

Table SIV. GSEA results of c5-reference gene sets for groups with high CCR5 expression.

GS follow link to MSigDB	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	227	0.644027	2.167779	<0.001	0.052766	0.038	5,211
GO_ADAPTIVE_IMMUNE_RESPONSE	261	0.683741	2.148318	<0.001	0.04424	0.06	4,815
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	83	0.629059	2.129852	<0.001	0.043367	0.074	3,570
GO_LYMPHOCYTE_DIFFERENTIATION	191	0.60992	2.120378	<0.001	0.040989	0.084	3,236
GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	27	0.727815	2.119218	<0.001	0.033573	0.087	3,173
GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	59	0.641365	2.118296	<0.001	0.027977	0.087	4,282
GO_LEUKOCYTE_PROLIFERATION	70	0.665175	2.113627	<0.001	0.026692	0.095	2,819
GO_LYMPHOCYTE_ACTIVATION	320	0.598321	2.105308	<0.001	0.026346	0.1	3,236
GO_T_CELL_DIFFERENTIATION	122	0.635494	2.104633	<0.001	0.023514	0.1	3,570
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_ OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	149	0.643679	2.103362	<0.001	0.021599	0.1	4,815
GO_LEUKOCYTE_ACTIVATION	387	0.571666	2.094341	<0.001	0.023708	0.118	3,236
GO_NATURAL_KILLER_CELL_ACTIVATION	39	0.703307	2.089424	<0.001	0.023755	0.124	2,871
GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	123	0.592513	2.089144	<0.001	0.022117	0.125	4,857
GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	22	0.756956	2.085798	<0.001	0.021515	0.131	3,173
GO_LEUKOCYTE_DIFFERENTIATION	272	0.563237	2.074412	<0.001	0.024743	0.146	3,236
GO_SIDE_OF_MEMBRANE	413	0.54057	2.06507	<0.001	0.027397	0.169	5,142
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	108	0.606109	2.060417	<0.001	0.027915	0.179	3,582
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	154	0.559447	2.058575	<0.001	0.027335	0.183	3,582
GO_CYTOKINE_PRODUCTION	116	0.575923	2.044277	<0.001	0.03209	0.213	3,450
GO_CYTOKINE_RECEPTOR_ACTIVITY	84	0.662274	2.043625	<0.001	0.030699	0.216	5,211
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	141	0.615386	2.042263	0.002004	0.029554	0.218	4,815
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	39	0.61584	2.039642	<0.001	0.029718	0.224	4,202
GO_LEUKOCYTE_CELL_CELL_ADHESION	236	0.584961	2.038452	<0.001	0.029077	0.225	5,025
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	51	0.6898	2.033769	<0.001	0.030015	0.234	2,586
GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	68	0.568692	2.025465	<0.001	0.03337	0.257	5,874
GO_LEUKOCYTE_MEDIATED_IMMUNITY	181	0.57989	2.02414	0.00202	0.032456	0.258	4,857
GO_REGULATION_OF_CELL_ACTIVATION	464	0.552668	2.023804	0.003976	0.031392	0.26	5,142
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	15	0.769027	2.02337	<0.001	0.030433	0.261	2,158
GO_PROTEIN_ACTIVATION_CASCADE	92	0.662735	2.020376	<0.001	0.031225	0.276	4,815
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	110	0.597635	2.017302	0.00198	0.031653	0.285	2,307
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	33	0.678658	2.012832	<0.001	0.032422	0.293	3,218
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	65	0.699566	2.012269	<0.001	0.031564	0.293	5,141
GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	195	0.54228	2.011616	<0.001	0.030852	0.295	5,662
GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	16	0.730956	2.010777	<0.001	0.030405	0.296	2,570
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.686646	2.009204	<0.001	0.030263	0.302	3,570

GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	24	0.676018	2.001798	<0.001	0.032852	0.324	2,375
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	98	0.574538	2.00081	<0.001	0.032219	0.325	4,162
GO_COMPLEMENT_ACTIVATION	71	0.71096	1.995946	<0.001	0.033728	0.337	5,142
GO_MYELOID_LEUKOCYTE_ACTIVATION	93	0.57614	1.995225	0.001972	0.033261	0.339	5,192
GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	40	0.626643	1.994359	<0.001	0.032726	0.341	3,527
GO_LEUKOCYTE_MIGRATION	252	0.533856	1.992876	0.001992	0.032549	0.347	4,606
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	45	0.640712	1.989929	<0.001	0.033009	0.354	3,570
GO_B_CELL_ACTIVATION	113	0.582481	1.989056	0.002024	0.03247	0.356	3,236
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	53	0.613731	1.986463	<0.001	0.033141	0.364	4,578
GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	16	0.689305	1.985943	<0.001	0.032572	0.365	2,002
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	33	0.741207	1.985452	<0.001	0.032144	0.367	2,307
GO_CORECEPTOR_ACTIVITY	35	0.723208	1.980048	<0.001	0.034105	0.383	2,926
GO_CYTOKINE_SECRETION	38	0.648685	1.978923	<0.001	0.033861	0.385	2,570
GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	47	0.569507	1.976471	<0.001	0.034097	0.393	4,202
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	299	0.578968	1.97587	0.006073	0.033632	0.395	4,226
GO_REGULATION_OF_CYTOKINE_SECRETION	136	0.551352	1.974938	<0.001	0.033443	0.399	4,787
GO_PEPTIDE_RECEPTOR_ACTIVITY	121	0.565342	1.974189	<0.001	0.033314	0.403	6,054
GO_REGULATION_OF_CELL_KILLING	61	0.659555	1.971225	0.004024	0.034249	0.415	4,162
GO_IMMUNE_EFFECTOR_PROCESS	452	0.514158	1.971089	0.002004	0.033731	0.416	4,869
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	64	0.591949	1.970635	<0.001	0.033227	0.418	4,680
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	38	0.646624	1.969562	<0.001	0.033141	0.421	4,526
GO_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	92	0.603566	1.967354	0.002008	0.03358	0.431	2,227
GO_LEUKOCYTE_CHEMOTAXIS	112	0.572423	1.965727	0.004008	0.033777	0.438	5,083
GO_B_CELL_MEDIATED_IMMUNITY	94	0.638907	1.962121	0.007937	0.03456	0.449	4

GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	285	0.495666	1.946775	<0.001	0.034475	0.49	3,582
GO_DETECTION_OF_BIOTIC_STIMULUS	25	0.773364	1.946077	<0.001	0.034339	0.492	3,191
GO_PHOSPHOLIPASE_C_ACTIVITY	31	0.597402	1.94571	0.002024	0.034062	0.493	1,832
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	62	0.644911	1.944497	0.002028	0.034091	0.5	2,187
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	22	0.821999	1.943802	<0.001	0.033936	0.5	2,750
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	130	0.588374	1.943276	0.004024	0.033646	0.5	4,202
GO_CELL_CHEMOTAXIS	156	0.545558	1.940071	0.00404	0.034524	0.51	4,059
GO_CELLULAR_DEFENSE_RESPONSE	54	0.664726	1.93921	<0.001	0.034658	0.513	3,990
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	57	0.55917	1.938187	0.003831	0.034637	0.514	2,375
GO_CYTOKINE_BINDING	87	0.587095	1.937845	<0.001	0.034336	0.516	5,083
GO_SINGLE_ORGANISM_CELL_ADHESION	431	0.482688	1.937348	<0.001	0.034175	0.519	5,025
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	42	0.632312	1.936979	0.003922	0.033867	0.519	3,140
GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	22	0.627191	1.93576	0.001953	0.033924	0.525	2,612
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	281	0.479834	1.935632	<0.001	0.03359	0.525	5,125
GO_REGULATION_OF_PLATELET_ACTIVATION	30	0.66946	1.934825	0.001969	0.033644	0.526	4,933
GO_B_CELL_DIFFERENTIATION	71	0.547218	1.933634	0.001969	0.033908	0.532	3,236
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	19	0.673897	1.932992	<0.001	0.033761	0.534	2,158
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	291	0.541907	1.932604	0.004008	0.03355	0.536	5,287
GO_MYELOID_LEUKOCYTE_MIGRATION	94	0.552649	1.9325	0.001984	0.033203	0.536	4,708
GO_RECEPTOR_COMPLEX	319	0.464545	1.932247	<0.001	0.032908	0.538	5,626
GO_ACTIVATION_OF_IMMUNE_RESPONSE	413	0.536524	1.931813	0.002037	0.032798	0.538	4,662
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	314	0.550109	1.929922	0.004008	0.033217	0.545	4,662
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	17	0.747437	1.929284	0.003929	0.033085	0.547	2,810
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN							

GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	150	0.53421	1.90364	0.001931	0.038048	0.616	5,098
GO_GRANULOCYTE_MIGRATION	70	0.566717	1.903409	0.005952	0.037844	0.616	4,991
GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	19	0.727329	1.903092	<0.001	0.037677	0.617	3,173
GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	74	0.568034	1.902011	0.002004	0.037817	0.62	5,617
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	19	0.770391	1.897448	<0.001	0.03959	0.631	2,307
GO_POSITIVE_REGULATION_OF_CELL_KILLING	37	0.682012	1.895854	<0.001	0.039886	0.635	4,680
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	361	0.491127	1.894025	0.006036	0.040306	0.637	5,287
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	38	0.603299	1.892704	<0.001	0.04054	0.643	4,502
GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	37	0.641642	1.891957	0.001965	0.040587	0.644	3,393
GO_MATURE_B_CELL_DIFFERENTIATION	17	0.695548	1.890939	0.001992	0.040765	0.647	3,236
GO_ANTIGEN_BINDING	106	0.652917	1.888784	0.008386	0.041569	0.654	4,756
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	0.689541	1.888506	0.003992	0.041384	0.654	2,466
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	74	0.564089	1.888171	<0.001	0.041229	0.654	6,971
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	149	0.528535	1.887495	0.003992	0.04125	0.656	5,287
GO_RESPIRATORY_BURST	15	0.787019	1.886741	0.006012	0.041255	0.658	1,654
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	67	0.584401	1.886263	0.004024	0.04119	0.658	1,714
GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	40	0.566089	1.884699	0.004082	0.041694	0.661	3,210
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	197	0.546676	1.884466	0.004016	0.041523	0.661	4,202
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	16	0.759357	1.884216	<0.001	0.041283	0.661	3,393
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	396	0.450916	1.883474	<0.001	0.041285	0.665	5,132
GO_T_CELL_HOMEOSTASIS	34	0.56725	1.881837	0.001988	0.041803	0.674	2,517
GO_MAST_CELL_GRANULE	20	0.695591	1.88084	0.005917	0.041863	0.676	5,909
GO_LIPID_PHOSPHORYLATION	97	0.476774	1.88039	<0.001	0.041752	0.678	5,874
GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	34	0.5955	1.879173	0.004065			

GO_SECOND_MESSENGER_MEDIATED_SIGNALING	152	0.501027	1.861848	<0.001	0.046303	0.723	6,753
GO_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	46	0.613635	1.861712	0.005894	0.046095	0.724	2,692
GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	54	0.560085	1.86167	0.005859	0.045828	0.724	6,283
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	146	0.483282	1.861171	<0.001	0.045898	0.727	6,974
GO_B_CELL_PROLIFERATION	21	0.761765	1.861013	0.001965	0.045709	0.728	2,529
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	83	0.567483	1.860911	0.006073	0.045455	0.728	3,527
GO_REGULATION_OF_NEUTROPHIL_MIGRATION	30	0.634176	1.860472	0.001988	0.045356	0.728	3,140
GO_CELLULAR_EXTRAVASATION	24	0.686894	1.858569	<0.001	0.045997	0.732	4,526
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	406	0.449814	1.858564	0.003976	0.045706	0.732	5,217
GO_ORGAN_MATURATION	18	0.624736	1.857482	<0.001	0.04596	0.736	3,820
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	51	0.61292	1.855871	0.005894	0.046414	0.74	4,162
GO_MACROPHAGE_ACTIVATION	31	0.632168	1.855255	<0.001	0.046437	0.741	3,730
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	28	0.602075	1.854534	0.004057	0.04653	0.742	1,733
GO_TAXIS	433	0.438533	1.852252	<0.001	0.047424	0.749	5,192
GO_REGULATION_OF_PLATELET_AGGREGATION	16	0.675219	1.850922	0.001957	0.047938	0.751	4,933
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	123	0.49001	1.850619	<0.001	0.04787	0.751	6,974
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	144	0.499807	1.850213	0.005964	0.047793	0.751	5,214
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	18	0.713901	1.847546	0.002033	0.048843	0.754	3,393
GO_T_CELL_MEDIATED_IMMUNITY	28	0.598264	1.847011	0.007707	0.048806	0.756	2,307
GO_LYMPHOCYTE_COSTIMULATION	76	0.654631	1.845286	0.010101	0.049539	0.761	5,025
GO_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	129	0.519599	1.845035	<0.001	0.049429	0.761	8,074
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	351	0.453444	1.844727	0.00198	0.049315	0.762	4,282
GO_LIPOPOLYSACCHARIDE_BINDING	20	0.641471	1.843406	0.001992	0.049716	0.764	4,174
GO_CCR_CHEMOKINE_RECEPTOR_BINDING	33	0.671294	1.843353	0.004065	0		

GO_CHEMOKINE_BINDING	17	0.744279	1.828923	<0.001	0.053053	0.794	1,733
GO_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	44	0.613704	1.828796	0.009921	0.052838	0.794	1,895
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	102	0.489026	1.827619	<0.001	0.053378	0.797	6,974
GO_REGULATION_OF_ION_HOMEOSTASIS	189	0.466312	1.827351	<0.001	0.053273	0.797	5,617
GO_PROTEIN_SECRETION	110	0.487224	1.826808	0.006024	0.053345	0.797	5,960
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	27	0.641511	1.825755	<0.001	0.05371	0.797	4,526
GO_REGULATION_OF_NEUTROPHIL_CHEMOTAXIS	25	0.675416	1.824474	0.001996	0.054068	0.802	5,574
GO_PHAGOCYTOSIS_RECOGNITION	33	0.721218	1.824222	0.00994	0.053904	0.802	5,142
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	17	0.725431	1.821275	0.001992	0.055434	0.81	4,831
GO_MONOCYTE_CHEMOTAXIS	39	0.618492	1.821166	0.014199	0.055234	0.81	4,708
GO_REGULATION_OF_TOLERANCE_INDUCION	17	0.740926	1.820319	0.007952	0.055435	0.812	2,152
GO_DENDRITIC_CELL_DIFFERENTIATION	32	0.608152	1.81836	0.004057	0.056312	0.817	2,494
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	107	0.514464	1.817402	0.006098	0.056495	0.818	3,543
GO_MAST_CELL_ACTIVATION	20	0.69441	1.81551	0.004024	0.057294	0.823	5,909
GO_CGMP_METABOLIC_PROCESS	21	0.683098	1.815369	<0.001	0.057091	0.824	6,283
GO_CYCLIC_NUCLEOTIDE_BINDING	33	0.546698	1.815199	0.006048	0.05694	0.826	3,862
GO_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY	92	0.552727	1.815161	0.011952	0.056696	0.826	4,226
GO_REFLEX	19	0.673393	1.814293	0.002	0.056857	0.826	7,000
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	79	0.552272	1.813804	0.006061	0.056874	0.827	3,543
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	198	0.461565	1.813265	<0.001	0.056876	0.828	5,689
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	493	0.426682	1.813155	<0.001	0.056654	0.828	5,810
GO_DENDRITIC_CELL_MIGRATION	20	0.720637	1.812003	0.002058	0.057002	0.829	1,962
GO_REGULATION_OF_HEMOPOIESIS	294	0.435876	1.810986	0.001953	0.057362	0.83	5,006
GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	20	0.682891	1.810324	0.00404	0.057482	0.831	2,885
GO_PHOSPHATIDYL							

GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	155	0.436417	1.800251	<0.001	0.059195	0.842	4,202
GO_REGULATION_OF_HEAT_GENERATION	15	0.623903	1.799859	0.00969	0.059184	0.842	1,186
GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	89	0.459661	1.799691	0.004149	0.059037	0.842	6,081
GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	40	0.567838	1.799609	0.009881	0.058813	0.842	3,218
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	353	0.462531	1.799202	0.004	0.058824	0.843	3,527
GO_PEPTIDYL_TYROSINE_MODIFICATION	182	0.428277	1.798999	<0.001	0.058702	0.844	4,472
GO_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	17	0.743413	1.798465	0.003984	0.05875	0.844	2,466
GO_RAC_PROTEIN_SIGNAL_TRANSDUCTION	18	0.638475	1.798428	0.004115	0.058526	0.844	3,561
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.669425	1.79221	0.008163	0.061995	0.854	4,799
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	36	0.559091	1.791961	0.009747	0.061885	0.854	3,099
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	154	0.467742	1.791604	0.005952	0.061893	0.854	7,024
GO_ADRENERGIC_RECEPTOR_BINDING	18	0.627616	1.790873	0.007547	0.062069	0.856	5,994
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	34	0.57621	1.790598	0.005906	0.061997	0.856	3,570
GO_REGULATION_OF_PHAGOCYTOSIS	66	0.498299	1.78874	0.002	0.06286	0.857	3,309
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	46	0.587833	1.788648	0.009653	0.062692	0.857	4,953
GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	15	0.645737	1.788272	0.007519	0.062627	0.857	3,972
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	223	0.430278	1.787669	0.003854	0.06272	0.857	6,075
GO_CALCIUM_ION_TRANSPORT	208	0.437373	1.786297	<0.001	0.063287	0.86	5,727
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	27	0.563694	1.785907	0.005964	0.063281	0.861	2,570
GO_POSITIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	28	0.599257	1.785405	0.008	0.063323	0.863	2,570
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	49	0.568441	1.785394	0.005803	0.063068	0.863	7,872
GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	95	0.471047	1.784853	0.002049	0.063156	0.863	3,756
GO_DETECTION_OF_OTHER_ORGANISM	17	0.748154	1.784783	0.001996	0.062935	0.863	2,228
GO_REGULATION_OF_T_CELL_DIFF							

GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	120	0.471185	1.776381	<0.001	0.064749	0.876	8,457
GO_REGULATION_OF_B_CELL_PROLIFERATION	54	0.581074	1.776353	0.00996	0.064541	0.876	3,720
GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	30	0.54285	1.774984	0.008032	0.065121	0.878	2,570
GO_DEFENSE_RESPONSE_TO_BACTERIUM	184	0.466077	1.774562	0.006048	0.06513	0.878	4,226
GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	25	0.615557	1.774185	0.006048	0.065185	0.88	3,527
GO_NEURON_CELL_CELL_ADHESION	16	0.782154	1.773987	<0.001	0.065028	0.88	4,831
GO_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	96	0.500031	1.772563	0.003968	0.065838	0.884	3,527
GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	20	0.597316	1.772522	0.005825	0.065617	0.884	2,641
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	87	0.501629	1.771957	0.003883	0.065759	0.885	5,617
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	21	0.698706	1.771137	0.015873	0.065995	0.886	3,955
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	25	0.610186	1.770617	0.006122	0.066057	0.887	2,187
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	16	0.699697	1.770481	0.01354	0.065931	0.887	3,393
GO_RECEPTOR_INTERNALIZATION	45	0.549392	1.769173	0.00404	0.066425	0.888	3,990
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	167	0.443678	1.768103	0.002028	0.066958	0.888	4,425
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	38	0.557668	1.767515	0.002016	0.067069	0.888	5,093
GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	21	0.677148	1.767447	0.008081	0.066867	0.888	1,714
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	122	0.482289	1.764859	0.007859	0.068334	0.89	2,519
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	19	0.660383	1.762452	0.005941	0.069672	0.892	6,123
GO_SIGNALING_ADAPTOR_ACTIVITY	73	0.488315	1.761961	0.003968	0.069776	0.893	4,307
GO_AXONAL_FASCICULATION	19	0.655601	1.76158	0.007813	0.069807	0.894	4,359
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	445	0.394359	1.761288	<0.001	0.069707	0.894	5,181
GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	29	0.53694	1.760442	0.005747	0.070043	0.894	6,069
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	69	0.504892	1.759515	0.00738	0.070358	0.894	6,546
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	21	0.704249	1.759216	0.009823	0.070291	0.896</	

GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	114	0.484683	1.747564	0.011765	0.07433	0.909	5,865
GO_REGULATION_OF_SEQUESTERING_OF_CALCIIUM_ION	100	0.487931	1.747491	0.005894	0.074145	0.909	5,617
GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	57	0.466222	1.747264	0.001919	0.074068	0.909	4,202
GO_POSITIVE_REGULATION_OF_STAT_CASCADE	68	0.494428	1.746853	0.010204	0.074148	0.91	4,532
GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	26	0.600338	1.746545	0.009785	0.074105	0.91	5,574
GO_MEGAKARYOCYTE_DIFFERENTIATION	20	0.633215	1.745991	0.012072	0.074242	0.912	7,227
GO_REGULATION_OF_LIPASE_ACTIVITY	83	0.48137	1.745495	0.007722	0.074274	0.912	5,574
GO_HETEROTYPIC_CELL_CELL_ADHESION	27	0.612149	1.744219	0.018072	0.074955	0.913	4,410
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	223	0.449917	1.74414	0.003929	0.074791	0.913	6,838
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	211	0.431856	1.743834	0.005587	0.074741	0.913	4,953
GO_B_CELL_HOMEOSTASIS	21	0.699971	1.743715	0.013889	0.074586	0.914	4,202
GO_INTERLEUKIN_1_PRODUCTION	15	0.697888	1.742709	0.01	0.075038	0.914	5,774
GO_CHEMOKINE_RECEPTOR_BINDING	53	0.551512	1.742326	0.015873	0.075081	0.916	4,708
GO_WALKING_BEHAVIOR	31	0.562413	1.742316	0.011765	0.074851	0.916	5,792
GO_TRANSMISSION_OF_NERVE_IMPULSE	53	0.540605	1.74135	0.007968	0.075238	0.916	6,647
GO_IMMUNOGLOBULIN_RECEPTOR_BINDING	25	0.7797	1.741158	0.021442	0.075127	0.916	5,142
GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	36	0.570619	1.741093	0.021739	0.074941	0.916	3,720
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	66	0.48557	1.740765	0.005736	0.074969	0.916	8,074
GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	65	0.510843	1.739999	0.00789	0.075284	0.917	8,074
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	39	0.495439	1.739948	0.003883	0.075089	0.918	4,202
GO_NEGATIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	121	0.419438	1.739751	0.004049	0.074995	0.918	5,363
GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	15	0.695984	1.739007	0.006	0.075249	0.918	5,192
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	196	0.427392	1.738891	<0.001	0.075114	0.918	6,069
GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	41	0.537212					

GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	98	0.488849	1.723066	0.012	0.082543	0.94	4,231
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	76	0.536681	1.7226	0.013889	0.082652	0.94	2,887
GO_POSITIVE_REGULATION_OF_PROTEIN_SECRETION	201	0.40524	1.722451	0.003861	0.082522	0.94	6,927
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	349	0.444872	1.72222	0.022222	0.082467	0.94	3,132
GO_T_CELL_RECEPTOR_COMPLEX	19	0.761069	1.721832	0.025845	0.082534	0.94	1,869
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	129	0.457911	1.721145	0.013889	0.082776	0.94	5,874
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	19	0.71321	1.720999	0.017893	0.082666	0.94	2,466
GO_REGULATION_OF_COAGULATION	86	0.470548	1.720749	0.015444	0.082573	0.94	5,132
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	170	0.404674	1.71781	0.001969	0.084374	0.94	5,973
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	31	0.579797	1.717746	0.015474	0.08418	0.94	6,945
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	23	0.563463	1.717322	0.013462	0.08427	0.941	4,191
GO_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	15	0.653752	1.717239	0.015748	0.08411	0.941	1,059
GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	43	0.480154	1.717122	0.001957	0.083994	0.941	2,375
GO_CIRCULATORY_SYSTEM_PROCESS	353	0.398149	1.716516	0.001898	0.084262	0.941	6,647
GO_DENDRITIC_CELL_CHEMOTAXIS	16	0.709554	1.71649	0.008163	0.084044	0.941	1,733
GO_GLOMERULUS_DEVELOPMENT	49	0.541719	1.716182	0.019048	0.084066	0.942	4,291
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	31	0.571274	1.716164	0.015968	0.083848	0.942	5,098
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	151	0.434399	1.716056	0.005952	0.083709	0.942	5,727
GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	61	0.506981	1.715959	0.003817	0.083548	0.942	7,324
GO_STAT_CASCADE	44	0.530495	1.715955	0.022727	0.083318	0.942	7,281
GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	36	0.555288	1.714068	0.001938	0.084475	0.942	6,546
GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	25	0.628758	1.714029	0.015717	0.084272	0.942	5,909
GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	30	0.626301	1.713616	0.018256	0.08437	0.942	4,202
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	248	0.410					

GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	113	0.429312	1.703064	0.005736	0.088668	0.955	3,375
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	28	0.589322	1.703042	0.017682	0.088453	0.955	6,362
GO_REGULATION_OF_CIRCADIAN_SLEEP_WAKE_CYCLE	23	0.590239	1.70304	0.018182	0.088226	0.955	6,867
GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	16	0.720661	1.702373	0.015152	0.088472	0.955	4,795
GO_NEGATIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	16	0.623756	1.701246	0.017682	0.089161	0.955	6,123
GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	28	0.524466	1.701035	0.017857	0.089052	0.955	2,940
GO_NUCLEUS_LOCALIZATION	20	0.622293	1.700514	0.018	0.08919	0.955	4,436
GO_REGULATION_OF_LYASE_ACTIVITY	81	0.447413	1.699635	0.011194	0.089657	0.956	8,226
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	82	0.46552	1.696928	0.00198	0.091657	0.957	8,457
GO_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	36	0.500737	1.696631	0.011516	0.091626	0.957	6,966
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	27	0.548943	1.69642	0.020408	0.091574	0.957	2,105
GO_RESPONSE_TO_PROSTAGLANDIN_E	25	0.561384	1.695791	0.022634	0.091869	0.958	3,140
GO_PROTEIN_TYROSINE_KINASE_BINDING	52	0.45157	1.695003	0.005837	0.092204	0.958	4,307
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	36	0.568723	1.694953	0.010204	0.092	0.958	4,137
GO_HEPARIN_BINDING	151	0.458135	1.694721	0.017476	0.09196	0.958	5,045
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	16	0.68967	1.693964	0.023301	0.092345	0.958	1,276
GO_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	51	0.578566	1.693616	0.026423	0.092327	0.958	3,945
GO_MELANOCYTE_DIFFERENTIATION	17	0.611162	1.693364	0.013807	0.092318	0.958	1,098
GO_NEGATIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	49	0.490555	1.691915	0.012024	0.093199	0.959	2,692
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	81	0.491377	1.691191	0.018904	0.093593	0.959	4,410
GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	47	0.510693	1.690585	0.016162	0.093887	0.96	4,815
GO_ADULT_BEHAVIOR	133	0.465086	1.690569	0.017857	0.093668	0.96	6,673
GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	34	0.521701	1.690331	0.017308	0.093619	0.96	3,492
GO_NEUROMUSCULAR_PROCESS	92	0.471049	1.690253	0.			

GO_REGULATION_OF_STAT_CASCADE	124	0.426052	1.681623	0.007843	0.096488	0.962	5,775
GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	39	0.534426	1.681079	0.034694	0.096659	0.962	3,206
GO_RENAL_SYSTEM_PROCESS	98	0.437854	1.681048	0.001976	0.096449	0.962	6,331
GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	18	0.663925	1.680782	0.010417	0.096416	0.962	2,488
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	55	0.521765	1.680507	0.020367	0.096373	0.962	1,150
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	118	0.412735	1.680452	0.006	0.096185	0.962	7,245
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	30	0.579019	1.679962	0.019881	0.096342	0.962	7,004
GO_POSITIVE_REGULATION_OF_LOCOMOTION	398	0.396766	1.679708	0.003817	0.096308	0.962	5,159
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	80	0.439244	1.679523	0.003861	0.096212	0.963	5,181
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	419	0.423833	1.679107	0.03854	0.096313	0.963	5,778
GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	32	0.533284	1.678985	0.012024	0.096233	0.963	6,283
GO_THYMOCYTE_AGGREGATION	44	0.524894	1.678247	0.01222	0.096587	0.964	2,386
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	77	0.452242	1.676026	0.003937	0.098095	0.966	3,990
GO_CYCLASE_ACTIVITY	19	0.59994	1.67596	0.02004	0.097932	0.966	6,001
GO_SCAVENGER_RECEPTOR_ACTIVITY	39	0.501809	1.675488	0.015873	0.098088	0.966	7,264
GO_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	204	0.384849	1.675201	0.001972	0.098095	0.966	4,202
GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	48	0.527727	1.674164	0.030829	0.098656	0.967	7,000
GO_LYSOSOME_LOCALIZATION	22	0.565285	1.673269	0.027426	0.099157	0.967	5,951
GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	19	0.609847	1.672632	0.022857	0.099455	0.967	2,828
GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	47	0.495499	1.671981	0.009785	0.099694	0.967	4,526
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	18	0.626395	1.671342	0.025948	0.099955	0.968	3,059
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	135	0.430517	1.669336	0.015748	0.101328	0.969	5,270
GO_IMMUNOGLOBULIN_COMPLEX	24	0.794555	1.668706	0.032129	0.10158	0.969	5,142
GO_CELLULAR_RESPONSE_TO_CAMP	49						

GO_SIALYLATION	20	0.586096	1.662741	0.026	0.102766	0.974	5,581
GO_REGULATION_OF_INTERLEUKIN_1_SECRETION	31	0.552537	1.661341	0.018947	0.103769	0.978	4,137
GO_LEUKOCYTE_DEGRANULATION	29	0.537004	1.660543	0.022634	0.104175	0.978	5,192
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	38	0.562918	1.660296	0.030303	0.104125	0.978	5,565
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	237	0.396001	1.659271	0.005803	0.104756	0.979	7,058
GO_NEGATIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	40	0.501413	1.658743	0.017045	0.104922	0.98	5,748
GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	17	0.678417	1.658728	0.021956	0.104702	0.98	1,733
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	49	0.481144	1.658558	0.013645	0.104655	0.98	3,972
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	78	0.444274	1.658396	0.007843	0.104556	0.98	4,202
GO_PHAGOCYTIC_CUP	17	0.60374	1.65837	0.035503	0.104354	0.98	2,023
GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	16	0.650513	1.657936	0.024145	0.104512	0.98	6,592
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	173	0.38834	1.656663	0.004	0.105293	0.98	4,890
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	253	0.388786	1.654474	0.004167	0.106779	0.98	5,727
GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	41	0.491325	1.654455	0.016129	0.106577	0.98	6,805
GO_BEHAVIOR	489	0.410406	1.65416	0.014028	0.106609	0.98	7,029
GO_REGULATION_OF_BONE_REMODELING	39	0.496246	1.654146	0.01232	0.106401	0.98	7,980
GO_FOREBRAIN_CELL_MIGRATION	59	0.48245	1.653018	0.013725	0.107084	0.98	4,121
GO_NEPHRIC_DUCT_DEVELOPMENT	15	0.596937	1.653012	0.031381	0.106869	0.98	1,563
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	41	0.511743	1.652684	0.028056	0.106887	0.98	5,098
GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	72	0.476271	1.652297	0.021654	0.106977	0.981	7,943
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	17	0.599232	1.651955	0.035088	0.107035	0.981	3,858
GO_REGULATION_OF_MITOCHONDRIAL_DEPOLARIZATION	17	0.570725	1.651075	0.017751	0.107501	0.981	4,924
GO_MEMBRANE_DEPOLARIZATION	59	0.492024	1.650626	0.02554	0.107623	0.981	5,689
GO_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	40	0.544465	1.649928	0.0			

GO_REGULATION_OF_TISSUE_REMODELING	58	0.453223	1.643009	0.007937	0.110114	0.981	2,692
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	49	0.443286	1.642682	0.017893	0.110121	0.981	2,105
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	109	0.429073	1.642619	0.004	0.109973	0.981	5,617
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	39	0.576806	1.642564	0.023576	0.109788	0.981	6,591
GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	95	0.445388	1.642399	0.026565	0.109696	0.981	5,728
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	30	0.516952	1.641352	0.01	0.110349	0.982	3,836
GO_GLYCOLIPID_BINDING	19	0.547563	1.640743	0.031809	0.110672	0.982	4,202
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	70	0.49165	1.640625	0.007968	0.110558	0.982	5,617
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	33	0.513568	1.640601	0.008264	0.11036	0.982	3,851
GO_SENSORY_PERCEPTION_OF_PAIN	71	0.474145	1.639829	0.021318	0.11082	0.984	7,456
GO_SINGLE_ORGANISM_BEHAVIOR	368	0.413259	1.639615	0.013861	0.110806	0.984	5,813
GO_ANCHORED_COMPONENT_OF_MEMBRANE	141	0.396628	1.639294	0.003891	0.110904	0.984	2,979
GO_PROTEOGLYCAN_BINDING	29	0.545187	1.638613	0.026365	0.111212	0.984	4,554
GO_REGULATION_OF_INTERLEUKIN_6_BIOSYNTHETIC_PROCESS	15	0.614217	1.637591	0.027311	0.111819	0.984	5,125
GO_BONE_GROWTH	20	0.562388	1.636688	0.022727	0.112409	0.985	4,159
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	33	0.558032	1.636145	0.033932	0.112626	0.986	2,227
GO_REGULATION_OF_ALPHA_AMINO_3_HYDROXY_5_METHYL_4_ISOXAZOLE_PROPIONATE_SELECTIVE_Glutamate_Receptor_Activity	19	0.616075	1.635413	0.032323	0.113034	0.987	5,374
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	42	0.485789	1.635337	0.023669	0.112868	0.987	6,647
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	26	0.613544	1.635321	0.047259	0.112671	0.987	5,565
GO_REGULATION_OF_CELL_SHAPE	134	0.424501	1.634954	0.015595	0.112753	0.987	3,756
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	17	0.64325	1.634699	0.025243	0.112733	0.987	6,411
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	49	0.467938	1.634528	0.017143	0.112648	0.987	5,574
GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	45	0.499897	1.634326	0.026369	0.112628	0.	

GO_PROTEIN_KINASE_B_SIGNALING	34	0.465664	1.622536	0.013487	0.119274	0.989	2,586
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	149	0.40623	1.622405	0.01711	0.119163	0.989	5,270
GO_NEURONAL_ACTION_POTENTIAL	27	0.536426	1.622212	0.043478	0.119099	0.989	5,663
GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	37	0.470545	1.622138	0.013917	0.118949	0.989	3,702
GO_POSITIVE_REGULATION_OF_OSSIFICATION	80	0.484535	1.622001	0.022901	0.11887	0.99	6,999
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	22	0.573456	1.621045	0.036585	0.11944	0.99	5,973
GO_THYMIC_T_CELL_SELECTION	19	0.667551	1.620992	0.05835	0.119282	0.99	1,830
GO_CATION_CHANNEL_ACTIVITY	280	0.400527	1.620611	0.021696	0.119417	0.99	7,182
GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	25	0.518526	1.620558	0.01875	0.119235	0.99	8,556
GO_REGULATION_OF_WOUND_HEALING	122	0.413663	1.620339	0.017682	0.119195	0.99	6,683
GO_COGNITION	239	0.418312	1.62021	0.010081	0.119116	0.99	6,130
GO_NEGATIVE_REGULATION_OF_CIRCADIAN_RHYTHM	15	0.549263	1.619448	0.027397	0.119558	0.99	8,657
GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	19	0.566758	1.619447	0.030738	0.11934	0.99	1,524
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	15	0.586658	1.619178	0.034156	0.119339	0.99	2,658
GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	34	0.550995	1.619012	0.05071	0.119268	0.99	4,815
GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	19	0.545016	1.6187	0.02381	0.119308	0.99	2,725
GO_PROTEIN_KINASE_C_ACTIVITY	16	0.542607	1.616675	0.015717	0.120977	0.99	2,375
GO_ENDOCYTIC_VESICLE_MEMBRANE	149	0.422073	1.616471	0.031809	0.120949	0.99	4,995
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	60	0.464949	1.616119	0.01711	0.121038	0.99	4,331
GO_CAMP_METABOLIC_PROCESS	33	0.52069	1.615431	0.037849	0.121487	0.99	6,001
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	26	0.551315	1.614801	0.02947	0.12185	0.99	5,093
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	20	0.622106	1.613902	0.047431	0.122375	0.99	4,606
GO_DENDRITE_MEMBRANE	18	0.599137	1.613484	0.030888	0.122578	0.991	6,673
GO_CELLULAR_RESPONSE_TO_DRUG	65	0.432753	1.613169	0.012526	0.122		

GO_COLLAGEN_TRIMER	83	0.527783	1.600806	0.05642	0.130701	0.995	8,696
GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	17	0.588154	1.600493	0.048356	0.130755	0.995	5,391
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	37	0.515713	1.600382	0.048638	0.130664	0.995	6,927
GO_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	30	0.558747	1.599927	0.050388	0.130865	0.995	4,202
GO_RECEPTOR_METABOLIC_PROCESS	76	0.436042	1.599069	0.020661	0.131403	0.995	3,990
GO_SULFUR_COMPOUND_BINDING	227	0.382917	1.598871	0.017682	0.131352	0.995	5,045
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	166	0.392946	1.596485	0.013889	0.133342	0.996	4,993
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	60	0.449192	1.596049	0.037109	0.133548	0.996	5,481
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	39	0.484455	1.595823	0.019531	0.133499	0.996	2,697
GO_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	41	0.500304	1.594913	0.039326	0.134082	0.996	7,959
GO_NEGATIVE_REGULATION_OF_AXONOGENESIS	64	0.413091	1.594772	0.013514	0.133981	0.996	5,070
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	49	0.460143	1.594113	0.03668	0.134392	0.997	4,027
GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	40	0.491752	1.593974	0.031496	0.134304	0.997	6,353
GO_BONE_CELL_DEVELOPMENT	22	0.5415	1.593798	0.045802	0.134225	0.997	7,227
GO_MHC_PROTEIN_COMPLEX	25	0.722162	1.593589	0.07113	0.134201	0.997	4,650
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	17	0.568203	1.593072	0.04466	0.134503	0.997	5,125
GO_PIGMENT_CELL_DIFFERENTIATION	25	0.495067	1.59306	0.033932	0.134278	0.997	1,098
GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	21	0.534445	1.592572	0.027132	0.134544	0.997	3,841
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	25	0.498644	1.591943	0.027559	0.134872	0.997	2,046
GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	34	0.475287	1.591539	0.021569	0.134997	0.997	5,719
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	238	0.384226	1.590696	0.02045	0.135531	0.997	6,318
GO_ACTIN_FILAMENT_POLYMERIZATION	21	0.503051	1.590624	0.04175	0.135368	0.997	2,082
GO_REGULATION_OF_VASOCONSTRICTION	64	0.440218	1.590605	0.024668	0.135167	0.997	4,371
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	295	0.389549	1				

GO_CLATHRIN_COATED_VESICLE_MEMBRANE	78	0.433193	1.580109	0.019569	0.141161	0.999	5,019
GO_SH2_DOMAIN_BINDING	28	0.503838	1.579987	0.028455	0.141042	0.999	6,043
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	84	0.444456	1.578814	0.044316	0.142024	0.999	8,881
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	22	0.551611	1.578699	0.055215	0.141922	0.999	3,981
GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	35	0.470305	1.578103	0.026667	0.142259	0.999	6,827
GO_POSITIVE_REGULATION_OF_VASODILATION	31	0.49561	1.577333	0.036511	0.142757	0.999	5,612
GO_REGULATION_OF_AMINE_TRANSPORT	68	0.476292	1.577331	0.034816	0.14253	0.999	6,226
GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSPORT	16	0.56905	1.576758	0.035573	0.142823	0.999	2,953
GO_EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	53	0.46742	1.576749	0.044444	0.142605	0.999	5,216
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	35	0.458952	1.576592	0.025591	0.14255	0.999	6,198
GO_DETECTION_OF ABIOTIC_STIMULUS	104	0.376988	1.576266	0.001984	0.142627	0.999	4,420
GO_GANGLIOSIDE_BIOSYNTHETIC_PROCESS	17	0.573979	1.576214	0.049801	0.142448	0.999	4,505
GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	18	0.541964	1.575563	0.03125	0.142842	0.999	2,641
GO_SECONDARY_METABOLIC_PROCESS	48	0.440853	1.575288	0.024952	0.142887	0.999	2,944
GO_REGULATION_OF_NOREPINEPHRINE_SECRETION	17	0.593018	1.575045	0.038388	0.142901	0.999	3,173
GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	439	0.359441	1.574978	0.027668	0.14274	0.999	7,580
GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	131	0.402757	1.5743	0.020243	0.143149	0.999	4,993
GO_NEGATIVE_REGULATION_OF_SECRETION	186	0.375352	1.574122	0.009823	0.1431	0.999	6,793
GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	54	0.43791	1.573143	0.028056	0.143876	0.999	4,584
GO_REGULATION_OF_CATECHOLAMINE_SECRETION	41	0.520048	1.573057	0.04931	0.143735	0.999	3,635
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_STIMULUS	24	0.526988	1.573	0.030242	0.143558	0.999	2,658
GO_RESPONSE_TO_GROWTH_HORMONE	28	0.509838	1.57273	0.042424	0.14356	0.999	4,202
GO_SPLEEN_DEVELOPMENT	38	0.456319	1.572065	0.026423	0.143955	0.999	6,542
GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	49	0.478094	1.571948	0.033797	0.143		

GO_MHC_PROTEIN_COMPLEX_BINDING	18	0.64253	1.564036	0.06544	0.148033	1	3,645
GO_PEPTIDE_ANTIGEN_BINDING	29	0.60179	1.563521	0.091684	0.148257	1	4,756
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	27	0.538465	1.562966	0.053719	0.14854	1	4,502
GO_REGULATION_OF_LIPID_STORAGE	39	0.446635	1.562822	0.034884	0.148459	1	3,013
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	46	0.466047	1.56272	0.04845	0.148342	1	1,714
GO_TRANSCRIPTIONAL_ACTIVATOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDING	23	0.500023	1.562709	0.025896	0.148129	1	1,976
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	46	0.488668	1.5607	0.058586	0.149923	1	3,206
GO_HYALURONIC_ACID_BINDING	20	0.558549	1.560684	0.034749	0.149718	1	4,903
GO_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	107	0.439234	1.560489	0.052738	0.149702	1	4,554
GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	34	0.46197	1.558925	0.019305	0.150966	1	2,297
GO_ENSHEATHMENT_OF_NEURONS	87	0.418664	1.558197	0.016293	0.151398	1	5,063
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	39	0.466849	1.558004	0.035644	0.151336	1	4,924
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	29	0.493342	1.557932	0.050813	0.151178	1	4,956
GO_REGULATION_OF_DENDRITE_DEVELOPMENT	116	0.3914	1.557106	0.031683	0.151833	1	5,214
GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	60	0.456544	1.556727	0.050193	0.151972	1	6,860
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	197	0.392589	1.556585	0.03055	0.151898	1	5,513
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	68	0.528906	1.556452	0.10101	0.151781	1	4,869
GO_SYNAPSE_ORGANIZATION	142	0.428122	1.55637	0.045276	0.151609	1	5,694
GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	79	0.386324	1.5555	0.017442	0.152319	1	5,490
GO_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	24	0.537137	1.555363	0.048733	0.152219	1	5,166
GO_RESPONSE_TO_DIETARY_EXCESS	20	0.515945	1.555111	0.050388	0.152224	1	5,666
GO_IMMUNOLOGICAL_SYNAPSE	31	0.574117	1.554861	0.059305	0.152258	1	4,184
GO_REGULATION_OF_SYSTEM_PROCESS	487	0.377203	1.554491	0.028791	0.152434	1	6,922
GO_GROWTH_FACTOR_BINDING	122	0.439044	1.552511	0.053846	0.154208	1	4,795
GO_REGULATION_OF_BLOOD_CIRCULATION	285	0.388407	1.552249				

GO_REGULATION_OF_JNK_CASCADE	156	0.354785	1.546762	0.017544	0.156528	1	3,155
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	16	0.562269	1.546615	0.023857	0.156432	1	3,385
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	81	0.44033	1.545209	0.051625	0.157676	1	5,118
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	277	0.36159	1.544086	0.016032	0.15853	1	5,694
GO_RECEPTOR_CLUSTERING	41	0.429228	1.543979	0.034483	0.158392	1	5,694
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	34	0.4672	1.543957	0.028736	0.158183	1	5,347
GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	19	0.539559	1.543845	0.053435	0.158076	1	5,784
GO_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	84	0.449162	1.543663	0.064777	0.158033	1	4,554
GO_AXON_EXTENSION	35	0.515201	1.542914	0.0625	0.158565	1	4,429
GO_INDOLALKYLAMINE_METABOLIC_PROCESS	16	0.543673	1.542301	0.044444	0.158952	1	8,556
GO_LYMPH_NODE_DEVELOPMENT	17	0.55786	1.541781	0.091093	0.159255	1	5,984
GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	16	0.534775	1.541181	0.055769	0.159637	1	3,017
GO_REGULATION_OF_VASODILATION	46	0.444949	1.54112	0.040486	0.159482	1	5,909
GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	26	0.522412	1.540884	0.044402	0.159504	1	7,943
GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	20	0.505659	1.540377	0.04931	0.159786	1	2,312
GO_EXTRACELLULAR_GLUTAMATE_GATED_ION_CHANNEL_ACTIVITY	20	0.557196	1.539068	0.041985	0.160935	1	5,166
GO_DEVELOPMENTAL_PIGMENTATION	36	0.459272	1.537587	0.034749	0.162155	1	1,710
GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	184	0.392424	1.537509	0.043478	0.161994	1	8,303
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	227	0.371809	1.536724	0.018109	0.162569	1	7,155
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	35	0.457331	1.536596	0.048096	0.162475	1	964
GO_DEVELOPMENTAL_MATURATION	179	0.351943	1.536078	0.02	0.162791	1	6,542
GO_POSITIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	21	0.534407	1.533592	0.058586	0.165132	1	5,662
GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	100	0.383721	1.53343	0.020325	0.165076	1	6,793
GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	22	0.469514	1.532556	0.06405	0.16568	1	5,492
GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	34						

GO_EXTRACELLULAR_MATRIX_ASSEMBLY	16	0.58399	1.524143	0.069721	0.170852	1	5,244
GO_RESPONSE_TO_PAIN	29	0.494812	1.523929	0.047904	0.170856	1	5,663
GO_REGULATION_OF_AXONOGENESIS	163	0.380662	1.523316	0.035573	0.171293	1	5,171
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	91	0.390231	1.523054	0.018868	0.171347	1	4,414
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	83	0.374284	1.522679	0.017442	0.171495	1	3,901
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	15	0.596424	1.522641	0.074951	0.171294	1	4,202
GO_ACTION_POTENTIAL	92	0.458052	1.521773	0.065606	0.171943	1	6,591
GO_CYTOKINE_ACTIVITY	184	0.390678	1.521462	0.045545	0.172029	1	7,572
GO_NEGATIVE_REGULATION_OF_ANTIGEN_							
RECEPTOR_MEDIATED_SIGNALING_PATHWAY	20	0.533048	1.521119	0.064182	0.172135	1	5,437
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	448	0.343984	1.520899	0.011628	0.172115	1	6,724
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	124	0.391775	1.520868	0.033531	0.171913	1	5,727
GO_RESPONSE_TO_DEXAMETHASONE	32	0.425554	1.520688	0.038776	0.171857	1	6,551
GO_FC_RECEPTOR_SIGNALING_PATHWAY	202	0.42459	1.520459	0.073069	0.171865	1	4,226
GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	121	0.369691	1.519531	0.023392	0.172542	1	5,195
GO_NEGATIVE_REGULATION_OF_GROWTH	227	0.330909	1.519435	0.017476	0.172406	1	4,939
GO_VACUOLAR_LUMEN	109	0.449441	1.518794	0.075758	0.172901	1	8,675
GO_HEMOSTASIS	287	0.353884	1.518372	0.022989	0.173159	1	5,031
GO_EXOCYTOSIS	297	0.34464	1.517191	0.023952	0.174163	1	6,192
GO_POSITIVE_REGULATION_OF_STRESS_							
ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	132	0.359442	1.516808	0.032	0.174342	1	5,999
GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	15	0.601956	1.516792	0.068898	0.174126	1	5,391
GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	227	0.376005	1.516495	0.039293	0.174221	1	5,719
GO_IONOTROPIC_Glutamate_Receptor_Complex	47	0.473	1.516482	0.050193	0.174004	1	7,116
GO_CARDIAC_MUSCLE_CELL_CONTRACTION	28	0.551872	1.516473	0.081673	0.173782	1	9,314
GO_SYNAPTIC_MEMBRANE	249	0.397286	1.				

GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	36	0.536028	1.510644	0.092	0.176576	1	6,591
GO_MULTI_ORGANISM_BEHAVIOR	70	0.408096	1.510349	0.021956	0.176663	1	6,949
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	483	0.336903	1.510019	0.025641	0.176825	1	4,371
GO_REGULATION_OF_TRANSPORTER_ACTIVITY	189	0.370859	1.50964	0.034413	0.17702	1	5,750
GO_AMPA_GLUTAMATE_RECEPTOR_COMPLEX	27	0.536089	1.508368	0.072266	0.17822	1	7,116
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	30	0.488853	1.508231	0.059055	0.178153	1	6,716
GO_IMMUNOGLOBULIN_PRODUCTION	44	0.494708	1.507411	0.075157	0.178835	1	3,091
GO_BLOOD_MICROPARTICLE	140	0.428056	1.506747	0.043738	0.179302	1	4,226
GO_RESPONSE_TO ESTRADIOL	143	0.346822	1.506646	0.015444	0.179194	1	3,472
GO_REGULATION_OF_BODY_FLUID_LEVELS	472	0.333616	1.506549	0.009785	0.179073	1	5,244
GO_PLASMA_MEMBRANE_RAFT	85	0.411464	1.506388	0.043825	0.179057	1	5,173
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	27	0.546374	1.505571	0.066667	0.179639	1	6,497
GO_REGULATION_OF_URINE_VOLUME	20	0.491886	1.504887	0.048193	0.180113	1	2,658
GO_COPULATION	15	0.541629	1.504806	0.057769	0.179983	1	5,574
GO_PRESYNAPTIC_MEMBRANE	52	0.494105	1.504651	0.081081	0.179925	1	7,984
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	28	0.465444	1.503821	0.035917	0.180607	1	6,949
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	222	0.353223	1.503811	0.045726	0.180387	1	4,715
GO_LYMPH_VESSEL_DEVELOPMENT	20	0.526555	1.503624	0.069632	0.18036	1	6,276
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	159	0.380495	1.50311	0.048356	0.180685	1	4,027
GO_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	22	0.53038	1.50291	0.078156	0.180671	1	5,253
GO_PLATELET_ALPHA_GRANULE	74	0.45633	1.502863	0.072266	0.180505	1	3,933
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	30	0.426332	1.501817	0.044118	0.181385	1	4,991
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	69	0.440151	1.501288	0.066019	0.1817	1	5,793
GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	69	0.384694	1.501204	0.034483	0.181546	1	6,191
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	62	0.42911					

GO_ANCHORED_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	21	0.543941	1.491543	0.078	0.188714	1	3,906
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	33	0.423304	1.491125	0.041667	0.188936	1	1,041
GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	461	0.320449	1.490828	0.017647	0.189004	1	5,194
GO_RECEPTOR_SIGNALING_PROTEIN_ACTIVITY	165	0.363856	1.49042	0.030612	0.189224	1	5,489
GO_NEURON_PROJECTION_MEMBRANE	34	0.488018	1.489529	0.075697	0.189915	1	6,673
GO_RESPONSE_TO_GLUCAGON	47	0.451227	1.4894	0.074747	0.189812	1	7,024
GO_ENDOCRINE_PROCESS	43	0.451825	1.488728	0.039526	0.190312	1	8,658
GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	22	0.564903	1.488689	0.089641	0.190131	1	7,279
GO_VASCULATURE_DEVELOPMENT	455	0.382357	1.488629	0.053846	0.189949	1	5,874
GO_POSTSYNAPTIC_MEMBRANE	197	0.380424	1.488605	0.061896	0.189739	1	7,004
GO_REGULATION_OF_DOPAMINE_SECRETION	21	0.535701	1.488393	0.050439	0.189747	1	3,635
GO_LAMELLIPODIUM_ASSEMBLY	28	0.437724	1.488223	0.047619	0.189708	1	3,720
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	66	0.415783	1.488051	0.057361	0.189641	1	5,393
GO_ANGIOGENESIS	283	0.386172	1.487628	0.070209	0.189883	1	5,874
GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	59	0.395851	1.487606	0.051823	0.18968	1	5,748
GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	36	0.447822	1.486866	0.057026	0.190241	1	3,911
GO_BRAIN_MORPHOGENESIS	33	0.429624	1.486763	0.042226	0.190108	1	6,838
GO_REGULATION_OF_PROTEIN_MATURATION	76	0.400968	1.48656	0.04902	0.190088	1	6,342
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	45	0.417873	1.486453	0.05988	0.189971	1	5,973
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDING	81	0.379339	1.48599	0.034205	0.190256	1	5,508
GO_CELLULAR_RESPONSE_TO ESTRADIOL_STIMULUS	27	0.446295	1.484879	0.064583	0.191291	1	3,283
GO_RESPONSE_TO_ALCOHOL	352	0.3273	1.484405	0.023256	0.191534	1	5,195
GO_NEGATIVE_REGULATION_OF_CALCIIUM_MEDIATED_SIGNALING	18	0.552695	1.483618	0.087398	0.19215	1	5,437
GO_POST_EMBRYONIC_DEVELOPMENT	85	0.39449	1.483616	0.050096	0.191922		

GO_SYNAPTIC_SIGNALING	401	0.363995	1.47795	0.074713	0.194591	1	7,447
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	15	0.55609	1.477897	0.09703	0.194423	1	5,662
GO_REGULATION_OF_T_CELL_MIGRATION	24	0.488997	1.477119	0.064257	0.195052	1	3,385
GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	82	0.416582	1.476602	0.066532	0.195373	1	5,750
GO_MUSCLE_HYPERTROPHY	28	0.482101	1.476061	0.057971	0.195807	1	9,571
GO_POSTSYNAPSE	364	0.366631	1.474794	0.066132	0.197001	1	6,903
GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	15	0.532376	1.47456	0.05973	0.197042	1	5,749
GO_PHOSPHOLIPID_BINDING	346	0.334388	1.474341	0.036217	0.197039	1	6,898
GO_KIDNEY_EPITHELIUM_DEVELOPMENT	125	0.362429	1.474293	0.038817	0.196856	1	2,812
GO_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	18	0.550582	1.474002	0.089796	0.196926	1	4,282
GO_NEUROMUSCULAR_JUNCTION	54	0.417842	1.473991	0.063953	0.196703	1	5,694
GO_RESPONSE_TO_FUNGUS	45	0.434924	1.473828	0.050201	0.196649	1	2,169
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	121	0.417961	1.473576	0.091451	0.196703	1	5,976
GO_REPLACEMENT_OSSIFICATION	25	0.510085	1.472234	0.085271	0.198069	1	3,017
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	389	0.320987	1.471694	0.033797	0.198478	1	5,287
GO_LYSOSOMAL_LUMEN	85	0.475308	1.471451	0.117988	0.198516	1	7,302
GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	19	0.524004	1.470894	0.068687	0.1989	1	5,195
GO_MONOCYTE_DIFFERENTIATION	16	0.503501	1.470538	0.071006	0.199058	1	3,087
GO_ACTIVATION_OF_MAPKK_ACTIVITY	48	0.445379	1.470052	0.076923	0.199396	1	6,043
GO_NEGATIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	19	0.540691	1.46988	0.071713	0.199357	1	4,064
GO_REGULATION_OF_MEMBRANE_POTENTIAL	329	0.360109	1.468955	0.059406	0.200206	1	5,808
GO_E_BOX_BINDING	26	0.452467	1.468893	0.072	0.200054	1	6,571
GO_TRANSLATION_REPRESSOR_ACTIVITY	20	0.537637	1.468721	0.072727	0.20005	1	6,727
GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	253	0.314937	1.467098	0.018939	0.201681	1	6,001
GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	24	0.491899	1.466632	0.0770			

GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	148	0.339176	1.45974	0.033074	0.206258	1	3,527
GO_PHASIC_SMOOTH_MUSCLE_CONTRACTION	16	0.548949	1.458889	0.085657	0.206931	1	2,994
GO_1_PHOSPHATIDYLINOSITOL_BINDING	19	0.545672	1.458118	0.125253	0.207573	1	8,162
GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	15	0.588622	1.457945	0.093626	0.207536	1	4,502
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	324	0.336815	1.4579	0.026975	0.207346	1	5,244
GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	26	0.436342	1.457459	0.046065	0.207651	1	3,207
GO_REGULATION_OF_SENSORY_PERCEPTION	33	0.464771	1.457184	0.078278	0.207749	1	2,553
GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	15	0.54733	1.456997	0.082677	0.20774	1	6,769
GO_RESPONSE_TO_NITRIC_OXIDE	21	0.440739	1.456759	0.03629	0.207785	1	2,274
GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	290	0.34343	1.456537	0.049603	0.207787	1	5,719
GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	23	0.489652	1.456485	0.1	0.20761	1	4,733
GO_POTASSIUM_CHANNEL_COMPLEX	86	0.430813	1.456477	0.093069	0.207385	1	6,609
GO_NEGATIVE_REGULATION_OF_TISSUE_REMODELING	17	0.500823	1.456368	0.069034	0.207279	1	4,003
GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	15	0.571168	1.455775	0.104563	0.207704	1	5,842
GO_ENDOTHELIUM_DEVELOPMENT	88	0.395107	1.45565	0.098425	0.207629	1	5,960
GO_PARTURITION	20	0.489877	1.455642	0.075435	0.207405	1	2,658
GO_SODIUM_CHANNEL_ACTIVITY	32	0.449616	1.455584	0.071856	0.207245	1	2,875
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	84	0.385691	1.454947	0.073077	0.207725	1	5,750
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIOTENSIN	21	0.527897	1.454411	0.072835	0.208103	1	3,835
GO_DEFINITIVE_HEMOPOIESIS	16	0.523381	1.454035	0.059524	0.208289	1	5,799
GO_POSITIVE_REGULATION_OF_SECRETION	353	0.325701	1.453993	0.017787	0.20811	1	7,024
GO_SENSORY_PERCEPTION	482	0.296562	1.453963	0.011858	0.207908	1	6,967
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	51	0.412479	1.453833	0.060311	0.207831	1	2,866
GO_CELL_BODY	481	0.335512	1.453626	0.057426	0.207844	1	5,182
GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	342						

GO_REGULATION_OF_CHEMOKINE_PRODUCTION	63	0.414744	1.448937	0.06012	0.209449	1	3,527
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	35	0.426741	1.448874	0.070707	0.209295	1	3,221
GO_RESPONSE_TO_CORTICOSTEROID	169	0.333136	1.448497	0.035156	0.209485	1	3,545
GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	352	0.360855	1.447914	0.063584	0.209937	1	7,481
GO_POSITIVE_REGULATION_OF_WOUND_HEALING	45	0.426034	1.447174	0.072125	0.210591	1	3,457
GO_NEGATIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	17	0.489071	1.446864	0.081028	0.210748	1	6,546
GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	331	0.387614	1.446738	0.095436	0.210666	1	3,132
GO_AXON	396	0.355712	1.446294	0.066532	0.210999	1	5,182
GO_DENDRITIC_SHAFT	36	0.456012	1.445129	0.068762	0.212169	1	4,384
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	222	0.3684	1.444812	0.069498	0.212301	1	7,456
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_ MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	61	0.403083	1.444313	0.090734	0.212651	1	2,187
GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	25	0.463666	1.444253	0.098232	0.212502	1	5,694
GO_NEURON_PROJECTION_MORPHOGENESIS	383	0.358933	1.444136	0.065385	0.212442	1	7,481
GO_REGULATION_OF_MITOCHONDRIAL_FISSION	15	0.520996	1.444129	0.091684	0.212226	1	1,334
GO_ENDOCARDIAL_CUSHION_FORMATION	15	0.545285	1.443723	0.093985	0.212512	1	5,960
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	479	0.322935	1.443617	0.035573	0.212401	1	7,033
GO_BETA_AMYLOID_BINDING	34	0.433762	1.443577	0.079848	0.212223	1	8,247
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	17	0.518408	1.443405	0.079208	0.212179	1	1,150
GO_VASOCONSTRICTION	27	0.461673	1.443207	0.076152	0.212207	1	6,647
GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	124	0.3381	1.443172	0.051823	0.21202	1	6,623
GO_TISSUE_REMODELING	85	0.391366	1.442392	0.059289	0.212711	1	5,960
GO_CAMP_BINDING	21	0.483822	1.441802	0.077689	0.213148	1	3,862
GO_REGULATION_OF_SYNAPSE_ORGANIZATION	105	0.390532	1.441338	0.06012	0.213466	1	6,110
GO_SODIUM_ION_HOMEOSTASIS	29	0.43409	1.441054	0.037182	0.213558	1	3,841
GO_TRANSPORTER_COMPLEX	306	0.350707	1.440756	0.083333	0.213614		

GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	22	0.449112	1.435488	0.084337	0.217004	1	3,966
GO_AXON_REGENERATION	23	0.502172	1.435261	0.095618	0.217033	1	6,475
GO_POTASSIUM_ION_IMPORT	29	0.463667	1.434802	0.089463	0.217321	1	6,591
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	44	0.431814	1.434557	0.080868	0.217411	1	5,666
GO_PROTEIN_AUTOPHOSPHORYLATION	188	0.344794	1.433674	0.057447	0.218242	1	3,768
GO_BONE_DEVELOPMENT	151	0.373149	1.433552	0.080078	0.218152	1	7,227
GO_NEPHRON_DEVELOPMENT	115	0.371073	1.433324	0.062382	0.218214	1	4,291
GO_STEM_CELL_DIFFERENTIATION	185	0.342687	1.432841	0.049808	0.218592	1	7,908
GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	22	0.482444	1.432234	0.090056	0.21913	1	5,370
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	26	0.43886	1.431886	0.069721	0.219251	1	2,227
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	118	0.335184	1.431744	0.034884	0.219204	1	6,017
GO_RESPONSE_TO_PH	36	0.442434	1.431165	0.094488	0.219659	1	8,033
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	191	0.378598	1.430938	0.074656	0.21967	1	7,263
GO_PHAGOCYTIC_VESICLE	85	0.419178	1.430566	0.102881	0.219848	1	4,162
GO_LYTIC_VACUOLE	494	0.338633	1.429891	0.079365	0.220456	1	6,277
GO_SMOOTH_MUSCLE_CONTRACTION	45	0.492352	1.429882	0.097847	0.220238	1	6,716
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	26	0.479046	1.429769	0.102767	0.220119	1	6,716
GO_NEURON_SPINE	116	0.375697	1.429436	0.075697	0.220266	1	5,975
GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	23	0.492432	1.429338	0.108871	0.220131	1	6,502
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	31	0.434946	1.428606	0.054656	0.220769	1	5,433
GO_LEARNING	125	0.3859	1.428552	0.075875	0.220605	1	6,130
GO_GABA_RECEPTOR_BINDING	15	0.515439	1.428433	0.104449	0.220543	1	3,817
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	45	0.408407	1.428085	0.07362	0.220762	1	4,032
GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	26	0.459119	1.427856	0.090909	0.220822	1	4,733
GO_CELLULAR_RESPONSE_TO_VITAMIN							

GO_POSITIVE_REGULATION_OF_AUTOPHAGY	74	0.391886	1.422386	0.099804	0.224033	1	3,529
GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	72	0.37838	1.422207	0.068323	0.224017	1	4,325
GO_DIGESTIVE_TRACT_MORPHOGENESIS	47	0.414249	1.422121	0.057884	0.223879	1	5,098
GO_FEMALE_SEX_DIFFERENTIATION	110	0.350434	1.421829	0.039216	0.224016	1	4,234
GO_NEGATIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	140	0.337653	1.421785	0.041588	0.223839	1	4,597
GO_FEEDING_BEHAVIOR	86	0.384447	1.421449	0.0587	0.224025	1	7,083
GO_METENCEPHALON_DEVELOPMENT	100	0.389603	1.421326	0.09505	0.223936	1	5,992
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	37	0.433288	1.42071	0.084778	0.224446	1	5,565
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	42	0.40724	1.42071	0.063872	0.224221	1	3,132
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	18	0.492071	1.420293	0.091429	0.224454	1	2,658
GO_REGULATION_OF_MAP_KINASE_ACTIVITY	310	0.327278	1.420196	0.045276	0.224342	1	5,147
GO_CAMP_MEDIATED_SIGNALING	36	0.448977	1.419758	0.086864	0.224628	1	6,727
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	30	0.416462	1.418974	0.066019	0.225323	1	6,838
GO_RESPONSE_TO_MONOAMINE	35	0.429573	1.418845	0.095808	0.225243	1	2,123
GO_REGULATION_OF_HEART_CONTRACTION	215	0.368449	1.418771	0.089147	0.225116	1	6,055
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	0.48102	1.418645	0.071984	0.225019	1	7,908
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	273	0.344523	1.418307	0.063918	0.225185	1	5,191
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	15	0.561295	1.418255	0.138833	0.225016	1	4,162
GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	54	0.380656	1.417754	0.075875	0.225387	1	6,551
GO_CALMODULIN_BINDING	175	0.34861	1.41748	0.07014	0.225509	1	6,389
GO_FERROUS_IRON_BINDING	22	0.472566	1.417415	0.114786	0.225368	1	5,595
GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	59	0.38508	1.417019	0.079365	0.225598	1	6,168
GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	24	0.472326	1.416766	0.097847	0.225651	1	2,725
GO_TELENCEPHALON_DEVELOPMENT	223	0.330959	1.413539	0.051331	0.2293	1	5,687

GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	21	0.535274	1.409077	0.134766	0.231326	1	8,270
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	21	0.42462	1.408276	0.079457	0.232089	1	5,303
GO_MESONEPHROS_DEVELOPMENT	90	0.372874	1.407731	0.08	0.232542	1	4,757
GO_GABA_RECEPTOR_COMPLEX	17	0.53603	1.407576	0.088353	0.232549	1	8,250
GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	194	0.319875	1.407168	0.050881	0.232828	1	3,155
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	98	0.343753	1.407162	0.06729	0.232606	1	7,304
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	20	0.498428	1.406576	0.134122	0.233095	1	875
GO_POSITIVE_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	16	0.562456	1.406493	0.145228	0.232961	1	5,061
GO_REGULATION_OF_SODIUM_ION_TRANSPORT	75	0.360425	1.405214	0.081553	0.234235	1	5,193
GO_REGULATION_OF_FILOPODIUM_ASSEMBLY	34	0.43234	1.404538	0.079918	0.234879	1	4,340
GO_DORSAL_SPINAL_CORD_DEVELOPMENT	17	0.487343	1.404219	0.083333	0.235031	1	5,159
GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	41	0.362472	1.404198	0.057769	0.234827	1	1,457
GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	275	0.32633	1.40273	0.066922	0.236284	1	5,919
GO_PHOSPHOTYROSINE_BINDING	15	0.522285	1.402263	0.120163	0.236589	1	4,602
GO_EXCITATORY_SYNAPSE	191	0.364818	1.40221	0.105159	0.236435	1	5,626
GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	18	0.505004	1.401656	0.088123	0.236894	1	6,194
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	30	0.453703	1.401624	0.126482	0.236702	1	1,108
GO_STEM_CELL_PROLIFERATION	59	0.378681	1.401174	0.058052	0.236994	1	4,869
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	400	0.325314	1.400901	0.073469	0.237058	1	6,673
GO_G_PROTEIN_ALPHA_SUBUNIT_BINDING	22	0.458784	1.400809	0.073359	0.236949	1	7,245
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	142	0.349119	1.400558	0.075397	0.237017	1	7,566
GO_RNA_DESTABILIZATION	15	0.486533	1.398911	0.093626	0.238734	1	5,719
GO GRANULOCYTE DIFFERENTIATION	15	0.452135	1.398759	0.091085	0.238697	1	4,799
GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	30	0.422896	1.398678	0.116183	0.238582	1	

GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	146	0.403769	1.395339	0.106719	0.239259	1	7,263
GO_RESPONSE_TO_ACID_CHEMICAL	303	0.304101	1.394611	0.04023	0.239887	1	6,662
GO_ACTIN_FILAMENT_BASED_MOVEMENT	90	0.378904	1.394368	0.084168	0.239956	1	4,889
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	108	0.385135	1.393967	0.091451	0.24023	1	5,314
GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	20	0.499401	1.393567	0.130081	0.240514	1	6,743
GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	49	0.424074	1.392579	0.135729	0.241552	1	5,842
GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	44	0.40618	1.392434	0.099804	0.241493	1	4,757
GO_INNERVATION	23	0.466438	1.3919	0.085317	0.241918	1	8,927
GO_CALCIIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	15	0.507404	1.39131	0.094567	0.242398	1	7,182
GO_RESPONSE_TO_ETHANOL	132	0.331397	1.39097	0.054545	0.242592	1	5,182
GO_PHOTORECEPTOR_OUTER_SEGMENT	63	0.342565	1.390953	0.047525	0.242391	1	6,059
GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	31	0.449555	1.390156	0.123732	0.243163	1	3,056
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	16	0.508166	1.38955	0.126506	0.243738	1	6,331
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	55	0.359821	1.388981	0.079922	0.244199	1	3,017
GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	88	0.333673	1.388147	0.043651	0.245001	1	5,635
GO_NEGATIVE_REGULATION_OF_TRANSPORT	431	0.309487	1.38722	0.040936	0.245902	1	5,768
GO_REGULATION_OF_FEEDING_BEHAVIOR	20	0.458536	1.386898	0.113949	0.246094	1	5,192
GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	23	0.47729	1.38618	0.121756	0.246781	1	4,255
GO_DENDRITE	434	0.326403	1.385977	0.083168	0.246823	1	7,456
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM_ION_INTO_CYTOSOL	36	0.421722	1.385964	0.097889	0.246617	1	5,574
GO_MEMBRANE_BIOGENESIS	30	0.442395	1.385876	0.099222	0.246508	1	5,042
GO_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	35	0.412495	1.385792	0.105477	0.24637	1	5,910
GO_NEUROTRANSMITTER_UPTAKE	15	0.537241	1.385736	0.117021	0.246193	1	5,314
GO_EMBRYONIC_DIGESTIVE_TRACT_MORPHOGENESIS	17	0.480271	1.38439	0.113949	0.247599	1	

GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	200	0.380762	1.379717	0.15735	0.250129	1	3,132
GO_RESPONSE_TO_CAMP	103	0.341957	1.37967	0.069246	0.249958	1	7,018
GO_ENDOSOME_LUMEN	24	0.47163	1.379643	0.10303	0.249765	1	10,355
GO_RESPONSE_TO_FLUID_SHEAR_STRESS	33	0.439688	1.37962	0.119231	0.249566	1	5,612
GO_POSITIVE_REGULATION_OF_BEHAVIOR	24	0.431614	1.378138	0.080483	0.251152	1	7,583
GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	39	0.392168	1.377514	0.099174	0.251679	1	2,116
GO_POSITIVE_REGULATION_OF_COAGULATION	24	0.496432	1.377369	0.133858	0.251617	1	4,338
GO_REGULATION_OF_MACROPHAGE_ACTIVATION	25	0.417255	1.376749	0.087121	0.252201	1	3,730
GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	117	0.324673	1.376557	0.058704	0.252232	1	5,874
GO_AMIDE_TRANSPORT	92	0.364453	1.375684	0.100823	0.253041	1	6,974
GO_KIDNEY_MORPHOGENESIS	82	0.351534	1.374504	0.072937	0.254286	1	4,109
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	164	0.322229	1.374493	0.07635	0.254072	1	6,662
GO_BIOMINERAL_TISSUE_DEVELOPMENT	67	0.355178	1.374436	0.090909	0.253915	1	5,986
GO_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	19	0.528902	1.374221	0.168337	0.253955	1	1,150
GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	66	0.383803	1.373836	0.085366	0.254171	1	5,663
GO_GLUTAMATE_RECEPTOR_BINDING	37	0.393927	1.37277	0.115163	0.255305	1	7,959
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	26	0.476631	1.371948	0.145161	0.25613	1	3,075
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	441	0.296161	1.371877	0.055985	0.256003	1	6,678
GO_CORTICAL_CYTOSKELETON_ORGANIZATION	35	0.419569	1.371641	0.10757	0.256059	1	4,273
GO_SYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	21	0.493883	1.371357	0.121032	0.256166	1	8,666
GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	26	0.454557	1.370981	0.118	0.256411	1	7,379
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT1_PROTEIN	15	0.4899	1.370671	0.128205	0.256575	1	3,527
GO_REGULATION_OF_ORGAN_GROWTH	70	0.35432	1.369668	0.066667	0.257522	1	5,960
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	266	0.304407	1.369323	0.060606	0.257741	1	3,860
GO_CELL_CELL_RECOGNITION	55	0.366297	1.368685				

GO_WOUND_HEALING	434	0.318972	1.361429	0.080769	0.264234	1	5,126
GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	278	0.301398	1.361092	0.05973	0.264449	1	5,181
GO_NEURONAL_POSTSYNAPTIC_DENSITY	51	0.448403	1.359968	0.180583	0.265654	1	8,252
GO_ENZYME_ACTIVATOR_ACTIVITY	445	0.288149	1.359145	0.056452	0.266519	1	6,736
GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	20	0.470866	1.357691	0.122407	0.268112	1	6,236
GO_GASTRULATION_WITH_MOUTH_FORMING_SECOND	25	0.437816	1.356641	0.120316	0.269342	1	5,508
GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	121	0.327445	1.355977	0.062868	0.269886	1	6,192
GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	44	0.383917	1.355858	0.098814	0.269799	1	6,546
GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	270	0.30146	1.35521	0.060784	0.270367	1	6,043
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	31	0.455516	1.355074	0.173116	0.270338	1	1,456
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	182	0.321985	1.354884	0.088757	0.270364	1	4,715
GO_VENTRAL_SPINAL_CORD_INTERNEURON_DIFFERENTIATION	15	0.512055	1.354732	0.12758	0.270339	1	10,986
GO_BLOOD_VESSEL_REMODELING	32	0.413737	1.354667	0.117534	0.27019	1	3,063
GO_NEUROTROPHIN_SIGNALING_PATHWAY	23	0.445308	1.354588	0.134538	0.270054	1	3,662
GO_JNK_CASCADE	79	0.338466	1.354417	0.078471	0.270042	1	3,765
GO_HEART TRABECULA MORPHOGENESIS	24	0.437005	1.354351	0.14611	0.269898	1	6,369
GO_REGULATION_OF_PEPTIDE_TRANSPORT	247	0.31353	1.354326	0.105788	0.269692	1	7,523
GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	33	0.416213	1.354072	0.103448	0.269791	1	8,140
GO_NEURON_PROJECTION_GUIDANCE	192	0.341428	1.354007	0.097276	0.269646	1	5,192
GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	39	0.430941	1.353641	0.168959	0.269859	1	7,133
GO_DRUG_BINDING	105	0.312779	1.353593	0.045817	0.269684	1	4,159
GO_RESPONSE_TO_FOLIC_ACID	15	0.468654	1.352717	0.141393	0.270598	1	5,814
GO_NEGATIVE_REGULATION_OF_OSSIFICATION	62	0.365836	1.351964	0.106509	0.2713	1	7,248
GO TRABECULA MORPHOGENESIS	37	0.397755	1.351326	0.137331	0.271844	1	6,369
GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	41	0.398997	1.35131				

GO_POTASSIUM_ION_HOMEOSTASIS	18	0.484702	1.343647	0.142857	0.278677	1	4,186
GO_PROTEOGLYCAN_METABOLIC_PROCESS	82	0.392819	1.343566	0.147448	0.27855	1	7,138
GO_VIRUS_RECEPTOR_ACTIVITY	64	0.375792	1.343419	0.142035	0.278498	1	2,612
GO_CELL_PROLIFERATION_IN_FOREBRAIN	27	0.431333	1.342998	0.132296	0.27885	1	4,436
GO_HINDBRAIN_MORPHOGENESIS	39	0.411342	1.342809	0.11068	0.278869	1	5,173
GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	118	0.317577	1.342512	0.083832	0.279001	1	4,305
GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	23	0.429853	1.342114	0.127237	0.279278	1	3,457
GO_NEGATIVE_CHEMOTAXIS	39	0.399829	1.340937	0.129278	0.280571	1	3,570
GO_NECROTIC_CELL_DEATH	28	0.408003	1.340613	0.148454	0.280753	1	3,239
GO_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	17	0.48162	1.340375	0.139489	0.280829	1	2,488
GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	48	0.387981	1.3403	0.145873	0.280699	1	6,280
GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	229	0.315598	1.340186	0.100806	0.280621	1	3,239
GO_ACTIN_FILAMENT	67	0.382191	1.340098	0.12426	0.280479	1	3,895
GO_RESPONSE_TO_ALKALOID	131	0.322392	1.339985	0.064646	0.280367	1	8,303
GO_NEGATIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	26	0.431622	1.339794	0.133745	0.280373	1	5,043
GO_AMIDE_BINDING	255	0.300059	1.339754	0.084813	0.280185	1	5,852
GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	60	0.335422	1.339637	0.090741	0.280094	1	4,662
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	33	0.417096	1.339303	0.148148	0.280321	1	3,690
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	140	0.343707	1.339041	0.131148	0.280418	1	3,690
GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	23	0.444189	1.338852	0.148221	0.280418	1	5,581
GO_POSITIVE_REGULATION_OF_GROWTH	226	0.304965	1.337964	0.084778	0.281388	1	7,155
GO_REGULATION_OF_VASCULAR_PERMEABILITY	30	0.403372	1.337651	0.105973	0.281547	1	1,674
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	25	0.455205	1.337369	0.149688	0.281685	1	4,270
GO_POSITIVE_REGULATION_OF_ACTIN_NUCLEATION	16	0.484983	1.337338	0.172485	0.281496	1	3,290
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION							

GO_PHOSPHATIDYLSERINE_BINDING	33	0.403574	1.332934	0.135135	0.284309	1	7,071
GO_TRANSCRIPTIONAL_ACTIVATOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	213	0.300593	1.33266	0.094697	0.284425	1	7,900
GO_CORONARY_VASCULATURE_DEVELOPMENT	36	0.427818	1.330738	0.177734	0.286726	1	5,686
GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	46	0.406033	1.330564	0.143678	0.286708	1	7,029
GO_RESPONSE_TO_AMMONIUM_ION	49	0.370033	1.329456	0.108949	0.287903	1	4,397
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	42	0.428792	1.329133	0.15619	0.288097	1	7,908
GO_RESPONSE_TO_ANTIBIOTIC	45	0.369688	1.329088	0.112167	0.287919	1	4,991
GO_SEGMENT_SPECIFICATION	16	0.485266	1.32908	0.16092	0.2877	1	2,164
GO_AXONAL_GROWTH_CONE	19	0.466743	1.32897	0.162933	0.2876	1	3,954
GO_RESPONSE_TO_ELECTRICAL_STIMULUS	41	0.372069	1.328853	0.072266	0.287534	1	7,560
GO_RESPONSE_TO_CARBOHYDRATE	159	0.310736	1.328756	0.073852	0.287408	1	6,191
GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	53	0.398721	1.32874	0.141129	0.2872	1	4,097
GO_REGULATION_OF_HORMONE_SECRETION	253	0.315462	1.32864	0.129845	0.287088	1	7,024
GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	42	0.351838	1.328483	0.08982	0.287073	1	4,991
GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	18	0.454894	1.327191	0.113821	0.288466	1	5,768
GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	166	0.351225	1.32698	0.137218	0.288536	1	6,546
GO_MAP_KINASE_KINASE_KINASE_ACTIVITY	18	0.457374	1.326939	0.173737	0.288357	1	5,287
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	71	0.434039	1.326727	0.204545	0.288382	1	6,955
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	16	0.492805	1.326671	0.137097	0.288222	1	3,937
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL_SIGNALING	69	0.34228	1.325929	0.117761	0.288951	1	7,943
GO_SULFOTRANSFERASE_ACTIVITY	50	0.362833	1.325916	0.118	0.28874	1	6,679
GO_ALCOHOL_BINDING	99	0.332541	1.325511	0.100402	0.289051	1	5,858
GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	56	0.352041	1.325483	0.116327	0.28886	1	5,724
GO_MEMBRANE_ASSEMBLY	25	0.447885	1.324998	0.159223	0.289273	1	5,042
GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16						

