:0009135	purine nucleoside diphosphate metabolic process	3/292	104/23328	0.14191039	0.09223741	3
BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	3/292	104/23328	0.14191039	0.09223741	3
BP	GO:0043488	regulation of mRNA stability	3/292	104/23328	0.14191039	0.09223741	3
BP	GO:0060349	bone morphogenesis	3/292	104/23328	0.14191039	0.09223741	3
BP	GO:0021795	cerebral cortex cell migration	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0048599	oocyte development	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0048701	embryonic cranial skeleton morphogenesis	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0048713	regulation of oligodendrocyte differentiation	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0050435	amyloid-beta metabolic process	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0052372	modulation by symbiont of entry into host	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:2000677	regulation of transcription regulatory region DNA binding	2/292	53/23328	0.14232088	0.09227669	2
BP	GO:0034248	regulation of cellular amide metabolic process	8/292	410/23328	0.14438668	0.09358322	8
BP	GO:0001708	cell fate specification	3/292	105/23328	0.14481738	0.09382941	3
BP	GO:0010948	negative regulation of cell cycle process	5/292	221/23328	0.14500155	0.09391576	5

BP	GO:0019439	aromatic compound catabolic process	8/292	411/23328	0.14576668	0.09437821	8
BP	GO:0046717	acid secretion	2/292	54/23328	0.14663584	0.09480789	2
BP	GO:0046834	lipid phosphorylation	2/292	54/23328	0.14663584	0.09480789	2
BP	GO:0048066	developmental pigmentation	2/292	54/23328	0.14663584	0.09480789	2
BP	GO:2000649	regulation of sodium ion transmembrane transporter activity	2/292	54/23328	0.14663584	0.09480789	2
BP	GO:0060070	canonical Wnt signaling pathway	6/292	284/23328	0.14727602	0.09518845	6
BP	GO:0000041	transition metal ion transport	3/292	106/23328	0.14774393	0.09539064	3
BP	GO:0006165	nucleoside diphosphate phosphorylation	3/292	106/23328	0.14774393	0.09539064	3
BP	GO:0035282	segmentation	3/292	106/23328	0.14774393	0.09539064	3
BP	GO:0030518	intracellular steroid hormone receptor signaling pathway	3/292	107/23328	0.15068965	0.09593443	3
BP	GO:0045017	glycerolipid biosynthetic process	4/292	164/23328	0.15079093	0.09593443	4
BP	GO:0010665	regulation of cardiac muscle cell apoptotic process	2/292	55/23328	0.15097745	0.09593443	2
BP	GO:0035176	social behavior	2/292	55/23328	0.15097745	0.09593443	2
BP	GO:0035306	positive regulation of dephosphorylation	2/292	55/23328	0.15097745	0.09593443	2

BP	GO:0045604	regulation of epidermal cell differentiation	2/292	55/23328	0.15097745	0.09593443	2
BP	GO:0002674	negative regulation of acute inflammatory response	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0002730	regulation of dendritic cell cytokine production	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0003093	regulation of glomerular filtration	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0003306	Wnt signaling pathway involved in heart development	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0006983	ER overload response	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0007183	SMAD protein complex assembly	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0009435	NAD biosynthetic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0010838	positive regulation of keratinocyte proliferation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0014841	skeletal muscle satellite cell proliferation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0032799	low-density lipoprotein receptor particle metabolic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0033083	regulation of immature T cell proliferation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0033262	regulation of nuclear cell cycle DNA replication	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0033280	response to vitamin D	1/292	13/23328	0.15108168	0.09593443	1

BP	GO:0035630	bone mineralization involved in bone maturation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0038094	Fc-gamma receptor signaling pathway	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0038166	angiotensin-activated signaling pathway	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0042402	cellular biogenic amine catabolic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0042541	hemoglobin biosynthetic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0042693	muscle cell fate commitment	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0042994	cytoplasmic sequestering of transcription factor	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0044090	positive regulation of vacuole organization	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0046007	negative regulation of activated T cell proliferation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0048340	paraxial mesoderm morphogenesis	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0048548	regulation of pinocytosis	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0055091	phospholipid homeostasis	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0060394	negative regulation of pathway-restricted SMAD protein phosphorylation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0061140	lung secretory cell differentiation	1/292	13/23328	0.15108168	0.09593443	1

BP	GO:0071073	positive regulation of phospholipid biosynthetic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0071281	cellular response to iron ion	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0071295	cellular response to vitamin	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0071380	cellular response to prostaglandin E stimulus	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0071838	cell proliferation in bone marrow	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0072160	nephron tubule epithelial cell differentiation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0090193	positive regulation of glomerulus development	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0097049	motor neuron apoptotic process	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:0150011	regulation of neuron projection arborization	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:1901096	regulation of autophagosome maturation	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:1901201	regulation of extracellular matrix assembly	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:1901678	iron coordination entity transport	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:1903025	regulation of RNA polymerase II regulatory region sequence-specific DNA binding	1/292	13/23328	0.15108168	0.09593443	1
BP	GO:1903430	negative regulation of cell maturation	1/292	13/23328	0.15108168	0.09593443	1

BP	GO:1903977	positive regulation of glial cell migration	1/292		13/23328	0.15108168	0.09593443	1
BP	GO:0006641	triglyceride metabolic process	3/292		108/23328	0.15365412	0.09746727	3
BP	GO:0009185	ribonucleoside diphosphate metabolic process	3/292		108/23328	0.15365412	0.09746727	3
BP	GO:0046939	nucleotide phosphorylation	3/292		108/23328	0.15365412	0.09746727	3
BP	GO:0006310	DNA recombination	6/292		288/23328	0.15413421	0.09773821	6
BP	GO:0001914	regulation of T cell mediated cytotoxicity	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0001954	positive regulation of cell-matrix adhesion	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0006023	aminoglycan biosynthetic process	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0021587	cerebellum morphogenesis	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0043647	inositol phosphate metabolic process	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0070265	necrotic cell death	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0098815	modulation of excitatory postsynaptic potential	2/292		56/23328	0.15534435	0.09826918	2
BP	GO:0050803	regulation of synapse structure or activity	6/292		289/23328	0.15587067	0.09856834	6
BP	GO:0021549	cerebellum development	3/292		109/23328	0.15663692	0.09898505	3

BP	GO:1905477	positive regulation of protein localization to membrane	3/292	109/23328	0.15663692	0.09898505	3
BP	GO:0032271	regulation of protein polymerization	5/292	227/23328	0.15675417	0.09899134	5
BP	GO:0033673	negative regulation of kinase activity	5/292	227/23328	0.15675417	0.09899134	5
BP	GO:0006275	regulation of DNA replication	3/292	110/23328	0.15963766	0.10043898	3
BP	GO:0009410	response to xenobiotic stimulus	3/292	110/23328	0.15963766	0.10043898	3
BP	GO:0006584	catecholamine metabolic process	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:0009712	catechol-containing compound metabolic process	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:0009994	oocyte differentiation	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:0043489	RNA stabilization	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:1902373	negative regulation of mRNA catabolic process	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:2000648	positive regulation of stem cell proliferation	2/292	57/23328	0.15973524	0.10043898	2
BP	GO:0002371	dendritic cell cytokine production	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0002829	negative regulation of type 2 immune response	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	1/292	14/23328	0.16171364	0.10043898	1

BP	GO:0007351	tripartite regional subdivision	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0008595	anterior/posterior axis specification, embryo	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0009310	amine catabolic process	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0010225	response to UV-C	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0010421	hydrogen peroxide-mediated programmed cell death	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0021936	regulation of cerebellar granule cell precursor proliferation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0031915	positive regulation of synaptic plasticity	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0032099	negative regulation of appetite	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0032736	positive regulation of interleukin-13 production	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0033079	immature T cell proliferation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0036498	IRE1-mediated unfolded protein response	1/292	14/23328	0.16171364	0.10043898	1

BP	GO:0045188	regulation of circadian sleep/wake cycle, non-REM sleep	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0045898	regulation of RNA polymerase II transcription preinitiation complex assembly	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0046835	carbohydrate phosphorylation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0048103	somatic stem cell division	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0048505	regulation of timing of cell differentiation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0048755	branching morphogenesis of a nerve	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0060019	radial glial cell differentiation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0060180	female mating behavior	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0060263	regulation of respiratory burst	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0061308	cardiac neural crest cell development involved in heart development	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0070207	protein homotrimerization	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0070365	hepatocyte differentiation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0071371	cellular response to gonadotropin stimulus	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0071803	positive regulation of podosome assembly	1/292	14/23328	0.16171364	0.10043898	1

BP	GO:0072224	metanephric glomerulus development	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0090153	regulation of sphingolipid biosynthetic process	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0090179	planar cell polarity pathway involved in neural tube closure	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0090331	negative regulation of platelet aggregation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0097468	programmed cell death in response to reactive oxygen species	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:1902563	regulation of neutrophil activation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:1903624	regulation of DNA catabolic process	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:1904948	midbrain dopaminergic neuron differentiation	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:1905038	regulation of membrane lipid metabolic process	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:2000052	positive regulation of non-canonical Wnt signaling pathway	1/292	14/23328	0.16171364	0.10043898	1
BP	GO:0031047	gene silencing by RNA	4/292	169/23328	0.16258772	0.10091393	4
BP	GO:0035303	regulation of dephosphorylation	4/292	169/23328	0.16258772	0.10091393	4
BP	GO:0008637	apoptotic mitochondrial changes	3/292	111/23328	0.16265593	0.10092232	3
BP	GO:0010662	regulation of striated muscle cell apoptotic process	2/292	58/23328	0.16414884	0.10167768	2

BP	GO:0035065	regulation of histone acetylation	2/292	58/23328	0.16414884	0.10167768	2
BP	GO:0035315	hair cell differentiation	2/292	58/23328	0.16414884	0.10167768	2
BP	GO:0043470	regulation of carbohydrate catabolic process	2/292	58/23328	0.16414884	0.10167768	2
BP	GO:0051703	intraspecies interaction between organisms	2/292	58/23328	0.16414884	0.10167768	2
BP	GO:0051604	protein maturation	6/292	294/23328	0.16468119	0.1019732	6
BP	GO:0007009	plasma membrane organization	3/292	112/23328	0.16569132	0.10256427	3
BP	GO:0072659	protein localization to plasma membrane	6/292	295/23328	0.16646848	0.10301078	6
BP	GO:0019827	stem cell population maintenance	4/292	171/23328	0.16739812	0.10355132	4
BP	GO:0007164	establishment of tissue polarity	2/292	59/23328	0.16858391	0.10418007	2
BP	GO:0007528	neuromuscular junction development	2/292	59/23328	0.16858391	0.10418007	2
BP	GO:0010659	cardiac muscle cell apoptotic process	2/292	59/23328	0.16858391	0.10418007	2
BP	GO:0060828	regulation of canonical Wnt signaling pathway	5/292	234/23328	0.17094187	0.10439491	5
BP	GO:0005976	polysaccharide metabolic process	3/292	114/23328	0.17181184	0.10439491	3
BP	GO:0043401	steroid hormone mediated signaling pathway	3/292	114/23328	0.17181184	0.10439491	3

BP	GO:0060078	regulation of postsynaptic membrane potential	3/292	114/23328	0.17181184	0.10439491	3
BP	GO:1903076	regulation of protein localization to plasma membrane	3/292	114/23328	0.17181184	0.10439491	3
BP	GO:0001771	immunological synapse formation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0006206	pyrimidine nucleobase metabolic process	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0007194	negative regulation of adenylate cyclase activity	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0010561	negative regulation of glycoprotein biosynthetic process	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0010885	regulation of cholesterol storage	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0014848	urinary tract smooth muscle contraction	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0014857	regulation of skeletal muscle cell proliferation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0030299	intestinal cholesterol absorption	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0030449	regulation of complement activation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0032096	negative regulation of response to food	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0032530	regulation of microvillus organization	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0032717	negative regulation of interleukin-8 production	1/292	15/23328	0.17221289	0.10439491	1

BP	GO:0033690	positive regulation of osteoblast proliferation	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0034162	toll-like receptor 9 signaling pathway	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0034433	steroid esterification	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0034434	sterol esterification	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0034435	cholesterol esterification	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0034698	response to gonadotropin	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0042748	circadian sleep/wake cycle, non-REM sleep	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0043129	surfactant homeostasis	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0044793	negative regulation by host of viral process	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0045591	positive regulation of regulatory T cell differentiation	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0045605	negative regulation of epidermal cell differentiation	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0045618	positive regulation of keratinocyte differentiation	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0047484	regulation of response to osmotic stress	1/292		15/23328	0.17221289	0.10439491	1
BP	GO:0048070	regulation of developmental pigmentation	1/292		15/23328	0.17221289	0.10439491	1

BP	GO:0048096	chromatin-mediated maintenance of transcription	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0050746	regulation of lipoprotein metabolic process	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060049	regulation of protein glycosylation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060330	regulation of response to interferon-gamma	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060334	regulation of interferon-gamma-mediated signaling pathway	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060396	growth hormone receptor signaling pathway	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060442	branching involved in prostate gland morphogenesis	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060732	positive regulation of inositol phosphate biosynthetic process	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0060742	epithelial cell differentiation involved in prostate gland development	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0061029	eyelid development in camera-type eye	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0061051	positive regulation of cell growth involved in cardiac muscle cell development	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0061307	cardiac neural crest cell differentiation involved in heart development	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0061318	renal filtration cell differentiation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0070307	lens fiber cell development	1/292	15/23328	0.17221289	0.10439491	1

BP	GO:0071378	cellular response to growth hormone stimulus	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0072112	glomerular visceral epithelial cell differentiation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0072311	glomerular epithelial cell differentiation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0072350	tricarboxylic acid metabolic process	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0090178	regulation of establishment of planar polarity involved in neural tube closure	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0097154	GABAergic neuron differentiation	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0098712	L-glutamate import across plasma membrane	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0098917	retrograde trans-synaptic signaling	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0150105	protein localization to cell-cell junction	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:1902969	mitotic DNA replication	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:1903961	positive regulation of anion transmembrane transport	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:1904478	regulation of intestinal absorption	1/292	15/23328	0.17221289	0.10439491	1
BP	GO:0007595	lactation	2/292	60/23328	0.17303922	0.10468947	2

BP	GO:0021575	hindbrain morphogenesis	2/292	60/23328	0.17303922	0.10468947	2
BP	GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	2/292	60/23328	0.17303922	0.10468947	2
BP	GO:0051893	regulation of focal adhesion assembly	2/292	60/23328	0.17303922	0.10468947	2
BP	GO:0090109	regulation of cell-substrate junction assembly	2/292	60/23328	0.17303922	0.10468947	2
BP	GO:1901016	regulation of potassium ion transmembrane transporter activity	2/292	60/23328	0.17303922	0.10468947	2
BP	GO:0030216	keratinocyte differentiation	3/292	115/23328	0.17489616	0.10574359	3
BP	GO:0031398	positive regulation of protein ubiquitination	3/292	115/23328	0.17489616	0.10574359	3
BP	GO:0098727	maintenance of cell number	4/292	175/23328	0.17716785	0.10708199	4
BP	GO:0007584	response to nutrient	2/292	61/23328	0.17751357	0.1072207	2
BP	GO:0051851	modulation by host of symbiont process	2/292	61/23328	0.17751357	0.1072207	2
BP	GO:0010171	body morphogenesis	2/292	62/23328	0.1820058	0.10861062	2
BP	GO:0010658	striated muscle cell apoptotic process	2/292	62/23328	0.1820058	0.10861062	2
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	2/292	62/23328	0.1820058	0.10861062	2
BP	GO:0032387	negative regulation of intracellular transport	2/292	62/23328	0.1820058	0.10861062	2

BP	GO:0048512	circadian behavior	2/292	62/23328	0.1820058	0.10861062	2
BP	GO:0001977	renal system process involved in regulation of blood volume	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0003161	cardiac conduction system development	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0006620	posttranslational protein targeting to endoplasmic reticulum membrane	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0006658	phosphatidylserine metabolic process	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0010224	response to UV-B	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0014733	regulation of skeletal muscle adaptation	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0014856	skeletal muscle cell proliferation	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0033089	positive regulation of T cell differentiation in thymus	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0035112	genitalia morphogenesis	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0039535	regulation of RIG-I signaling pathway	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0040034	regulation of development, heterochronic	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0042308	negative regulation of protein import into nucleus	1/292	16/23328	0.18258109	0.10861062	1

BP	GO:0043217	myelin maintenance	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0043518	negative regulation of DNA damage response, signal transduction by p53 class mediator	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0044068	modulation by symbiont of host cellular process	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0045655	regulation of monocyte differentiation	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0051938	L-glutamate import	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0060026	convergent extension	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0060100	positive regulation of phagocytosis, engulfment	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0060391	positive regulation of SMAD protein signal transduction	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0060856	establishment of blood-brain barrier	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0061000	negative regulation of dendritic spine development	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0071243	cellular response to arsenic-containing substance	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0071404	cellular response to low-density lipoprotein particle stimulus	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0071498	cellular response to fluid shear stress	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0071599	otic vesicle development	1/292	16/23328	0.18258109	0.10861062	1

BP	GO:0071731	response to nitric oxide	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:0090083	regulation of inclusion body assembly	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:0090136	epithelial cell-cell adhesion	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:0090177	establishment of planar polarity involved in neural tube closure	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:0090494	dopamine uptake	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1903729	regulation of plasma membrane organization	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1903779	regulation of cardiac conduction	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1904590	negative regulation of protein import	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1905048	regulation of metallopeptidase activity	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1905155	positive regulation of membrane invagination	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:1905941	positive regulation of gonad development	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:2000628	regulation of miRNA metabolic process	1/292		16/23328	0.18258109	0.10861062	1
BP	GO:2001212	regulation of vasculogenesis	1/292		16/23328	0.18258109	0.10861062	1

BP	GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	1/292	16/23328	0.18258109	0.10861062	1
BP	GO:0030111	regulation of Wnt signaling pathway	6/292	304/23328	0.18291662	0.10877515	6
BP	GO:0018107	peptidyl-threonine phosphorylation	3/292	118/23328	0.18424062	0.10949192	3
BP	GO:0030317	flagellated sperm motility	3/292	118/23328	0.18424062	0.10949192	3
BP	GO:0050954	sensory perception of mechanical stimulus	6/292	305/23328	0.18478319	0.10977901	6
BP	GO:0006661	phosphatidylinositol biosynthetic process	2/292	63/23328	0.18651475	0.11066521	2
BP	GO:0030104	water homeostasis	2/292	63/23328	0.18651475	0.11066521	2
BP	GO:0060999	positive regulation of dendritic spine development	2/292	63/23328	0.18651475	0.11066521	2
BP	GO:0150116	regulation of cell-substrate junction organization	2/292	63/23328	0.18651475	0.11066521	2
BP	GO:0007622	rhythmic behavior	2/292	64/23328	0.19103933	0.11248922	2
BP	GO:0015909	long-chain fatty acid transport	2/292	64/23328	0.19103933	0.11248922	2
BP	GO:1902305	regulation of sodium ion transmembrane transport	2/292	64/23328	0.19103933	0.11248922	2
BP	GO:1901361	organic cyclic compound catabolic process	8/292	442/23328	0.19162172	0.11248922	8
BP	GO:0007266	Rho protein signal transduction	4/292	181/23328	0.19217187	0.11248922	4

BP	GO:0050853	B cell receptor signaling pathway	4/292	181/23328	0.19217187	0.11248922	4
BP	GO:0001710	mesodermal cell fate commitment	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0001821	histamine secretion	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0001886	endothelial cell morphogenesis	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0001967	suckling behavior	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0006704	glucocorticoid biosynthetic process	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0007096	regulation of exit from mitosis	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0010310	regulation of hydrogen peroxide metabolic process	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0010878	cholesterol storage	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0019359	nicotinamide nucleotide biosynthetic process	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0031280	negative regulation of cyclase activity	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0032105	negative regulation of response to extracellular stimulus	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0032108	negative regulation of response to nutrient levels	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0032682	negative regulation of chemokine production	1/292	17/23328	0.19281986	0.11248922	1

BP	GO:0033623	regulation of integrin activation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0034755	iron ion transmembrane transport	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0035313	wound healing, spreading of epidermal cells	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0036035	osteoclast development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0042074	cell migration involved in gastrulation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0043278	response to morphine	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0045198	establishment of epithelial cell apical/basal polarity	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0045653	negative regulation of megakaryocyte differentiation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0045725	positive regulation of glycogen biosynthetic process	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0045836	positive regulation of meiotic nuclear division	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0046755	viral budding	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0048368	lateral mesoderm development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0048875	chemical homeostasis within a tissue	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0050665	hydrogen peroxide biosynthetic process	1/292	17/23328	0.19281986	0.11248922	1

BP	GO:0051004	regulation of lipoprotein lipase activity	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0060788	ectodermal placode formation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0070206	protein trimerization	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0071697	ectodermal placode morphogenesis	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0072010	glomerular epithelium development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0072234	metanephric nephron tubule development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0072672	neutrophil extravasation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0090185	negative regulation of kidney development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0090192	regulation of glomerulus development	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0090336	positive regulation of brown fat cell differentiation	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0090493	catecholamine uptake	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:0098814	spontaneous synaptic transmission	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:1900016	negative regulation of cytokine production involved in inflammatory response	1/292	17/23328	0.19281986	0.11248922	1
BP	GO:1900221	regulation of amyloid-beta clearance	1/292	17/23328	0.19281986	0.11248922	1

BP	GO:1900452	regulation of long-term synaptic depression	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:1902894	negative regulation of pri-miRNA transcription by RNA polymerase II	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:1904889	regulation of excitatory synapse assembly	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:2000047	regulation of cell-cell adhesion mediated by cadherin	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:2000380	regulation of mesoderm development	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:2000479	regulation of cAMP-dependent protein kinase activity	1/292		17/23328	0.19281986	0.11248922	1
BP	GO:0022037	metencephalon development	3/292		121/23328	0.19371395	0.11290373	3
BP	GO:0097722	sperm motility	3/292		121/23328	0.19371395	0.11290373	3
BP	GO:1901136	carbohydrate derivative catabolic process	3/292		121/23328	0.19371395	0.11290373	3
BP	GO:0006836	neurotransmitter transport	5/292		245/23328	0.19418891	0.11314482	5
BP	GO:0048592	eye morphogenesis	4/292		182/23328	0.19471085	0.11341312	4
BP	GO:1903828	negative regulation of cellular protein localization	3/292		122/23328	0.19689854	0.11465119	3
BP	GO:0009132	nucleoside diphosphate metabolic process	3/292		123/23328	0.20009588	0.11631317	3
BP	GO:0010921	regulation of phosphatase activity	3/292		123/23328	0.20009588	0.11631317	3

BP	GO:0046474	glycerophospholipid biosynthetic process	3/292		123/23328	0.20009588	0.11631317	3
BP	GO:0042440	pigment metabolic process	2/292		66/23328	0.20013097	0.11631317	2
BP	GO:0050433	regulation of catecholamine secretion	2/292		66/23328	0.20013097	0.11631317	2
BP	GO:2000736	regulation of stem cell differentiation	2/292		66/23328	0.20013097	0.11631317	2
BP	GO:0071229	cellular response to acid chemical	4/292		185/23328	0.2023896	0.1168729	4
BP	GO:0001820	serotonin secretion	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0002283	neutrophil activation involved in immune response	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0003128	heart field specification	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0009886	post-embryonic animal morphogenesis	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0010002	cardioblast differentiation	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0010867	positive regulation of triglyceride biosynthetic process	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0010919	regulation of inositol phosphate biosynthetic process	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0014072	response to isoquinoline alkaloid	1/292		18/23328	0.20293082	0.1168729	1
BP	GO:0021542	dentate gyrus development	1/292		18/23328	0.20293082	0.1168729	1

BP	GO:0021702	cerebellar Purkinje cell differentiation	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0021756	striatum development	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0030033	microvillus assembly	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0033631	cell-cell adhesion mediated by integrin	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0035633	maintenance of blood-brain barrier	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0042249	establishment of planar polarity of embryonic epithelium	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0044241	lipid digestion	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0044406	adhesion of symbiont to host	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0045019	negative regulation of nitric oxide biosynthetic process	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0050855	regulation of B cell receptor signaling pathway	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0050872	white fat cell differentiation	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0060416	response to growth hormone	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0070102	interleukin-6-mediated signaling pathway	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0071696	ectodermal placode development	1/292	18/23328	0.20293082	0.1168729	1

BP	GO:0072148	epithelial cell fate commitment	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0098856	intestinal lipid absorption	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:1904406	negative regulation of nitric oxide metabolic process	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:2000319	regulation of T-helper 17 cell differentiation	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	1/292	18/23328	0.20293082	0.1168729	1
BP	GO:0051963	regulation of synapse assembly	3/292	124/23328	0.20330559	0.1170522	3
BP	GO:0021695	cerebellar cortex development	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:0030239	myofibril assembly	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:0086003	cardiac muscle cell contraction	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:0090307	mitotic spindle assembly	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:1903307	positive regulation of regulated secretory pathway	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:2000756	regulation of peptidyl-lysine acetylation	2/292	67/23328	0.20469593	0.11763247	2
BP	GO:0051321	meiotic cell cycle	6/292	317/23328	0.20774856	0.11934955	6
BP	GO:0007566	embryo implantation	2/292	68/23328	0.20927228	0.11988899	2

BP	GO:0030032	lamellipodium assembly	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0033692	cellular polysaccharide biosynthetic process	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0043949	regulation of cAMP-mediated signaling	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0048641	regulation of skeletal muscle tissue development	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0050432	catecholamine secretion	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0071868	cellular response to monoamine stimulus	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0071870	cellular response to catecholamine stimulus	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:1902369	negative regulation of RNA catabolic process	2/292	68/23328	0.20927228	0.11988899	2
BP	GO:0036294	cellular response to decreased oxygen levels	3/292	126/23328	0.20976059	0.12013143	3
BP	GO:0031669	cellular response to nutrient levels	4/292	188/23328	0.21015701	0.12032113	4
BP	GO:0048705	skeletal system morphogenesis	5/292	253/23328	0.21175345	0.12075284	5
BP	GO:0001975	response to amphetamine	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0002031	G protein-coupled receptor internalization	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0006309	apoptotic DNA fragmentation	1/292	19/23328	0.21291556	0.12075284	1

BP	GO:0006525	arginine metabolic process	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0006590	thyroid hormone generation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0009074	aromatic amino acid family catabolic process	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0010544	negative regulation of platelet activation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0014061	regulation of norepinephrine secretion	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0016486	peptide hormone processing	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0017121	plasma membrane phospholipid scrambling	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0021694	cerebellar Purkinje cell layer formation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0030502	negative regulation of bone mineralization	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0032823	regulation of natural killer cell differentiation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0034111	negative regulation of homotypic cell-cell adhesion	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0046068	cGMP metabolic process	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0046321	positive regulation of fatty acid oxidation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0048243	norepinephrine secretion	1/292	19/23328	0.21291556	0.12075284	1

BP	GO:0048712	negative regulation of astrocyte differentiation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0051350	negative regulation of lyase activity	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0060033	anatomical structure regression	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0060044	negative regulation of cardiac muscle cell proliferation	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0060099	regulation of phagocytosis, engulfment	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0070875	positive regulation of glycogen metabolic process	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0071071	regulation of phospholipid biosynthetic process	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0090201	negative regulation of release of cytochrome c from mitochondria	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:1903960	negative regulation of anion transmembrane transport	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:1904424	regulation of GTP binding	1/292	19/23328	0.21291556	0.12075284	1
BP	GO:0008277	regulation of G protein-coupled receptor signaling pathway	3/292	127/23328	0.21300512	0.12075284	3
BP	GO:0018210	peptidyl-threonine modification	3/292	127/23328	0.21300512	0.12075284	3
BP	GO:0060048	cardiac muscle contraction	3/292	127/23328	0.21300512	0.12075284	3
BP	GO:0060996	dendritic spine development	3/292	127/23328	0.21300512	0.12075284	3

BP	GO:0001913	T cell mediated cytotoxicity	2/292	69/23328	0.21385902	0.12105097	2
BP	GO:0008542	visual learning	2/292	69/23328	0.21385902	0.12105097	2
BP	GO:0031638	zymogen activation	2/292	69/23328	0.21385902	0.12105097	2
BP	GO:0071867	response to monoamine	2/292	69/23328	0.21385902	0.12105097	2
BP	GO:0071869	response to catecholamine	2/292	69/23328	0.21385902	0.12105097	2
BP	GO:0006401	RNA catabolic process	5/292	254/23328	0.21398452	0.12108487	5
BP	GO:0120032	regulation of plasma membrane bounded cell projection assembly	4/292	190/23328	0.21538198	0.12183827	4
BP	GO:0051592	response to calcium ion	3/292	128/23328	0.2162605	0.12226027	3
BP	GO:0061013	regulation of mRNA catabolic process	3/292	128/23328	0.2162605	0.12226027	3
BP	GO:0043954	cellular component maintenance	2/292	70/23328	0.21845519	0.12338761	2
BP	GO:0055117	regulation of cardiac muscle contraction	2/292	70/23328	0.21845519	0.12338761	2
BP	GO:2000179	positive regulation of neural precursor cell proliferation	2/292	70/23328	0.21845519	0.12338761	2
BP	GO:0032273	positive regulation of protein polymerization	3/292	129/23328	0.21952636	0.12391676	3
BP	GO:0060294	cilium movement involved in cell motility	3/292	129/23328	0.21952636	0.12391676	3

BP	GO:0060491	regulation of cell projection assembly	4/292	192/23328	0.2206425	0.12450871	4
BP	GO:0001505	regulation of neurotransmitter levels	5/292	257/23328	0.22072228	0.12451565	5
BP	GO:0009150	purine ribonucleotide metabolic process	6/292	324/23328	0.22159447	0.12481145	6
BP	GO:0001696	gastric acid secretion	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0006828	manganese ion transport	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0006883	cellular sodium ion homeostasis	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0019363	pyridine nucleotide biosynthetic process	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0021535	cell migration in hindbrain	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0030002	cellular anion homeostasis	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0030320	cellular monovalent inorganic anion homeostasis	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0030852	regulation of granulocyte differentiation	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0032095	regulation of response to food	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0035584	calcium-mediated signaling using intracellular calcium source	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0045217	cell-cell junction maintenance	1/292	20/23328	0.22277564	0.12481145	1

BP	GO:0045722	positive regulation of gluconeogenesis	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0048172	regulation of short-term neuronal synaptic plasticity	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0048557	embryonic digestive tract morphogenesis	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0051608	histamine transport	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0072079	nephron tubule formation	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0090030	regulation of steroid hormone biosynthetic process	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0140448	signaling receptor ligand precursor processing	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:1900746	regulation of vascular endothelial growth factor signaling pathway	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:1903909	regulation of receptor clustering	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:1905153	regulation of membrane invagination	1/292	20/23328	0.22277564	0.12481145	1
BP	GO:0042177	negative regulation of protein catabolic process	3/292	130/23328	0.22280232	0.12481145	3
BP	GO:0006635	fatty acid beta-oxidation	2/292	71/23328	0.22305983	0.12491778	2
BP	GO:1903305	regulation of regulated secretory pathway	4/292	193/23328	0.22328561	0.12500628	4
BP	GO:0051348	negative regulation of transferase activity	5/292	260/23328	0.2275244	0.12734073	5

BP	GO:0051453	regulation of intracellular pH	2/292	72/23328	0.22767201	0.1273461	2
BP	GO:1904888	cranial skeletal system development	2/292	72/23328	0.22767201	0.1273461	2
BP	GO:1905475	regulation of protein localization to membrane	4/292	195/23328	0.22859656	0.12782449	4
BP	GO:0072521	purine-containing compound metabolic process	7/292	396/23328	0.22924542	0.12814848	7
BP	GO:0045055	regulated exocytosis	5/292	261/23328	0.22980553	0.12842268	5
BP	GO:0002090	regulation of receptor internalization	2/292	73/23328	0.23229083	0.12899789	2
BP	GO:0007632	visual behavior	2/292	73/23328	0.23229083	0.12899789	2
BP	GO:0009988	cell-cell recognition	2/292	73/23328	0.23229083	0.12899789	2
BP	GO:0001502	cartilage condensation	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0007035	vacuolar acidification	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0007625	grooming behavior	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0014075	response to amine	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	1/292	21/23328	0.23251262	0.12899789	1

BP	GO:0019430	removal of superoxide radicals	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0031065	positive regulation of histone deacetylation	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0031290	retinal ganglion cell axon guidance	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0032332	positive regulation of chondrocyte differentiation	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0033605	positive regulation of catecholamine secretion	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0035089	establishment of apical/basal cell polarity	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0035357	peroxisome proliferator activated receptor signaling pathway	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0042053	regulation of dopamine metabolic process	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0043931	ossification involved in bone maturation	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0045948	positive regulation of translational initiation	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0046174	polyol catabolic process	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0048569	post-embryonic animal organ development	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0051900	regulation of mitochondrial depolarization	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	1/292	21/23328	0.23251262	0.12899789	1

BP	GO:1903209	positive regulation of oxidative stress-induced cell death	1/292	21/23328	0.23251262	0.12899789	1
BP	GO:0046928	regulation of neurotransmitter secretion	3/292	134/23328	0.2359999	0.13089328	3
BP	GO:0009060	aerobic respiration	2/292	74/23328	0.2369154	0.1313221	2
BP	GO:2001021	negative regulation of response to DNA damage stimulus	2/292	74/23328	0.2369154	0.1313221	2
BP	GO:0009314	response to radiation	7/292	401/23328	0.23846608	0.13214195	7
BP	GO:0043467	regulation of generation of precursor metabolites and energy	3/292	135/23328	0.23932092	0.13253604	3
BP	GO:0072331	signal transduction by p53 class mediator	3/292	135/23328	0.23932092	0.13253604	3
BP	GO:0009116	nucleoside metabolic process	2/292	75/23328	0.24154486	0.13317137	2
BP	GO:0009259	ribonucleotide metabolic process	6/292	334/23328	0.24188456	0.13317137	6
BP	GO:0099173	postsynapse organization	4/292	200/23328	0.24200935	0.13317137	4
BP	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0006516	glycoprotein catabolic process	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0007141	male meiosis I	1/292	22/23328	0.24212803	0.13317137	1

BP	GO:0008356	asymmetric cell division	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0014850	response to muscle activity	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0014912	negative regulation of smooth muscle cell migration	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0015813	L-glutamate transmembrane transport	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0019320	hexose catabolic process	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0021516	dorsal spinal cord development	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0042438	melanin biosynthetic process	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0046597	negative regulation of viral entry into host cell	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0048857	neural nucleus development	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0051220	cytoplasmic sequestering of protein	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0060009	Sertoli cell development	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0060080	inhibitory postsynaptic potential	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0060438	trachea development	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	1/292	22/23328	0.24212803	0.13317137	1

BP	GO:1902547	regulation of cellular response to vascular endothelial growth factor stimulus	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	1/292	22/23328	0.24212803	0.13317137	1
BP	GO:0001539	cilium or flagellum-dependent cell motility	3/292	136/23328	0.24264988	0.13337887	3
BP	GO:0060285	cilium-dependent cell motility	3/292	136/23328	0.24264988	0.13337887	3
BP	GO:1901606	alpha-amino acid catabolic process	2/292	76/23328	0.24617836	0.1352781	2
BP	GO:0006639	acylglycerol metabolic process	3/292	138/23328	0.24933019	0.13672301	3
BP	GO:0009411	response to UV	3/292	138/23328	0.24933019	0.13672301	3
BP	GO:0030218	erythrocyte differentiation	3/292	138/23328	0.24933019	0.13672301	3
BP	GO:0035023	regulation of Rho protein signal transduction	3/292	138/23328	0.24933019	0.13672301	3
BP	GO:0001756	somitogenesis	2/292	77/23328	0.25081509	0.13672301	2
BP	GO:0010822	positive regulation of mitochondrion organization	2/292	77/23328	0.25081509	0.13672301	2
BP	GO:0031397	negative regulation of protein ubiquitination	2/292	77/23328	0.25081509	0.13672301	2
BP	GO:0032410	negative regulation of transporter activity	2/292	77/23328	0.25081509	0.13672301	2
BP	GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	2/292	77/23328	0.25081509	0.13672301	2

BP	GO:0048844	artery morphogenesis	2/292		77/23328	0.25081509	0.13672301	2
BP	GO:0006907	pinocytosis	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0009065	glutamine family amino acid catabolic process	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0010866	regulation of triglyceride biosynthetic process	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0010996	response to auditory stimulus	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0021692	cerebellar Purkinje cell layer morphogenesis	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0023019	signal transduction involved in regulation of gene expression	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0030539	male genitalia development	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0032331	negative regulation of chondrocyte differentiation	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0034383	low-density lipoprotein particle clearance	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0034405	response to fluid shear stress	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0039529	RIG-I signaling pathway	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0042069	regulation of catecholamine metabolic process	1/292		23/23328	0.25162338	0.13672301	1
BP	GO:0042537	benzene-containing compound metabolic process	1/292		23/23328	0.25162338	0.13672301	1

BP	GO:0043501	skeletal muscle adaptation	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0043576	regulation of respiratory gaseous exchange	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0045026	plasma membrane fusion	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0045056	transcytosis	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0045606	positive regulation of epidermal cell differentiation	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0051450	myoblast proliferation	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0061162	establishment of monopolar cell polarity	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0070977	bone maturation	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0071450	cellular response to oxygen radical	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0071451	cellular response to superoxide	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0097062	dendritic spine maintenance	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:0098703	calcium ion import across plasma membrane	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:1903306	negative regulation of regulated secretory pathway	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:2000316	regulation of T-helper 17 type immune response	1/292	23/23328	0.25162338	0.13672301	1

BP	GO:2000810	regulation of bicellular tight junction assembly	1/292	23/23328	0.25162338	0.13672301	1
BP	GO:1903322	positive regulation of protein modification by small protein conjugation or removal	3/292	139/23328	0.25268086	0.13725719	3
BP	GO:0005977	glycogen metabolic process	2/292	78/23328	0.25545423	0.13855975	2
BP	GO:0006073	cellular glucan metabolic process	2/292	78/23328	0.25545423	0.13855975	2
BP	GO:0044042	glucan metabolic process	2/292	78/23328	0.25545423	0.13855975	2
BP	GO:0046718	viral entry into host cell	2/292	78/23328	0.25545423	0.13855975	2
BP	GO:1901983	regulation of protein acetylation	2/292	78/23328	0.25545423	0.13855975	2
BP	GO:0016236	macroautophagy	4/292	205/23328	0.25559656	0.13859621	4
BP	GO:0006638	neutral lipid metabolic process	3/292	140/23328	0.25603807	0.13867262	3
BP	GO:0050905	neuromuscular process	3/292	140/23328	0.25603807	0.13867262	3
BP	GO:0071453	cellular response to oxygen levels	3/292	140/23328	0.25603807	0.13867262	3
BP	GO:1904375	regulation of protein localization to cell periphery	3/292	140/23328	0.25603807	0.13867262	3
BP	GO:0010038	response to metal ion	5/292	274/23328	0.2600251	0.14020725	5
BP	GO:0045471	response to ethanol	2/292	79/23328	0.2600095	0.14020725	2

BP	GO:0002903	negative regulation of B cell apoptotic process	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0006582	melanin metabolic process	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0021544	subpallium development	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0022403	cell cycle phase	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0030859	polarized epithelial cell differentiation	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0030903	notochord development	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0031670	cellular response to nutrient	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0032691	negative regulation of interleukin-1 beta production	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0035455	response to interferon-alpha	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0042474	middle ear morphogenesis	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0043586	tongue development	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0044331	cell-cell adhesion mediated by cadherin	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0044550	secondary metabolite biosynthetic process	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	1/292	24/23328	0.26100016	0.14020725	1

BP	GO:0046823	negative regulation of nucleocytoplasmic transport	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0051882	mitochondrial depolarization	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0061339	establishment or maintenance of monopolar cell polarity	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0070841	inclusion body assembly	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0071392	cellular response to estradiol stimulus	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0072525	pyridine-containing compound biosynthetic process	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0090330	regulation of platelet aggregation	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0097150	neuronal stem cell population maintenance	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0098869	cellular oxidant detoxification	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:1900409	positive regulation of cellular response to oxidative stress	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:1902656	calcium ion import into cytosol	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:1903077	negative regulation of protein localization to plasma membrane	1/292	24/23328	0.26100016	0.14020725	1
BP	GO:0001101	response to acid chemical	4/292	207/23328	0.26107502	0.14020725	4
BP	GO:0010821	regulation of mitochondrion organization	3/292	142/23328	0.26277077	0.14099483	3

BP	GO:0016052	carbohydrate catabolic process	3/292	142/23328	0.26277077	0.14099483	3
BP	GO:1902850	microtubule cytoskeleton organization involved in mitosis	3/292	142/23328	0.26277077	0.14099483	3
BP	GO:0010923	negative regulation of phosphatase activity	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:0030641	regulation of cellular pH	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:0032465	regulation of cytokinesis	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:0048041	focal adhesion assembly	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:0051965	positive regulation of synapse assembly	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:1900542	regulation of purine nucleotide metabolic process	2/292	80/23328	0.26473664	0.14180052	2
BP	GO:0019693	ribose phosphate metabolic process	6/292	345/23328	0.26481025	0.14180052	6
BP	GO:0008037	cell recognition	5/292	277/23328	0.26713178	0.14300216	5
BP	GO:0006140	regulation of nucleotide metabolic process	2/292	81/23328	0.2693784	0.14375917	2
BP	GO:0051881	regulation of mitochondrial membrane potential	2/292	81/23328	0.2693784	0.14375917	2
BP	GO:0007274	neuromuscular synaptic transmission	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0007413	axonal fasciculation	1/292	25/23328	0.27025986	0.14375917	1

BP	GO:0010640	regulation of platelet-derived growth factor receptor signaling pathway	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0010884	positive regulation of lipid storage	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0019068	virion assembly	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0032480	negative regulation of type I interferon production	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0032515	negative regulation of phosphoprotein phosphatase activity	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0032897	negative regulation of viral transcription	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0036342	post-anal tail morphogenesis	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0042430	indole-containing compound metabolic process	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0046496	nicotinamide nucleotide metabolic process	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0048642	negative regulation of skeletal muscle tissue development	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0051123	RNA polymerase II preinitiation complex assembly	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0051894	positive regulation of focal adhesion assembly	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0060004	reflex	1/292	25/23328	0.27025986	0.14375917	1
BP	GO:0070633	transepithelial transport	1/292	25/23328	0.27025986	0.14375917	1

BP	GO:0071108	protein K48-linked deubiquitination	1/292		25/23328	0.27025986	0.14375917	1
BP	GO:0071880	adenylate cyclase-activating adrenergic receptor signaling pathway	1/292		25/23328	0.27025986	0.14375917	1
BP	GO:0098743	cell aggregation	1/292		25/23328	0.27025986	0.14375917	1
BP	GO:0106030	neuron projection fasciculation	1/292		25/23328	0.27025986	0.14375917	1
BP	GO:0044409	entry into host	2/292		82/23328	0.27401955	0.14567507	2
BP	GO:1901019	regulation of calcium ion transmembrane transporter activity	2/292		82/23328	0.27401955	0.14567507	2
BP	GO:0001738	morphogenesis of a polarized epithelium	2/292		83/23328	0.27865939	0.14764426	2
BP	GO:0003333	amino acid transmembrane transport	2/292		83/23328	0.27865939	0.14764426	2
BP	GO:0044106	cellular amine metabolic process	2/292		83/23328	0.27865939	0.14764426	2
BP	GO:0051899	membrane depolarization	2/292		83/23328	0.27865939	0.14764426	2
BP	GO:0000002	mitochondrial genome maintenance	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0000303	response to superoxide	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0000737	DNA catabolic process, endonucleolytic	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0032104	regulation of response to extracellular stimulus	1/292		26/23328	0.27940392	0.14764426	1

BP	GO:0032107	regulation of response to nutrient levels	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0033622	integrin activation	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0046365	monosaccharide catabolic process	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0055094	response to lipoprotein particle	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0070193	synaptonemal complex organization	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0090344	negative regulation of cell aging	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0098901	regulation of cardiac muscle cell action potential	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0140058	neuron projection arborization	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:1904030	negative regulation of cyclin-dependent protein kinase activity	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:1904376	negative regulation of protein localization to cell periphery	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:2000050	regulation of non-canonical Wnt signaling pathway	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:2000311	regulation of AMPA receptor activity	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:2000679	positive regulation of transcription regulatory region DNA binding	1/292		26/23328	0.27940392	0.14764426	1
BP	GO:0034655	nucleobase-containing compound catabolic process	6/292		352/23328	0.27968225	0.14774903	6

BP	GO:0070830	bicellular tight junction assembly	2/292	84/23328	0.28329722	0.14961589	2
BP	GO:0006163	purine nucleotide metabolic process	6/292	354/23328	0.28396689	0.14992665	6
BP	GO:0006417	regulation of translation	6/292	355/23328	0.28611472	0.15101743	6
BP	GO:0009117	nucleotide metabolic process	7/292	427/23328	0.28816458	0.15124645	7
BP	GO:0000305	response to oxygen radical	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0015874	norepinephrine transport	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0030194	positive regulation of blood coagulation	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0031342	negative regulation of cell killing	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0032528	microvillus organization	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0033688	regulation of osteoblast proliferation	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0042044	fluid transport	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0045780	positive regulation of bone resorption	1/292	27/23328	0.2884338	0.15124645	1

BP	GO:0046852	positive regulation of bone remodeling	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0046885	regulation of hormone biosynthetic process	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0048745	smooth muscle tissue development	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0048799	animal organ maturation	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0060008	Sertoli cell differentiation	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0060716	labyrinthine layer blood vessel development	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0061298	retina vasculature development in camera-type eye	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0071361	cellular response to ethanol	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:1900048	positive regulation of hemostasis	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:1902884	positive regulation of response to oxidative stress	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:1903010	regulation of bone development	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:1905809	negative regulation of synapse organization	1/292	27/23328	0.2884338	0.15124645	1
BP	GO:0006970	response to osmotic stress	2/292	86/23328	0.29256417	0.15332516	2
BP	GO:0097581	lamellipodium organization	2/292	86/23328	0.29256417	0.15332516	2

BP	GO:0016055	Wnt signaling pathway	7/292	430/23328	0.29405819	0.15406438	7
BP	GO:0035304	regulation of protein dephosphorylation	2/292	87/23328	0.297192	0.15482242	2
BP	GO:0006837	serotonin transport	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0008340	determination of adult lifespan	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0010155	regulation of proton transport	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0010458	exit from mitosis	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0019362	pyridine nucleotide metabolic process	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0019835	cytolysis	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0030224	monocyte differentiation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0032801	receptor catabolic process	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0033233	regulation of protein sumoylation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0042744	hydrogen peroxide catabolic process	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0045663	positive regulation of myoblast differentiation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0045992	negative regulation of embryonic development	1/292	28/23328	0.29735089	0.15482242	1

BP	GO:0060037	pharyngeal system development	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0060384	innervation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0061436	establishment of skin barrier	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0071168	protein localization to chromatin	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0071402	cellular response to lipoprotein particle stimulus	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0071875	adrenergic receptor signaling pathway	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:1901532	regulation of hematopoietic progenitor cell differentiation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:1903131	mononuclear cell differentiation	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:1903861	positive regulation of dendrite extension	1/292	28/23328	0.29735089	0.15482242	1
BP	GO:0198738	cell-cell signaling by wnt	7/292	432/23328	0.2980024	0.15511787	7
BP	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	2/292	88/23328	0.30181522	0.1569697	2
BP	GO:0035914	skeletal muscle cell differentiation	2/292	88/23328	0.30181522	0.1569697	2
BP	GO:1903312	negative regulation of mRNA metabolic process	2/292	88/23328	0.30181522	0.1569697	2
BP	GO:2001020	regulation of response to DNA damage stimulus	4/292	222/23328	0.30278547	0.15742995	4

BP	GO:1990778	protein localization to cell periphery	6/292	363/23328	0.30341871	0.15771475	6
BP	GO:0007163	establishment or maintenance of cell polarity	4/292	223/23328	0.30559661	0.15820206	4
BP	GO:0006753	nucleoside phosphate metabolic process	7/292	436/23328	0.30592495	0.15820206	7
BP	GO:0007214	gamma-aminobutyric acid signaling pathway	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0010586	miRNA metabolic process	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0030262	apoptotic nuclear changes	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0031063	regulation of histone deacetylation	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0033141	positive regulation of peptidyl-serine phosphorylation of STAT protein	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0033198	response to ATP	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0033273	response to vitamin	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0045187	regulation of circadian sleep/wake cycle, sleep	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0045761	regulation of adenylate cyclase activity	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0048643	positive regulation of skeletal muscle tissue development	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0061050	regulation of cell growth involved in cardiac muscle cell development	1/292	29/23328	0.30615663	0.15820206	1

BP	GO:0070296	sarcoplasmic reticulum calcium ion transport	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0070897	transcription preinitiation complex assembly	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0090208	positive regulation of triglyceride metabolic process	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0090312	positive regulation of protein deacetylation	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0090314	positive regulation of protein targeting to membrane	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0150117	positive regulation of cell-substrate junction organization	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:1900027	regulation of ruffle assembly	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:2000272	negative regulation of signaling receptor activity	1/292	29/23328	0.30615663	0.15820206	1
BP	GO:0042770	signal transduction in response to DNA damage	2/292	89/23328	0.30643322	0.15830065	2
BP	GO:0007044	cell-substrate junction assembly	2/292	90/23328	0.31104543	0.16054844	2
BP	GO:0009063	cellular amino acid catabolic process	2/292	90/23328	0.31104543	0.16054844	2
BP	GO:0043242	negative regulation of protein-containing complex disassembly	2/292	90/23328	0.31104543	0.16054844	2
BP	GO:0005979	regulation of glycogen biosynthetic process	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0006921	cellular component disassembly involved in execution phase of apoptosis	1/292	30/23328	0.31485238	0.16201492	1

BP	GO:0010922	positive regulation of phosphatase activity	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0010955	negative regulation of protein processing	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0010962	regulation of glucan biosynthetic process	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0035162	embryonic hemopoiesis	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0050802	circadian sleep/wake cycle, sleep	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0050820	positive regulation of coagulation	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:1902751	positive regulation of cell cycle G2/M phase transition	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:1903318	negative regulation of protein maturation	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:1903579	negative regulation of ATP metabolic process	1/292	30/23328	0.31485238	0.16201492	1
BP	GO:0002385	mucosal immune response	2/292	91/23328	0.31565124	0.16238071	2
BP	GO:0071241	cellular response to inorganic substance	4/292	227/23328	0.31686762	0.16296102	4
BP	GO:0009416	response to light stimulus	5/292	298/23328	0.31791068	0.1634519	5
BP	GO:0000045	autophagosome assembly	2/292	92/23328	0.32025012	0.16460884	2
BP	GO:0007569	cell aging	3/292	159/23328	0.32063602	0.1647613	3

BP	GO:0000132	establishment of mitotic spindle orientation	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0001832	blastocyst growth	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0001958	endochondral ossification	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0021533	cell differentiation in hindbrain	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0022011	myelination in peripheral nervous system	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0032292	peripheral nervous system axon ensheathment	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0033687	osteoblast proliferation	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0036075	replacement ossification	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0042168	heme metabolic process	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0044788	modulation by host of viral process	1/292		31/23328	0.32343951	0.16532715	1
BP	GO:0045920	negative regulation of exocytosis	1/292		31/23328	0.32343951	0.16532715	1

BP	GO:0051497	negative regulation of stress fiber assembly	1/292	31/23328	0.32343951	0.16532715	1
BP	GO:0060117	auditory receptor cell development	1/292	31/23328	0.32343951	0.16532715	1
BP	GO:0060795	cell fate commitment involved in formation of primary germ layer	1/292	31/23328	0.32343951	0.16532715	1
BP	GO:0098810	neurotransmitter reuptake	1/292	31/23328	0.32343951	0.16532715	1
BP	GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	1/292	31/23328	0.32343951	0.16532715	1
BP	GO:0035305	negative regulation of dephosphorylation	2/292	93/23328	0.3248415	0.16590591	2
BP	GO:0043297	apical junction assembly	2/292	93/23328	0.3248415	0.16590591	2
BP	GO:0150115	cell-substrate junction organization	2/292	93/23328	0.3248415	0.16590591	2
BP	GO:0070252	actin-mediated cell contraction	2/292	94/23328	0.32942486	0.16820021	2
BP	GO:0001556	oocyte maturation	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0006099	tricarboxylic acid cycle	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0010614	negative regulation of cardiac muscle hypertrophy	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0016242	negative regulation of macroautophagy	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0021697	cerebellar cortex formation	1/292	32/23328	0.33191939	0.16881991	1

BP	GO:0033139	regulation of peptidyl-serine phosphorylation of STAT protein	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0045815	positive regulation of gene expression, epigenetic	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0051491	positive regulation of filopodium assembly	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0055022	negative regulation of cardiac muscle tissue growth	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0061117	negative regulation of heart growth	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0070536	protein K63-linked deubiquitination	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:1901797	negative regulation of signal transduction by p53 class mediator	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:1903859	regulation of dendrite extension	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:1905476	negative regulation of protein localization to membrane	1/292	32/23328	0.33191939	0.16881991	1
BP	GO:0055013	cardiac muscle cell development	2/292	95/23328	0.33399969	0.16983117	2
BP	GO:0002244	hematopoietic progenitor cell differentiation	3/292	163/23328	0.33431964	0.16994703	3
BP	GO:0061053	somite development	2/292	96/23328	0.33856546	0.17205794	2
BP	GO:0001779	natural killer cell differentiation	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0007617	mating behavior	1/292	33/23328	0.34029334	0.17241372	1

BP	GO:0022410	circadian sleep/wake cycle process	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0033081	regulation of T cell differentiation in thymus	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0033561	regulation of water loss via skin	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0045652	regulation of megakaryocyte differentiation	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0045745	positive regulation of G protein-coupled receptor signaling pathway	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0051642	centrosome localization	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0060487	lung epithelial cell differentiation	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0060914	heart formation	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0072524	pyridine-containing compound metabolic process	1/292	33/23328	0.34029334	0.17241372	1
BP	GO:0006575	cellular modified amino acid metabolic process	3/292	165/23328	0.34115825	0.17280449	3
BP	GO:0045930	negative regulation of mitotic cell cycle	4/292	236/23328	0.34233674	0.17335383	4
BP	GO:1905037	autophagosome organization	2/292	97/23328	0.34312171	0.17370366	2
BP	GO:0098739	import across plasma membrane	3/292	166/23328	0.34457584	0.17439196	3
BP	GO:1901657	glycosyl compound metabolic process	2/292	98/23328	0.34766795	0.17583102	2

BP	GO:0001964	startle response	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0006884	cell volume homeostasis	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0014044	Schwann cell development	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0014741	negative regulation of muscle hypertrophy	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0019884	antigen processing and presentation of exogenous antigen	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0019934	cGMP-mediated signaling	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0044275	cellular carbohydrate catabolic process	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0060479	lung cell differentiation	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0061842	microtubule organizing center localization	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0090162	establishment of epithelial cell polarity	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0097352	autophagosome maturation	1/292	34/23328	0.34856268	0.17583102	1
BP	GO:0045185	maintenance of protein location	2/292	99/23328	0.35220371	0.17761917	2
BP	GO:0002082	regulation of oxidative phosphorylation	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0007026	negative regulation of microtubule depolymerization	1/292	35/23328	0.35672872	0.17911792	1

BP	GO:0009187	cyclic nucleotide metabolic process	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0010719	negative regulation of epithelial to mesenchymal transition	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0021846	cell proliferation in forebrain	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0032094	response to food	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0034331	cell junction maintenance	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0035308	negative regulation of protein dephosphorylation	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0040001	establishment of mitotic spindle localization	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0045686	negative regulation of glial cell differentiation	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0045746	negative regulation of Notch signaling pathway	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0060292	long-term synaptic depression	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0071320	cellular response to cAMP	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:0090313	regulation of protein targeting to membrane	1/292	35/23328	0.35672872	0.17911792	1
BP	GO:1900181	negative regulation of protein localization to nucleus	1/292	35/23328	0.35672872	0.17911792	1

BP	GO:0009062	fatty acid catabolic process	2/292	101/23328	0.36124205	0.18118691	2
BP	GO:0031058	positive regulation of histone modification	2/292	101/23328	0.36124205	0.18118691	2
BP	GO:0055006	cardiac cell development	2/292	101/23328	0.36124205	0.18118691	2
BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	2/292	101/23328	0.36124205	0.18118691	2
BP	GO:0007143	female meiotic nuclear division	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0009112	nucleobase metabolic process	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0032232	negative regulation of actin filament bundle assembly	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0033260	nuclear DNA replication	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0034381	plasma lipoprotein particle clearance	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0050779	RNA destabilization	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:0071158	positive regulation of cell cycle arrest	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:2000171	negative regulation of dendrite development	1/292	36/23328	0.36479274	0.18247184	1
BP	GO:2000785	regulation of autophagosome assembly	1/292	36/23328	0.36479274	0.18247184	1

BP	GO:0008654	phospholipid biosynthetic process	3/292	172/23328	0.36504152	0.18249734	3
BP	GO:0060041	retina development in camera-type eye	3/292	172/23328	0.36504152	0.18249734	3
BP	GO:0044264	cellular polysaccharide metabolic process	2/292	103/23328	0.37023326	0.18504274	2
BP	GO:0002931	response to ischemia	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0009072	aromatic amino acid family metabolic process	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0009954	proximal/distal pattern formation	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0030574	collagen catabolic process	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0030866	cortical actin cytoskeleton organization	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0042501	serine phosphorylation of STAT protein	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0045047	protein targeting to ER	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0051294	establishment of spindle orientation	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0070873	regulation of glycogen metabolic process	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0098751	bone cell development	1/292	37/23328	0.37275601	0.18564991	1

BP	GO:1903427	negative regulation of reactive oxygen species biosynthetic process	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:1990748	cellular detoxification	1/292	37/23328	0.37275601	0.18564991	1
BP	GO:0052126	movement in host environment	2/292	104/23328	0.37471018	0.1865225	2
BP	GO:1902106	negative regulation of leukocyte differentiation	2/292	104/23328	0.37471018	0.1865225	2
BP	GO:0019432	triglyceride biosynthetic process	1/292	38/23328	0.38061979	0.18920896	1
BP	GO:0031114	regulation of microtubule depolymerization	1/292	38/23328	0.38061979	0.18920896	1
BP	GO:0033238	regulation of cellular amine metabolic process	1/292	38/23328	0.38061979	0.18920896	1
BP	GO:0043267	negative regulation of potassium ion transport	1/292	38/23328	0.38061979	0.18920896	1
BP	GO:0071391	cellular response to estrogen stimulus	1/292	38/23328	0.38061979	0.18920896	1
BP	GO:0016042	lipid catabolic process	5/292	324/23328	0.38213767	0.18991235	5
BP	GO:0043473	pigmentation	2/292	106/23328	0.3836247	0.19060003	2
BP	GO:0006778	porphyrin-containing compound metabolic process	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:0009651	response to salt stress	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:0031279	regulation of cyclase activity	1/292	39/23328	0.38838531	0.19260229	1

BP	GO:0042398	cellular modified amino acid biosynthetic process	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:0046320	regulation of fatty acid oxidation	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:1901385	regulation of voltage-gated calcium channel activity	1/292	39/23328	0.38838531	0.19260229	1
BP	GO:0003341	cilium movement	3/292	180/23328	0.39215674	0.19432168	3
BP	GO:1901605	alpha-amino acid metabolic process	3/292	180/23328	0.39215674	0.19432168	3
BP	GO:0006119	oxidative phosphorylation	2/292	108/23328	0.39248434	0.19432168	2
BP	GO:0021987	cerebral cortex development	2/292	108/23328	0.39248434	0.19432168	2
BP	GO:0034754	cellular hormone metabolic process	2/292	108/23328	0.39248434	0.19432168	2
BP	GO:0048704	embryonic skeletal system morphogenesis	2/292	108/23328	0.39248434	0.19432168	2
BP	GO:1903362	regulation of cellular protein catabolic process	4/292	254/23328	0.39333471	0.19469046	4
BP	GO:0000578	embryonic axis specification	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0001835	blastocyst hatching	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0003009	skeletal muscle contraction	1/292	40/23328	0.3960538	0.19545961	1

BP	GO:0006984	ER-nucleus signaling pathway	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0031076	embryonic camera-type eye development	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0035188	hatching	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0035307	positive regulation of protein dephosphorylation	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0048520	positive regulation of behavior	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0071684	organism emergence from protective structure	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:0090175	regulation of establishment of planar polarity	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:1901021	positive regulation of calcium ion transmembrane transporter activity	1/292	40/23328	0.3960538	0.19545961	1
BP	GO:1900006	positive regulation of dendrite development	2/292	109/23328	0.39689271	0.19576891	2
BP	GO:1901800	positive regulation of proteasomal protein catabolic process	2/292	109/23328	0.39689271	0.19576891	2
BP	GO:2001022	positive regulation of response to DNA damage stimulus	2/292	110/23328	0.40128632	0.19788318	2
BP	GO:0000082	G1/S transition of mitotic cell cycle	3/292	183/23328	0.40225345	0.1983071	3
BP	GO:0044786	cell cycle DNA replication	1/292	41/23328	0.40362647	0.19871853	1
BP	GO:0046164	alcohol catabolic process	1/292	41/23328	0.40362647	0.19871853	1

BP	GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	1/292	41/23328	0.40362647	0.19871853	1
BP	GO:0072595	maintenance of protein localization in organelle	1/292	41/23328	0.40362647	0.19871853	1
BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	1/292	41/23328	0.40362647	0.19871853	1
BP	GO:0051225	spindle assembly	2/292	112/23328	0.41002801	0.20181637	2
BP	GO:0051339	regulation of lyase activity	1/292	42/23328	0.41110451	0.20218444	1
BP	GO:2000279	negative regulation of DNA biosynthetic process	1/292	42/23328	0.41110451	0.20218444	1
BP	GO:2000772	regulation of cellular senescence	1/292	42/23328	0.41110451	0.20218444	1
BP	GO:0014003	oligodendrocyte development	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:0032008	positive regulation of TOR signaling	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:0045880	positive regulation of smoothened signaling pathway	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:0046782	regulation of viral transcription	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:0055026	negative regulation of cardiac muscle tissue development	1/292	43/23328	0.41848909	0.20543296	1
BP	GO:2001258	negative regulation of cation channel activity	1/292	43/23328	0.41848909	0.20543296	1

BP	GO:0010927	cellular component assembly involved in morphogenesis	2/292	114/23328	0.41870698	0.20548525	2
BP	GO:0007269	neurotransmitter secretion	3/292	189/23328	0.42229888	0.20713784	3
BP	GO:0099643	signal release from synapse	3/292	189/23328	0.42229888	0.20713784	3
BP	GO:0014904	myotube cell development	1/292	44/23328	0.42578139	0.20856881	1
BP	GO:0043403	skeletal muscle tissue regeneration	1/292	44/23328	0.42578139	0.20856881	1
BP	GO:0046621	negative regulation of organ growth	1/292	44/23328	0.42578139	0.20856881	1
BP	GO:1901998	toxin transport	1/292	44/23328	0.42578139	0.20856881	1
BP	GO:2000144	positive regulation of DNA-templated transcription, initiation	1/292	44/23328	0.42578139	0.20856881	1
BP	GO:0007052	mitotic spindle organization	2/292	116/23328	0.42732092	0.20926739	2
BP	GO:0010639	negative regulation of organelle organization	6/292	420/23328	0.42974141	0.21039692	6
BP	GO:0006612	protein targeting to membrane	2/292	117/23328	0.43160283	0.21119618	2
BP	GO:1905269	positive regulation of chromatin organization	2/292	117/23328	0.43160283	0.21119618	2
BP	GO:0021696	cerebellar cortex morphogenesis	1/292	45/23328	0.43298255	0.21159077	1
BP	GO:0042149	cellular response to glucose starvation	1/292	45/23328	0.43298255	0.21159077	1

BP	GO:0044088	regulation of vacuole organization	1/292	45/23328	0.43298255	0.21159077	1
BP	GO:0051293	establishment of spindle localization	1/292	45/23328	0.43298255	0.21159077	1
BP	GO:0097178	ruffle assembly	1/292	45/23328	0.43298255	0.21159077	1
BP	GO:0006576	cellular biogenic amine metabolic process	1/292	46/23328	0.44009371	0.21478146	1
BP	GO:0010259	multicellular organism aging	1/292	46/23328	0.44009371	0.21478146	1
BP	GO:0019083	viral transcription	1/292	46/23328	0.44009371	0.21478146	1
BP	GO:0019228	neuronal action potential	1/292	46/23328	0.44009371	0.21478146	1
BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	1/292	46/23328	0.44009371	0.21478146	1
BP	GO:0090407	organophosphate biosynthetic process	6/292	427/23328	0.44522282	0.2172272	6
BP	GO:0009101	glycoprotein biosynthetic process	4/292	273/23328	0.44648989	0.21763299	4
BP	GO:0001941	postsynaptic membrane organization	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0030520	intracellular estrogen receptor signaling pathway	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0033013	tetrapyrrole metabolic process	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0045332	phospholipid translocation	1/292	47/23328	0.44711599	0.21763299	1

BP	GO:0045581	negative regulation of T cell differentiation	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0046460	neutral lipid biosynthetic process	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0046463	acylglycerol biosynthetic process	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0072666	establishment of protein localization to vacuole	1/292	47/23328	0.44711599	0.21763299	1
BP	GO:0072329	monocarboxylic acid catabolic process	2/292	121/23328	0.44855761	0.21826992	2
BP	GO:0050773	regulation of dendrite development	3/292	197/23328	0.44866111	0.21826992	3
BP	GO:0003382	epithelial cell morphogenesis	1/292	48/23328	0.45405049	0.22060101	1
BP	GO:0007339	binding of sperm to zona pellucida	1/292	48/23328	0.45405049	0.22060101	1
BP	GO:0031111	negative regulation of microtubule polymerization or depolymerization	1/292	48/23328	0.45405049	0.22060101	1
BP	GO:0070527	platelet aggregation	1/292	48/23328	0.45405049	0.22060101	1
BP	GO:0090329	regulation of DNA-dependent DNA replication	1/292	48/23328	0.45405049	0.22060101	1
BP	GO:0071805	potassium ion transmembrane transport	3/292	200/23328	0.45842371	0.22266712	3
BP	GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	1/292	49/23328	0.46089831	0.223607	1
BP	GO:0014888	striated muscle adaptation	1/292	49/23328	0.46089831	0.223607	1

BP	GO:0034204	lipid translocation	1/292		49/23328	0.46089831	0.223607	1
BP	GO:1902808	positive regulation of cell cycle G1/S phase transition	1/292		49/23328	0.46089831	0.223607	1
BP	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	2/292		124/23328	0.4610858	0.223607	2
BP	GO:1905039	carboxylic acid transmembrane transport	2/292		124/23328	0.4610858	0.223607	2
BP	GO:0044843	cell cycle G1/S phase transition	3/292		201/23328	0.46166175	0.22376869	3
BP	GO:0070507	regulation of microtubule cytoskeleton organization	3/292		201/23328	0.46166175	0.22376869	3
BP	GO:0016458	gene silencing	4/292		279/23328	0.46299778	0.22435734	4
BP	GO:1903825	organic acid transmembrane transport	2/292		125/23328	0.46522497	0.22537739	2
BP	GO:0002762	negative regulation of myeloid leukocyte differentiation	1/292		50/23328	0.46766053	0.22620098	1
BP	GO:0007140	male meiotic nuclear division	1/292		50/23328	0.46766053	0.22620098	1
BP	GO:0043392	negative regulation of DNA binding	1/292		50/23328	0.46766053	0.22620098	1
BP	GO:0046128	purine ribonucleoside metabolic process	1/292		50/23328	0.46766053	0.22620098	1
BP	GO:0051653	spindle localization	1/292		50/23328	0.46766053	0.22620098	1
BP	GO:1903573	negative regulation of response to endoplasmic reticulum stress	1/292		50/23328	0.46766053	0.22620098	1

BP	GO:0030048	actin filament-based movement	2/292	126/23328	0.46934536	0.22695642	2
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0031648	protein destabilization	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0035088	establishment or maintenance of apical/basal cell polarity	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0046470	phosphatidylcholine metabolic process	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0051489	regulation of filopodium assembly	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0061245	establishment or maintenance of bipolar cell polarity	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0071470	cellular response to osmotic stress	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0072527	pyrimidine-containing compound metabolic process	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0090311	regulation of protein deacetylation	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0098754	detoxification	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:2000142	regulation of DNA-templated transcription, initiation	1/292	51/23328	0.47433821	0.22865173	1
BP	GO:0030857	negative regulation of epithelial cell differentiation	1/292	52/23328	0.48093242	0.23170936	1

BP	GO:0065002	intracellular protein transmembrane transport	1/292	52/23328	0.48093242	0.23170936	1
BP	GO:0008203	cholesterol metabolic process	2/292	130/23328	0.48563575	0.23385328	2
BP	GO:0090305	nucleic acid phosphodiester bond hydrolysis	2/292	130/23328	0.48563575	0.23385328	2
BP	GO:0001662	behavioral fear response	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0030514	negative regulation of BMP signaling pathway	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0034605	cellular response to heat	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0043666	regulation of phosphoprotein phosphatase activity	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0045839	negative regulation of mitotic nuclear division	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0046148	pigment biosynthetic process	1/292	53/23328	0.48744418	0.23435716	1
BP	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	2/292	131/23328	0.48965975	0.23536106	2
BP	GO:0099175	regulation of postsynapse organization	2/292	132/23328	0.49366401	0.23689328	2
BP	GO:0002209	behavioral defense response	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:0007019	microtubule depolymerization	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:0010823	negative regulation of mitochondrion organization	1/292	54/23328	0.49387452	0.23689328	1

BP	GO:0014014	negative regulation of gliogenesis	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:0042278	purine nucleoside metabolic process	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:0071806	protein transmembrane transport	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:1900271	regulation of long-term synaptic potentiation	1/292	54/23328	0.49387452	0.23689328	1
BP	GO:0006754	ATP biosynthetic process	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0009948	anterior/posterior axis specification	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0031529	ruffle organization	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0035036	sperm-egg recognition	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0046580	negative regulation of Ras protein signal transduction	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0050891	multicellular organismal water homeostasis	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0086001	cardiac muscle cell action potential	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0097035	regulation of membrane lipid distribution	1/292	55/23328	0.50022447	0.23944119	1
BP	GO:0009119	ribonucleoside metabolic process	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0015872	dopamine transport	1/292	56/23328	0.50649502	0.24194061	1

BP	GO:0030199	collagen fibril organization	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0030219	megakaryocyte differentiation	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0042446	hormone biosynthetic process	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0045620	negative regulation of lymphocyte differentiation	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0048538	thymus development	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:1903533	regulation of protein targeting	1/292	56/23328	0.50649502	0.24194061	1
BP	GO:0044772	mitotic cell cycle phase transition	5/292	376/23328	0.50845366	0.24281336	5
BP	GO:0006402	mRNA catabolic process	3/292	217/23328	0.51224872	0.24445548	3
BP	GO:0019748	secondary metabolic process	1/292	57/23328	0.51268715	0.24445548	1
BP	GO:0035567	non-canonical Wnt signaling pathway	1/292	57/23328	0.51268715	0.24445548	1
BP	GO:0042775	mitochondrial ATP synthesis coupled electron transport	1/292	57/23328	0.51268715	0.24445548	1
BP	GO:0050879	multicellular organismal movement	1/292	57/23328	0.51268715	0.24445548	1
BP	GO:0050881	musculoskeletal movement	1/292	57/23328	0.51268715	0.24445548	1
BP	GO:0001736	establishment of planar polarity	1/292	58/23328	0.51880186	0.24698812	1

BP	GO:0006493	protein O-linked glycosylation	1/292	58/23328	0.51880186	0.24698812	1
BP	GO:0010656	negative regulation of muscle cell apoptotic process	1/292	58/23328	0.51880186	0.24698812	1
BP	GO:0035019	somatic stem cell population maintenance	1/292	58/23328	0.51880186	0.24698812	1
BP	GO:0042596	fear response	1/292	58/23328	0.51880186	0.24698812	1
BP	GO:0099172	presynapse organization	1/292	58/23328	0.51880186	0.24698812	1
BP	GO:0016125	sterol metabolic process	2/292	139/23328	0.52113034	0.24803266	2
BP	GO:0051656	establishment of organelle localization	5/292	382/23328	0.52244401	0.24859378	5
BP	GO:1901616	organic hydroxy compound catabolic process	1/292	60/23328	0.53080283	0.25250603	1
BP	GO:0016358	dendrite development	4/292	306/23328	0.5348518	0.25436658	4
BP	GO:0035725	sodium ion transmembrane transport	2/292	143/23328	0.53637315	0.2549784	2
BP	GO:0006446	regulation of translational initiation	1/292	61/23328	0.53669098	0.2549784	1
BP	GO:0042773	ATP synthesis coupled electron transport	1/292	61/23328	0.53669098	0.2549784	1
BP	GO:1902017	regulation of cilium assembly	1/292	61/23328	0.53669098	0.2549784	1
BP	GO:0043624	cellular protein complex disassembly	2/292	144/23328	0.54013156	0.25654694	2

BP	GO:0006081	cellular aldehyde metabolic process	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0015695	organic cation transport	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0019080	viral gene expression	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0030865	cortical cytoskeleton organization	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0032835	glomerulus development	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0043966	histone H3 acetylation	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0046513	ceramide biosynthetic process	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0051058	negative regulation of small GTPase mediated signal transduction	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0061337	cardiac conduction	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0072665	protein localization to vacuole	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:1903078	positive regulation of protein localization to plasma membrane	1/292	62/23328	0.54250549	0.25690868	1
BP	GO:0007286	spermatid development	3/292	227/23328	0.54256386	0.25690868	3
BP	GO:0016573	histone acetylation	2/292	146/23328	0.54758516	0.25921978	2
BP	GO:0070936	protein K48-linked ubiquitination	1/292	63/23328	0.54824728	0.25940013	1

BP	GO:0071260	cellular response to mechanical stimulus	1/292	63/23328	0.54824728	0.25940013	1
BP	GO:0009064	glutamine family amino acid metabolic process	1/292	64/23328	0.55391725	0.26201566	1
BP	GO:0009952	anterior/posterior pattern specification	3/292	231/23328	0.55438286	0.2621687	3
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	1/292	65/23328	0.55951629	0.26439303	1
BP	GO:0045454	cell redox homeostasis	1/292	65/23328	0.55951629	0.26439303	1
BP	GO:0090398	cellular senescence	1/292	65/23328	0.55951629	0.26439303	1
BP	GO:0001824	blastocyst development	2/292	150/23328	0.56223778	0.26561102	2
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	1/292	66/23328	0.5650453	0.26673248	1
BP	GO:0070972	protein localization to endoplasmic reticulum	1/292	66/23328	0.5650453	0.26673248	1
BP	GO:0097006	regulation of plasma lipoprotein particle levels	1/292	66/23328	0.5650453	0.26673248	1
BP	GO:0048515	spermatid differentiation	3/292	236/23328	0.56889918	0.26848304	3
BP	GO:0006475	internal protein amino acid acetylation	2/292	152/23328	0.56943606	0.26859902	2
BP	GO:0018393	internal peptidyl-lysine acetylation	2/292	152/23328	0.56943606	0.26859902	2
BP	GO:0046847	filopodium assembly	1/292	67/23328	0.57050514	0.26896579	1

BP	GO:0070613	regulation of protein processing	1/292	67/23328	0.57050514	0.26896579	1
BP	GO:0000209	protein polyubiquitination	3/292	237/23328	0.57176747	0.26949207	3
BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:0030968	endoplasmic reticulum unfolded protein response	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:0032413	negative regulation of ion transmembrane transporter activity	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:0032507	maintenance of protein location in cell	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	1/292	68/23328	0.57589667	0.27102293	1
BP	GO:0045600	positive regulation of fat cell differentiation	1/292	69/23328	0.58122075	0.27338905	1
BP	GO:1904377	positive regulation of protein localization to cell periphery	1/292	69/23328	0.58122075	0.27338905	1
BP	GO:0009267	cellular response to starvation	2/292	156/23328	0.58357521	0.27442657	2
BP	GO:0006367	transcription initiation from RNA polymerase II promoter	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:0019369	arachidonic acid metabolic process	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	1/292	70/23328	0.58647823	0.2753006	1

BP	GO:0048488	synaptic vesicle endocytosis	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:0050885	neuromuscular process controlling balance	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:0140238	presynaptic endocytosis	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:1903317	regulation of protein maturation	1/292	70/23328	0.58647823	0.2753006	1
BP	GO:0006260	DNA replication	3/292	244/23328	0.59151239	0.27745532	3
BP	GO:0042733	embryonic digit morphogenesis	1/292	71/23328	0.59166992	0.27745532	1
BP	GO:0043113	receptor clustering	1/292	71/23328	0.59166992	0.27745532	1
BP	GO:1901796	regulation of signal transduction by p53 class mediator	1/292	71/23328	0.59166992	0.27745532	1
BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	2/292	159/23328	0.5939537	0.27845551	2
BP	GO:0044770	cell cycle phase transition	5/292	415/23328	0.59603131	0.27935855	5
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	1/292	72/23328	0.59679665	0.27964623	1
BP	GO:0000910	cytokinesis	2/292	160/23328	0.59737012	0.27984389	2
BP	GO:0030178	negative regulation of Wnt signaling pathway	2/292	161/23328	0.60076498	0.28136281	2
BP	GO:0045739	positive regulation of DNA repair	1/292	73/23328	0.60185923	0.28180377	1

BP	GO:0034976	response to endoplasmic reticulum stress	3/292	249/23328	0.60525282	0.28332083	3
BP	GO:0018394	peptidyl-lysine acetylation	2/292	163/23328	0.60749009	0.28415186	2
BP	GO:0031056	regulation of histone modification	2/292	163/23328	0.60749009	0.28415186	2
BP	GO:1902904	negative regulation of supramolecular fiber organization	2/292	163/23328	0.60749009	0.28415186	2
BP	GO:0006520	cellular amino acid metabolic process	3/292	250/23328	0.60796407	0.28430149	3
BP	GO:0043279	response to alkaloid	1/292	75/23328	0.61179513	0.28602053	1
BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	1/292	76/23328	0.61667002	0.28815358	1
BP	GO:0051865	protein autoubiquitination	1/292	76/23328	0.61667002	0.28815358	1
BP	GO:0003407	neural retina development	1/292	77/23328	0.6214839	0.29018253	1
BP	GO:0016575	histone deacetylation	1/292	77/23328	0.6214839	0.29018253	1
BP	GO:0030433	ubiquitin-dependent ERAD pathway	1/292	77/23328	0.6214839	0.29018253	1
BP	GO:0009142	nucleoside triphosphate biosynthetic process	1/292	78/23328	0.62623753	0.29225419	1
BP	GO:0046785	microtubule polymerization	1/292	78/23328	0.62623753	0.29225419	1
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	1/292	79/23328	0.63093167	0.29437041	1

BP	GO:0051494	negative regulation of cytoskeleton organization	2/292	171/23328	0.63353068	0.2955083	2
BP	GO:0036465	synaptic vesicle recycling	1/292	80/23328	0.63556705	0.29623351	1
BP	GO:1901880	negative regulation of protein depolymerization	1/292	80/23328	0.63556705	0.29623351	1
BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	1/292	80/23328	0.63556705	0.29623351	1
BP	GO:0071230	cellular response to amino acid stimulus	2/292	173/23328	0.63982676	0.29814106	2
BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	1/292	81/23328	0.64014441	0.29814106	1
BP	GO:0022904	respiratory electron transport chain	1/292	81/23328	0.64014441	0.29814106	1
BP	GO:0007033	vacuole organization	2/292	174/23328	0.64294285	0.29936885	2
BP	GO:0015914	phospholipid transport	1/292	82/23328	0.64466447	0.30009475	1
BP	GO:1901990	regulation of mitotic cell cycle phase transition	3/292	265/23328	0.64713469	0.30116868	3
BP	GO:0006637	acyl-CoA metabolic process	1/292	83/23328	0.64912794	0.30179186	1
BP	GO:0009199	ribonucleoside triphosphate metabolic process	1/292	83/23328	0.64912794	0.30179186	1
BP	GO:0035383	thioester metabolic process	1/292	83/23328	0.64912794	0.30179186	1
BP	GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	1/292	83/23328	0.64912794	0.30179186	1

BP	GO:1903311	regulation of mRNA metabolic process	3/292	266/23328	0.64964526	0.30195629	3
BP	GO:0022900	electron transport chain	1/292	84/23328	0.65353554	0.30345875	1
BP	GO:0030148	sphingolipid biosynthetic process	1/292	84/23328	0.65353554	0.30345875	1
BP	GO:0046530	photoreceptor cell differentiation	1/292	84/23328	0.65353554	0.30345875	1
BP	GO:0061515	myeloid cell development	1/292	84/23328	0.65353554	0.30345875	1
BP	GO:0042594	response to starvation	2/292	178/23328	0.65519525	0.30415287	2
BP	GO:0007051	spindle organization	2/292	179/23328	0.65820557	0.30547346	2
BP	GO:1905897	regulation of response to endoplasmic reticulum stress	1/292	86/23328	0.66218589	0.30724346	1
BP	GO:0002455	humoral immune response mediated by circulating immunoglobulin	2/292	181/23328	0.66416324	0.30808345	2
BP	GO:0007605	sensory perception of sound	3/292	274/23328	0.66927286	0.31037561	3
BP	GO:0009144	purine nucleoside triphosphate metabolic process	1/292	88/23328	0.67062098	0.31074694	1
BP	GO:0032526	response to retinoic acid	1/292	88/23328	0.67062098	0.31074694	1
BP	GO:0034502	protein localization to chromosome	1/292	88/23328	0.67062098	0.31074694	1
BP	GO:0018205	peptidyl-lysine modification	4/292	364/23328	0.67074718	0.31074694	4

BP	GO:0006672	ceramide metabolic process	1/292	90/23328	0.67884615	0.31426237	1
BP	GO:0009593	detection of chemical stimulus	1/292	90/23328	0.67884615	0.31426237	1
BP	GO:0032024	positive regulation of insulin secretion	1/292	90/23328	0.67884615	0.31426237	1
BP	GO:0043200	response to amino acid	2/292	187/23328	0.68153638	0.31542864	2
BP	GO:0031110	regulation of microtubule polymerization or depolymerization	1/292	91/23328	0.68288165	0.315972	1
BP	GO:0035773	insulin secretion involved in cellular response to glucose stimulus	1/292	92/23328	0.68686661	0.31773619	1
BP	GO:0061136	regulation of proteasomal protein catabolic process	2/292	189/23328	0.68716243	0.31779336	2
BP	GO:0016311	dephosphorylation	4/292	374/23328	0.69120644	0.31958351	4
BP	GO:1901879	regulation of protein depolymerization	1/292	94/23328	0.69468744	0.32111251	1
BP	GO:0006473	protein acetylation	2/292	192/23328	0.69544865	0.3213034	2
BP	GO:2001252	positive regulation of chromosome organization	2/292	192/23328	0.69544865	0.3213034	2
BP	GO:1902600	proton transmembrane transport	1/292	95/23328	0.69852454	0.3226437	1
BP	GO:1902749	regulation of cell cycle G2/M phase transition	1/292	97/23328	0.70605517	0.32604044	1
BP	GO:0006911	phagocytosis, engulfment	2/292	197/23328	0.70885618	0.32725199	2

BP	GO:0140029	exocytic process	1/292	98/23328	0.70974988	0.3275007	1
BP	GO:1903008	organelle disassembly	1/292	98/23328	0.70974988	0.3275007	1
BP	GO:0033865	nucleoside bisphosphate metabolic process	1/292	99/23328	0.71339831	0.32877313	1
BP	GO:0033875	ribonucleoside bisphosphate metabolic process	1/292	99/23328	0.71339831	0.32877313	1
BP	GO:0034032	purine nucleoside bisphosphate metabolic process	1/292	99/23328	0.71339831	0.32877313	1
BP	GO:0036503	ERAD pathway	1/292	99/23328	0.71339831	0.32877313	1
BP	GO:0097061	dendritic spine organization	1/292	99/23328	0.71339831	0.32877313	1
BP	GO:0006476	protein deacetylation	1/292	100/23328	0.71700103	0.33010369	1
BP	GO:0032006	regulation of TOR signaling	1/292	100/23328	0.71700103	0.33010369	1
BP	GO:0098659	inorganic cation import across plasma membrane	1/292	100/23328	0.71700103	0.33010369	1
BP	GO:0099587	inorganic ion import across plasma membrane	1/292	100/23328	0.71700103	0.33010369	1
BP	GO:0009566	fertilization	2/292	201/23328	0.71922518	0.33104508	2
BP	GO:0006352	DNA-templated transcription, initiation	1/292	101/23328	0.72055862	0.33149346	1
BP	GO:0007041	lysosomal transport	1/292	101/23328	0.72055862	0.33149346	1

BP	GO:1901987	regulation of cell cycle phase transition	3/292	297/23328	0.72118763	0.33170014	3
BP	GO:0009165	nucleotide biosynthetic process	2/292	204/23328	0.72679708	0.33419683	2
BP	GO:0006821	chloride transport	1/292	103/23328	0.72754065	0.33428883	1
BP	GO:0015748	organophosphate ester transport	1/292	103/23328	0.72754065	0.33428883	1
BP	GO:2000300	regulation of synaptic vesicle exocytosis	1/292	103/23328	0.72754065	0.33428883	1
BP	GO:0006413	translational initiation	1/292	104/23328	0.73096619	0.33577918	1
BP	GO:0099024	plasma membrane invagination	2/292	206/23328	0.73174874	0.336055	2
BP	GO:0021510	spinal cord development	1/292	106/23328	0.73768903	0.33861453	1
BP	GO:0106027	neuron projection organization	1/292	106/23328	0.73768903	0.33861453	1
BP	GO:1901293	nucleoside phosphate biosynthetic process	2/292	209/23328	0.73903355	0.33914732	2
BP	GO:1902275	regulation of chromatin organization	2/292	210/23328	0.74142413	0.34015978	2
BP	GO:0009141	nucleoside triphosphate metabolic process	1/292	109/23328	0.74746066	0.34275885	1
BP	GO:0051668	localization within membrane	1/292	109/23328	0.74746066	0.34275885	1
BP	GO:0010324	membrane invagination	2/292	213/23328	0.74848408	0.34314288	2

BP	GO:1990830	cellular response to leukemia inhibitory factor	3/292	311/23328	0.74956406	0.34355265	3
BP	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	1/292	110/23328	0.75063657	0.34387339	1
BP	GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	1/292	110/23328	0.75063657	0.34387339	1
BP	GO:1990823	response to leukemia inhibitory factor	3/292	312/23328	0.7514999	0.34418344	3
BP	GO:0001676	long-chain fatty acid metabolic process	1/292	111/23328	0.75377268	0.3449675	1
BP	GO:0035601	protein deacylation	1/292	111/23328	0.75377268	0.3449675	1
BP	GO:0098732	macromolecule deacylation	1/292	111/23328	0.75377268	0.3449675	1
BP	GO:0044242	cellular lipid catabolic process	2/292	219/23328	0.76210927	0.34869629	2
BP	GO:0016579	protein deubiquitination	1/292	115/23328	0.76592891	0.35035706	1
BP	GO:0098656	anion transmembrane transport	2/292	221/23328	0.76650719	0.35044784	2
BP	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	2/292	221/23328	0.76650719	0.35044784	2
BP	GO:2000045	regulation of G1/S transition of mitotic cell cycle	1/292	116/23328	0.76887332	0.35144256	1
BP	GO:0051259	protein complex oligomerization	2/292	223/23328	0.77083448	0.35225173	2
BP	GO:0000086	G2/M transition of mitotic cell cycle	1/292	117/23328	0.77178083	0.35250959	1

BP	GO:0007127	meiosis I	1/292	117/23328	0.77178083	0.35250959	1
BP	GO:0046467	membrane lipid biosynthetic process	1/292	121/23328	0.78305085	0.35756864	1
BP	GO:0031109	microtubule polymerization or depolymerization	1/292	122/23328	0.7857806	0.35854896	1
BP	GO:0031929	TOR signaling	1/292	122/23328	0.7857806	0.35854896	1
BP	GO:0061982	meiosis I cell cycle process	1/292	122/23328	0.7857806	0.35854896	1
BP	GO:0099504	synaptic vesicle cycle	2/292	231/23328	0.78745304	0.35922326	2
BP	GO:0000723	telomere maintenance	1/292	123/23328	0.78847611	0.35951221	1
BP	GO:0051261	protein depolymerization	1/292	123/23328	0.78847611	0.35951221	1
BP	GO:0090150	establishment of protein localization to membrane	2/292	233/23328	0.79143896	0.360774	2
BP	GO:0010212	response to ionizing radiation	1/292	125/23328	0.79376615	0.36156688	1
BP	GO:0032200	telomere organization	1/292	125/23328	0.79376615	0.36156688	1
BP	GO:1902414	protein localization to cell junction	1/292	125/23328	0.79376615	0.36156688	1
BP	GO:0006470	protein dephosphorylation	2/292	235/23328	0.79535899	0.36220302	2
BP	GO:0051053	negative regulation of DNA metabolic process	1/292	126/23328	0.79636152	0.36248065	1

BP	GO:0120254	olefinic compound metabolic process	1/292	126/23328	0.79636152	0.36248065	1
BP	GO:0006611	protein export from nucleus	1/292	127/23328	0.79892433	0.36337827	1
BP	GO:0042157	lipoprotein metabolic process	1/292	127/23328	0.79892433	0.36337827	1
BP	GO:0090090	negative regulation of canonical Wnt signaling pathway	1/292	127/23328	0.79892433	0.36337827	1
BP	GO:0043543	protein acylation	2/292	237/23328	0.79921393	0.36342041	2
BP	GO:0006282	regulation of DNA repair	1/292	128/23328	0.801455	0.36434969	1
BP	GO:0006665	sphingolipid metabolic process	1/292	131/23328	0.80885814	0.36753414	1
BP	GO:0007093	mitotic cell cycle checkpoint	1/292	131/23328	0.80885814	0.36753414	1
BP	GO:0006261	DNA-dependent DNA replication	1/292	132/23328	0.8112642	0.36853667	1
BP	GO:0044839	cell cycle G2/M phase transition	1/292	134/23328	0.81598615	0.37049931	1
BP	GO:1902806	regulation of cell cycle G1/S phase transition	1/292	134/23328	0.81598615	0.37049931	1
BP	GO:0070646	protein modification by small protein removal	1/292	135/23328	0.81830279	0.37145977	1
BP	GO:0060291	long-term synaptic potentiation	2/292	248/23328	0.81928817	0.37181561	2
BP	GO:0007034	vacuolar transport	1/292	140/23328	0.82945717	0.37633803	1

BP	GO:0009152	purine ribonucleotide biosynthetic process	1/292	141/23328	0.83160477	0.37712697	1
BP	GO:0016079	synaptic vesicle exocytosis	1/292	141/23328	0.83160477	0.37712697	1
BP	GO:0034401	chromatin organization involved in regulation of transcription	1/292	143/23328	0.83581944	0.37894516	1
BP	GO:0099003	vesicle-mediated transport in synapse	2/292	260/23328	0.83912503	0.3803504	2
BP	GO:0051168	nuclear export	1/292	146/23328	0.84194515	0.38144129	1
BP	GO:0098693	regulation of synaptic vesicle cycle	1/292	146/23328	0.84194515	0.38144129	1
BP	GO:0010498	proteasomal protein catabolic process	4/292	470/23328	0.84251849	0.38160734	4
BP	GO:0031333	negative regulation of protein-containing complex assembly	1/292	147/23328	0.843936	0.38215559	1
BP	GO:0009260	ribonucleotide biosynthetic process	1/292	150/23328	0.84975986	0.38460402	1
BP	GO:0061025	membrane fusion	1/292	150/23328	0.84975986	0.38460402	1
BP	GO:0048593	camera-type eye morphogenesis	1/292	151/23328	0.85165261	0.38536616	1
BP	GO:0007005	mitochondrion organization	4/292	481/23328	0.85506949	0.38681741	4
BP	GO:0006605	protein targeting	2/292	271/23328	0.85555938	0.38694417	2
BP	GO:0007338	single fertilization	1/292	154/23328	0.85718946	0.38758641	1

BP	GO:0016050	vesicle organization	2/292	275/23328	0.8611466	0.38928028	2
BP	GO:0046390	ribose phosphate biosynthetic process	1/292	157/23328	0.86252033	0.38961493	1
BP	GO:0050657	nucleic acid transport	1/292	157/23328	0.86252033	0.38961493	1
BP	GO:0050658	RNA transport	1/292	157/23328	0.86252033	0.38961493	1
BP	GO:0007018	microtubule-based movement	3/292	385/23328	0.86310116	0.38978188	3
BP	GO:0043484	regulation of RNA splicing	1/292	158/23328	0.86425284	0.39020649	1
BP	GO:0006164	purine nucleotide biosynthetic process	1/292	160/23328	0.86765286	0.39154998	1
BP	GO:0051236	establishment of RNA localization	1/292	160/23328	0.86765286	0.39154998	1
BP	GO:0040029	regulation of gene expression, epigenetic	1/292	163/23328	0.87259441	0.3936837	1
BP	GO:0072522	purine-containing compound biosynthetic process	1/292	165/23328	0.87578619	0.39502713	1
BP	GO:0006338	chromatin remodeling	1/292	167/23328	0.87889827	0.39633397	1
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	3/292	405/23328	0.88477988	0.39873284	3
BP	GO:0065004	protein-DNA complex assembly	1/292	171/23328	0.88489124	0.39873284	1
BP	GO:0071214	cellular response to abiotic stimulus	2/292	294/23328	0.88508228	0.39873284	2

BP	GO:0104004	cellular response to environmental stimulus	2/292	294/23328	0.88508228	0.39873284	2
BP	GO:0051260	protein homooligomerization	1/292	173/23328	0.88777595	0.39984873	1
BP	GO:0006643	membrane lipid metabolic process	1/292	174/23328	0.88919117	0.40038841	1
BP	GO:0010256	endomembrane system organization	3/292	410/23328	0.88969956	0.40051959	3
BP	GO:0000075	cell cycle checkpoint	1/292	180/23328	0.89731667	0.4038501	1
BP	GO:0006403	RNA localization	1/292	182/23328	0.89989098	0.40490994	1
BP	GO:0006956	complement activation	1/292	187/23328	0.90604883	0.40758131	1
BP	GO:0006486	protein glycosylation	1/292	193/23328	0.91294193	0.410382	1
BP	GO:0015931	nucleobase-containing compound transport	1/292	193/23328	0.91294193	0.410382	1
BP	GO:0043413	macromolecule glycosylation	1/292	193/23328	0.91294193	0.410382	1
BP	GO:0034660	ncRNA metabolic process	3/292	444/23328	0.91845455	0.41275946	3
BP	GO:0006364	rRNA processing	1/292	206/23328	0.9261964	0.41613735	1
BP	GO:0070085	glycosylation	1/292	208/23328	0.92804875	0.4168681	1
BP	GO:0071824	protein-DNA complex subunit organization	1/292	214/23328	0.93333238	0.41913941	1

BP	GO:0016072	rRNA metabolic process	1/292	215/23328	0.93417459	0.41941556	1
BP	GO:0034470	ncRNA processing	2/292	355/23328	0.93849926	0.42125471	2
BP	GO:0033044	regulation of chromosome organization	2/292	369/23328	0.94689538	0.42492003	2
BP	GO:0006790	sulfur compound metabolic process	1/292	279/23328	0.97085779	0.43556725	1
BP	GO:0031647	regulation of protein stability	1/292	287/23328	0.97368405	0.43672905	1
BP	GO:0042254	ribosome biogenesis	1/292	296/23328	0.97653831	0.43790284	1
BP	GO:0016570	histone modification	2/292	448/23328	0.97723594	0.4381092	2
BP	GO:0060271	cilium assembly	1/292	310/23328	0.98037722	0.43934394	1
BP	GO:0016569	covalent chromatin modification	2/292	462/23328	0.98046631	0.43934394	2
BP	GO:0006281	DNA repair	2/292	481/23328	0.98414952	0.44088732	2
BP	GO:0044782	cilium organization	1/292	343/23328	0.98712755	0.4421141	1
BP	GO:0008380	RNA splicing	1/292	386/23328	0.99257529	0.44444616	1
BP	GO:0022613	ribonucleoprotein complex biogenesis	1/292	409/23328	0.99447074	0.44518685	1
CC	GO:0043235	receptor complex	32/294	403/23271	1.31E-16	3.02E-14	32

CC	GO:0045121	membrane raft	25/294	379/23271	1.93E-11	1.57E-09	25
CC	GO:0098857	membrane microdomain	25/294	380/23271	2.04E-11	1.57E-09	25
CC	GO:0098589	membrane region	25/294	393/23271	4.19E-11	2.42E-09	25
CC	GO:0005901	caveola	9/294	97/23271	3.92E-06	0.0018085	9
CC	GO:0044853	plasma membrane raft	10/294	130/23271	6.24E-06	0.0023961	10
CC	GO:0098802	plasma membrane signaling receptor complex	11/294	187/23271	2.76E-05	0.0090885	11
CC	GO:0062023	collagen-containing extracellular matrix	16/294	385/23271	3.50E-05	0.0100984	16
CC	GO:0005788	endoplasmic reticulum lumen	7/294	85/23271	0.00010177	0.0026068	7
CC	GO:0043204	perikaryon	8/294	140/23271	0.00041767	0.00962837	8
CC	GO:0030141	secretory granule	14/294	401/23271	0.00062979	0.01319844	14
CC	GO:0098992	neuronal dense core vesicle	3/294	16/23271	0.00098943	0.01900738	3
CC	GO:0044306	neuron projection terminus	9/294	213/23271	0.00161665	0.02741179	9
CC	GO:0043034	costamere	3/294	19/23271	0.00166473	0.02741179	3
CC	GO:0005796	Golgi lumen	3/294	21/23271	0.00224269	0.03446663	3

CC	GO:0043679	axon terminus	8/294	192/23271	0.00315635	0.04547641	8
CC	GO:0030139	endocytic vesicle	8/294	200/23271	0.00403981	0.05478126	8
CC	GO:0042383	sarcolemma	7/294	164/23271	0.00494264	0.06330052	7
CC	GO:0045177	apical part of cell	13/294	454/23271	0.0053945	0.06545127	13
CC	GO:0008180	COP9 signalosome	3/294	34/23271	0.00894314	0.09817286	3
CC	GO:0031045	dense core granule	3/294	34/23271	0.00894314	0.09817286	3
CC	GO:0150034	distal axon	11/294	384/23271	0.01005731	0.10538526	11
CC	GO:0032809	neuronal cell body membrane	3/294	37/23271	0.01129498	0.10899576	3
CC	GO:0032589	neuron projection membrane	4/294	69/23271	0.0113475	0.10899576	4
CC	GO:0044298	cell body membrane	3/294	40/23271	0.01397048	0.1288225	3
CC	GO:0043196	varicosity	2/294	16/23271	0.01698433	0.1505898	2
CC	GO:0005635	nuclear envelope	11/294	421/23271	0.01872503	0.15987451	11
CC	GO:0032590	dendrite membrane	3/294	48/23271	0.02272429	0.18709097	3
CC	GO:0043292	contractile fiber	7/294	226/23271	0.02521967	0.2004758	7

CC	GO:0043195	terminal bouton	4/294	91/23271	0.0283398	0.21151077	4
CC	GO:0070062	extracellular exosome	4/294	92/23271	0.02934353	0.21151077	4
CC	GO:0031252	cell leading edge	10/294	395/23271	0.0293604	0.21151077	10
CC	GO:0005791	rough endoplasmic reticulum	4/294	93/23271	0.03036812	0.21214095	4
CC	GO:0005667	transcription regulator complex	11/294	460/23271	0.03287552	0.22290214	11
CC	GO:0031965	nuclear membrane	7/294	246/23271	0.03737266	0.24415224	7
CC	GO:1903561	extracellular vesicle	4/294	100/23271	0.03812788	0.24415224	4
CC	GO:0045334	clathrin-coated endocytic vesicle	2/294	26/23271	0.04236131	0.26392967	2
CC	GO:0043230	extracellular organelle	4/294	110/23271	0.05100647	0.29626249	4
CC	GO:0005942	phosphatidylinositol 3-kinase complex	2/294	29/23271	0.05163612	0.29626249	2
CC	GO:0045335	phagocytic vesicle	4/294	111/23271	0.05241012	0.29626249	4
CC	GO:0030016	myofibril	6/294	212/23271	0.053013	0.29626249	6
CC	GO:0005925	focal adhesion	5/294	161/23271	0.05397659	0.29626249	5
CC	GO:0005604	basement membrane	4/294	114/23271	0.05674642	0.30422195	4

CC	GO:0030315	T-tubule	3/294	70/23271	0.05888471	0.30851082	3
CC	GO:0005921	gap junction	2/294	33/23271	0.06499875	0.32899094	2
CC	GO:0000323	lytic vacuole	10/294	460/23271	0.06832418	0.32899094	10
CC	GO:0005764	lysosome	10/294	460/23271	0.06832418	0.32899094	10
CC	GO:0097225	sperm midpiece	2/294	34/23271	0.06850222	0.32899094	2
CC	GO:0030055	cell-substrate junction	5/294	174/23271	0.07034111	0.33092811	5
CC	GO:0001650	fibrillar center	4/294	125/23271	0.07423082	0.34224313	4
CC	GO:0016324	apical plasma membrane	8/294	350/23271	0.07745939	0.35012604	8
CC	GO:0098636	protein complex involved in cell adhesion	2/294	39/23271	0.08689066	0.38520355	2
CC	GO:0044291	cell-cell contact zone	3/294	85/23271	0.09287394	0.38948823	3
CC	GO:0044304	main axon	3/294	85/23271	0.09287394	0.38948823	3
CC	GO:0005884	actin filament	4/294	136/23271	0.09411516	0.38948823	4
CC	GO:0001772	immunological synapse	2/294	41/23271	0.0946154	0.38948823	2
CC	GO:0031225	anchored component of membrane	5/294	198/23271	0.10687992	0.43225673	5

CC	GO:0030175	filopodium	3/294	93/23271	0.1136412	0.45167736	3
CC	GO:0033116	endoplasmic reticulum-Golgi intermediate compartment membrane	1/294	10/23271	0.11941348	0.45879917	1
CC	GO:0072562	blood microparticle	1/294	10/23271	0.11941348	0.45879917	1
CC	GO:0031256	leading edge membrane	4/294	150/23271	0.12263492	0.46221837	4
CC	GO:0045211	postsynaptic membrane	7/294	330/23271	0.1262278	0.46221837	7
CC	GO:0031594	neuromuscular junction	3/294	98/23271	0.12743256	0.46221837	3
CC	GO:0035631	CD40 receptor complex	1/294	11/23271	0.13054337	0.46221837	1
CC	GO:0099544	perisynaptic space	1/294	11/23271	0.13054337	0.46221837	1
CC	GO:0043209	myelin sheath	5/294	213/23271	0.13361395	0.46221837	5
CC	GO:0005902	microvillus	3/294	101/23271	0.13598048	0.46221837	3
CC	GO:0034663	endoplasmic reticulum chaperone complex	1/294	12/23271	0.14153307	0.46221837	1
CC	GO:0036128	CatSper complex	1/294	12/23271	0.14153307	0.46221837	1
CC	GO:0043020	NADPH oxidase complex	1/294	12/23271	0.14153307	0.46221837	1
CC	GO:0090575	RNA polymerase II transcription regulator complex	4/294	159/23271	0.14268829	0.46221837	4

CC	GO:0098858	actin-based cell projection	5/294	221/23271	0.14898514	0.46221837	5
CC	GO:0002199	zona pellucida receptor complex	1/294	13/23271	0.15238432	0.46221837	1
CC	GO:0005916	fascia adherens	1/294	13/23271	0.15238432	0.46221837	1
CC	GO:0034774	secretory granule lumen	1/294	13/23271	0.15238432	0.46221837	1
CC	GO:0060205	cytoplasmic vesicle lumen	1/294	13/23271	0.15238432	0.46221837	1
CC	GO:0098878	neurotransmitter receptor complex	2/294	56/23271	0.15762667	0.47191033	2
CC	GO:0030061	mitochondrial crista	1/294	14/23271	0.16309887	0.47593141	1
CC	GO:0098871	postsynaptic actin cytoskeleton	1/294	14/23271	0.16309887	0.47593141	1
CC	GO:0031983	vesicle lumen	1/294	15/23271	0.17367843	0.49956851	1
CC	GO:0009925	basal plasma membrane	2/294	60/23271	0.17553332	0.49956851	2
CC	GO:0015629	actin cytoskeleton	9/294	497/23271	0.1795115	0.50466005	9
CC	GO:0072687	meiotic spindle	1/294	16/23271	0.18412471	0.5046788	1
CC	GO:0014704	intercalated disc	2/294	62/23271	0.184604	0.5046788	2
CC	GO:0008021	synaptic vesicle	5/294	239/23271	0.1860859	0.5046788	5

CC	GO:0005614	interstitial matrix	1/294	17/23271	0.19443936	0.52120221	1
CC	GO:0016328	lateral plasma membrane	2/294	66/23271	0.20293309	0.53771745	2
CC	GO:0031091	platelet alpha granule	1/294	19/23271	0.21468042	0.54808609	1
CC	GO:0099571	postsynaptic cytoskeleton	1/294	19/23271	0.21468042	0.54808609	1
CC	GO:0016607	nuclear speck	6/294	320/23271	0.21955787	0.54808609	6
CC	GO:0005882	intermediate filament	3/294	129/23271	0.22346029	0.54808609	3
CC	GO:0097449	astrocyte projection	1/294	20/23271	0.22461005	0.54808609	1
CC	GO:0016323	basolateral plasma membrane	5/294	259/23271	0.23074615	0.54808609	5
CC	GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	2/294	72/23271	0.23076752	0.54808609	2
CC	GO:0043197	dendritic spine	4/294	195/23271	0.23344429	0.54808609	4
CC	GO:0005640	nuclear outer membrane	1/294	21/23271	0.23441456	0.54808609	1
CC	GO:0030673	axolemma	1/294	21/23271	0.23441456	0.54808609	1
CC	GO:0031362	anchored component of external side of plasma membrane	1/294	21/23271	0.23441456	0.54808609	1
CC	GO:0070382	exocytic vesicle	5/294	261/23271	0.2353767	0.54808609	5

CC	GO:0001891	phagocytic cup	1/294	22/23271	0.24409552	0.55164178	1
CC	GO:0016605	PML body	2/294	75/23271	0.24478069	0.55164178	2
CC	GO:0044309	neuron spine	4/294	200/23271	0.24705	0.55164178	4
CC	GO:0001673	male germ cell nucleus	1/294	23/23271	0.25365446	0.55164178	1
CC	GO:0005865	striated muscle thin filament	1/294	23/23271	0.25365446	0.55164178	1
CC	GO:0016327	apicolateral plasma membrane	1/294	23/23271	0.25365446	0.55164178	1
CC	GO:0097524	sperm plasma membrane	1/294	23/23271	0.25365446	0.55164178	1
CC	GO:0030133	transport vesicle	6/294	339/23271	0.25883076	0.55642059	6
CC	GO:0031233	intrinsic component of external side of plasma membrane	1/294	24/23271	0.26309293	0.55642059	1
CC	GO:0035327	transcriptionally active chromatin	1/294	24/23271	0.26309293	0.55642059	1
CC	GO:0005777	peroxisome	3/294	145/23271	0.27748806	0.57579811	3
CC	GO:0042579	microbody	3/294	145/23271	0.27748806	0.57579811	3
CC	GO:0030670	phagocytic vesicle membrane	1/294	26/23271	0.28161449	0.57579811	1
CC	GO:0045178	basal part of cell	2/294	83/23271	0.28224624	0.57579811	2

CC	GO:0002102	podosome	1/294	27/23271	0.29070054	0.58273152	1
CC	GO:0036379	myofilament	1/294	27/23271	0.29070054	0.58273152	1
CC	GO:0030667	secretory granule membrane	2/294	88/23271	0.3056031	0.60732377	2
CC	GO:0044305	calyx of Held	1/294	29/23271	0.30853049	0.60790083	1
CC	GO:0043073	germ cell nucleus	1/294	30/23271	0.31727724	0.61462819	1
CC	GO:0061827	sperm head	1/294	30/23271	0.31727724	0.61462819	1
CC	GO:0043296	apical junction complex	3/294	158/23271	0.32225008	0.61905936	3
CC	GO:0099092	postsynaptic density, intracellular component	1/294	31/23271	0.32591373	0.62092306	1
CC	GO:0045111	intermediate filament cytoskeleton	3/294	165/23271	0.34641139	0.6545651	3
CC	GO:0097228	sperm principal piece	1/294	34/23271	0.35117532	0.65752033	1
CC	GO:1902911	protein kinase complex	2/294	99/23271	0.35638101	0.65752033	2
CC	GO:0015030	Cajal body	1/294	35/23271	0.3593844	0.65752033	1
CC	GO:0097386	glial cell projection	1/294	35/23271	0.3593844	0.65752033	1
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	4/294	241/23271	0.36288597	0.65869894	4

CC	GO:0005790	smooth endoplasmic reticulum	1/294	36/23271	0.36748997	0.6618446	1
CC	GO:0099091	postsynaptic specialization, intracellular component	1/294	37/23271	0.37549333	0.66978786	1
CC	GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	2/294	104/23271	0.37903989	0.66978786	2
CC	GO:0016235	aggresome	1/294	38/23271	0.38339575	0.66978786	1
CC	GO:0097060	synaptic membrane	7/294	470/23271	0.38352236	0.66978786	7
CC	GO:0030136	clathrin-coated vesicle	2/294	106/23271	0.38801105	0.67253201	2
CC	GO:0005891	voltage-gated calcium channel complex	1/294	40/23271	0.39890287	0.67910451	1
CC	GO:0031941	filamentous actin	1/294	40/23271	0.39890287	0.67910451	1
CC	GO:0032154	cleavage furrow	1/294	41/23271	0.40651006	0.67910451	1
CC	GO:0005720	nuclear heterochromatin	1/294	42/23271	0.4140213	0.67910451	1
CC	GO:0032993	protein-DNA complex	3/294	186/23271	0.41808565	0.67910451	3
CC	GO:0098562	cytoplasmic side of membrane	3/294	186/23271	0.41808565	0.67910451	3
CC	GO:0005778	peroxisomal membrane	1/294	43/23271	0.42143779	0.67910451	1
CC	GO:0031903	microbody membrane	1/294	43/23271	0.42143779	0.67910451	1

CC	GO:0030017	sarcomere	3/294	188/23271	0.42479651	0.67910451	3
CC	GO:0030666	endocytic vesicle membrane	1/294	44/23271	0.42876073	0.67910451	1
CC	GO:0030672	synaptic vesicle membrane	2/294	116/23271	0.43195377	0.67910451	2
CC	GO:0099056	integral component of presynaptic membrane	2/294	116/23271	0.43195377	0.67910451	2
CC	GO:0099501	exocytic vesicle membrane	2/294	116/23271	0.43195377	0.67910451	2
CC	GO:0005637	nuclear inner membrane	1/294	45/23271	0.4359913	0.67910451	1
CC	GO:0030285	integral component of synaptic vesicle membrane	1/294	45/23271	0.4359913	0.67910451	1
CC	GO:0022627	cytosolic small ribosomal subunit	1/294	46/23271	0.44313065	0.68102184	1
CC	GO:0034707	chloride channel complex	1/294	46/23271	0.44313065	0.68102184	1
CC	GO:0019867	outer membrane	3/294	196/23271	0.45135931	0.68454077	3
CC	GO:0031968	organelle outer membrane	3/294	196/23271	0.45135931	0.68454077	3
CC	GO:0030018	Z disc	2/294	125/23271	0.47002872	0.70474982	2
CC	GO:0000791	euchromatin	1/294	50/23271	0.47079863	0.70474982	1
CC	GO:0098889	intrinsic component of presynaptic membrane	2/294	128/23271	0.48237952	0.71742692	2

CC	GO:0030426	growth cone	3/294	209/23271	0.4933994	0.72911248	3
CC	GO:0030427	site of polarized growth	3/294	216/23271	0.51537002	0.74050305	3
CC	GO:0034702	ion channel complex	4/294	296/23271	0.51602315	0.74050305	4
CC	GO:0005923	bicellular tight junction	2/294	137/23271	0.51834542	0.74050305	2
CC	GO:0036464	cytoplasmic ribonucleoprotein granule	3/294	218/23271	0.52155398	0.74050305	3
CC	GO:0031674	I band	2/294	138/23271	0.5222382	0.74050305	2
CC	GO:0005770	late endosome	3/294	219/23271	0.52462989	0.74050305	3
CC	GO:0036126	sperm flagellum	2/294	141/23271	0.53378971	0.74050305	2
CC	GO:0034703	cation channel complex	3/294	222/23271	0.53379223	0.74050305	3
CC	GO:0031253	cell projection membrane	4/294	304/23271	0.53699391	0.74050305	4
CC	GO:0032153	cell division site	1/294	61/23271	0.54002185	0.74050305	1
CC	GO:0034704	calcium channel complex	1/294	61/23271	0.54002185	0.74050305	1
CC	GO:0070160	tight junction	2/294	146/23271	0.55261467	0.74050305	2
CC	GO:0035770	ribonucleoprotein granule	3/294	229/23271	0.55477862	0.74050305	3

CC	GO:0030496	midbody	2/294	147/23271	0.55631493	0.74050305	2
CC	GO:0030658	transport vesicle membrane	2/294	147/23271	0.55631493	0.74050305	2
CC	GO:0098563	intrinsic component of synaptic vesicle membrane	1/294	64/23271	0.55728167	0.74050305	1
CC	GO:1902495	transmembrane transporter complex	4/294	312/23271	0.55750209	0.74050305	4
CC	GO:0001726	ruffle	2/294	149/23271	0.5636503	0.74050305	2
CC	GO:0014069	postsynaptic density	5/294	400/23271	0.5715841	0.74050305	5
CC	GO:0032421	stereocilium bundle	1/294	67/23271	0.57389597	0.74050305	1
CC	GO:1990351	transporter complex	4/294	319/23271	0.57504242	0.74050305	4
CC	GO:0019898	extrinsic component of membrane	4/294	320/23271	0.57751621	0.74050305	4
CC	GO:0030176	integral component of endoplasmic reticulum membrane	2/294	153/23271	0.57805939	0.74050305	2
CC	GO:0097729	9+2 motile cilium	2/294	154/23271	0.58160698	0.74050305	2
CC	GO:0032279	asymmetric synapse	5/294	405/23271	0.58262202	0.74050305	5
CC	GO:0005905	clathrin-coated pit	1/294	69/23271	0.58462546	0.74050305	1
CC	GO:0099061	integral component of postsynaptic density membrane	1/294	71/23271	0.59508568	0.74963339	1

CC	GO:0005776	autophagosome	1/294	73/23271	0.60528336	0.75121792	1
CC	GO:0031227	intrinsic component of endoplasmic reticulum membrane	2/294	161/23271	0.60582587	0.75121792	2
CC	GO:0005844	polysome	1/294	74/23271	0.6102858	0.75121792	1
CC	GO:0030659	cytoplasmic vesicle membrane	4/294	337/23271	0.61828977	0.75121792	4
CC	GO:0000932	P-body	1/294	76/23271	0.62010193	0.75121792	1
CC	GO:0016234	inclusion body	1/294	76/23271	0.62010193	0.75121792	1
CC	GO:0046658	anchored component of plasma membrane	1/294	77/23271	0.62491719	0.75121792	1
CC	GO:0099146	intrinsic component of postsynaptic density membrane	1/294	77/23271	0.62491719	0.75121792	1
CC	GO:0015935	small ribosomal subunit	1/294	78/23271	0.62967163	0.75121792	1
CC	GO:0009898	cytoplasmic side of plasma membrane	2/294	169/23271	0.63218933	0.75121792	2
CC	GO:0099055	integral component of postsynaptic membrane	2/294	169/23271	0.63218933	0.75121792	2
CC	GO:0098984	neuron to neuron synapse	5/294	433/23271	0.64148667	0.7531427	5
CC	GO:0005581	collagen trimer	1/294	81/23271	0.64357757	0.7531427	1
CC	GO:0005741	mitochondrial outer membrane	2/294	175/23271	0.65104723	0.7531427	2

CC	GO:0005758	mitochondrial intermembrane space	1/294	83/23271	0.65255783	0.7531427	1
CC	GO:1902554	serine/threonine protein kinase complex	1/294	83/23271	0.65255783	0.7531427	1
CC	GO:0099572	postsynaptic specialization	5/294	439/23271	0.65341148	0.7531427	5
CC	GO:0098936	intrinsic component of postsynaptic membrane	2/294	178/23271	0.66018502	0.75586191	2
CC	GO:0001725	stress fiber	1/294	86/23271	0.66560716	0.75586191	1
CC	GO:0097517	contractile actin filament bundle	1/294	86/23271	0.66560716	0.75586191	1
CC	GO:0016363	nuclear matrix	1/294	88/23271	0.67403419	0.75610084	1
CC	GO:0012506	vesicle membrane	4/294	363/23271	0.67570355	0.75610084	4
CC	GO:0005811	lipid droplet	1/294	89/23271	0.67816799	0.75610084	1
CC	GO:0019897	extrinsic component of plasma membrane	2/294	189/23271	0.69205696	0.75610084	2
CC	GO:0005769	early endosome	3/294	284/23271	0.6986459	0.75610084	3
CC	GO:0030135	coated vesicle	2/294	192/23271	0.70031153	0.75610084	2
CC	GO:0000792	heterochromatin	1/294	95/23271	0.70189635	0.75610084	1
CC	GO:0000795	synaptonemal complex	1/294	95/23271	0.70189635	0.75610084	1

CC	GO:0032432	actin filament bundle	1/294	95/23271	0.70189635	0.75610084	1
CC	GO:0042641	actomyosin	1/294	95/23271	0.70189635	0.75610084	1
CC	GO:0099086	synaptonemal structure	1/294	95/23271	0.70189635	0.75610084	1
CC	GO:0031970	organelle envelope lumen	1/294	96/23271	0.70567796	0.75663879	1
CC	GO:0098839	postsynaptic density membrane	1/294	97/23271	0.70941175	0.75712073	1
CC	GO:0042734	presynaptic membrane	2/294	198/23271	0.7162711	0.76091861	2
CC	GO:0098982	GABA-ergic synapse	1/294	105/23271	0.73763165	0.77645437	1
CC	GO:0099060	integral component of postsynaptic specialization membrane	1/294	105/23271	0.73763165	0.77645437	1
CC	GO:1990204	oxidoreductase complex	1/294	110/23271	0.75386437	0.78887495	1
CC	GO:0098948	intrinsic component of postsynaptic specialization membrane	1/294	111/23271	0.75698876	0.78887495	1
CC	GO:0034399	nuclear periphery	1/294	113/23271	0.76311944	0.78887495	1
CC	GO:0098685	Schaffer collateral - CA1 synapse	1/294	113/23271	0.76311944	0.78887495	1
CC	GO:0022626	cytosolic ribosome	1/294	115/23271	0.76909598	0.79150385	1
CC	GO:0031514	motile cilium	2/294	222/23271	0.77312462	0.79211364	2

CC	GO:0005814	centriole	1/294	119/23271	0.78060195	0.79371469	1
CC	GO:0099699	integral component of synaptic membrane	2/294	226/23271	0.78157339	0.79371469	2
CC	GO:0005765	lysosomal membrane	1/294	130/23271	0.80938093	0.81477556	1
CC	GO:0098852	lytic vacuole membrane	1/294	130/23271	0.80938093	0.81477556	1
CC	GO:0099240	intrinsic component of synaptic membrane	2/294	244/23271	0.81626642	0.81813431	2
CC	GO:0072686	mitotic spindle	1/294	135/23271	0.82118694	0.81822852	1
CC	GO:0099634	postsynaptic specialization membrane	1/294	136/23271	0.8234592	0.81822852	1
CC	GO:0005912	adherens junction	1/294	138/23271	0.82791775	0.81912802	1
CC	GO:0031301	integral component of organelle membrane	3/294	368/23271	0.84642759	0.83386254	3
CC	GO:0055037	recycling endosome	1/294	153/23271	0.85796755	0.84163446	1
CC	GO:0000794	condensed nuclear chromosome	1/294	159/23271	0.86846754	0.84637272	1
CC	GO:0097730	non-motile cilium	1/294	160/23271	0.87014072	0.84637272	1
CC	GO:0036064	ciliary basal body	1/294	166/23271	0.8797436	0.84864581	1
CC	GO:0031300	intrinsic component of organelle membrane	3/294	403/23271	0.88652733	0.84864581	3

CC	GO:0030027	lamellipodium	1/294	171/23271	0.88720301	0.84864581	1
CC	GO:0032838	plasma membrane bounded cell projection cytoplasm	1/294	171/23271	0.88720301	0.84864581	1
CC	GO:0005819	spindle	2/294	297/23271	0.89156035	0.84928976	2
CC	GO:0005774	vacuolar membrane	1/294	183/23271	0.90327757	0.85691049	1
CC	GO:0044391	ribosomal subunit	1/294	198/23271	0.92019774	0.86773731	1
CC	GO:0098862	cluster of actin-based cell projections	1/294	200/23271	0.92221854	0.86773731	1
CC	GO:0000793	condensed chromosome	1/294	210/23271	0.93158266	0.87225621	1
CC	GO:0099568	cytoplasmic region	1/294	223/23271	0.94209622	0.87225621	1
CC	GO:0010008	endosome membrane	1/294	227/23271	0.94499483	0.87225621	1
CC	GO:0005802	trans-Golgi network	1/294	231/23271	0.94774881	0.87225621	1
CC	GO:0019866	organelle inner membrane	3/294	489/23271	0.94827747	0.87225621	3
CC	GO:0005840	ribosome	1/294	234/23271	0.94972372	0.87225621	1
CC	GO:0005759	mitochondrial matrix	1/294	273/23271	0.96954675	0.8834754	1
CC	GO:0005874	microtubule	2/294	430/23271	0.97349409	0.8834754	2

CC	GO:0098791	Golgi apparatus subcompartment	1/294	295/23271	0.97705712	0.8834754	1
CC	GO:0005743	mitochondrial inner membrane	2/294	444/23271	0.97726902	0.8834754	2
CC	GO:0031984	organelle subcompartment	1/294	321/23271	0.9835885	0.88571497	1
MF	GO:0048018	receptor ligand activity	111/292	499/22669	8.78E-109	2.64E-106	111
MF	GO:0005125	cytokine activity	56/292	231/22669	2.00E-55	3.00E-53	56
MF	GO:0005126	cytokine receptor binding	60/292	314/22669	8.92E-53	8.95E-51	60
MF	GO:0140375	immune receptor activity	37/292	123/22669	1.57E-40	1.18E-38	37
MF	GO:0008083	growth factor activity	39/292	147/22669	2.75E-40	1.65E-38	39
MF	GO:0019955	cytokine binding	36/292	136/22669	3.42E-37	1.72E-35	36
MF	GO:0004896	cytokine receptor activity	32/292	98/22669	1.82E-36	7.81E-35	32
MF	GO:0001664	G protein-coupled receptor binding	39/292	310/22669	4.18E-27	1.57E-25	39
MF	GO:0008528	G protein-coupled peptide receptor activity	28/292	144/22669	4.61E-25	1.54E-23	28
MF	GO:0001653	peptide receptor activity	28/292	151/22669	1.85E-24	5.56E-23	28
MF	GO:0070851	growth factor receptor binding	27/292	149/22669	2.42E-23	6.62E-22	27

MF	GO:0005179	hormone activity	23/292	130/22669	8.40E-20	2.11E-18	23
MF	GO:0008009	chemokine activity	16/292	44/22669	1.15E-19	2.66E-18	16
MF	GO:0042379	chemokine receptor binding	18/292	78/22669	5.98E-18	1.29E-16	18
MF	GO:0016493	C-C chemokine receptor activity	12/292	24/22669	3.92E-17	7.87E-16	12
MF	GO:0001637	G protein-coupled chemoattractant receptor activity	12/292	25/22669	7.46E-17	1.25E-15	12
MF	GO:0004950	chemokine receptor activity	12/292	25/22669	7.46E-17	1.25E-15	12
MF	GO:0019957	C-C chemokine binding	12/292	25/22669	7.46E-17	1.25E-15	12
MF	GO:0019956	chemokine binding	13/292	33/22669	9.37E-17	1.48E-15	13
MF	GO:0004879	nuclear receptor activity	14/292	53/22669	3.89E-15	5.57E-14	14
MF	GO:0098531	ligand-activated transcription factor activity	14/292	53/22669	3.89E-15	5.57E-14	14
MF	GO:0019838	growth factor binding	20/292	147/22669	4.47E-15	6.12E-14	20
MF	GO:0003707	steroid hormone receptor activity	14/292	54/22669	5.19E-15	6.79E-14	14
MF	GO:0045499	chemorepellent activity	11/292	29/22669	3.78E-14	4.74E-13	11
MF	GO:0032813	tumor necrosis factor receptor superfamily binding	12/292	48/22669	7.67E-13	9.24E-12	12

MF	GO:0030215	semaphorin receptor binding	9/292	22/22669	3.71E-12	4.29E-11	9
MF	GO:0045236	CXCR chemokine receptor binding	8/292	15/22669	4.10E-12	4.57E-11	8
MF	GO:0042562	hormone binding	13/292	88/22669	1.04E-10	1.12E-09	13
MF	GO:0042277	peptide binding	22/292	318/22669	1.87E-10	1.94E-09	22
MF	GO:0008201	heparin binding	16/292	156/22669	2.01E-10	2.01E-09	16
MF	GO:0005164	tumor necrosis factor receptor binding	9/292	33/22669	2.54E-10	2.47E-09	9
MF	GO:0005539	glycosaminoglycan binding	18/292	213/22669	3.60E-10	3.39E-09	18
MF	GO:0042056	chemoattractant activity	9/292	38/22669	1.01E-09	9.25E-09	9
MF	GO:0033218	amide binding	23/292	391/22669	1.71E-09	1.51E-08	23
MF	GO:0048020	CCR chemokine receptor binding	10/292	56/22669	2.28E-09	1.96E-08	10
MF	GO:1901681	sulfur compound binding	18/292	260/22669	8.69E-09	7.27E-08	18
MF	GO:0071855	neuropeptide receptor binding	8/292	34/22669	9.35E-09	7.61E-08	8
MF	GO:0017046	peptide hormone binding	9/292	53/22669	2.33E-08	1.84E-07	9
MF	GO:0005154	epidermal growth factor receptor binding	7/292	36/22669	3.32E-07	2.56E-06	7

MF	GO:0051427	hormone receptor binding	13/292	181/22669	6.91E-07	5.20E-06	13
MF	GO:0001223	transcription coactivator binding	6/292	28/22669	1.29E-06	9.23E-06	6
MF	GO:0005184	neuropeptide hormone activity	6/292	28/22669	1.29E-06	9.23E-06	6
MF	GO:0005178	integrin binding	11/292	136/22669	1.57E-06	1.10E-05	11
MF	GO:0019199	transmembrane receptor protein kinase activity	8/292	77/22669	6.71E-06	4.59E-05	8
MF	GO:0001221	transcription cofactor binding	7/292	59/22669	1.05E-05	7.05E-05	7
MF	GO:0005160	transforming growth factor beta receptor binding	5/292	25/22669	1.47E-05	9.65E-05	5
MF	GO:0005165	neurotrophin receptor binding	4/292	15/22669	3.29E-05	0.00021082	4
MF	GO:0030971	receptor tyrosine kinase binding	7/292	73/22669	4.31E-05	0.00027061	7
MF	GO:1990782	protein tyrosine kinase binding	8/292	105/22669	6.52E-05	0.0004004	8
MF	GO:0044389	ubiquitin-like protein ligase binding	14/292	324/22669	8.73E-05	0.00051696	14
MF	GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	13/292	284/22669	8.76E-05	0.00051696	13
MF	GO:0001540	amyloid-beta binding	6/292	58/22669	0.00010008	0.00057943	6
MF	GO:0005123	death receptor binding	4/292	20/22669	0.00011104	0.00061903	4

MF	GO:0051428	peptide hormone receptor binding	4/292	20/22669	0.00011104	0.00061903	4
MF	GO:0005200	structural constituent of cytoskeleton	6/292	64/22669	0.00017381	0.00095135	6
MF	GO:0031625	ubiquitin protein ligase binding	13/292	306/22669	0.00018348	0.0009864	13
MF	GO:0051787	misfolded protein binding	4/292	23/22669	0.00019685	0.00103969	4
MF	GO:0034713	type I transforming growth factor beta receptor binding	3/292	10/22669	0.00023739	0.00123217	3
MF	GO:0004713	protein tyrosine kinase activity	8/292	130/22669	0.00028794	0.00146922	8
MF	GO:0044183	protein folding chaperone	4/292	26/22669	0.00032239	0.00161762	4
MF	GO:0050839	cell adhesion molecule binding	12/292	284/22669	0.00033905	0.00167332	12
MF	GO:0038024	cargo receptor activity	6/292	76/22669	0.00044556	0.00216348	6
MF	GO:0005520	insulin-like growth factor binding	4/292	29/22669	0.00049686	0.00237432	4
MF	GO:0004875	complement receptor activity	3/292	13/22669	0.00054978	0.00258611	3
MF	GO:0044548	S100 protein binding	3/292	14/22669	0.00069306	0.0031767	3
MF	GO:0016922	nuclear receptor binding	7/292	114/22669	0.00069643	0.0031767	7
MF	GO:0033612	receptor serine/threonine kinase binding	4/292	32/22669	0.0007298	0.00327923	4

MF	GO:0003725	double-stranded RNA binding	6/292	85/22669	0.00080946	0.00355657	6
MF	GO:0035257	nuclear hormone receptor binding	8/292	152/22669	0.00081515	0.00355657	8
MF	GO:0005496	steroid binding	7/292	119/22669	0.00089796	0.00386189	7
MF	GO:0140297	DNA-binding transcription factor binding	13/292	365/22669	0.00096858	0.00406335	13
MF	GO:0004714	transmembrane receptor protein tyrosine kinase activity	5/292	59/22669	0.0009718	0.00406335	5
MF	GO:0004953	icosanoid receptor activity	3/292	16/22669	0.0010461	0.00425583	3
MF	GO:0030296	protein tyrosine kinase activator activity	3/292	16/22669	0.0010461	0.00425583	3
MF	GO:0004675	transmembrane receptor protein serine/threonine kinase activity	3/292	18/22669	0.00149554	0.00577228	3
MF	GO:0016500	protein-hormone receptor activity	3/292	18/22669	0.00149554	0.00577228	3
MF	GO:0050135	NAD(P)+ nucleosidase activity	3/292	18/22669	0.00149554	0.00577228	3
MF	GO:0061809	NAD+ nucleotidase, cyclic ADP-ribose generating	3/292	18/22669	0.00149554	0.00577228	3
MF	GO:0008188	neuropeptide receptor activity	4/292	40/22669	0.00171097	0.00652014	4
MF	GO:0003953	NAD+ nucleosidase activity	3/292	20/22669	0.00204997	0.00761914	3
MF	GO:0035259	glucocorticoid receptor binding	3/292	20/22669	0.00204997	0.00761914	3

MF	GO:0001784	phosphotyrosine residue binding	4/292	45/22669	0.00265262	0.00973877	4
MF	GO:0005044	scavenger receptor activity	4/292	46/22669	0.00287622	0.01043245	4
MF	GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	3/292	24/22669	0.00350393	0.01241019	3
MF	GO:0070696	transmembrane receptor protein serine/threonine kinase binding	3/292	24/22669	0.00350393	0.01241019	3
MF	GO:0001046	core promoter sequence-specific DNA binding	4/292	50/22669	0.00389948	0.01365057	4
MF	GO:0030295	protein kinase activator activity	5/292	83/22669	0.00439042	0.01493951	5
MF	GO:0005104	fibroblast growth factor receptor binding	3/292	26/22669	0.00441656	0.01493951	3
MF	GO:0017134	fibroblast growth factor binding	3/292	26/22669	0.00441656	0.01493951	3
MF	GO:0015026	coreceptor activity	3/292	27/22669	0.0049218	0.01628264	3
MF	GO:0042923	neuropeptide binding	3/292	27/22669	0.0049218	0.01628264	3
MF	GO:0030247	polysaccharide binding	3/292	28/22669	0.00546049	0.01786843	3
MF	GO:0019209	kinase activator activity	5/292	90/22669	0.00618119	0.0199715	5
MF	GO:0045309	protein phosphorylated amino acid binding	4/292	57/22669	0.00623586	0.0199715	4
MF	GO:0004955	prostaglandin receptor activity	2/292	11/22669	0.00842273	0.02641338	2

MF	GO:0005024	transforming growth factor beta-activated receptor activity	2/292	11/22669	0.00842273	0.02641338	2
MF	GO:0051059	NF-kappaB binding	3/292	33/22669	0.00867466	0.02692297	3
MF	GO:0001224	RNA polymerase II transcription cofactor binding	2/292	12/22669	0.01002188	0.02987241	2
MF	GO:0004954	prostanoid receptor activity	2/292	12/22669	0.01002188	0.02987241	2
MF	GO:0017154	semaphorin receptor activity	2/292	12/22669	0.01002188	0.02987241	2
MF	GO:0023023	MHC protein complex binding	2/292	12/22669	0.01002188	0.02987241	2
MF	GO:0031072	heat shock protein binding	6/292	146/22669	0.01174273	0.03378912	6
MF	GO:0036312	phosphatidylinositol 3-kinase regulatory subunit binding	2/292	13/22669	0.01174408	0.03378912	2
MF	GO:0043121	neurotrophin binding	2/292	13/22669	0.01174408	0.03378912	2
MF	GO:0016799	hydrolase activity, hydrolyzing N-glycosyl compounds	3/292	37/22669	0.01189708	0.03378912	3
MF	GO:0017080	sodium channel regulator activity	3/292	37/22669	0.01189708	0.03378912	3
MF	GO:0051721	protein phosphatase 2A binding	3/292	38/22669	0.01279596	0.03600242	3
MF	GO:0005161	platelet-derived growth factor receptor binding	2/292	14/22669	0.01358592	0.03718251	2
MF	GO:0048185	activin binding	2/292	14/22669	0.01358592	0.03718251	2

MF	GO:0070700	BMP receptor binding	2/292	14/22669	0.01358592	0.03718251	2
MF	GO:0002020	protease binding	6/292	152/22669	0.01409638	0.03823201	6
MF	GO:0046935	1-phosphatidylinositol-3-kinase regulator activity	2/292	15/22669	0.01554404	0.04178192	2
MF	GO:0043548	phosphatidylinositol 3-kinase binding	3/292	41/22669	0.01572034	0.04188185	3
MF	GO:0019207	kinase regulator activity	7/292	202/22669	0.01606511	0.04242494	7
MF	GO:0020037	heme binding	6/292	159/22669	0.01723616	0.04512165	6
MF	GO:0005172	vascular endothelial growth factor receptor binding	2/292	16/22669	0.01761518	0.04532561	2
MF	GO:0008179	adenylate cyclase binding	2/292	16/22669	0.01761518	0.04532561	2
MF	GO:0005149	interleukin-1 receptor binding	2/292	17/22669	0.01979611	0.05050568	2
MF	GO:0004715	non-membrane spanning protein tyrosine kinase activity	3/292	45/22669	0.02015658	0.05099322	3
MF	GO:0046906	tetrapyrrole binding	6/292	168/22669	0.0219388	0.05503945	6
MF	GO:0051082	unfolded protein binding	4/292	84/22669	0.02329738	0.05796477	4
MF	GO:0001222	transcription corepressor binding	2/292	19/22669	0.0244748	0.06039511	2
MF	GO:0047485	protein N-terminus binding	5/292	129/22669	0.02593519	0.06347853	5

MF	GO:0035014	phosphatidylinositol 3-kinase regulator activity	2/292	20/22669	0.02696645	0.06519036	2
MF	GO:0035258	steroid hormone receptor binding	4/292	88/22669	0.02706768	0.06519036	4
MF	GO:0046965	retinoid X receptor binding	2/292	22/22669	0.03223951	0.07703006	2
MF	GO:0004709	MAP kinase kinase kinase activity	2/292	23/22669	0.03501516	0.08171632	2
MF	GO:0038187	pattern recognition receptor activity	2/292	23/22669	0.03501516	0.08171632	2
MF	GO:0050431	transforming growth factor beta binding	2/292	23/22669	0.03501516	0.08171632	2
MF	GO:0001848	complement binding	2/292	24/22669	0.03787981	0.08772168	2
MF	GO:0005112	Notch binding	2/292	25/22669	0.04083074	0.0938336	2
MF	GO:0050840	extracellular matrix binding	3/292	61/22669	0.04405439	0.10047493	3
MF	GO:0051219	phosphoprotein binding	4/292	104/22669	0.04562398	0.10327232	4
MF	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	2/292	28/22669	0.0501746	0.11272533	2
MF	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	2/292	29/22669	0.05344433	0.1191819	2
MF	GO:0035254	glutamate receptor binding	3/292	67/22669	0.0554809	0.12281375	3
MF	GO:0001968	fibronectin binding	2/292	31/22669	0.06020157	0.13229081	2

MF	GO:0035035	histone acetyltransferase binding	2/292	32/22669	0.06368429	0.13793037	2
MF	GO:0042974	retinoic acid receptor binding	2/292	32/22669	0.06368429	0.13793037	2
MF	GO:0070491	repressing transcription factor binding	3/292	73/22669	0.0681689	0.14658877	3
MF	GO:0019902	phosphatase binding	6/292	223/22669	0.06937126	0.14714431	6
MF	GO:0019887	protein kinase regulator activity	5/292	170/22669	0.06940478	0.14714431	5
MF	GO:0097718	disordered domain specific binding	2/292	34/22669	0.07084632	0.14915015	2
MF	GO:0019903	protein phosphatase binding	5/292	176/22669	0.07789233	0.16284507	5
MF	GO:0033293	monocarboxylic acid binding	3/292	82/22669	0.08940358	0.1851586	3
MF	GO:0035255	ionotropic glutamate receptor binding	2/292	39/22669	0.08979545	0.1851586	2
MF	GO:0042805	actinin binding	2/292	40/22669	0.09374745	0.19069538	2
MF	GO:0051539	4 iron, 4 sulfur cluster binding	2/292	40/22669	0.09374745	0.19069538	2
MF	GO:0033613	activating transcription factor binding	3/292	85/22669	0.09702744	0.19488441	3
MF	GO:0001965	G-protein alpha-subunit binding	2/292	41/22669	0.09774884	0.19488441	2
MF	GO:0043028	cysteine-type endopeptidase regulator activity involved in apoptotic process	2/292	41/22669	0.09774884	0.19488441	2

MF	GO:0005048	signal sequence binding	2/292	44/22669	0.11003037	0.21650283	2
MF	GO:0042169	SH2 domain binding	2/292	44/22669	0.11003037	0.21650283	2
MF	GO:0016247	channel regulator activity	4/292	143/22669	0.11369138	0.22225383	4
MF	GO:0003727	single-stranded RNA binding	3/292	93/22669	0.118569	0.22462103	3
MF	GO:0001849	complement component C1q complex binding	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0005381	iron ion transmembrane transporter activity	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0008296	3'-5'-exodeoxyribonuclease activity	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0016175	superoxide-generating NAD(P)H oxidase activity	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0034511	U3 snoRNA binding	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0050544	arachidonic acid binding	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0061578	Lys63-specific deubiquitinase activity	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0070697	activin receptor binding	1/292	10/22669	0.12161737	0.22462103	1
MF	GO:0005201	extracellular matrix structural constituent	4/292	148/22669	0.12454762	0.22863042	4
MF	GO:0001102	RNA polymerase II activating transcription factor binding	2/292	49/22669	0.13131628	0.23404083	2

MF	GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0017128	phospholipid scramblase activity	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0032052	bile acid binding	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0043560	insulin receptor substrate binding	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0050542	icosanoid binding	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0050543	icosatetraenoic acid binding	1/292	11/22669	0.13293683	0.23404083	1
MF	GO:0005522	profilin binding	1/292	12/22669	0.14411092	0.24717746	1
MF	GO:0008656	cysteine-type endopeptidase activator activity involved in apoptotic process	1/292	12/22669	0.14411092	0.24717746	1
MF	GO:0031386	protein tag	1/292	12/22669	0.14411092	0.24717746	1
MF	GO:0033691	sialic acid binding	1/292	12/22669	0.14411092	0.24717746	1
MF	GO:0005504	fatty acid binding	2/292	52/22669	0.14450375	0.24717746	2
MF	GO:0004601	peroxidase activity	2/292	53/22669	0.14895944	0.2533595	2
MF	GO:0031994	insulin-like growth factor I binding	1/292	13/22669	0.15514149	0.25522269	1
MF	GO:0035256	G protein-coupled glutamate receptor binding	1/292	13/22669	0.15514149	0.25522269	1

MF	GO:0035497	cAMP response element binding	1/292	13/22669	0.15514149	0.25522269	1
MF	GO:0042301	phosphate ion binding	1/292	13/22669	0.15514149	0.25522269	1
MF	GO:0051139	metal ion:proton antiporter activity	1/292	13/22669	0.15514149	0.25522269	1
MF	GO:1901338	catecholamine binding	1/292	13/22669	0.15514149	0.25522269	1
MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	7/292	344/22669	0.1574237	0.25565478	7
MF	GO:0031593	polyubiquitin modification-dependent protein binding	2/292	55/22669	0.15795175	0.25565478	2
MF	GO:0032934	sterol binding	2/292	55/22669	0.15795175	0.25565478	2
MF	GO:0001217	DNA-binding transcription repressor activity	7/292	345/22669	0.15904458	0.256047	7
MF	GO:0005159	insulin-like growth factor receptor binding	1/292	14/22669	0.16603038	0.25898384	1
MF	GO:0005523	tropomyosin binding	1/292	14/22669	0.16603038	0.25898384	1
MF	GO:0008191	metalloendopeptidase inhibitor activity	1/292	14/22669	0.16603038	0.25898384	1
MF	GO:0016505	peptidase activator activity involved in apoptotic process	1/292	14/22669	0.16603038	0.25898384	1
MF	GO:0036122	BMP binding	1/292	14/22669	0.16603038	0.25898384	1
MF	GO:0051378	serotonin binding	1/292	14/22669	0.16603038	0.25898384	1

MF	GO:0031406	carboxylic acid binding	5/292	226/22669	0.16796999	0.2606588	5
MF	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	2/292	58/22669	0.1716214	0.26226941	2
MF	GO:0022824	transmitter-gated ion channel activity	2/292	58/22669	0.1716214	0.26226941	2
MF	GO:0022835	transmitter-gated channel activity	2/292	58/22669	0.1716214	0.26226941	2
MF	GO:0019215	intermediate filament binding	1/292	15/22669	0.1767794	0.2674367	1
MF	GO:0045125	bioactive lipid receptor activity	1/292	15/22669	0.1767794	0.2674367	1
MF	GO:0016863	intramolecular oxidoreductase activity, transposing C=C bonds	1/292	16/22669	0.18739035	0.27790324	1
MF	GO:0043176	amine binding	1/292	16/22669	0.18739035	0.27790324	1
MF	GO:0048019	receptor antagonist activity	1/292	16/22669	0.18739035	0.27790324	1
MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	1/292	16/22669	0.18739035	0.27790324	1
MF	GO:0001846	opsonin binding	1/292	17/22669	0.19786499	0.29057451	1
MF	GO:0016290	palmitoyl-CoA hydrolase activity	1/292	17/22669	0.19786499	0.29057451	1
MF	GO:0043177	organic acid binding	5/292	241/22669	0.20069844	0.29330483	5
MF	GO:0004435	phosphatidylinositol phospholipase C activity	1/292	18/22669	0.20820506	0.29524214	1

MF	GO:0004629	phospholipase C activity	1/292	18/22669	0.20820506	0.29524214	1
MF	GO:0015299	solute:proton antiporter activity	1/292	18/22669	0.20820506	0.29524214	1
MF	GO:0008144	drug binding	3/292	122/22669	0.20827229	0.29524214	3
MF	GO:0043621	protein self-association	2/292	66/22669	0.20888897	0.29524214	2
MF	GO:0051536	iron-sulfur cluster binding	2/292	66/22669	0.20888897	0.29524214	2
MF	GO:0051540	metal cluster binding	2/292	66/22669	0.20888897	0.29524214	2
MF	GO:0042288	MHC class I protein binding	1/292	19/22669	0.2184123	0.30673131	1
MF	GO:0004252	serine-type endopeptidase activity	4/292	186/22669	0.21905549	0.30673131	4
MF	GO:0005230	extracellular ligand-gated ion channel activity	2/292	70/22669	0.22782606	0.3098515	2
MF	GO:1990841	promoter-specific chromatin binding	2/292	70/22669	0.22782606	0.3098515	2
MF	GO:0001091	RNA polymerase II general transcription initiation factor binding	1/292	20/22669	0.2284884	0.3098515	1
MF	GO:0008307	structural constituent of muscle	1/292	20/22669	0.2284884	0.3098515	1
MF	GO:0016641	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	1/292	20/22669	0.2284884	0.3098515	1
MF	GO:0036041	long-chain fatty acid binding	1/292	20/22669	0.2284884	0.3098515	1

MF	GO:0099186	structural constituent of postsynapse	1/292	20/22669	0.2284884	0.3098515	1
MF	GO:0004529	exodeoxyribonuclease activity	1/292	21/22669	0.23843504	0.3204531	1
MF	GO:0016895	exodeoxyribonuclease activity, producing 5'-phosphomonoesters	1/292	21/22669	0.23843504	0.3204531	1
MF	GO:0008139	nuclear localization sequence binding	1/292	22/22669	0.24825387	0.32636455	1
MF	GO:0019865	immunoglobulin binding	1/292	22/22669	0.24825387	0.32636455	1
MF	GO:0048156	tau protein binding	1/292	22/22669	0.24825387	0.32636455	1
MF	GO:0050998	nitric-oxide synthase binding	1/292	22/22669	0.24825387	0.32636455	1
MF	GO:0070530	K63-linked polyubiquitin modification-dependent protein binding	1/292	22/22669	0.24825387	0.32636455	1
MF	GO:0004527	exonuclease activity	2/292	75/22669	0.25164848	0.32796293	2
MF	GO:0043130	ubiquitin binding	2/292	75/22669	0.25164848	0.32796293	2
MF	GO:0016638	oxidoreductase activity, acting on the CH-NH2 group of donors	1/292	23/22669	0.25794654	0.33472192	1
MF	GO:0015491	cation:cation antiporter activity	1/292	24/22669	0.26751466	0.33981431	1
MF	GO:0031681	G-protein beta-subunit binding	1/292	24/22669	0.26751466	0.33981431	1
MF	GO:0051861	glycolipid binding	1/292	24/22669	0.26751466	0.33981431	1

MF	GO:0070412	R-SMAD binding	1/292	24/22669	0.26751466	0.33981431	1
MF	GO:0140303	intramembrane lipid transporter activity	1/292	24/22669	0.26751466	0.33981431	1
MF	GO:0016798	hydrolase activity, acting on glycosyl bonds	3/292	140/22669	0.26975165	0.34120343	3
MF	GO:0000062	fatty-acyl-CoA binding	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0005212	structural constituent of eye lens	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0009975	cyclase activity	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0016849	phosphorus-oxygen lyase activity	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0031435	mitogen-activated protein kinase kinase kinase binding	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0048027	mRNA 5'-UTR binding	1/292	25/22669	0.27695982	0.34120343	1
MF	GO:0008236	serine-type peptidase activity	4/292	207/22669	0.27767517	0.34120343	4
MF	GO:0030246	carbohydrate binding	5/292	274/22669	0.27897015	0.34140121	5
MF	GO:0017025	TBP-class protein binding	1/292	26/22669	0.2862836	0.34613025	1
MF	GO:0019825	oxygen binding	1/292	26/22669	0.2862836	0.34613025	1
MF	GO:0047617	acyl-CoA hydrolase activity	1/292	26/22669	0.2862836	0.34613025	1

MF	GO:0008081	phosphoric diester hydrolase activity	2/292	83/22669	0.28984927	0.34903954	2
MF	GO:0017171	serine hydrolase activity	4/292	212/22669	0.29201658	0.35022562	4
MF	GO:0016209	antioxidant activity	2/292	84/22669	0.29461492	0.35022562	2
MF	GO:0046332	SMAD binding	2/292	84/22669	0.29461492	0.35022562	2
MF	GO:0046625	sphingolipid binding	1/292	27/22669	0.29548756	0.35022562	1
MF	GO:0016289	CoA hydrolase activity	1/292	28/22669	0.30457322	0.35678043	1
MF	GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	1/292	28/22669	0.30457322	0.35678043	1
MF	GO:0120227	acyl-CoA binding	1/292	28/22669	0.30457322	0.35678043	1
MF	GO:0015298	solute:cation antiporter activity	1/292	29/22669	0.31354211	0.3658631	1
MF	GO:0000175	3'-5'-exoribonuclease activity	1/292	30/22669	0.32239572	0.37124981	1
MF	GO:0001530	lipopolysaccharide binding	1/292	30/22669	0.32239572	0.37124981	1
MF	GO:0098918	structural constituent of synapse	1/292	30/22669	0.32239572	0.37124981	1
MF	GO:0008013	beta-catenin binding	2/292	90/22669	0.32309118	0.37124981	2
MF	GO:0030515	snoRNA binding	1/292	31/22669	0.33113553	0.37904647	1

MF	GO:0051213	dioxygenase activity	2/292	92/22669	0.33252345	0.3791934	2
MF	GO:0004620	phospholipase activity	2/292	93/22669	0.33722574	0.38310452	2
MF	GO:0016896	exoribonuclease activity, producing 5'-phosphomonoesters	1/292	32/22669	0.33976299	0.38453587	1
MF	GO:0032182	ubiquitin-like protein binding	2/292	95/22669	0.34659997	0.39080461	2
MF	GO:0004532	exoribonuclease activity	1/292	33/22669	0.34827954	0.3912331	1
MF	GO:0030547	receptor inhibitor activity	1/292	34/22669	0.35668661	0.39918752	1
MF	GO:1901567	fatty acid derivative binding	1/292	35/22669	0.36498559	0.40696249	1
MF	GO:0099094	ligand-gated cation channel activity	2/292	100/22669	0.36983501	0.41002256	2
MF	GO:0016504	peptidase activator activity	1/292	36/22669	0.37317788	0.41002256	1
MF	GO:0030551	cyclic nucleotide binding	1/292	36/22669	0.37317788	0.41002256	1
MF	GO:0042287	MHC protein binding	1/292	36/22669	0.37317788	0.41002256	1
MF	GO:0043394	proteoglycan binding	1/292	38/22669	0.38924781	0.42457999	1
MF	GO:0046915	transition metal ion transmembrane transporter activity	1/292	38/22669	0.38924781	0.42457999	1
MF	GO:0004712	protein serine/threonine/tyrosine kinase activity	1/292	39/22669	0.39712813	0.4316118	1

MF	GO:0004180	carboxypeptidase activity	1/292	40/22669	0.40490712	0.43848329	1
MF	GO:0005109	frizzled binding	1/292	41/22669	0.41258608	0.44360759	1
MF	GO:0017069	snRNA binding	1/292	41/22669	0.41258608	0.44360759	1
MF	GO:0030594	neurotransmitter receptor activity	2/292	111/22669	0.41971405	0.44554011	2
MF	GO:0043539	protein serine/threonine kinase activator activity	1/292	42/22669	0.42016629	0.44554011	1
MF	GO:0051019	mitogen-activated protein kinase binding	1/292	42/22669	0.42016629	0.44554011	1
MF	GO:0016887	ATPase activity	6/292	404/22669	0.42030322	0.44554011	6
MF	GO:0004540	ribonuclease activity	2/292	114/22669	0.43297294	0.45633651	2
MF	GO:0004177	aminopeptidase activity	1/292	44/22669	0.43503548	0.45633651	1
MF	GO:0048487	beta-tubulin binding	1/292	44/22669	0.43503548	0.45633651	1
MF	GO:0140296	general transcription initiation factor binding	1/292	46/22669	0.44952465	0.46989784	1
MF	GO:0005548	phospholipid transporter activity	1/292	47/22669	0.45662975	0.47403307	1
MF	GO:0070888	E-box binding	1/292	47/22669	0.45662975	0.47403307	1
MF	GO:0030331	estrogen receptor binding	1/292	48/22669	0.46364346	0.47638595	1

MF	GO:0050661	NADP binding	1/292	48/22669	0.46364346	0.47638595	1
MF	GO:0051879	Hsp90 protein binding	1/292	48/22669	0.46364346	0.47638595	1
MF	GO:0004518	nuclease activity	3/292	197/22669	0.46725871	0.4781806	3
MF	GO:0008408	3'-5' exonuclease activity	1/292	49/22669	0.47056695	0.4781806	1
MF	GO:0015459	potassium channel regulator activity	1/292	49/22669	0.47056695	0.4781806	1
MF	GO:0042826	histone deacetylase binding	2/292	123/22669	0.47174355	0.4781806	2
MF	GO:0016790	thiolester hydrolase activity	1/292	50/22669	0.47740136	0.47907645	1
MF	GO:0016860	intramolecular oxidoreductase activity	1/292	50/22669	0.47740136	0.47907645	1
MF	GO:0030544	Hsp70 protein binding	1/292	50/22669	0.47740136	0.47907645	1
MF	GO:0016763	transferase activity, transferring pentosyl groups	1/292	51/22669	0.48414785	0.48103625	1
MF	GO:0016796	exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	1/292	51/22669	0.48414785	0.48103625	1
MF	GO:0030374	nuclear receptor transcription coactivator activity	1/292	51/22669	0.48414785	0.48103625	1
MF	GO:0016298	lipase activity	2/292	128/22669	0.49258662	0.48781085	2
MF	GO:0004674	protein serine/threonine kinase activity	6/292	439/22669	0.49918803	0.49272744	6

MF	GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	2/292	131/22669	0.50484156	0.49667934	2
MF	GO:0015276	ligand-gated ion channel activity	2/292	132/22669	0.50888385	0.49876686	2
MF	GO:0035591	signaling adaptor activity	1/292	55/22669	0.51027686	0.49876686	1
MF	GO:0046982	protein heterodimerization activity	4/292	290/22669	0.51519038	0.50168998	4
MF	GO:0016836	hydro-lyase activity	1/292	56/22669	0.51660034	0.50168998	1
MF	GO:0004866	endopeptidase inhibitor activity	3/292	213/22669	0.51901782	0.50241698	3
MF	GO:0022834	ligand-gated channel activity	2/292	135/22669	0.52088094	0.50260441	2
MF	GO:0004536	deoxyribonuclease activity	1/292	58/22669	0.52900422	0.50881186	1
MF	GO:0001098	basal transcription machinery binding	1/292	59/22669	0.53508669	0.51139446	1
MF	GO:0001099	basal RNA polymerase II transcription machinery binding	1/292	59/22669	0.53508669	0.51139446	1
MF	GO:0030414	peptidase inhibitor activity	3/292	219/22669	0.53772125	0.51228607	3
MF	GO:0008047	enzyme activator activity	6/292	460/22669	0.54475166	0.51530182	6
MF	GO:0004521	endoribonuclease activity	1/292	61/22669	0.54701779	0.51530182	1
MF	GO:0005507	copper ion binding	1/292	61/22669	0.54701779	0.51530182	1

MF	GO:0061135	endopeptidase regulator activity	3/292	223/22669	0.54995829	0.51530182	3
MF	GO:0044325	ion channel binding	2/292	143/22669	0.55190385	0.51530182	2
MF	GO:0030145	manganese ion binding	1/292	62/22669	0.55286841	0.51530182	1
MF	GO:0043022	ribosome binding	1/292	62/22669	0.55286841	0.51530182	1
MF	GO:0005080	protein kinase C binding	1/292	63/22669	0.55864372	0.51907766	1
MF	GO:0043021	ribonucleoprotein complex binding	2/292	146/22669	0.563168	0.52115783	2
MF	GO:0008227	G protein-coupled amine receptor activity	1/292	64/22669	0.56434468	0.52115783	1
MF	GO:0001085	RNA polymerase II transcription factor binding	1/292	65/22669	0.56997226	0.5247451	1
MF	GO:0004386	helicase activity	2/292	150/22669	0.57786969	0.53039388	2
MF	GO:0016835	carbon-oxygen lyase activity	1/292	67/22669	0.58101099	0.5316562	1
MF	GO:0004869	cysteine-type endopeptidase inhibitor activity	1/292	69/22669	0.59176731	0.5398579	1
MF	GO:0016597	amino acid binding	1/292	70/22669	0.59704182	0.54302421	1
MF	GO:0005518	collagen binding	1/292	71/22669	0.60224842	0.54610985	1
MF	GO:0005089	Rho guanyl-nucleotide exchange factor activity	1/292	73/22669	0.61246132	0.54926771	1

MF	GO:0005254	chloride channel activity	1/292	73/22669	0.61246132	0.54926771	1
MF	GO:0017022	myosin binding	1/292	73/22669	0.61246132	0.54926771	1
MF	GO:0008234	cysteine-type peptidase activity	2/292	160/22669	0.61302886	0.54926771	2
MF	GO:0015297	antiporter activity	1/292	74/22669	0.61746935	0.5499727	1
MF	GO:0097110	scaffold protein binding	1/292	74/22669	0.61746935	0.5499727	1
MF	GO:0061134	peptidase regulator activity	3/292	254/22669	0.63799801	0.56658106	3
MF	GO:0016811	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	1/292	80/22669	0.64619163	0.57216968	1
MF	GO:0048029	monosaccharide binding	1/292	82/22669	0.65527982	0.57851529	1
MF	GO:0005253	anion channel activity	1/292	83/22669	0.65973629	0.57905349	1
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	1/292	83/22669	0.65973629	0.57905349	1
MF	GO:0048306	calcium-dependent protein binding	1/292	89/22669	0.68529482	0.59973782	1
MF	GO:0008238	exopeptidase activity	1/292	91/22669	0.69338178	0.60505626	1
MF	GO:0004175	endopeptidase activity	5/292	453/22669	0.696556066	0.60606941	5
MF	GO:0016829	lyase activity	2/292	188/22669	0.69948571	0.6068646	2

MF	GO:0031490	chromatin DNA binding	1/292	94/22669	0.70512553	0.6099997	1
MF	GO:0140030	modification-dependent protein binding	2/292	192/22669	0.71043961	0.61283586	2
MF	GO:0004197	cysteine-type endopeptidase activity	1/292	96/22669	0.71270456	0.6130331	1
MF	GO:0051117	ATPase binding	1/292	97/22669	0.71642096	0.61447412	1
MF	GO:0004843	thiol-dependent ubiquitin-specific protease activity	1/292	99/22669	0.72371064	0.61896305	1
MF	GO:0101005	ubiquitinyl hydrolase activity	1/292	100/22669	0.72728514	0.62025809	1
MF	GO:0015108	chloride transmembrane transporter activity	1/292	102/22669	0.73429647	0.62270953	1
MF	GO:0051087	chaperone binding	1/292	102/22669	0.73429647	0.62270953	1
MF	GO:0003823	antigen binding	2/292	208/22669	0.75096468	0.63334795	2
MF	GO:0008242	omega peptidase activity	1/292	107/22669	0.7510488	0.63334795	1
MF	GO:0099106	ion channel regulator activity	1/292	110/22669	0.76059053	0.63949868	1
MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2/292	213/22669	0.76259099	0.63949868	2
MF	GO:0015078	proton transmembrane transporter activity	1/292	112/22669	0.7667483	0.64119887	1
MF	GO:0030674	protein-macromolecule adaptor activity	2/292	222/22669	0.78233743	0.65242311	2

MF	GO:0004519	endonuclease activity	1/292	121/22669	0.79256217	0.65912411	1
MF	GO:0003713	transcription coactivator activity	2/292	232/22669	0.80257834	0.66421914	2
MF	GO:0005088	Ras guanyl-nucleotide exchange factor activity	1/292	125/22669	0.80310133	0.66421914	1
MF	GO:0004867	serine-type endopeptidase inhibitor activity	1/292	129/22669	0.81310677	0.66881949	1
MF	GO:0017124	SH3 domain binding	1/292	129/22669	0.81310677	0.66881949	1
MF	GO:0003712	transcription coregulator activity	4/292	441/22669	0.82246731	0.67467561	4
MF	GO:0015103	inorganic anion transmembrane transporter activity	1/292	136/22669	0.8294123	0.67843021	1
MF	GO:0019842	vitamin binding	1/292	137/22669	0.83162291	0.67843021	1
MF	GO:0005319	lipid transporter activity	1/292	138/22669	0.83380497	0.67843021	1
MF	GO:0042393	histone binding	2/292	265/22669	0.8580131	0.69624556	2
MF	GO:0016853	isomerase activity	1/292	153/22669	0.86334886	0.69869206	1
MF	GO:0019001	guanyl nucleotide binding	3/292	379/22669	0.8689001	0.69942423	3
MF	GO:0032561	guanyl ribonucleotide binding	3/292	379/22669	0.8689001	0.69942423	3
MF	GO:0017137	Rab GTPase binding	1/292	163/22669	0.88007444	0.70652994	1

MF	GO:0004857	enzyme inhibitor activity	3/292	392/22669	0.88320571	0.70685211	3
MF	GO:0017048	Rho GTPase binding	1/292	168/22669	0.88765559	0.70685211	1
MF	GO:0003714	transcription corepressor activity	1/292	176/22669	0.89880435	0.70685211	1
MF	GO:0061630	ubiquitin protein ligase activity	2/292	299/22669	0.8999471	0.70685211	2
MF	GO:0004842	ubiquitin-protein transferase activity	3/292	418/22669	0.90771938	0.70685211	3
MF	GO:0061659	ubiquitin-like protein ligase activity	2/292	307/22669	0.9079814	0.70685211	2
MF	GO:0140097	catalytic activity, acting on DNA	1/292	184/22669	0.90885015	0.70685211	1
MF	GO:0005216	ion channel activity	3/292	421/22669	0.91022689	0.70685211	3
MF	GO:0031267	small GTPase binding	3/292	424/22669	0.91267263	0.70685211	3
MF	GO:0060090	molecular adaptor activity	2/292	316/22669	0.91629862	0.70685211	2
MF	GO:0005516	calmodulin binding	1/292	192/22669	0.91790177	0.70685211	1
MF	GO:0003779	actin binding	3/292	434/22669	0.9203952	0.70685211	3
MF	GO:0019787	ubiquitin-like protein transferase activity	3/292	435/22669	0.92113225	0.70685211	3
MF	GO:0022836	gated channel activity	2/292	323/22669	0.92227513	0.70685211	2

MF	GO:0000287	magnesium ion binding	1/292	197/22669	0.92309817	0.70685211	1
MF	GO:0016758	transferase activity, transferring hexosyl groups	1/292	199/22669	0.92508374	0.70685211	1
MF	GO:0005261	cation channel activity	2/292	327/22669	0.92550794	0.70685211	2
MF	GO:0005085	guanyl-nucleotide exchange factor activity	1/292	201/22669	0.92701822	0.70685211	1
MF	GO:0140098	catalytic activity, acting on RNA	2/292	332/22669	0.92937119	0.70685211	2
MF	GO:0051015	actin filament binding	1/292	210/22669	0.93512544	0.70685211	1
MF	GO:0015267	channel activity	3/292	461/22669	0.93823863	0.70685211	3
MF	GO:0022803	passive transmembrane transporter activity	3/292	461/22669	0.93823863	0.70685211	3
MF	GO:0022853	active ion transmembrane transporter activity	1/292	218/22669	0.94157491	0.70685211	1
MF	GO:0005525	GTP binding	2/292	355/22669	0.94483075	0.70685211	2
MF	GO:0042578	phosphoric ester hydrolase activity	2/292	357/22669	0.94601149	0.70685211	2
MF	GO:0032550	purine ribonucleoside binding	2/292	362/22669	0.94885922	0.70685211	2
MF	GO:0032549	ribonucleoside binding	2/292	365/22669	0.95049868	0.70685211	2
MF	GO:0015291	secondary active transmembrane transporter activity	1/292	231/22669	0.95072036	0.70685211	1

MF	GO:0001883	purine nucleoside binding	2/292	366/22669	0.95103397	0.70685211	2
MF	GO:0008022	protein C-terminus binding	1/292	233/22669	0.95199465	0.70685211	1
MF	GO:0005096	GTPase activator activity	1/292	238/22669	0.95503856	0.70685211	1
MF	GO:0001882	nucleoside binding	2/292	375/22669	0.95560968	0.70685211	2
MF	GO:0030695	GTPase regulator activity	1/292	258/22669	0.96540773	0.71084035	1
MF	GO:0008017	microtubule binding	1/292	260/22669	0.96630331	0.71084035	1
MF	GO:0017016	Ras GTPase binding	2/292	409/22669	0.96947605	0.71084035	2
MF	GO:0016757	transferase activity, transferring glycosyl groups	1/292	270/22669	0.97044621	0.71084035	1
MF	GO:0003924	GTPase activity	1/292	296/22669	0.97899317	0.71402536	1
MF	GO:0060589	nucleoside-triphosphatase regulator activity	1/292	298/22669	0.97953794	0.71402536	1
MF	GO:0008509	anion transmembrane transporter activity	1/292	336/22669	0.98758517	0.71419849	1
MF	GO:0022804	active transmembrane transporter activity	1/292	341/22669	0.9883759	0.71419849	1
MF	GO:0003729	mRNA binding	1/292	345/22669	0.98897218	0.71419849	1
MF	GO:0015077	monovalent inorganic cation transmembrane transporter activity	1/292	361/22669	0.99106758	0.71419849	1

MF	GO:0015631	tubulin binding	1/292	366/22669	0.99163713	0.71419849	1
MF	GO:0046873	metal ion transmembrane transporter activity	1/292	426/22669	0.99621133	0.71578053	1

Table S9 Significant Enrichment Results of KEGG of FRGs

ID	Description	GeneRatio	BgRatio	pvalue	qvalue	Count
mmu04216	Ferroptosis	9/48	40/8939	4.06E-13	4.70E-11	9
mmu04140	Autophagy - animal	7/48	142/8939	9.41E-06	0.0005445	7
mmu04657	IL-17 signaling pathway	5/48	91/8939	0.00011867	0.00449769	5
mmu01210	2-Oxocarboxylic acid metabolism	3/48	20/8939	0.00015537	0.00449769	3
mmu04668	TNF signaling pathway	5/48	113/8939	0.00032794	0.00659257	5
mmu04066	HIF-1 signaling pathway	5/48	114/8939	0.00034161	0.00659257	5
mmu05230	Central carbon metabolism in cancer	4/48	69/8939	0.00048984	0.00680123	4
mmu01523	Antifolate resistance	3/48	30/8939	0.00053288	0.00680123	3
mmu00480	Glutathione metabolism	4/48	72/8939	0.0005761	0.00680123	4
mmu00020	Citrate cycle (TCA cycle)	3/48	32/8939	0.00064612	0.00680123	3
mmu04136	Autophagy - other	3/48	32/8939	0.00064612	0.00680123	3

mmu05167	Kaposi sarcoma-associated herpesvirus infection	6/48	224/8939	0.00117885	0.01137491	6
mmu04064	NF-kappa B signaling pathway	4/48	105/8939	0.00235195	0.02040769	4
mmu05146	Amoebiasis	4/48	107/8939	0.00251931	0.02040769	4
mmu04931	Insulin resistance	4/48	110/8939	0.00278546	0.02040769	4
mmu00270	Cysteine and methionine metabolism	3/48	53/8939	0.00281997	0.02040769	3
mmu05134	Legionellosis	3/48	61/8939	0.00420438	0.02863667	3
mmu05206	MicroRNAs in cancer	6/48	303/8939	0.00534251	0.03350613	6
mmu04137	Mitophagy - animal	3/48	68/8939	0.00570315	0.03350613	3
mmu05417	Lipid and atherosclerosis	5/48	216/8939	0.00578742	0.03350613	5
mmu04920	Adipocytokine signaling pathway	3/48	71/8939	0.0064316	0.03546246	3
mmu05162	Measles	4/48	146/8939	0.00761413	0.04007435	4
mmu05418	Fluid shear stress and atherosclerosis	4/48	148/8939	0.00798205	0.04018422	4
mmu01230	Biosynthesis of amino acids	3/48	79/8939	0.00863661	0.04166785	3

mmu04146	Peroxisome	3/48	86/8939	0.01088889	0.05043277	3
mmu03320	PPAR signaling pathway	3/48	89/8939	0.01194874	0.05216797	3
mmu05022	Pathways of neurodegeneration - multiple diseases	7/48	471/8939	0.01216462	0.05216797	7
mmu00630	Glyoxylate and dicarboxylate metabolism	2/48	32/8939	0.01263966	0.05226926	2
mmu04217	Necroptosis	4/48	176/8939	0.01440882	0.05753067	4
mmu04659	Th17 cell differentiation	3/48	105/8939	0.01858379	0.07172691	3
mmu04625	C-type lectin receptor signaling pathway	3/48	112/8939	0.02201517	0.08222984	3
mmu04621	NOD-like receptor signaling pathway	4/48	211/8939	0.02613582	0.09439954	4
mmu01200	Carbon metabolism	3/48	121/8939	0.02690387	0.09439954	3
mmu04726	Serotonergic synapse	3/48	131/8939	0.03296401	0.11197638	3
mmu04978	Mineral absorption	2/48	54/8939	0.03384741	0.11197638	2
mmu05169	Epstein-Barr virus infection	4/48	231/8939	0.03483813	0.11205246	4
mmu04370	VEGF signaling pathway	2/48	58/8939	0.03857466	0.11780677	2
mmu04936	Alcoholic liver disease	3/48	141/8939	0.03967946	0.11780677	3

mmu05017	Spinocerebellar ataxia	3/48	141/8939	0.03967946	0.11780677	3
mmu01212	Fatty acid metabolism	2/48	62/8939	0.04353846	0.12067683	2
mmu05321	Inflammatory bowel disease	2/48	62/8939	0.04353846	0.12067683	2
mmu05166	Human T-cell leukemia virus 1 infection	4/48	250/8939	0.04450506	0.12067683	4
mmu04623	Cytosolic DNA-sensing pathway	2/48	63/8939	0.04481499	0.12067683	2
mmu04150	mTOR signaling pathway	3/48	156/8939	0.05095623	0.13226261	3
mmu05211	Renal cell carcinoma	2/48	68/8939	0.05140206	0.13226261	2
mmu05010	Alzheimer disease	5/48	383/8939	0.05335479	0.13335257	5
mmu05140	Leishmaniasis	2/48	70/8939	0.05412902	0.13335257	2
mmu04918	Thyroid hormone synthesis	2/48	74/8939	0.05973335	0.1440936	2
mmu05133	Pertussis	2/48	77/8939	0.06406295	0.14941598	2
mmu04141	Protein processing in endoplasmic reticulum	3/48	172/8939	0.06452054	0.14941598	3
mmu00430	Taurine and hypotaurine metabolism	1/48	13/8939	0.06764507	0.15358014	1

mmu04218	Cellular senescence	3/48	184/8939	0.07568383	0.16852674	3
mmu00590	Arachidonic acid metabolism	2/48	86/8939	0.07765543	0.16965436	2
mmu05323	Rheumatoid arthritis	2/48	87/8939	0.07921824	0.16986367	2
mmu05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	2/48	88/8939	0.08079101	0.17008634	2
mmu04211	Longevity regulating pathway	2/48	90/8939	0.08396584	0.17361357	2
mmu05222	Small cell lung cancer	2/48	93/8939	0.08879913	0.17841483	2
mmu04640	Hematopoietic cell lineage	2/48	94/8939	0.0904286	0.17841483	2
mmu04061	Viral protein interaction with cytokine and cytokine receptor	2/48	95/8939	0.09206703	0.17841483	2
mmu00120	Primary bile acid biosynthesis	1/48	18/8939	0.09245132	0.17841483	1
mmu00061	Fatty acid biosynthesis	1/48	19/8939	0.09733444	0.18434349	1
mmu05215	Prostate cancer	2/48	99/8939	0.09870756	0.18434349	2
mmu04620	Toll-like receptor signaling pathway	2/48	100/8939	0.10038872	0.18450725	2

mmu04933	AGE-RAGE signaling pathway in diabetic complications	2/48	101/8939	0.10207802	0.18468063	2
mmu05142	Chagas disease	2/48	103/8939	0.10548053	0.18790055	2

Table S10 Significant Enrichment Results of KEGG of IRGs

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
mmu04060	Cytokine-cytokine receptor interaction	89/259	292/8939	6.35E-70	1.42E-67	8.09E-68	89
mmu04061	Viral protein interaction with cytokine and cytokine receptor	39/259	95/8939	1.01E-35	1.13E-33	6.41E-34	39
mmu05323	Rheumatoid arthritis	25/259	87/8939	9.79E-19	7.31E-17	4.15E-17	25
mmu04062	Chemokine signaling pathway	33/259	192/8939	5.69E-17	2.94E-15	1.67E-15	33
mmu04630	JAK-STAT signaling pathway	31/259	168/8939	6.57E-17	2.94E-15	1.67E-15	31
mmu04668	TNF signaling pathway	25/259	113/8939	9.01E-16	3.36E-14	1.91E-14	25
mmu04657	IL-17 signaling pathway	22/259	91/8939	7.09E-15	2.27E-13	1.29E-13	22
mmu05321	Inflammatory bowel disease	18/259	62/8939	6.80E-14	1.90E-12	1.08E-12	18
mmu04659	Th17 cell differentiation	22/259	105/8939	1.71E-13	4.26E-12	2.42E-12	22
mmu04010	MAPK signaling pathway	35/259	294/8939	6.30E-13	1.41E-11	8.02E-12	35
mmu04064	NF-kappa B signaling pathway	21/259	105/8939	1.63E-12	3.32E-11	1.89E-11	21
mmu04080	Neuroactive ligand-receptor interaction	39/259	376/8939	2.26E-12	4.22E-11	2.40E-11	39
mmu04620	Toll-like receptor signaling pathway	20/259	100/8939	5.65E-12	9.73E-11	5.53E-11	20

mmu04380	Osteoclast differentiation	22/259	128/8939	1.16E-11	1.85E-10	1.05E-10	22
mmu05417	Lipid and atherosclerosis	28/259	216/8939	1.99E-11	2.97E-10	1.69E-10	28
mmu05144	Malaria	15/259	57/8939	4.22E-11	5.91E-10	3.36E-10	15
mmu04672	Intestinal immune network for IgA production	12/259	43/8939	1.87E-09	2.47E-08	1.40E-08	12
mmu04660	T cell receptor signaling pathway	17/259	103/8939	5.23E-09	6.50E-08	3.70E-08	17
mmu04151	PI3K-Akt signaling pathway	32/259	359/8939	1.16E-08	1.36E-07	7.76E-08	32
mmu05134	Legionellosis	13/259	61/8939	1.43E-08	1.60E-07	9.09E-08	13
mmu05164	Influenza A	21/259	173/8939	2.41E-08	2.57E-07	1.46E-07	21
mmu05167	Kaposi sarcoma-associated herpesvirus infection	24/259	224/8939	2.77E-08	2.82E-07	1.61E-07	24
mmu04625	C-type lectin receptor signaling pathway	16/259	112/8939	1.23E-07	1.19E-06	6.79E-07	16
mmu04933	AGE-RAGE signaling pathway in diabetic complications	15/259	101/8939	1.82E-07	1.70E-06	9.65E-07	15
mmu04658	Th1 and Th2 cell differentiation	14/259	88/8939	1.96E-07	1.70E-06	9.67E-07	14
mmu05162	Measles	18/259	146/8939	1.97E-07	1.70E-06	9.67E-07	18
mmu05146	Amoebiasis	15/259	107/8939	3.95E-07	3.27E-06	1.86E-06	15
mmu05145	Toxoplasmosis	15/259	110/8939	5.69E-07	4.55E-06	2.59E-06	15
mmu05142	Chagas disease	14/259	103/8939	1.42E-06	1.10E-05	6.24E-06	14
mmu04640	Hematopoietic cell lineage	13/259	94/8939	2.79E-06	2.08E-05	1.18E-05	13
mmu05161	Hepatitis B	17/259	163/8939	4.59E-06	3.16E-05	1.79E-05	17
mmu04622	RIG-I-like receptor signaling pathway	11/259	70/8939	4.65E-06	3.16E-05	1.79E-05	11
mmu05140	Leishmaniasis	11/259	70/8939	4.65E-06	3.16E-05	1.79E-05	11
mmu05418	Fluid shear stress and atherosclerosis	16/259	148/8939	5.53E-06	3.55E-05	2.02E-05	16

mmu04024	cAMP signaling pathway	20/259	220/8939	5.55E-06	3.55E-05	2.02E-05	20
mmu05135	Yersinia infection	15/259	134/8939	7.10E-06	4.42E-05	2.51E-05	15
mmu04623	Cytosolic DNA-sensing pathway	10/259	63/8939	1.16E-05	7.01E-05	3.98E-05	10
mmu04014	Ras signaling pathway	20/259	232/8939	1.23E-05	7.23E-05	4.11E-05	20
mmu05143	African trypanosomiasis	8/259	39/8939	1.26E-05	7.23E-05	4.11E-05	8
mmu04015	Rap1 signaling pathway	19/259	214/8939	1.35E-05	7.54E-05	4.29E-05	19
mmu05163	Human cytomegalovirus infection	21/259	256/8939	1.60E-05	8.71E-05	4.96E-05	21
mmu05205	Proteoglycans in cancer	18/259	205/8939	2.65E-05	0.00014134	8.04E-05	18
mmu05171	Coronavirus disease - COVID-19	20/259	247/8939	3.08E-05	0.00016048	9.12E-05	20
mmu04920	Adipocytokine signaling pathway	10/259	71/8939	3.41E-05	0.00017361	9.87E-05	10
mmu05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	11/259	88/8939	4.34E-05	0.00021593	0.00012278	11
mmu04650	Natural killer cell mediated cytotoxicity	13/259	121/8939	4.53E-05	0.00022057	0.00012542	13
mmu04917	Prolactin signaling pathway	10/259	74/8939	4.92E-05	0.00023428	0.00013322	10
mmu04936	Alcoholic liver disease	14/259	141/8939	5.59E-05	0.00026093	0.00014837	14
mmu05310	Asthma	6/259	25/8939	6.22E-05	0.00028428	0.00016165	6
mmu04360	Axon guidance	16/259	181/8939	6.89E-05	0.00030868	0.00017552	16
mmu05166	Human T-cell leukemia virus 1 infection	19/259	250/8939	0.00011447	0.00050275	0.00028587	19
mmu05169	Epstein-Barr virus infection	18/259	231/8939	0.00012649	0.0005449	0.00030984	18
mmu04012	ErbB signaling pathway	10/259	84/8939	0.00014653	0.00061928	0.00035213	10
mmu04020	Calcium signaling pathway	18/259	240/8939	0.00020454	0.00084844	0.00048243	18
mmu05160	Hepatitis C	14/259	165/8939	0.00030045	0.00122363	0.00069577	14

mmu04621	NOD-like receptor signaling pathway	16/259	211/8939	0.00040727	0.0016291	0.00092632	16
mmu04662	B cell receptor signaling pathway	9/259	81/8939	0.00052809	0.00207531	0.00118004	9
mmu04932	Non-alcoholic fatty liver disease	13/259	156/8939	0.00058426	0.00225647	0.00128305	13
mmu05152	Tuberculosis	14/259	180/8939	0.00072472	0.00275149	0.00156452	14
mmu05224	Breast cancer	12/259	147/8939	0.00113164	0.0042248	0.00240226	12
mmu05220	Chronic myeloid leukemia	8/259	76/8939	0.00153041	0.00561986	0.0031955	8
mmu05133	Pertussis	8/259	77/8939	0.00166598	0.00595142	0.00338403	8
mmu04350	TGF-beta signaling pathway	9/259	95/8939	0.00167384	0.00595142	0.00338403	9
mmu04210	Apoptosis	11/259	136/8939	0.00194296	0.00677363	0.00385155	11
mmu01521	EGFR tyrosine kinase inhibitor resistance	8/259	79/8939	0.00196556	0.00677363	0.00385155	8
mmu04722	Neurotrophin signaling pathway	10/259	121/8939	0.002634	0.00893965	0.00508317	10
mmu05226	Gastric cancer	11/259	150/8939	0.00416686	0.01393101	0.0079213	11
mmu04612	Antigen processing and presentation	8/259	90/8939	0.00444819	0.01455565	0.00827647	8
mmu04931	Insulin resistance	9/259	110/8939	0.00454685	0.01455565	0.00827647	9
mmu04514	Cell adhesion molecules	12/259	174/8939	0.00463126	0.01455565	0.00827647	12
mmu04068	FoxO signaling pathway	10/259	131/8939	0.00466908	0.01455565	0.00827647	10
mmu05218	Melanoma	7/259	72/8939	0.0046786	0.01455565	0.00827647	7
mmu05410	Hypertrophic cardiomyopathy	8/259	91/8939	0.00475797	0.01459981	0.00830158	8
mmu04923	Regulation of lipolysis in adipocytes	6/259	56/8939	0.00538805	0.01630976	0.00927388	6
mmu04924	Renin secretion	7/259	76/8939	0.00629849	0.01881148	0.01069638	7
mmu04213	Longevity regulating pathway - multiple species	6/259	62/8939	0.00883708	0.02604614	0.01481007	6

mmu05332	Graft-versus-host disease	6/259	63/8939	0.00953683	0.02774349	0.0157752	6
mmu01523	Antifolate resistance	4/259	30/8939	0.01043061	0.02995457	0.01703244	4
mmu04072	Phospholipase D signaling pathway	10/259	149/8939	0.01125613	0.03191611	0.01814779	10
mmu04930	Type II diabetes mellitus	5/259	48/8939	0.0121807	0.03410595	0.01939295	5
mmu04926	Relaxin signaling pathway	9/259	129/8939	0.01251334	0.0346048	0.0196766	9
mmu05202	Transcriptional misregulation in cancer	13/259	223/8939	0.01286491	0.03500507	0.0199042	13
mmu04928	Parathyroid hormone synthesis, secretion and action	8/259	108/8939	0.01297063	0.03500507	0.0199042	8
mmu05210	Colorectal cancer	7/259	88/8939	0.0136679	0.03644772	0.0207245	7
mmu04510	Focal adhesion	12/259	201/8939	0.01391571	0.03667199	0.02085202	12
mmu04915	Estrogen signaling pathway	9/259	134/8939	0.01573927	0.0409953	0.0233103	9
mmu04066	HIF-1 signaling pathway	8/259	114/8939	0.01750642	0.045074	0.02562948	8
mmu01522	Endocrine resistance	7/259	93/8939	0.01807476	0.04600847	0.02616083	7
mmu05414	Dilated cardiomyopathy	7/259	94/8939	0.0190634	0.04789771	0.02723507	7
mmu04935	Growth hormone synthesis, secretion and action	8/259	116/8939	0.01924461	0.04789771	0.02723507	8
mmu05340	Primary immunodeficiency	4/259	36/8939	0.01959326	0.04822957	0.02742377	4
mmu04550	Signaling pathways regulating pluripotency of stem cells	9/259	140/8939	0.02037222	0.04960191	0.0282041	9
mmu04670	Leukocyte transendothelial migration	8/259	118/8939	0.02110281	0.05082827	0.02890141	8
mmu05212	Pancreatic cancer	6/259	76/8939	0.02252692	0.05368117	0.0305236	6
mmu04270	Vascular smooth muscle contraction	9/259	144/8939	0.02396324	0.05650279	0.0321288	9
mmu05215	Prostate cancer	7/259	99/8939	0.02457906	0.05735113	0.03261037	7
mmu05320	Autoimmune thyroid disease	6/259	79/8939	0.02667999	0.06161152	0.03503287	6

mmu05225	Hepatocellular carcinoma	10/259	174/8939	0.0298089	0.06813462	0.03874196	10
mmu05207	Chemical carcinogenesis - receptor activation	12/259	225/8939	0.03052237	0.06906071	0.03926854	12
mmu05330	Allograft rejection	5/259	63/8939	0.03534014	0.07916191	0.04501218	5
mmu04664	Fc epsilon RI signaling pathway	5/259	66/8939	0.0419433	0.09302276	0.05289358	5
mmu04211	Longevity regulating pathway	6/259	90/8939	0.04612893	0.1007788	0.05730374	6
mmu05170	Human immunodeficiency virus 1 infection	12/259	240/8939	0.04634025	0.1007788	0.05730374	12
mmu04610	Complement and coagulation cascades	6/259	93/8939	0.05264229	0.1133834	0.06447082	6
mmu04710	Circadian rhythm	3/259	30/8939	0.05492658	0.1162333	0.06609131	3
mmu04810	Regulation of actin cytoskeleton	11/259	220/8939	0.05500326	0.1162333	0.06609131	11
mmu05132	Salmonella infection	12/259	253/8939	0.06401739	0.1340177	0.07620368	12
mmu04370	VEGF signaling pathway	4/259	58/8939	0.08677339	0.17997443	0.10233509	4
mmu05416	Viral myocarditis	5/259	88/8939	0.11160563	0.2293547	0.13041315	5
mmu05211	Renal cell carcinoma	4/259	68/8939	0.13410525	0.27308706	0.15527977	4
mmu04217	Necroptosis	8/259	176/8939	0.13882372	0.28014876	0.15929511	8
mmu04940	Type I diabetes mellitus	4/259	70/8939	0.14463013	0.28926026	0.164476	4
mmu04520	Adherens junction	4/259	71/8939	0.15001092	0.29599743	0.16830681	4
mmu04071	Sphingolipid signaling pathway	6/259	124/8939	0.15064155	0.29599743	0.16830681	6
mmu04152	AMPK signaling pathway	6/259	126/8939	0.15874438	0.30920644	0.17581757	6
mmu04218	Cellular senescence	8/259	184/8939	0.1651806	0.31896944	0.1813689	8
mmu04390	Hippo signaling pathway	7/259	157/8939	0.17074727	0.32690075	0.18587872	7
mmu05100	Bacterial invasion of epithelial cells	4/259	76/8939	0.1780053	0.3352138	0.19060559	4

mmu05168	Herpes simplex virus 1 infection	17/259	459/8939	0.17808233	0.3352138	0.19060559	17
mmu04950	Maturity onset diabetes of the young	2/259	27/8939	0.18353871	0.34260559	0.19480863	2