Table SI. Gene Set Enrichment Analysis results of the c2 reference gene set for high expression of glutathione S-transferase Mu 5 in gastric cancer tissues.

Name	Size	ES	NES	NOM P-value	FDR q-value
KEGG_CELL_CYCLE	124	-0.673	-2.372	<0.001	0.000
KEGG_RNA_DEGRADATION	56	-0.665	-2.162	<0.001	0.002
KEGG_SPLICEOSOME	123	-0.687	-2.132	<0.001	0.003
KEGG_BASE_EXCISION_REPAIR	33	-0.739	-2.109	<0.001	0.002
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.688	-2.103	<0.001	0.002
KEGG_PYRIMIDINE_METABOLISM	96	-0.579	-2.101	<0.001	0.002
KEGG_DNA_REPLICATION	36	-0.805	-2.031	<0.001	0.006
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.723	-2.018	<0.001	0.006
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.719	-2.006	0.004	0.006
KEGG_MISMATCH_REPAIR	23	-0.765	-1.985	<0.001	0.008
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	-0.736	-1.982	<0.001	0.007
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	130	-0.452	-1.875	0.002	0.020
KEGG_RNA_POLYMERASE	29	-0.615	-1.813	0.010	0.036
KEGG_PROTEASOME	43	-0.698	-1.792	0.002	0.040
KEGG_BASAL_TRANSCRIPTION_FACTORS	35	-0.525	-1.763	0.012	0.049
KEGG_P53_SIGNALING_PATHWAY	66	-0.437	-1.690	0.018	0.082
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	32	-0.505	-1.675	0.016	0.087
KEGG_SELENOAMINO_ACID_METABOLISM	25	-0.528	-1.665	0.010	0.088
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	-0.640	-1.639	0.042	0.098
KEGG_LYSINE_DEGRADATION	39	-0.473	-1.611	0.034	0.113
KEGG_THYROID_CANCER	29	-0.466	-1.606	0.024	0.111
KEGG_OOCYTE_MEIOSIS	108	-0.387	-1.599	0.023	0.111
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.501	-1.589	0.039	0.113
KEGG_PROTEIN_EXPORT	22	-0.608	-1.537	0.078	0.149
KEGG_PURINE_METABOLISM	154	-0.343	-1.503	0.033	0.174
KEGG_STEROID_BIOSYNTHESIS	16	-0.584	-1.501	0.083	0.168
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.490	-1.499	0.067	0.164
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.590	-1.479	0.092	0.177
KEGG_PROGESTERONE_MEDIATED_O	83	-0.355	-1.476	0.039	0.174

OCYTE_MATURATION					
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	-0.434	-1.464	0.055	0.180
KEGG_PEROXISOME	78	-0.422	-1.450	0.107	0.187
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	-0.567	-1.417	0.127	0.213
KEGG_RIBOFLAVIN_METABOLISM	16	-0.479	-1.413	0.090	0.210
KEGG_HUNTINGTONS_DISEASE	172	-0.387	-1.359	0.199	0.261
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	42	-0.397	-1.355	0.144	0.258
KEGG_PENTOSE_PHOSPHATE_PATHWAY	26	-0.457	-1.354	0.138	0.252
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	-0.448	-1.348	0.185	0.252
KEGG_PYRUVATE_METABOLISM	38	-0.412	-1.337	0.165	0.258
KEGG_ARGININE_AND_PROLINE_METABOLISM	51	-0.367	-1.293	0.166	0.301
KEGG_SPHINGOLIPID_METABOLISM	36	-0.372	-1.289	0.160	0.299
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	51	-0.374	-1.284	0.142	0.297
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	-0.406	-1.276	0.203	0.300
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	40	-0.384	-1.220	0.229	0.363
KEGG_PROPANOATE_METABOLISM	32	-0.392	-1.181	0.272	0.407
KEGG_BUTANOATE_METABOLISM	33	-0.379	-1.177	0.274	0.403
KEGG_OXIDATIVE_PHOSPHORYLATION	116	-0.416	-1.158	0.370	0.422
KEGG_ALZHEIMERS_DISEASE	156	-0.325	-1.149	0.333	0.425
KEGG_PARKINSONS_DISEASE	111	-0.404	-1.148	0.369	0.417
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	44	-0.345	-1.112	0.337	0.461
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	-0.352	-1.068	0.342	0.518
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	68	-0.364	-1.060	0.399	0.519
KEGG_GLUTATHIONE_METABOLISM	47	-0.313	-1.036	0.406	0.549
KEGG_GALACTOSE_METABOLISM	25	-0.324	-1.032	0.402	0.545
KEGG_NITROGEN_METABOLISM	23	-0.336	-1.020	0.427	0.555
KEGG_BLADDER_CANCER	40	-0.278	-1.005	0.423	0.567
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	59	-0.279	-0.985	0.471	0.588
KEGG_RIBOSOME	87	-0.432	-0.937	0.555	0.657
KEGG_MATURITY_ONSET_DIABETES_	24	-0.342	-0.919	0.544	0.676

OF_THE_YOUNG					
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	-0.255	-0.879	0.623	0.731
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	-0.274	-0.879	0.614	0.720
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	-0.298	-0.879	0.588	0.709
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	-0.233	-0.877	0.628	0.700
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	52	-0.217	-0.873	0.669	0.695
KEGG_VIBRIO_CHOLERAE_INFECTION	52	-0.227	-0.871	0.626	0.687
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	60	-0.222	-0.821	0.668	0.760
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	-0.257	-0.819	0.688	0.750
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	56	-0.209	-0.782	0.752	0.797
KEGG_O_GLYCAN_BIOSYNTHESIS	27	-0.234	-0.731	0.778	0.861
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	71	-0.176	-0.730	0.928	0.849
KEGG_GLYCEROLIPID_METABOLISM	41	-0.194	-0.717	0.879	0.854
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	27	-0.240	-0.665	0.835	0.901
KEGG_OTHER_GLYCAN_DEGRADATION	16	-0.216	-0.593	0.918	0.949
KEGG_FATTY_ACID_METABOLISM	42	-0.174	-0.542	0.959	0.964

ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SII. Gene Set Enrichment Analysis results of the c5 reference gene set for high expression of glutathione S-transferase Mu 5 in gastric cancer tissues.

Name	Size	ES	NES	NOM P-value	FDR q-value
GO_SARCOLEMMA	124	0.641	2.280	<0.001	0.020
GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	344	0.649	2.274	<0.001	0.012
GO_EXTRACELLULAR_MATRIX	411	0.640	2.254	<0.001	0.010
GO_HEPARIN_BINDING	151	0.610	2.199	<0.001	0.018
GO_SIALYLATION	21	0.744	2.185	<0.001	0.019
GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	195	0.574	2.175	<0.001	0.018
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	223	0.532	2.172	<0.001	0.016
GO_GLYCOSAMINOGLYCAN_BINDING	194	0.593	2.168	<0.001	0.015
GO_INTEGRIN_BINDING	101	0.631	2.157	<0.001	0.016
GO_POSITIVE_REGULATION_OF_OSSIFICATION	81	0.623	2.152	<0.001	0.015
GO_EXTRACELLULAR_MATRIX_COMPONENT	122	0.675	2.152	<0.001	0.014
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	36	0.643	2.150	<0.001	0.013
GO_DIGESTIVE_TRACT_MORPHOGENESIS	47	0.624	2.145	<0.001	0.013
GO_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	102	0.575	2.142	<0.001	0.013
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	295	0.597	2.137	<0.001	0.014
GO_GLOMERULUS_DEVELOPMENT	49	0.679	2.135	<0.001	0.013
GO_MUSCLE_SYSTEM_PROCESS	277	0.526	2.135	<0.001	0.013
GO_NEPHRON_DEVELOPMENT	115	0.569	2.133	<0.001	0.012
GO_GROWTH_FACTOR_BINDING	122	0.610	2.132	<0.001	0.012
GO_VASCULATURE_DEVELOPMENT	457	0.532	2.131	<0.001	0.011
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	88	0.588	2.130	<0.001	0.011
GO_REGULATION_OF_OSSIFICATION	170	0.562	2.129	<0.001	0.010
GO_REGULATION_OF_ION_HOMEOSTASIS	193	0.514	2.128	<0.001	0.010
GO_CELL_ADHESION_MOLECULE_BINDING	176	0.564	2.127	<0.001	0.010
GO_EMBRYONIC_DIGESTIVE_TRACT_	32	0.659	2.118	<0.001	0.011

DEVELOPMENT					
GO_BASEMENT_MEMBRANE	90	0.646	2.113	<0.001	0.012
GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	57	0.650	2.111	<0.001	0.011
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	129	0.591	2.110	<0.001	0.011
GO_CELL_SUBSTRATE_ADHESION	161	0.542	2.105	<0.001	0.012
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	73	0.670	2.102	<0.001	0.012
GO_MUSCLE_CONTRACTION	228	0.531	2.102	<0.001	0.012
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	55	0.574	2.099	<0.001	0.012
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	108	0.556	2.099	<0.001	0.011
GO_ANGIOGENESIS	284	0.544	2.091	<0.001	0.012
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	160	0.510	2.089	<0.001	0.012
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	249	0.512	2.089	<0.001	0.012
GO_CELL_MATRIX_ADHESION	116	0.564	2.086	<0.001	0.012
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	75	0.583	2.086	<0.001	0.012
GO_REGULATION_OF_HEART_CONTRACTION	216	0.520	2.086	<0.001	0.011
GO_CIRCULATORY_SYSTEM_PROCESS	354	0.489	2.085	<0.001	0.011
GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	107	0.572	2.082	<0.001	0.011
GO_BLOOD_VESSEL_MORPHOGENESIS	355	0.528	2.080	<0.001	0.011
GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	56	0.658	2.078	<0.001	0.012
GO_MUSCLE_ORGAN_DEVELOPMENT	259	0.504	2.076	<0.001	0.012
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	71	0.592	2.076	<0.001	0.012
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	35	0.662	2.076	<0.001	0.011
GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	52	0.611	2.074	<0.001	0.011
GO_SMOOTHENED_SIGNALING_PATHWAY	69	0.565	2.073	<0.001	0.011
GO_SULFUR_COMPOUND_BINDING	227	0.495	2.073	<0.001	0.011
GO_REGULATION_OF_BLOOD_CIRCULATION	285	0.509	2.071	<0.001	0.011

GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	49	0.590	2.069	<0.001	0.011
GO_COLLAGEN_TRIMER	86	0.670	2.069	<0.001	0.011
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	199	0.515	2.068	<0.001	0.011
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	22	0.723	2.067	<0.001	0.011
GO_CGMP_METABOLIC_PROCESS	23	0.748	2.057	<0.001	0.012
GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	57	0.613	2.056	<0.001	0.012
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	42	0.648	2.054	<0.001	0.012
GO_OUTFLOW_TRACT_MORPHOGENESIS	56	0.592	2.053	<0.001	0.012
GO_NEURON_RECOGNITION	33	0.672	2.052	<0.001	0.012
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	223	0.545	2.052	<0.001	0.012
GO_PLATELET_DEGRANULATION	103	0.601	2.051	<0.001	0.012
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	71	0.571	2.051	<0.001	0.011
GO_MELANOCYTE_DIFFERENTIATION	17	0.705	2.048	<0.001	0.012
GO_ACTION_POTENTIAL	92	0.543	2.047	<0.001	0.012
GO_REGULATION_OF_SYSTEM_PROCESS	490	0.487	2.047	<0.001	0.011
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	121	0.538	2.047	<0.001	0.011
GO_EMBRYONIC_DIGESTIVE_TRACT_MORPHOGENESIS	17	0.725	2.045	<0.001	0.012
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	119	0.523	2.044	<0.001	0.011
GO_REGULATION_OF_CARDIAC_CONDUCTION	66	0.599	2.043	0.002	0.011
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	153	0.543	2.043	<0.001	0.011
GO_MUSCLE_STRUCTURE_DEVELOPMENT	411	0.481	2.041	<0.001	0.011
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	110	0.527	2.041	<0.001	0.011
GO_CALCIUM_MEDIATED_SIGNALING	84	0.568	2.039	0.002	0.011
GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	42	0.655	2.036	<0.001	0.012
GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THR	200	0.486	2.036	<0.001	0.012

EONINE_KINASE_SIGNALING_PATHWAY					
GO_PEPTIDE_RECEPTOR_ACTIVITY	126	0.567	2.032	<0.001	0.012
GO_REGULATION_OF_MUSCLE_CONTRACTION	144	0.520	2.032	<0.001	0.012
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	64	0.616	2.030	<0.001	0.012
GO_MESONEPHROS_DEVELOPMENT	90	0.537	2.028	<0.001	0.012
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	65	0.577	2.025	0.002	0.013
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	227	0.479	2.023	<0.001	0.013
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	26	0.680	2.023	<0.001	0.013
GO_DIGESTIVE_SYSTEM_DEVELOPMENT	142	0.492	2.023	<0.001	0.012
GO_T_TUBULE	45	0.640	2.022	0.002	0.012
GO_FIBRIL_ORGANIZATION	19	0.758	2.022	<0.001	0.012
GO_BONE_DEVELOPMENT	150	0.505	2.021	<0.001	0.012
GO_NEGATIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	41	0.609	2.020	<0.001	0.012
GO_PLATELET_ALPHA_GRANULE	74	0.624	2.019	<0.001	0.012
GO_REGULATION_OF_SMAD_PROTEIN_IMPORT_INTO_NUCLEUS	16	0.738	2.017	<0.001	0.012
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	55	0.609	2.017	<0.001	0.012
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	81	0.557	2.017	<0.001	0.012
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	38	0.611	2.015	0.002	0.012
GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	158	0.518	2.015	<0.001	0.012
GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	34	0.668	2.013	<0.001	0.012
GO_FOREBRAIN_NEURON_DEVELOPMENT	34	0.625	2.012	<0.001	0.012
GO_MESENCHYME_DEVELOPMENT	183	0.522	2.011	<0.001	0.013
GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	59	0.597	2.011	<0.001	0.012
GO_ATRIAL_SEPTUM_DEVELOPMENT	17	0.721	2.010	<0.001	0.013

GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	37	0.612	2.009	<0.001	0.013
GO_GANGLIOSIDE_BIOSYNTHETIC_PROCESS	18	0.716	2.009	<0.001	0.013
GO_POSITIVE_REGULATION_OF_LOCOMOTION	397	0.474	2.008	<0.001	0.013
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	135	0.500	2.008	<0.001	0.013
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	102	0.523	2.008	<0.001	0.012
GO_RESPONSE_TO_PROSTAGLANDIN	34	0.622	2.007	<0.001	0.012
GO_COLLAGEN_BINDING	60	0.653	2.006	0.004	0.012
GO_EXTRACELLULAR_MATRIX_ASSEMBLY	16	0.812	2.006	<0.001	0.012
GO_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	95	0.537	2.004	<0.001	0.013
GO_REGULATION_OF_BLOOD_PRESSURE	164	0.506	2.004	<0.001	0.013
GO_REGULATION_OF_METAL_ION_TRANSPORT	312	0.467	2.004	<0.001	0.012
GO_CARTILAGE_DEVELOPMENT	143	0.535	2.003	<0.001	0.012
GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	29	0.701	2.002	<0.001	0.012
GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	165	0.504	2.002	<0.001	0.012
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	81	0.578	2.002	<0.001	0.012
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	19	0.642	2.000	<0.001	0.012
GO_SMOOTH_MUSCLE_CONTRACTION	45	0.658	1.998	<0.001	0.013
GO_KIDNEY_EPITHELIUM_DEVELOPMENT	125	0.510	1.998	<0.001	0.013
GO_SENSORY_PERCEPTION_OF_PAIN	72	0.558	1.997	<0.001	0.013
GO_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	135	0.565	1.997	<0.001	0.013
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	295	0.479	1.996	<0.001	0.013
GO_ENDOTHELIUM_DEVELOPMENT	88	0.552	1.995	0.004	0.013
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	49	0.556	1.995	<0.001	0.013
GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	19	0.816	1.994	<0.001	0.013

GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	61	0.536	1.994	<0.001	0.012
GO_CATION_CHANNEL_COMPLEX	159	0.542	1.994	<0.001	0.012
GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	24	0.649	1.994	<0.001	0.012
GO_CONTRACTILE_FIBER	205	0.528	1.990	0.002	0.013
GO_AMINOGLYCAN_CATABOLIC_PROCESS	66	0.552	1.989	<0.001	0.013
GO_MESENCHYMAL_CELL_DIFFERENTIATION	131	0.520	1.989	<0.001	0.013
GO_CONNECTIVE_TISSUE_DEVELOPMENT	188	0.516	1.987	<0.001	0.013
GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	328	0.461	1.985	<0.001	0.013
GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	41	0.599	1.983	0.002	0.013
GO_MULTICELLULAR_ORGANISM_METABOLIC_PROCESS	87	0.623	1.983	0.002	0.013
GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	54	0.623	1.983	<0.001	0.013
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	86	0.560	1.981	<0.001	0.013
GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	30	0.605	1.980	<0.001	0.014
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	101	0.510	1.979	<0.001	0.014
GO_CGMP_BIOSYNTHETIC_PROCESS	15	0.752	1.978	<0.001	0.014
GO_KIDNEY_MORPHOGENESIS	82	0.521	1.978	<0.001	0.014
GO_REGULATION_OF_SYNAPSE_ASSEMBLY	72	0.565	1.978	<0.001	0.014
GO_CALCIUM_ION_TRANSPORT	209	0.477	1.977	<0.001	0.014
GO_NEPHRON_EPITHELIUM_DEVELOPMENT	93	0.516	1.975	<0.001	0.014
GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	35	0.607	1.975	<0.001	0.014
GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	62	0.577	1.975	<0.001	0.014
GO_BASAL_PART_OF_CELL	49	0.558	1.975	<0.001	0.014
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	39	0.553	1.973	<0.001	0.014
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	35	0.622	1.973	<0.001	0.014
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCES	106	0.542	1.972	<0.001	0.014

S					
GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	199	0.463	1.972	<0.001	0.014
GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	39	0.699	1.972	<0.001	0.014
GO_NEURAL_CREST_CELL_DIFFERENTIATION	74	0.541	1.972	<0.001	0.014
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	101	0.515	1.972	0.004	0.014
GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	46	0.607	1.971	<0.001	0.014
GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLED_TO_CYCLIC_NUCLEOTIDE_SECOND_MESSENGER	161	0.551	1.970	<0.001	0.014
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	151	0.526	1.969	<0.001	0.014
GO_REGULATION_OF_VASOCONSTRICTION	65	0.578	1.969	<0.001	0.014
GO_RENAL_SYSTEM_PROCESS	98	0.513	1.968	<0.001	0.014
GO_PLATELET_DENSE_GRANULE	19	0.687	1.967	0.002	0.014
GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	58	0.561	1.967	<0.001	0.014
GO_POTASSIUM_CHANNEL_COMPLEX	88	0.564	1.967	<0.001	0.014
GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	25	0.725	1.966	<0.001	0.014
GO_REGULATION_OF_CALCIUM_ION_IMPORT	97	0.510	1.965	0.002	0.014
GO_SECRETORY_GRANULE_LUMEN	80	0.608	1.965	0.002	0.014
GO_REGULATION_OF_AMINE_TRANSPORT	69	0.570	1.964	<0.001	0.014
GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	18	0.713	1.964	0.002	0.014
GO_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	91	0.500	1.964	<0.001	0.014
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	128	0.522	1.962	<0.001	0.014
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	53	0.620	1.962	<0.001	0.014
GO_NEGATIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	16	0.712	1.961	0.004	0.014
GO_BONE_GROWTH	20	0.687	1.961	0.002	0.014

GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	191	0.488	1.961	<0.001	0.014
GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	67	0.571	1.961	<0.001	0.014
GO_CARDIAC_CHAMBER_MORPHOGENESIS	101	0.488	1.961	<0.001	0.014
GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	37	0.628	1.961	0.002	0.014
GO_ENSHEATHMENT_OF_NEURONS	87	0.509	1.960	<0.001	0.014
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	83	0.499	1.960	<0.001	0.014
GO_RESPONSE_TO_BMP	88	0.549	1.960	<0.001	0.014
GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	73	0.515	1.960	<0.001	0.014
GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	36	0.600	1.960	<0.001	0.014
GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	25	0.663	1.959	<0.001	0.014
GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	126	0.488	1.959	<0.001	0.014
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	49	0.612	1.957	<0.001	0.014
GO_FIBRONECTIN_BINDING	26	0.697	1.956	<0.001	0.014
GO_REGULATION_OF_CALCINEURIN_NFAT_SIGNALING_CASCADE	16	0.693	1.956	0.004	0.014
GO_I_BAND	118	0.572	1.955	0.004	0.014
GO_LUNG_ALVEOLUS_DEVELOPMENT	40	0.589	1.955	0.002	0.014
GO_REGULATION_OF_CHEMOTAXIS	176	0.515	1.955	0.002	0.014
GO_REGULATION_OF_SYNAPSE_ORGANIZATION	105	0.522	1.954	<0.001	0.014
GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	126	0.535	1.953	<0.001	0.014
GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	95	0.541	1.953	<0.001	0.014
GO_RESPONSE_TO_PROSTAGLANDIN_E	25	0.631	1.953	<0.001	0.014
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	81	0.506	1.951	<0.001	0.014
GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	21	0.696	1.951	0.002	0.014
GO_NEGATIVE_CHEMOTAXIS	39	0.603	1.950	0.002	0.014
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A_CHEMICAL_SIGNAL	45	0.579	1.950	<0.001	0.014

GO_HEART_DEVELOPMENT	449	0.450	1.949	<0.001	0.014
GO_REGULATION_OF_MEMBRANE_POTENTIAL	329	0.444	1.949	<0.001	0.014
GO_RESPONSE_TO_FLUID_SHEAR_STRESS	33	0.623	1.949	<0.001	0.014
GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	45	0.565	1.949	<0.001	0.014
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	82	0.523	1.948	<0.001	0.014
GO_MUSCLE_TISSUE_DEVELOPMENT	261	0.455	1.947	<0.001	0.015
GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	35	0.640	1.946	<0.001	0.014
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	413	0.447	1.946	<0.001	0.014
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	64	0.556	1.946	<0.001	0.014
GO_GOLGI_LUMEN	84	0.515	1.946	<0.001	0.014
GO_ARTERY_DEVELOPMENT	75	0.559	1.946	<0.001	0.014
GO_PLATELET_ALPHA_GRANULE_LUMEN	54	0.656	1.945	<0.001	0.014
GO_MEMBRANE_DEPOLARIZATION	59	0.564	1.945	<0.001	0.014
GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	30	0.615	1.945	<0.001	0.014
GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	39	0.604	1.942	0.002	0.015
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	202	0.472	1.942	<0.001	0.015
GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	59	0.564	1.942	<0.001	0.015
GO_COLLAGEN_FIBRIL_ORGANIZATION	36	0.716	1.941	0.004	0.015
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	18	0.709	1.940	0.002	0.015
GO_CARDIAC_CONDUCTION	81	0.530	1.940	0.002	0.015
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	39	0.626	1.940	<0.001	0.015
GO_REGULATION_OF_VASCULAR_PERMEABILITY	30	0.616	1.939	<0.001	0.015
GO_PHASIC_SMOOTH_MUSCLE_CONTRACTION	16	0.709	1.939	<0.001	0.015
GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	66	0.591	1.937	<0.001	0.015
GO_SULFUR_COMPOUND_CATABOLIC_	39	0.583	1.936	<0.001	0.015

PROCESS					
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	68	0.555	1.934	<0.001	0.015
GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	74	0.550	1.932	0.002	0.016
GO_RETINAL_GANGLION_CELL_AXON_GUIDANCE	18	0.687	1.932	0.002	0.016
GO_CARDIAC_CHAMBER_DEVELOPMENT	140	0.473	1.931	<0.001	0.016
GO_CALCIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	16	0.675	1.928	0.002	0.016
GO_POSITIVE_REGULATION_OF_AXONOGENESIS	68	0.518	1.928	<0.001	0.016
GO_NEGATIVE_REGULATION_OF_OSSIFICATION	64	0.544	1.927	<0.001	0.016
GO_POSITIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	24	0.628	1.927	<0.001	0.016
GO_SKELETAL_SYSTEM_DEVELOPMENT	441	0.438	1.927	<0.001	0.016
GO_MAIN_AXON	57	0.535	1.926	<0.001	0.017
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	123	0.465	1.925	<0.001	0.017
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	27	0.687	1.925	<0.001	0.017
GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	20	0.655	1.925	<0.001	0.017
GO_RESPONSE_TO_PAIN	29	0.621	1.924	<0.001	0.017
GO_CAMP_METABOLIC_PROCESS	34	0.644	1.924	<0.001	0.016
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	66	0.561	1.923	<0.001	0.017
GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	21	0.680	1.923	0.004	0.017
GO_ENDOTHELIAL_CELL_DIFFERENTIATION	70	0.541	1.922	0.002	0.017
GO_REGULATION_OF_HEART_RATE	83	0.515	1.922	<0.001	0.017
GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	25	0.611	1.922	0.002	0.017
GO_ANCHORED_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	19	0.674	1.919	0.008	0.017
GO_REGULATION_OF_OSTEOBLAST_PROLIFERATION	22	0.644	1.919	0.002	0.017
GO_NEGATIVE_REGULATION_OF_ANIO	32	0.587	1.919	0.002	0.017

N_TRANSPORT					
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	42	0.594	1.919	0.002	0.017
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	38	0.596	1.918	0.002	0.017
GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	65	0.579	1.918	<0.001	0.017
GO_LONG_TERM_SYNAPTIC_POTENTIATION	39	0.572	1.917	<0.001	0.017
GO_MULTICELLULAR_ORGANISMAL_MACROMOLECULE_METABOLIC_PROCESS	73	0.640	1.917	0.006	0.017
GO_CYCLASE_ACTIVITY	20	0.721	1.916	0.002	0.017
GO_CHANNEL_REGULATOR_ACTIVITY	125	0.465	1.916	<0.001	0.017
GO_REGULATION_OF_LYASE_ACTIVITY	83	0.509	1.913	<0.001	0.018
GO_TAXIS	443	0.443	1.913	0.002	0.018
GO_CYTOKINE_BINDING	88	0.595	1.913	<0.001	0.018
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	297	0.427	1.913	<0.001	0.017
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	451	0.421	1.912	<0.001	0.018
GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	288	0.436	1.912	<0.001	0.018
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	222	0.465	1.912	<0.001	0.018
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	39	0.571	1.912	<0.001	0.018
GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	225	0.461	1.910	<0.001	0.018
GO_REGULATION_OF_LIPASE_ACTIVITY	83	0.569	1.910	<0.001	0.018
GO_CELL_CELL_CONTACT_ZONE	64	0.519	1.909	0.004	0.018
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	39	0.574	1.909	0.006	0.018
GO_MESONEPHRIC_TUBULE_MORPHOGENESIS	53	0.540	1.908	0.004	0.018
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_IMPORT	51	0.551	1.908	0.002	0.018
GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	52	0.545	1.908	0.002	0.018
GO_POSITIVE_REGULATION_OF_BLOO	25	0.650	1.907	0.006	0.018

D_VESSEL_ENDOTHELIAL_CELL_MIGRATION					
GO_DENDRITE_MEMBRANE	18	0.676	1.907	<0.001	0.018
GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	395	0.438	1.906	<0.001	0.018
GO_TRABECULA_MORPHOGENESIS	37	0.558	1.906	0.006	0.018
GO_FILOPODIUM_MEMBRANE	18	0.660	1.905	<0.001	0.018
GO_NEURON_PROJECTION_MORPHOGENESIS	391	0.460	1.905	0.002	0.018
GO_ANCHORED_COMPONENT_OF_MEMBRANE	144	0.458	1.905	<0.001	0.018
GO_CALCIUM_ION_IMPORT	61	0.516	1.904	0.002	0.018
GO_STEM_CELL_DIFFERENTIATION	186	0.467	1.904	<0.001	0.018
GO_MEMBRANE_MICRODOMAIN	283	0.439	1.903	<0.001	0.018
GO_SARCOPLASM	66	0.527	1.903	0.004	0.018
GO_LEARNING	125	0.487	1.902	<0.001	0.018
GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	49	0.573	1.902	<0.001	0.018
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	449	0.426	1.902	<0.001	0.018
GO_GROWTH_FACTOR_ACTIVITY	149	0.470	1.902	0.002	0.018
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	118	0.536	1.902	0.002	0.018
GO_HEART_MORPHOGENESIS	208	0.451	1.901	<0.001	0.018
GO_REGULATED_EXOCYTOSIS	213	0.471	1.900	<0.001	0.019
GO_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	55	0.540	1.900	<0.001	0.018
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	499	0.428	1.899	<0.001	0.019
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	40	0.526	1.896	<0.001	0.019
GO_TEMPERATURE_HOMEOSTASIS	26	0.592	1.896	<0.001	0.019
GO_REGULATION_OF_CELL_MATRIX_ADHESION	87	0.505	1.895	<0.001	0.019
GO_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	105	0.511	1.895	<0.001	0.019
GO_CARDIAC_ATRIUM_DEVELOPMENT	28	0.597	1.895	<0.001	0.019
GO_MUSCLE_CELL_DIFFERENTIATION	226	0.464	1.895	0.002	0.019
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	23	0.684	1.895	0.004	0.019
GO_INTERCALATED_DISC	51	0.537	1.894	0.006	0.019
GO_POSITIVE_REGULATION_OF_ACTIN	46	0.510	1.894	<0.001	0.019

_FILAMENT_BUNDLE_ASSEMBLY					
GO_EMBRYONIC_HEMOPOIESIS	18	0.674	1.894	0.002	0.019
GO_NEUROMUSCULAR_JUNCTION	54	0.528	1.894	0.002	0.019
GO_REGULATION_OF_MAP_KINASE_ACTIVITY	312	0.416	1.893	<0.001	0.019
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	147	0.543	1.892	<0.001	0.019
GO_RESPONSE_TO_PH	37	0.545	1.892	0.002	0.019
GO_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	130	0.480	1.891	<0.001	0.019
GO_WOUND_HEALING	439	0.428	1.889	<0.001	0.020
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	183	0.453	1.889	0.002	0.019
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	67	0.515	1.889	0.004	0.020
GO_RESPONSE_TO_MECHANICAL_STIMULUS	206	0.432	1.888	<0.001	0.020
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	107	0.497	1.888	<0.001	0.020
GO_POSITIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	28	0.579	1.887	0.002	0.020
GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	38	0.575	1.887	0.002	0.020
GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	45	0.589	1.886	0.004	0.020
GO_REGULATION_OF_CATECHOLAMINE_SECRETION	41	0.613	1.886	<0.001	0.020
GO_HEART_PROCESS	83	0.491	1.886	0.006	0.020
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	74	0.560	1.885	0.006	0.020
GO_VASCULOGENESIS	57	0.553	1.885	0.004	0.020
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	228	0.425	1.884	<0.001	0.020
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	50	0.511	1.883	<0.001	0.020
GO_ORGAN_GROWTH	65	0.554	1.883	<0.001	0.020
GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	359	0.456	1.883	0.002	0.020
GO_EXTRACELLULAR_MATRIX_DISASSEMBLY	73	0.576	1.882	<0.001	0.020

GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	50	0.542	1.881	<0.001	0.020
GO_NEURON_SPINE	116	0.463	1.881	0.002	0.020
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_STIMULUS	24	0.628	1.881	0.002	0.020
GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	44	0.561	1.880	0.004	0.020
GO_TRANSMISSION_OF_NERVE_IMPULSE	53	0.559	1.880	0.002	0.020
GO_TISSUE_REMODELING	87	0.499	1.880	0.002	0.020
GO_CGMP_BINDING	15	0.694	1.880	0.002	0.020
GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	50	0.537	1.880	0.004	0.020
GO_PROTEOGLYCAN_METABOLIC_PROCESS	81	0.530	1.879	<0.001	0.020
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	257	0.443	1.879	<0.001	0.020
GO_COGNITION	240	0.447	1.879	<0.001	0.020
GO_FOREBRAIN_CELL_MIGRATION	60	0.531	1.879	0.002	0.020
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	97	0.463	1.878	<0.001	0.020
GO_ARTERY_MORPHOGENESIS	51	0.542	1.877	<0.001	0.020
GO_RECEPTOR_COMPLEX	322	0.441	1.877	<0.001	0.020
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	151	0.482	1.877	<0.001	0.020
GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	155	0.448	1.877	0.002	0.020
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	37	0.521	1.877	0.002	0.020
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	408	0.420	1.877	<0.001	0.020
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_SARCOPLASMIC_RETICULUM	25	0.709	1.876	0.004	0.020
GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	32	0.569	1.875	0.002	0.021
GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	17	0.708	1.875	<0.001	0.021
GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	91	0.517	1.875	<0.001	0.020
GO_POSITIVE_REGULATION_OF_VASO	35	0.624	1.874	0.002	0.020

CONSTRICTION					
GO_ACTIN_FILAMENT_BASED_MOVEMENT	91	0.489	1.873	0.004	0.021
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	49	0.579	1.873	0.008	0.021
GO_CELL_RECOGNITION	123	0.464	1.873	0.002	0.021
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	31	0.616	1.872	<0.001	0.021
GO_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	57	0.565	1.871	0.004	0.021
GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	26	0.637	1.871	0.004	0.021
GO_NEURON_CELL_CELL_ADHESION	16	0.776	1.871	<0.001	0.021
GO_GLIAL_CELL_MIGRATION	35	0.590	1.869	0.002	0.021
GO_PLATELET_ACTIVATION	139	0.476	1.869	<0.001	0.021
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	30	0.588	1.869	<0.001	0.021
GO_REGULATION_OF_CELL_FATE_COMMITMENT	26	0.559	1.866	0.002	0.022
GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	26	0.604	1.866	0.008	0.022
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	193	0.490	1.865	<0.001	0.022
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	482	0.496	1.864	0.008	0.022
GO_GLYCOPROTEIN_COMPLEX	21	0.665	1.864	0.008	0.022
GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	26	0.611	1.863	0.006	0.022
GO_SINGLE_ORGANISM_CELL_ADHESION	434	0.444	1.862	<0.001	0.022
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	147	0.493	1.862	<0.001	0.022
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	325	0.422	1.862	<0.001	0.022
GO_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	201	0.427	1.862	<0.001	0.022
GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	24	0.611	1.862	0.010	0.022
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	19	0.643	1.861	0.004	0.022
GO_POSTSYNAPSE	366	0.428	1.860	<0.001	0.022

GO_REGULATION_OF_DOPAMINE_SECRETION	21	0.658	1.859	<0.001	0.023
GO_RENAL_TUBULE_DEVELOPMENT	78	0.495	1.859	0.006	0.023
GO_VASOCONSTRICTION	28	0.603	1.859	<0.001	0.023
GO_CILIARY_MEMBRANE	73	0.490	1.858	<0.001	0.023
GO_NEURAL_CREST_CELL_MIGRATION	50	0.551	1.857	0.002	0.023
GO_DENDRITIC_SHAFT	36	0.574	1.857	0.004	0.023
GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	64	0.497	1.857	0.002	0.023
GO_METANEPHROS_DEVELOPMENT	81	0.499	1.856	<0.001	0.023
GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	275	0.421	1.856	<0.001	0.023
GO_RESPIRATORY_SYSTEM_DEVELOPMENT	194	0.430	1.855	<0.001	0.023
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	95	0.472	1.855	<0.001	0.023
GO_SPROUTING_ANGIOGENESIS	43	0.594	1.855	0.008	0.023
GO_TRABECULA_FORMATION	22	0.634	1.854	0.006	0.023
GO_ACTIN_FILAMENT_BUNDLE	50	0.569	1.854	0.010	0.023
GO_POTASSIUM_CHANNEL_ACTIVITY	116	0.499	1.854	0.002	0.023
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	17	0.718	1.853	0.004	0.023
GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	161	0.475	1.853	<0.001	0.023
GO_HORMONE_BINDING	63	0.506	1.852	0.002	0.023
GO_NEGATIVE_REGULATION_OF_STAT_CASCADE	44	0.523	1.851	0.002	0.024
GO_REGULATION_OF_TRANSPORTER_ACTIVITY	188	0.425	1.851	<0.001	0.024
GO_PROTEIN_KINASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	31	0.576	1.851	0.002	0.023
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	65	0.488	1.850	0.004	0.024
GO_PIGMENT_CELL_DIFFERENTIATION	25	0.559	1.850	<0.001	0.024
GO_PROTEOGLYCAN_BINDING	28	0.611	1.850	<0.001	0.024
GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	41	0.605	1.850	0.010	0.024
GO_RESPONSE_TO_TRANSFORMING_G	142	0.454	1.848	<0.001	0.024

ROWTH_FACTOR_BETA					
GO_CELL_GROWTH	130	0.458	1.848	<0.001	0.024
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_BINDING	28	0.620	1.848	<0.001	0.024
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	70	0.511	1.847	<0.001	0.024
GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	77	0.480	1.847	<0.001	0.024
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	28	0.578	1.847	0.004	0.024
GO_CHEMOREPELLENT_ACTIVITY	27	0.584	1.847	0.002	0.024
GO_EXTRACELLULAR_MATRIX_BINDING	48	0.582	1.846	0.008	0.024
GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	36	0.529	1.846	0.008	0.024
GO_ACTOMYOSIN	57	0.569	1.845	0.004	0.024
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	148	0.467	1.845	<0.001	0.024
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	90	0.491	1.845	<0.001	0.024
GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	67	0.544	1.845	<0.001	0.024
GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	17	0.697	1.845	0.004	0.024
GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	40	0.547	1.844	<0.001	0.024
GO_AXONAL_FASCICULATION	20	0.678	1.841	0.002	0.025
GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	15	0.735	1.840	<0.001	0.025
GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	58	0.475	1.840	0.004	0.025
GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	25	0.620	1.840	0.004	0.025
GO_UROGENITAL_SYSTEM_DEVELOPMENT	296	0.422	1.840	<0.001	0.025
GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	28	0.607	1.838	0.008	0.025
GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	16	0.801	1.838	0.004	0.025
GO_AMINOGLYCAN_BIOSYNTHETIC_P	104	0.506	1.838	0.004	0.025

ROCESS					
GO_MYOFIBRIL_ASSEMBLY	45	0.592	1.838	0.009	0.025
GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	36	0.587	1.837	0.012	0.025
GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	290	0.413	1.837	<0.001	0.025
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	44	0.547	1.836	0.002	0.025
GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	40	0.517	1.836	<0.001	0.025
GO_MODULATION_OF_SYNAPTIC_TRANSMISSION	291	0.444	1.836	0.002	0.025
GO_ACTIN_MEDIATED_CELL_CONTRACTION	72	0.515	1.835	0.002	0.025
GO_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	38	0.572	1.835	0.008	0.025
GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	25	0.608	1.835	0.002	0.025
GO_NEURON_PROJECTION_GUIDANCE	199	0.457	1.835	0.002	0.025
GO_BASAL_PLASMA_MEMBRANE	31	0.545	1.834	0.010	0.025
GO_CATION_CHANNEL_ACTIVITY	285	0.468	1.834	0.002	0.025
GO_CORECEPTOR_ACTIVITY	35	0.650	1.833	0.008	0.026
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	39	0.577	1.832	0.004	0.026
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	16	0.681	1.831	0.008	0.026
GO_WNT_PROTEIN_BINDING	29	0.632	1.831	<0.001	0.026
GO_TUBE_MORPHOGENESIS	320	0.406	1.830	<0.001	0.026
GO_RESPONSE_TO_AXON_INJURY	46	0.519	1.826	0.008	0.027
GO_SYNAPTIC_MEMBRANE	251	0.445	1.826	0.002	0.027
GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	29	0.574	1.825	0.006	0.027
GO_RESPONSE_TO_PROGESTERONE	48	0.511	1.825	0.004	0.028
GO_ACTIVATION_OF_MAPKK_ACTIVITY	48	0.508	1.824	<0.001	0.028
GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	49	0.531	1.824	0.006	0.028
GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	35	0.548	1.824	0.002	0.028
GO_POSTSYNAPTIC_MEMBRANE	199	0.448	1.823	0.002	0.028
GO_REGULATION_OF_TISSUE_REMODELING	59	0.484	1.822	<0.001	0.028
GO_PLASMA_MEMBRANE_RAFT	83	0.483	1.822	0.002	0.028

GO_CARDIAC_VENTRICLE_MORPHOGENESIS	60	0.477	1.822	0.002	0.028
GO_REGULATION_OF_STAT_CASCADE	129	0.442	1.820	<0.001	0.028
GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	25	0.578	1.819	0.004	0.029
GO_SINGLE_ORGANISM_BEHAVIOR	373	0.423	1.819	<0.001	0.029
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL_SIGNALING	70	0.489	1.818	<0.001	0.029
GO_CHONDROCYTE_DIFFERENTIATION	59	0.520	1.815	0.006	0.030
GO_INOSITOL_LIPID_MEDIATED_SIGNALING	115	0.447	1.815	<0.001	0.030
GO_GROWTH_FACTOR_RECEPTOR_BINDING	126	0.432	1.814	<0.001	0.030
GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	16	0.827	1.814	<0.001	0.030
GO_RECEPTOR_INTERNALIZATION	46	0.540	1.813	0.006	0.030
GO_AMINOGLYCAN_METABOLIC_PROCESS	162	0.452	1.812	<0.001	0.030
GO_RELAXATION_OF_MUSCLE	20	0.607	1.812	0.010	0.030
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	85	0.506	1.811	0.002	0.030
GO_CARDIAC_MUSCLE_CELL_CONTRACTION	28	0.608	1.810	0.004	0.031
GO_BEHAVIOR	496	0.409	1.809	<0.001	0.031
GO_SULFOTRANSFERASE_ACTIVITY	52	0.516	1.809	0.002	0.031
GO_REGULATION_OF_BEHAVIOR	61	0.529	1.809	<0.001	0.031
GO_SCAVENGER_RECEPTOR_ACTIVITY	39	0.548	1.808	0.008	0.031
GO_NEGATIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	26	0.601	1.808	0.010	0.031
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	29	0.612	1.807	0.006	0.031
GO_GLIOGENESIS	168	0.440	1.806	0.002	0.031
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	78	0.464	1.806	<0.001	0.031
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	398	0.430	1.806	0.004	0.031
GO_REGULATION_OF_PROTEIN_MATURATION	78	0.464	1.805	0.002	0.031
GO_PHAGOCYTOSIS_RECOGNITION	15	0.678	1.805	0.008	0.031
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RE	29	0.542	1.804	0.002	0.031

CEPTOR_SIGNALING_PATHWAY					
GO_REGULATION_OF_EXCRETION	28	0.595	1.804	0.011	0.031
GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	67	0.466	1.804	0.002	0.031
GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	51	0.480	1.803	<0.001	0.032
GO_REGULATION_OF_N_METHYL_D_ASPARTATE_SELECTIVE_GLUTAMATE_RECEPTOR_ACTIVITY	15	0.674	1.803	0.006	0.032
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	254	0.400	1.803	0.002	0.032
GO_MUSCLE_HYPERTROPHY	28	0.585	1.802	0.008	0.032
GO_ORGAN_FORMATION	34	0.533	1.802	0.010	0.032
GO_METANEPHRIC_NEPHRON_DEVELOPMENT	32	0.563	1.802	0.002	0.032
GO_RECEPTOR_CLUSTERING	41	0.513	1.802	0.002	0.032
GO_CARDIOCYTE_DIFFERENTIATION	93	0.453	1.802	<0.001	0.032
GO_MESENCHYME_MORPHOGENESIS	38	0.573	1.802	0.012	0.032
GO_HISTONE_ACETYLTRANSFERASE_BINDING	28	0.569	1.801	0.004	0.032
GO_REGULATION_OF_SENSORY_PERCEPTION	33	0.545	1.801	0.004	0.032
GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	71	0.507	1.799	0.002	0.032
GO_REGULATION_OF_AXONOGENESIS	165	0.449	1.798	<0.001	0.032
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	20	0.626	1.798	0.006	0.032
GO_SENSORY_ORGAN_DEVELOPMENT	478	0.393	1.797	<0.001	0.033
GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	35	0.541	1.797	0.006	0.033
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	47	0.491	1.796	0.002	0.033
GO_LYSOSOMAL_LUMEN	86	0.522	1.795	0.004	0.033
GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	103	0.480	1.795	0.008	0.033
GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	29	0.568	1.795	0.010	0.033
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	19	0.640	1.794	0.004	0.033
GO_EYE_DEVELOPMENT	316	0.406	1.794	<0.001	0.033
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_THE_RELEASE_OF_SEQUESTERED_	19	0.718	1.793	0.006	0.033

CALCIUM_ION					
GO_SH3_DOMAIN_BINDING	113	0.432	1.793	0.006	0.033
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	290	0.442	1.793	0.006	0.033
GO_MUSCLE_CELL_DEVELOPMENT	119	0.466	1.792	0.006	0.033
GO_PARTURITION	20	0.606	1.792	0.006	0.033
GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	121	0.436	1.792	<0.001	0.033
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	166	0.413	1.792	0.002	0.033
GO_CARDIAC_SEPTUM_DEVELOPMENT	83	0.477	1.792	<0.001	0.033
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	15	0.667	1.792	0.010	0.033
GO_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	44	0.524	1.791	<0.001	0.033
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	282	0.446	1.790	0.004	0.034
GO_BLOOD_VESSEL_REMODELING	32	0.558	1.790	0.002	0.034
GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	19	0.614	1.787	0.008	0.034
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	48	0.483	1.787	0.004	0.034
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	293	0.413	1.786	0.002	0.035
GO_CELL_LEADING_EDGE	337	0.402	1.786	<0.001	0.035
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	16	0.644	1.786	0.006	0.035
GO_REGULATION_OF_RESPIRATORY_SYSTEM_PROCESS	15	0.712	1.785	0.009	0.034
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	207	0.490	1.785	0.010	0.035
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	38	0.561	1.785	0.008	0.035
GO_EPITHELIAL_CELL_MORPHOGENESIS	42	0.506	1.785	0.004	0.035
GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	25	0.607	1.785	0.006	0.034
GO_RESPONSE_TO_OXYGEN_LEVELS	302	0.385	1.784	<0.001	0.035
GO_ACTIN_FILAMENT_BASED_PROCESS	430	0.391	1.784	0.002	0.035
GO_REGULATION_OF_PROTEIN_KINAS	115	0.418	1.783	0.002	0.035

E_B_SIGNALING					
GO_GLIAL_CELL_DEVELOPMENT	73	0.463	1.783	0.002	0.035
GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	136	0.429	1.781	<0.001	0.035
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	17	0.677	1.781	0.012	0.035
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	22	0.608	1.781	0.004	0.035
GO_AORTA_DEVELOPMENT	41	0.536	1.781	0.004	0.035
GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	114	0.444	1.781	0.004	0.035
GO_CARDIAC_VENTRICLE_DEVELOPMENT	103	0.431	1.781	<0.001	0.035
GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	99	0.465	1.780	0.006	0.035
GO_REGULATION_OF_ORGAN_FORMATION	32	0.539	1.780	0.002	0.035
GO_GLYCOLIPID_BINDING	18	0.572	1.779	0.004	0.036
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	29	0.545	1.779	0.004	0.036
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	46	0.507	1.779	0.008	0.036
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	35	0.563	1.778	0.006	0.036
GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	38	0.522	1.778	0.006	0.036
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	273	0.420	1.778	0.002	0.036
GO_RESPONSE_TO_GROWTH_FACTOR	461	0.385	1.776	<0.001	0.036
GO_REGULATION_OF_GASTRULATION	32	0.553	1.776	0.010	0.036
GO_CELL_PROJECTION_MEMBRANE	285	0.373	1.776	<0.001	0.036
GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	255	0.411	1.775	<0.001	0.036
GO_BETA_AMYLOID_BINDING	33	0.519	1.775	0.002	0.036
GO_REGULATION_OF_SODIUM_ION_TRANSPORT	76	0.455	1.775	0.002	0.036
GO_BONE_CELL_DEVELOPMENT	21	0.608	1.775	0.014	0.036
GO_DEVELOPMENTAL_PIGMENTATION	36	0.509	1.775	0.002	0.036
GO_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	16	0.641	1.772	0.008	0.037
GO_REGULATION_OF_FAT_CELL_DIFFE	98	0.446	1.772	0.002	0.037

RENTIATION					
GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	27	0.556	1.772	0.013	0.037
GO_NEGATIVE_REGULATION_OF_CELL_GROWTH	163	0.408	1.772	0.002	0.037
GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	130	0.483	1.772	0.004	0.037
GO_HEART_GROWTH	23	0.610	1.772	0.004	0.037
GO_PEPTIDE_HORMONE_BINDING	36	0.577	1.771	0.011	0.037
GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	448	0.409	1.771	0.002	0.037
GO_NEURONAL_ACTION_POTENTIAL	27	0.575	1.770	0.006	0.037
GO_REFLEX	20	0.618	1.770	0.008	0.037
GO_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	204	0.408	1.770	0.002	0.037
GO_COMPLEX_OF_COLLAGEN_TRIMERS	23	0.771	1.769	0.012	0.037
GO_E_BOX_BINDING	30	0.540	1.768	0.008	0.037
GO_REGULATION_OF_MYOBLAST_FUSION	18	0.634	1.768	0.012	0.038
GO_REGULATION_OF_RECEPTOR_INTERNALIZATION	37	0.488	1.767	0.004	0.038
GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	35	0.532	1.767	0.014	0.038
GO_CELL_CELL_JUNCTION	365	0.375	1.766	0.002	0.038
GO_EXTRACELLULAR_GLUTAMATE_GATED_ION_CHANNEL_ACTIVITY	20	0.627	1.765	0.002	0.038
GO_EXCITATORY_SYNAPSE	191	0.429	1.765	0.002	0.038
GO_CYTOKINE_RECEPTOR_ACTIVITY	85	0.555	1.764	0.012	0.039
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	360	0.430	1.763	0.006	0.039
GO_A_BAND	32	0.550	1.763	0.017	0.039
GO_NEURON_PROJECTION_REGENERATION	31	0.562	1.762	0.010	0.039
GO_REGULATION_OF_CELL_SHAPE	135	0.441	1.761	0.002	0.039
GO_TRANSPORTER_COMPLEX	310	0.419	1.761	0.002	0.039
GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	17	0.625	1.761	0.014	0.039
GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	72	0.440	1.761	0.002	0.039
GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	39	0.509	1.761	<0.001	0.039
GO_ENDOCARDIAL_CUSHION_DEVEL	32	0.566	1.761	0.018	0.039

OPMENT					
GO_MEMORY	95	0.449	1.760	0.002	0.039
GO_PERIKARYON	99	0.471	1.759	<0.001	0.039
GO_EYE_MORPHOGENESIS	131	0.422	1.758	<0.001	0.040
GO_AXIS_ELONGATION	27	0.568	1.758	0.008	0.040
GO_OSSIFICATION	245	0.403	1.758	<0.001	0.040
GO_BASAL_LAMINA	21	0.636	1.758	0.016	0.040
GO_ALPHA_ACTININ_BINDING	21	0.630	1.758	0.009	0.040
GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	165	0.440	1.757	0.002	0.040
GO_POTASSIUM_ION_TRANSPORT	149	0.452	1.756	0.004	0.040
GO_RESPONSE_TO_ACID_CHEMICAL	308	0.366	1.756	<0.001	0.040
GO_REGULATION_OF_CELLULAR_EXTRAVASATION	22	0.609	1.756	0.015	0.040
GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	145	0.414	1.755	0.002	0.040
GO_LYMPH_VESSEL_DEVELOPMENT	20	0.647	1.754	0.008	0.041
GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	222	0.420	1.754	0.006	0.041
GO_REGULATION_OF_AXON_GUIDANCE	39	0.550	1.753	0.008	0.041
GO_CORONARY_VASCULATURE_DEVELOPMENT	36	0.553	1.753	0.010	0.041
GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	31	0.561	1.753	0.004	0.041
GO_CELLULAR_RESPONSE_TO_VITAMIN	26	0.564	1.753	0.015	0.041
GO_NEGATIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	50	0.485	1.752	0.006	0.041
GO_GANGLIOSIDE_METABOLIC_PROCESS	26	0.537	1.752	0.004	0.041
GO_REGULATION_OF_FATTY_ACID_OXIDATION	27	0.559	1.752	0.006	0.041
GO_PEPTIDYL_TYROSINE_MODIFICATION	184	0.391	1.751	<0.001	0.041
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	59	0.489	1.751	0.006	0.041
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	35	0.554	1.751	0.016	0.041
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	24	0.528	1.751	0.006	0.041
GO_NEURONAL_CELL_BODY_MEMBRANE	20	0.638	1.751	0.008	0.041

GO_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	24	0.580	1.751	0.006	0.041
GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	28	0.540	1.751	0.008	0.041
GO_INNERVATION	23	0.589	1.750	0.011	0.041
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	33	0.580	1.749	0.006	0.041
GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	81	0.467	1.749	0.008	0.041
GO_DERMATAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	16	0.680	1.748	0.012	0.042
GO_AXON_REGENERATION	22	0.602	1.747	0.012	0.042
GO_ANATOMICAL_STRUCTURE_MATURATION	39	0.525	1.747	0.008	0.042
GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	17	0.618	1.746	0.007	0.042
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	144	0.472	1.746	0.018	0.042
GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	58	0.515	1.745	0.010	0.042
GO_DENDRITE	436	0.385	1.744	0.004	0.042
GO_GATED_CHANNEL_ACTIVITY	316	0.432	1.744	0.002	0.042
GO_POLYSACCHARIDE_BINDING	21	0.593	1.744	0.004	0.042
GO_SYNAPSE_ORGANIZATION	143	0.473	1.743	0.008	0.042
GO_RESPIRATORY_GASEOUS_EXCHANGE	47	0.454	1.743	0.010	0.043
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	122	0.418	1.743	0.002	0.042
GO_ACTIN_BINDING	378	0.389	1.743	0.004	0.043
GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	185	0.411	1.742	0.002	0.043
GO_DEVELOPMENTAL_CELL_GROWTH	75	0.479	1.741	0.008	0.043
GO_CYCLIC_NUCLEOTIDE_BINDING	34	0.534	1.740	0.011	0.043
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	452	0.371	1.740	0.002	0.043
GO_MEMBRANE_BIOGENESIS	30	0.542	1.740	0.021	0.043
GO_RESPONSE_TO_MUSCLE_STRETCH	19	0.611	1.740	0.008	0.043
GO_NEUROMUSCULAR_PROCESS	94	0.434	1.739	0.002	0.043
GO_CAMP_BIOSYNTHETIC_PROCESS	17	0.668	1.739	0.016	0.043
GO_VESICLE_LUMEN	101	0.517	1.739	0.010	0.043
GO_FUCOSYLATION	21	0.560	1.738	0.020	0.043
GO_PALATE_DEVELOPMENT	85	0.470	1.738	0.004	0.044
GO_REGULATION_OF_RYANODINE_SE	26	0.596	1.738	0.016	0.044

NSITIVE_CALCIUM_RELEASE_CHANNEL_ACTIVITY					
GO_ENDOCRINE_PROCESS	44	0.512	1.738	0.010	0.044
GO_SYNAPTIC_SIGNALING	409	0.411	1.736	0.004	0.044
GO_REGULATION_OF_PLATELET_ACTIVATION	30	0.559	1.735	0.014	0.044
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	123	0.460	1.735	0.011	0.044
GO_GLYCOPROTEIN_BINDING	98	0.446	1.735	0.004	0.044
GO_COMPLEMENT_ACTIVATION	46	0.566	1.735	0.014	0.044
GO_REGULATION_OF_RECEPTOR_ACTIVITY	115	0.411	1.735	0.002	0.044
GO_REGULATION_OF_RENAL_SODIUM_EXCRETION	23	0.599	1.734	0.013	0.044
GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	18	0.603	1.734	0.014	0.044
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	110	0.408	1.734	<0.001	0.044
GO_STRIATED_MUSCLE_CONTRACTION	95	0.427	1.734	0.008	0.044
GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	23	0.608	1.734	0.016	0.044
GO_NODE_OF_RANVIER	15	0.620	1.733	0.008	0.044
GO_HEART_TRABECULA_MORPHOGENESIS	24	0.553	1.733	0.014	0.045
GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	24	0.535	1.733	0.004	0.045
GO_LAMELLIPODIUM	166	0.419	1.732	0.010	0.045
GO_COCHLEA_DEVELOPMENT	39	0.502	1.732	0.008	0.045
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	174	0.389	1.732	<0.001	0.045
GO_LEADING_EDGE_MEMBRANE	129	0.402	1.732	<0.001	0.045
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	136	0.392	1.732	0.002	0.045
GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	21	0.554	1.731	0.010	0.045
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	163	0.432	1.731	0.007	0.045
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	21	0.546	1.731	0.006	0.045
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDI	86	0.420	1.730	0.004	0.045

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GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	19	0.583	1.730	0.014	0.045
GO_MEGAKARYOCYTE_DEVELOPMENT	15	0.629	1.729	0.014	0.045
GO_MORPHOGENESIS_OF_AN_EPITHELIUM	391	0.377	1.729	<0.001	0.045
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	80	0.500	1.728	0.012	0.046
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	21	0.553	1.728	0.010	0.046
GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	47	0.483	1.727	0.010	0.046
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	30	0.534	1.727	0.016	0.046
GO_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	25	0.615	1.727	0.019	0.046
GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	63	0.456	1.725	0.009	0.046
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	83	0.429	1.725	0.008	0.046
GO_CAMP_MEDIATED_SIGNALING	36	0.557	1.725	0.011	0.046
GO_VACUOLAR_LUMEN	110	0.477	1.724	0.011	0.047
GO_AXON_EXTENSION	36	0.584	1.723	0.023	0.047
GO_MEMBRANE_ASSEMBLY	25	0.560	1.723	0.029	0.047
GO_REGULATION_OF_URINE_VOLUME	20	0.598	1.723	0.012	0.047
GO_REGULATION_OF_EMBRYONIC_DEVELOPMENT	108	0.438	1.723	0.014	0.047
GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	70	0.465	1.722	0.006	0.047
GO_CARDIAC_SEPTUM_MORPHOGENESIS	48	0.501	1.721	0.010	0.047
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	165	0.431	1.720	0.004	0.048
GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	37	0.561	1.719	0.014	0.048
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	281	0.386	1.719	<0.001	0.048
GO_FRIZZLED_BINDING	36	0.517	1.719	0.012	0.048
GO_NEGATIVE_REGULATION_OF_GROWTH	229	0.378	1.717	0.002	0.048
GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIG	22	0.579	1.717	0.014	0.048

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GO_ION_CHANNEL_BINDING	107	0.421	1.717	0.008	0.048
GO_MYELOID_CELL_DEVELOPMENT	40	0.475	1.717	0.011	0.048
GO_PROTEIN_ACTIVATION_CASCADE	67	0.549	1.716	0.010	0.049
GO_NEGATIVE_REGULATION_OF_CATECHOLAMINE_SECRETION	16	0.643	1.716	0.006	0.049
GO_STRIATED_MUSCLE_ADAPTATION	23	0.571	1.715	0.011	0.049
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	30	0.585	1.715	0.027	0.049
GO_REGULATION_OF_BODY_FLUID_LEVELS	478	0.377	1.715	<0.001	0.049
GO_RESPONSE_TO_FATTY_ACID	83	0.421	1.715	0.004	0.049
GO_EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	55	0.517	1.714	0.014	0.049
GO_ADHERENS_JUNCTION_ASSEMBLY	33	0.539	1.714	0.012	0.049
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	26	0.547	1.713	0.021	0.049
GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	113	0.386	1.713	<0.001	0.049
GO_SODIUM_CHANNEL_COMPLEX	17	0.639	1.713	0.012	0.049
GO_MUSCLE_CELL_MIGRATION	18	0.604	1.713	0.015	0.049
GO_REGULATION_OF_CELL_GROWTH	375	0.352	1.711	<0.001	0.050
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	137	0.424	1.711	0.004	0.050
GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	16	0.617	1.710	0.023	0.050
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	28	0.558	1.710	0.004	0.050
GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	17	0.649	1.709	0.016	0.050
GO_TRANSCRIPTIONAL_ACTIVATOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	223	0.381	1.709	<0.001	0.050
GO_CAMERA_TYPE_EYE_MORPHOGENESIS	97	0.424	1.709	0.002	0.050
GO_SECRETION_BY_CELL	467	0.368	1.709	<0.001	0.050
GO_EPITHELIAL_CELL_DEVELOPMENT	180	0.384	1.709	0.004	0.050
GO_RESPONSE_TO_VITAMIN_D	33	0.523	1.708	0.011	0.051
GO_GROWTH	391	0.372	1.707	0.002	0.051
GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	47	0.479	1.707	0.020	0.051
GO_NEURON_MIGRATION	106	0.436	1.707	0.017	0.051

GO_REGULATION_OF_KIDNEY_DEVELOPMENT	55	0.470	1.707	0.010	0.051
GO_REGULATION_OF_ALPHA_AMINO_3_HYDROXY_5_METHYL_4_ISOXAZOLE_PROPIONATE_SELECTIVE_GLUTAMATE_RECEPTOR_ACTIVITY	19	0.631	1.706	0.012	0.051
GO_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	53	0.481	1.706	0.008	0.051
GO_REGULATION_OF_ENDOCYTOSIS	197	0.398	1.706	0.004	0.051
GO_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	65	0.453	1.705	0.008	0.051
GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	22	0.583	1.705	0.013	0.051
GO_PHAGOCYTOSIS_ENGULFMENT	19	0.642	1.705	0.021	0.051
GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	43	0.459	1.705	0.006	0.051
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	245	0.387	1.705	<0.001	0.051
GO_ENDOPLASMIC_RETICULUM_LUMEN	190	0.438	1.704	0.012	0.051
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	42	0.523	1.703	0.017	0.051
GO_RESPONSE_TO_CAMP	103	0.415	1.703	0.006	0.052
GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	185	0.439	1.703	0.004	0.052
GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	17	0.658	1.703	0.014	0.052
GO_SIDE_OF_MEMBRANE	392	0.408	1.702	0.013	0.052
GO_HEMOSTASIS	290	0.395	1.702	0.006	0.052
GO_AMEBOIDAL_TYPE_CELL_MIGRATION	150	0.421	1.702	0.010	0.052
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	52	0.445	1.702	0.006	0.052
GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	113	0.402	1.701	0.010	0.052
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	159	0.442	1.701	0.010	0.052
GO_REGULATION_OF_CATENIN_IMPORT_INTO_NUCLEUS	27	0.526	1.701	0.010	0.052
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	30	0.540	1.700	0.016	0.052

GO_MEGAKARYOCYTE_DIFFERENTIATION	19	0.567	1.700	0.008	0.052
GO_CYTOKINE_ACTIVITY	193	0.432	1.700	0.006	0.052
GO_ACTININ_BINDING	29	0.534	1.699	0.029	0.052
GO_NEURONAL_POSTSYNAPTIC_DENSITY	51	0.519	1.699	0.014	0.052
GO_REGULATION_OF_HOMEOSTATIC_PROCESS	429	0.343	1.699	<0.001	0.052
GO_REGULATION_OF_FILOPODIUM_ASSEMBLY	34	0.485	1.698	0.016	0.052
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	34	0.507	1.698	0.017	0.053
GO_REGULATION_OF_GLIAL_CELL_PROLIFERATION	21	0.503	1.697	0.012	0.053
GO_NEGATIVE_REGULATION_OF_TRANSPORT	431	0.357	1.697	<0.001	0.053
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	108	0.415	1.696	0.006	0.053
GO_NEURON_PROJECTION_MEMBRANE	34	0.526	1.696	0.011	0.053
GO_CELL_CELL_ADHERENS_JUNCTION	50	0.491	1.696	0.014	0.053
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	30	0.547	1.695	0.015	0.053
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	40	0.484	1.695	0.008	0.053
GO_WNT_ACTIVATED_RECEPTOR_ACTIVITY	22	0.590	1.695	0.014	0.053
GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	70	0.437	1.694	0.008	0.053
GO_RESPONSE_TO_CALCIUM_ION	112	0.403	1.693	0.002	0.054
GO_NEPHRIC_DUCT_DEVELOPMENT	15	0.612	1.693	0.018	0.054
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	22	0.692	1.692	0.037	0.054
GO_ACTIVATION_OF_MAPK_ACTIVITY	133	0.400	1.692	<0.001	0.054
GO_BODY_MORPHOGENESIS	43	0.513	1.691	0.015	0.055
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	18	0.634	1.690	0.024	0.055
GO_ENDOTHELIAL_CELL_DEVELOPMENT	44	0.492	1.690	0.016	0.055
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_ION_SIGNALING	23	0.616	1.689	0.040	0.055
GO_T_CELL_SELECTION	36	0.617	1.688	0.041	0.055

GO_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	81	0.406	1.687	0.004	0.056
GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	18	0.601	1.687	0.008	0.056
GO_KERATAN_SULFATE_METABOLIC_PROCESS	32	0.521	1.687	0.016	0.056
GO_CELLULAR_RESPONSE_TO_NUTRIENT	38	0.475	1.686	0.022	0.056
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	40	0.519	1.686	0.004	0.056
GO_ADHERENS_JUNCTION_ORGANIZATION	65	0.447	1.685	0.002	0.057
GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	19	0.589	1.685	0.012	0.057
GO_REGULATION_OF_BONE_REMODELING	39	0.469	1.682	0.008	0.058
GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	180	0.412	1.682	0.008	0.058
GO_ORGAN_MATURATION	18	0.574	1.681	0.015	0.058
GO_CELL_BODY	482	0.360	1.681	0.002	0.058
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	18	0.591	1.680	0.018	0.058
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	93	0.482	1.680	0.031	0.058
GO_RESPONSE_TO_ESTROGEN	215	0.364	1.680	0.002	0.058
GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	34	0.558	1.679	0.024	0.058
GO_OVULATION	17	0.620	1.679	0.023	0.058
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	418	0.342	1.679	<0.001	0.058
GO_PROSTATE_GLAND_MORPHOGENESIS	23	0.552	1.679	0.018	0.058
GO_SYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	21	0.604	1.678	0.013	0.058
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	101	0.404	1.678	0.006	0.058
GO_RESPONSE_TO_STEROL	23	0.545	1.678	0.021	0.058
GO_REGULATION_OF_NEUTROPHIL_MIGRATION	30	0.541	1.678	0.035	0.058
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	21	0.579	1.678	0.024	0.058
GO_REGULATION_OF_CIRCADIAN_SLEEP_WAKE_CYCLE	23	0.576	1.677	0.010	0.059

GO_EAR_DEVELOPMENT	191	0.388	1.676	0.004	0.059
GO_INTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	27	0.524	1.676	0.013	0.059
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	22	0.562	1.676	0.024	0.059
GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	271	0.360	1.676	<0.001	0.059
GO_GLIAL_CELL_DIFFERENTIATION	131	0.408	1.676	0.006	0.059
GO_REGULATION_OF_FIBROBLAST_MIGRATION	27	0.532	1.674	0.014	0.059
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	158	0.391	1.674	0.008	0.059
GO_NEGATIVE_REGULATION_OF_STEM_CELL_PROLIFERATION	16	0.577	1.674	0.008	0.059
GO_OLFACTORY_BULB_INTERNEURON_DIFFERENTIATION	15	0.622	1.674	0.026	0.060
GO_CELL_FATE_COMMITMENT	223	0.388	1.673	0.002	0.060
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	15	0.597	1.673	0.020	0.060
GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	61	0.456	1.673	0.009	0.060
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	112	0.465	1.673	0.025	0.060
GO_PRESYNAPTIC_MEMBRANE	52	0.511	1.671	0.025	0.060
GO_REGULATION_OF_NEUROTRANSMITTER_SECRETION	45	0.492	1.671	0.021	0.060
GO_LIGAND_GATED_CHANNEL_ACTIVITY	137	0.423	1.671	0.010	0.060
GO_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	22	0.527	1.671	0.015	0.060
GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	27	0.516	1.670	0.006	0.060
GO_CARBOHYDRATE_BINDING	255	0.390	1.670	0.006	0.060
GO_CELL_FATE_SPECIFICATION	70	0.436	1.670	0.004	0.060
GO_DEVELOPMENTAL_MATURATION	181	0.376	1.670	0.004	0.060
GO_ESTROUS_CYCLE	19	0.578	1.668	0.017	0.061
GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	26	0.541	1.668	0.014	0.061
GO_FOREBRAIN_GENERATION_OF_NEURONS	66	0.460	1.667	0.010	0.061
GO_POSITIVE_REGULATION_OF_EPITH	55	0.439	1.667	0.008	0.061

ELIAL_CELL_DIFFERENTIATION					
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	132	0.370	1.667	0.002	0.061
GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	106	0.433	1.667	0.012	0.061
GO_RESPONSE_TO_NICOTINE	51	0.447	1.667	0.002	0.061
GO_PLATELET_AGGREGATION	38	0.515	1.666	0.022	0.062
GO_NEGATIVE_REGULATION_OF_SECRETION	185	0.373	1.665	<0.001	0.062
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	28	0.551	1.665	0.016	0.062
GO_REGULATION_OF_GLUCOSE_IMPORT	56	0.449	1.665	0.016	0.062
GO_NEGATIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	140	0.397	1.664	0.008	0.062
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	22	0.607	1.664	0.020	0.062
GO_STRIATUM_DEVELOPMENT	16	0.569	1.664	0.023	0.062
GO_TRANSCRIPTIONAL_ACTIVATOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_REGULATORY_REGION_SEQUENCE_SPECIFIC_BINDING	308	0.361	1.664	<0.001	0.062
GO_RESPONSE_TO_GLUCAGON	48	0.479	1.664	0.012	0.062
GO_OVULATION_CYCLE	110	0.391	1.663	<0.001	0.062
GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	79	0.425	1.663	0.004	0.062
GO_SUBPALLIUM_DEVELOPMENT	22	0.552	1.663	0.006	0.062
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	46	0.480	1.662	0.016	0.063
GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	40	0.545	1.662	0.027	0.063
GO_HETEROTYPIC_CELL_CELL_ADHESION	27	0.558	1.662	0.029	0.063
GO_MUSCLE_ORGAN_MORPHOGENESIS	67	0.426	1.661	0.006	0.063
GO_DEVELOPMENTAL_GROWTH	319	0.373	1.661	0.004	0.063
GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	126	0.406	1.661	0.004	0.063
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	31	0.531	1.661	0.021	0.063
GO_CELL_SUBSTRATE_ADHERENS_JUNCTION_ASSEMBLY	23	0.541	1.660	0.018	0.063
GO_REGULATION_OF_TYROSINE_PHOS	19	0.555	1.659	0.019	0.063

PHORYLATION_OF_STAT5_PROTEIN					
GO_DETECTION_OF_BIOTIC_STIMULUS	25	0.617	1.658	0.027	0.064
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_IMPORT	23	0.513	1.657	0.018	0.064
GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	24	0.557	1.657	0.022	0.064
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	42	0.444	1.655	0.004	0.065
GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	21	0.531	1.655	0.012	0.065
GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	22	0.579	1.654	0.018	0.065
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	26	0.545	1.654	0.028	0.065
GO_CONNEXON_COMPLEX	20	0.564	1.654	0.019	0.065
GO_RESPONSE_TO_WATER	18	0.539	1.653	0.018	0.065
GO_REGULATION_OF_CELL_SIZE	167	0.380	1.653	0.006	0.065
GO_ENDOCARDIAL_CUSHION_FORMATION	15	0.655	1.653	0.010	0.066
GO_SKELETAL_SYSTEM_MORPHOGENESIS	196	0.403	1.650	0.012	0.067
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	99	0.428	1.650	0.011	0.067
GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	96	0.437	1.650	0.027	0.067
GO_NEGATIVE_REGULATION_OF_AXONOGENESIS	64	0.441	1.649	0.012	0.067
GO_POSITIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	15	0.622	1.649	0.022	0.067
GO_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	52	0.446	1.649	0.008	0.067
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	44	0.472	1.649	0.014	0.067
GO_NEGATIVE_REGULATION_OF_RECEPTOR_ACTIVITY	29	0.470	1.649	0.017	0.067
GO_REGULATION_OF_BONE_DEVELOPMENT	16	0.602	1.648	0.033	0.067
GO_DETECTION_OF_MECHANICAL_STIMULUS	39	0.514	1.647	0.047	0.067
GO_VASODILATION	26	0.534	1.647	0.014	0.067

GO_G_PROTEIN_ALPHA_SUBUNIT_BINDING	22	0.536	1.647	0.030	0.067
GO_ATRIOVENTRICULAR_VALVE_MORPHOGENESIS	16	0.595	1.647	0.030	0.067
GO_REGULATION_OF_STEM_CELL_PROLIFERATION	85	0.408	1.647	0.004	0.067
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	28	0.519	1.646	0.021	0.068
GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	37	0.477	1.646	0.017	0.068
GO_EXPLORATION_BEHAVIOR	23	0.573	1.646	0.008	0.067
GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	47	0.453	1.646	0.018	0.067
GO_COSTAMERE	19	0.701	1.646	0.038	0.067
GO_RESPONSE_TO_ORGANOPHOSPHORUS	138	0.390	1.645	0.004	0.068
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	17	0.592	1.644	0.024	0.068
GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	15	0.624	1.644	0.034	0.068
GO_PHOSPHATIDYLSERINE_BINDING	32	0.477	1.644	0.012	0.068
GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	44	0.461	1.644	0.017	0.068
GO_EXOCYTOSIS	297	0.363	1.643	0.004	0.068
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	48	0.454	1.643	0.024	0.068
GO_POSITIVE_REGULATION_OF_STAT_CASCADE	70	0.445	1.643	0.018	0.068
GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	48	0.483	1.642	0.026	0.069
GO_ACTIN_CYTOSKELETON	425	0.362	1.642	0.008	0.069
GO_REGULATION_OF_MITOCHONDRIAL_DEPOLARIZATION	17	0.578	1.642	0.016	0.069
GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	17	0.560	1.641	0.013	0.069
GO_EMBRYONIC_ORGAN_MORPHOGENESIS	276	0.374	1.641	0.008	0.069
GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	20	0.597	1.641	0.028	0.069
GO_CELL_JUNCTION_ORGANIZATION	177	0.399	1.641	0.012	0.069
GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	257	0.364	1.639	0.002	0.070
GO_ADULT_BEHAVIOR	133	0.427	1.639	0.013	0.070
GO_SMAD_BINDING	70	0.442	1.639	0.022	0.070

GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	463	0.333	1.638	<0.001	0.070
GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	27	0.569	1.638	0.025	0.070
GO_DENDRITE_MORPHOGENESIS	42	0.495	1.636	0.026	0.071
GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	30	0.521	1.636	0.021	0.070
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	150	0.386	1.636	0.004	0.071
GO_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	30	0.572	1.636	0.045	0.071
GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	90	0.396	1.635	0.006	0.071
GO_CATECHOLAMINE_METABOLIC_PROCESS	41	0.452	1.635	0.013	0.071
GO_SITE_OF_POLARIZED_GROWTH	141	0.382	1.634	0.004	0.071
GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	54	0.439	1.634	0.015	0.071
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_MOVEMENT	32	0.472	1.634	0.016	0.071
GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	156	0.371	1.633	0.002	0.071
GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	23	0.519	1.633	0.036	0.071
GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	98	0.389	1.633	0.011	0.071
GO_LOCOMOTORY_BEHAVIOR	176	0.407	1.633	0.004	0.071
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	30	0.484	1.633	0.018	0.071
GO_MONOCYTE_DIFFERENTIATION	16	0.554	1.632	0.030	0.072
GO_RESPONSE_TO_KETONE	179	0.370	1.631	0.004	0.072
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	43	0.464	1.631	0.021	0.072
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	119	0.377	1.631	0.002	0.072
GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	16	0.575	1.630	0.045	0.072
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	30	0.505	1.630	0.024	0.072
GO_SECRETORY_VESICLE	441	0.349	1.630	0.002	0.072
GO_NEUROPEPTIDE_RECEPTOR_ACTIVITY	41	0.509	1.630	0.021	0.072
GO_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	98	0.405	1.629	0.016	0.073

GO_DEFINITIVE_HEMOPOIESIS	16	0.573	1.628	0.024	0.073
GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	19	0.544	1.628	0.036	0.073
GO_CELL_SUBSTRATE_JUNCTION	388	0.385	1.628	0.029	0.073
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	27	0.555	1.628	0.023	0.073
GO_DENDRITE_DEVELOPMENT	79	0.425	1.627	0.012	0.073
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	107	0.458	1.627	0.032	0.073
GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	24	0.559	1.627	0.046	0.073
GO_REGULATION_OF_ENDOCRINE_PROCESS	47	0.470	1.626	0.010	0.073
GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	56	0.465	1.626	0.016	0.073
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	24	0.488	1.626	0.026	0.073
GO_TISSUE_MIGRATION	81	0.430	1.625	0.017	0.074
GO_NEGATIVE_REGULATION_OF_CELL_MATRIX_ADHESION	28	0.521	1.625	0.029	0.074
GO_LEUKOCYTE_DIFFERENTIATION	274	0.418	1.625	0.050	0.074
GO_LAMELLIPODIUM_MEMBRANE	19	0.586	1.625	0.018	0.074
GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	24	0.530	1.625	0.042	0.074
GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	279	0.346	1.625	0.002	0.073
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	73	0.447	1.624	0.034	0.074
GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	16	0.593	1.624	0.045	0.074
GO_DETECTION_OF_OTHER_ORGANISM	17	0.654	1.623	0.035	0.074
GO_CEREBRAL_CORTEX_CELL_MIGRATION	41	0.465	1.623	0.029	0.074
GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	22	0.581	1.622	0.025	0.074
GO_GLAND_MORPHOGENESIS	97	0.415	1.622	0.010	0.074
GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	23	0.541	1.621	0.021	0.075
GO_RESPONSE_TO_CORTICOSTEROID	173	0.366	1.621	0.004	0.075
GO_POSITIVE_REGULATION_OF_RECE	24	0.487	1.621	0.016	0.075

PTOR_INTERNALIZATION					
GO_REGULATION_OF_AMINO_ACID_TRANSPORT	25	0.515	1.621	0.013	0.075
GO_PROTEIN_TARGETING_TO_PLASMA_MEMBRANE	23	0.516	1.620	0.025	0.075
GO_REGULATION_OF_JUN_KINASE_ACTIVITY	78	0.429	1.620	0.014	0.075
GO_CARGO_RECEPTOR_ACTIVITY	60	0.450	1.619	0.031	0.075
GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	27	0.500	1.619	0.020	0.076
GO_REGULATION_OF_NOREPINEPHRINE_SECRETION	17	0.590	1.619	0.014	0.076
GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	21	0.550	1.619	0.020	0.076
GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	47	0.440	1.618	0.008	0.076
GO_BRANCH_ELONGATION_OF_AN_EPITHELIUM	17	0.565	1.617	0.025	0.076
GO_CELLULAR_RESPONSE_TO_PH	16	0.530	1.616	0.018	0.077
GO_ANCHORING_JUNCTION	474	0.371	1.616	0.021	0.077
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	27	0.544	1.616	0.033	0.076
GO_ASSOCIATIVE_LEARNING	70	0.424	1.616	0.012	0.076
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	149	0.433	1.616	0.033	0.076
GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	28	0.494	1.616	0.022	0.077
GO_CILIARY_BASE	22	0.511	1.616	0.040	0.077
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	94	0.406	1.615	0.012	0.077
GO_CALMODULIN_BINDING	177	0.381	1.615	0.008	0.077
GO_NEURON_PROJECTION_EXTENSION	52	0.471	1.615	0.043	0.077
GO_OLIGODENDROCYTE_DIFFERENTIATION	57	0.430	1.614	0.012	0.077
GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	173	0.392	1.613	0.018	0.077
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	38	0.509	1.612	0.025	0.078
GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	48	0.422	1.612	0.013	0.078
GO_REGULATION_OF_CAMP_MEDIATE	23	0.536	1.611	0.026	0.078

D_SIGNALING					
GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	72	0.417	1.611	0.018	0.078
GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSPORT	16	0.559	1.611	0.035	0.079
GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	41	0.493	1.610	0.033	0.079
GO_LYMPHOCYTE_DIFFERENTIATION	194	0.439	1.610	0.055	0.079
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	18	0.556	1.609	0.026	0.079
GO_HMG_BOX_DOMAIN_BINDING	18	0.549	1.609	0.029	0.079
GO_SEMAPHORIN_RECEPTOR_BINDING	22	0.531	1.609	0.024	0.079
GO_KINASE_INHIBITOR_ACTIVITY	86	0.391	1.609	0.002	0.079
GO_NEGATIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	15	0.629	1.608	0.034	0.080
GO_EMBRYONIC_ORGAN_DEVELOPMENT	398	0.349	1.607	0.004	0.080
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	15	0.598	1.606	0.030	0.080
GO_REGULATION_OF_NEUTROPHIL_CHEMOTAXIS	25	0.563	1.606	0.057	0.080
GO_HEAD_MORPHOGENESIS	35	0.495	1.605	0.035	0.081
GO_DENDRITIC_CELL_DIFFERENTIATION	32	0.556	1.605	0.047	0.081
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	37	0.467	1.605	0.032	0.081
GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	58	0.432	1.605	0.008	0.081
GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	51	0.419	1.604	0.013	0.081
GO_REGULATION_OF_ACTION_POTENTIAL	36	0.465	1.604	0.035	0.081
GO_MACROPHAGE_ACTIVATION	31	0.540	1.603	0.035	0.081
GO_REGULATION_OF_NEUROBLAST_PROLIFERATION	27	0.477	1.603	0.015	0.081
GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	15	0.643	1.603	0.028	0.081
GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	26	0.510	1.603	0.030	0.081
GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	19	0.609	1.603	0.045	0.081
GO_OLIGODENDROCYTE_DEVELOPME	32	0.459	1.602	0.016	0.081

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GO_HEART_VALVE_DEVELOPMENT	32	0.495	1.601	0.020	0.082
GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	70	0.422	1.601	0.027	0.082
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	133	0.426	1.600	0.032	0.082
GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	19	0.540	1.600	0.031	0.083
GO_SECRETORY_GRANULE	334	0.347	1.599	0.006	0.083
GO_CELL_JUNCTION_ASSEMBLY	126	0.417	1.599	0.024	0.083
GO_CARBOXYPEPTIDASE_ACTIVITY	37	0.466	1.598	0.028	0.083
GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	18	0.569	1.598	0.040	0.083
GO_REGULATION_OF_PROTEIN_IMPORT	177	0.359	1.597	0.004	0.083
GO_NEGATIVE_REGULATION_OF_AXON_GUIDANCE	27	0.510	1.597	0.037	0.084
GO_PLASMA_MEMBRANE_ORGANIZATION	201	0.344	1.596	0.014	0.084
GO_ACTIN_FILAMENT_BINDING	115	0.385	1.595	0.012	0.084
GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	19	0.541	1.595	0.044	0.084
GO_SYNAPSE_ASSEMBLY	68	0.459	1.595	0.049	0.084
GO_POSITIVE_T_CELL_SELECTION	21	0.625	1.595	0.063	0.084
GO_NEUROPEPTIDE_SIGNALING_PATHWAY	88	0.442	1.594	0.010	0.085
GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	409	0.322	1.594	<0.001	0.085
GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	122	0.395	1.594	0.010	0.085
GO_RESPONSE_TO_STEROID_HORMONE	485	0.316	1.594	<0.001	0.085
GO_ENDOCYTIC_VESICLE_MEMBRANE	148	0.399	1.594	0.036	0.085
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	36	0.470	1.593	0.028	0.085
GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	24	0.498	1.593	0.042	0.085
GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENESIS	25	0.510	1.593	0.023	0.085
GO_SENSORY_ORGAN_MORPHOGENESIS	233	0.368	1.592	0.013	0.085
GO_VOLTAGE_GATED_CALCIUM_CHA	42	0.505	1.591	0.030	0.086

NNEL_ACTIVITY					
GO_SPECIFICATION_OF_SYMMETRY	112	0.396	1.591	0.006	0.086
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	52	0.416	1.591	0.015	0.086
GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	31	0.497	1.590	0.041	0.086
GO_SULFURIC_ESTER_HYDROLASE_ACTIVITY	17	0.572	1.589	0.041	0.086
GO_CELL_FATE_DETERMINATION	43	0.455	1.589	0.030	0.086
GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	21	0.500	1.589	0.026	0.087
GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	32	0.454	1.588	0.018	0.087
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	16	0.639	1.588	0.049	0.087
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	489	0.327	1.588	0.004	0.087
GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	55	0.447	1.588	0.039	0.087
GO_REGULATION_OF_PROTEIN_SECRETION	369	0.340	1.588	0.009	0.087
GO_BROWN_FAT_CELL_DIFFERENTIATION	28	0.490	1.587	0.033	0.087
GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	17	0.549	1.587	0.038	0.087
GO_REGULATION_OF_JNK_CASCADE	155	0.367	1.586	0.008	0.087
GO_POSITIVE_REGULATION_OF_VASODILATION	29	0.500	1.586	0.039	0.088
GO_POSITIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	22	0.498	1.585	0.028	0.088
GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	16	0.552	1.584	0.052	0.089
GO_EXCRETION	44	0.457	1.582	0.016	0.089
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	93	0.407	1.582	0.023	0.090
GO_CARDIAC_CELL_DEVELOPMENT	47	0.458	1.582	0.033	0.090
GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	23	0.520	1.581	0.031	0.090
GO_VISUAL_BEHAVIOR	48	0.423	1.581	0.023	0.090
GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	32	0.485	1.581	0.028	0.090

GO_M_BAND	20	0.518	1.581	0.040	0.090
GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	44	0.473	1.580	0.035	0.090
GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	197	0.336	1.580	<0.001	0.090
GO_PERIPHERAL_NERVOUS_SYSTEM_AXON_ENSHEATHMENT	21	0.525	1.579	0.025	0.090
GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	15	0.578	1.579	0.030	0.091
GO_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	49	0.454	1.578	0.025	0.091
GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	132	0.373	1.578	0.024	0.091
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	15	0.568	1.578	0.035	0.091
GO_POSITIVE_REGULATION_OF_PROTEIN_MATURATION	16	0.526	1.576	0.023	0.092
GO_SPINAL_CORD_DEVELOPMENT	103	0.416	1.576	0.021	0.092
GO_NERVE_DEVELOPMENT	66	0.422	1.575	0.034	0.092
GO_VENTRAL_SPINAL_CORD_INTERNEURON_DIFFERENTIATION	17	0.589	1.575	0.037	0.092
GO_RESPONSE_TO_AMINO_ACID	107	0.365	1.575	0.014	0.093
GO_REGULATION_OF_WOUND_HEALING	123	0.414	1.574	0.018	0.093
GO_CORTICAL_CYTOSKELETON	79	0.405	1.574	0.022	0.093
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	98	0.445	1.574	0.048	0.093
GO_MYOTUBE_DIFFERENTIATION	50	0.442	1.573	0.023	0.093
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	92	0.366	1.573	0.004	0.093
GO_MONOOXYGENASE_ACTIVITY	92	0.407	1.573	0.026	0.093
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	65	0.427	1.573	0.019	0.093
GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	16	0.557	1.573	0.028	0.093
GO_LIPID_PHOSPHORYLATION	96	0.379	1.572	0.016	0.093
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	38	0.468	1.572	0.040	0.093
GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	22	0.509	1.572	0.030	0.093
GO_REGULATION_OF_THE_FORCE_OF_	28	0.480	1.572	0.033	0.093

HEART_CONTRACTION					
GO_CELLULAR_EXTRAVASATION	24	0.594	1.571	0.052	0.094
GO_REGULATION_OF_VASODILATION	44	0.461	1.571	0.020	0.094
GO_BONE_MORPHOGENESIS	78	0.435	1.570	0.036	0.094
GO_TISSUE_REGENERATION	48	0.429	1.570	0.035	0.094
GO_CALCIUM_CHANNEL_COMPLEX	56	0.452	1.569	0.027	0.094
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	202	0.379	1.569	0.022	0.095
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	34	0.486	1.569	0.045	0.095
GO_CELL_AGGREGATION	20	0.538	1.568	0.029	0.095
GO_NEUROTROPHIN_SIGNALING_PATHWAY	23	0.520	1.568	0.049	0.095
GO_RECEPTOR_METABOLIC_PROCESS	77	0.402	1.568	0.016	0.095
GO_ACTIN_FILAMENT	67	0.417	1.568	0.032	0.095
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	16	0.629	1.568	0.048	0.095
GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	64	0.414	1.567	0.006	0.095
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	54	0.470	1.566	0.072	0.096
GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	46	0.420	1.566	0.027	0.095
GO_MYOBLAST_DIFFERENTIATION	37	0.467	1.566	0.038	0.096
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COACTIVATOR_ACTIVITY	35	0.495	1.564	0.015	0.096
GO_MIDDLE_EAR_MORPHOGENESIS	20	0.525	1.564	0.051	0.096
GO_SIGNALING_ADAPTOR_ACTIVITY	73	0.426	1.564	0.040	0.096
GO_RESPONSE_TO_ALCOHOL	358	0.322	1.564	0.006	0.096
GO_REGULATION_OF_CELL_ACTIVATION	443	0.393	1.564	0.062	0.096
GO_FACE_DEVELOPMENT	49	0.446	1.564	0.022	0.096
GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	168	0.338	1.564	0.007	0.096
GO_INFLAMMATORY_RESPONSE	431	0.404	1.563	0.042	0.096
GO_LUNG_MORPHOGENESIS	45	0.437	1.563	0.028	0.096
GO_CHANNEL_INHIBITOR_ACTIVITY	34	0.426	1.563	0.021	0.096
GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	28	0.481	1.563	0.030	0.096
GO_RECEPTOR_AGONIST_ACTIVITY	16	0.547	1.563	0.033	0.096
GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	22	0.589	1.563	0.066	0.096
GO_LIGAND_GATED_CALCIUM_CHAN	16	0.584	1.562	0.063	0.097

NEL_ACTIVITY					
GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	207	0.360	1.562	0.004	0.097
GO_NEGATIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	122	0.378	1.562	0.026	0.097
GO_REGULATION_OF_MUSCLE_HYPERTROPHY	36	0.456	1.561	0.023	0.097
GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	68	0.380	1.561	0.006	0.097
GO_GABA_RECEPTOR_BINDING	15	0.543	1.561	0.044	0.097
GO_LEUKOCYTE_MIGRATION	254	0.404	1.560	0.049	0.097
GO_JNK_CASCADE	79	0.380	1.560	0.017	0.097
GO_ENDODERM_FORMATION	50	0.454	1.559	0.043	0.098
GO_PODOSOME	23	0.517	1.559	0.067	0.098
GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	95	0.373	1.559	0.020	0.098
GO_TELENCEPHALON_DEVELOPMENT	225	0.346	1.558	0.016	0.098
GO_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	46	0.486	1.558	0.044	0.098
GO_MAST_CELL_GRANULE	21	0.551	1.558	0.065	0.098
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	218	0.385	1.557	0.048	0.098
GO_SARCOMERE_ORGANIZATION	25	0.526	1.557	0.065	0.098
GO_CARDIAC_MYOFIBRIL_ASSEMBLY	16	0.586	1.557	0.047	0.098
GO_POSITIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	16	0.547	1.557	0.056	0.098
GO_POSITIVE_REGULATION_OF_RECEPTOR_ACTIVITY	44	0.399	1.556	0.014	0.099
GO_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	21	0.513	1.556	0.045	0.099
GO_CYTOKINE_RECEPTOR_BINDING	243	0.361	1.556	0.012	0.099
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	166	0.361	1.555	0.030	0.099
GO_EAR_MORPHOGENESIS	111	0.383	1.555	0.023	0.099
GO_MAMMARY_GLAND_MORPHOGENESIS	40	0.454	1.555	0.036	0.099
GO_MUSCLE_ADAPTATION	29	0.457	1.554	0.038	0.099
GO_ADAPTATION_OF_SIGNALING_PATHWAY	20	0.508	1.554	0.042	0.099
GO_LAMININ_BINDING	29	0.504	1.554	0.036	0.099
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	125	0.423	1.553	0.070	0.100
GO_POSITIVE_REGULATION_OF_HEAR	35	0.430	1.553	0.016	0.100

T_CONTRACTION					
GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	19	0.523	1.553	0.038	0.100
GO_NEGATIVE_REGULATION_OF_MACROAUTOPHAGY	20	0.465	1.551	0.031	0.101
GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	23	0.511	1.551	0.044	0.101
GO_NEGATIVE_REGULATION_OF_TISSUE_REMODELING	17	0.546	1.550	0.033	0.101
GO_REGULATION_OF_PHAGOCYTOSIS	67	0.425	1.550	0.033	0.101
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_CONTRACTION	27	0.473	1.548	0.049	0.102
GO_CHEMOATTRACTANT_ACTIVITY	26	0.507	1.548	0.038	0.102
GO_TRANSMITTER_GATED_CHANNEL_ACTIVITY	26	0.529	1.548	0.042	0.103
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	36	0.477	1.547	0.054	0.103
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	35	0.484	1.546	0.025	0.104
GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	35	0.435	1.546	0.038	0.104
GO_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	132	0.367	1.545	0.012	0.104
GO_THYMIC_T_CELL_SELECTION	19	0.594	1.545	0.075	0.104
GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	22	0.560	1.545	0.057	0.104
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	59	0.425	1.545	0.040	0.104
GO_NEURON_MATURATION	30	0.464	1.545	0.046	0.104
GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	15	0.545	1.544	0.060	0.104
GO_REGULATION_OF_GLUTAMATE_SECRETION	15	0.557	1.544	0.049	0.104
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	481	0.314	1.542	0.004	0.105
GO_OVULATION_CYCLE_PROCESS	85	0.366	1.542	0.006	0.105
GO_HOMOTYPIC_CELL_CELL_ADHESION	49	0.434	1.542	0.047	0.105
GO_REGULATION_OF_HEAT_GENERATION	15	0.572	1.542	0.060	0.105
GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	60	0.390	1.541	0.031	0.106

GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	51	0.440	1.541	0.027	0.106
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	46	0.426	1.541	0.035	0.106
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	59	0.438	1.541	0.048	0.106
GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	20	0.518	1.541	0.039	0.105
GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	34	0.481	1.540	0.028	0.105
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	29	0.526	1.540	0.096	0.105
GO_FOREBRAIN_DEVELOPMENT	352	0.345	1.540	0.015	0.105
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	211	0.353	1.539	0.029	0.106
GO_FILOPODIUM	89	0.375	1.539	0.046	0.106
GO_OLFACTORY_LOBE_DEVELOPMENT	36	0.446	1.538	0.023	0.107
GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	17	0.525	1.536	0.045	0.108
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	79	0.451	1.536	0.064	0.108
GO_AXON	398	0.341	1.536	0.020	0.108
GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	26	0.531	1.536	0.066	0.108
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	38	0.506	1.535	0.062	0.108
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	76	0.450	1.534	0.071	0.108
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	33	0.459	1.534	0.045	0.109
GO_RENAL_WATER_HOMEOSTASIS	34	0.449	1.534	0.041	0.109
GO_EPHRIN_RECEPTOR_ACTIVITY	19	0.508	1.534	0.040	0.109
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	353	0.359	1.533	0.044	0.109
GO_MEMBRANE_INVAGINATION	29	0.493	1.532	0.047	0.109
GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	15	0.582	1.532	0.078	0.109
GO_REGULATION_OF_HEART_GROWT	41	0.424	1.532	0.027	0.109

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GO_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	458	0.309	1.532	0.004	0.109
GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	16	0.550	1.532	0.051	0.109
GO_SCHWANN_CELL_DEVELOPMENT	25	0.494	1.531	0.040	0.110
GO_PROTEIN_KINASE_B_SIGNALING	34	0.455	1.531	0.042	0.110
GO_REGULATION_OF_CHOLESTEROL_EFFLUX	20	0.510	1.530	0.041	0.110
GO_MRNA_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	15	0.534	1.530	0.050	0.110
GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	193	0.334	1.530	0.008	0.110
GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	41	0.432	1.530	0.053	0.110
GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	41	0.474	1.530	0.051	0.110
GO_METANEPHRIC_NEPHRON_MORPHOGENESIS	21	0.504	1.528	0.031	0.111
GO_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	70	0.394	1.528	0.034	0.111
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	403	0.345	1.527	0.017	0.112
GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	33	0.448	1.527	0.053	0.111
GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	52	0.404	1.526	0.038	0.112
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	19	0.585	1.526	0.066	0.112
GO_METANEPHROS_MORPHOGENESIS	28	0.474	1.525	0.052	0.113
GO_CHEMOKINE_BINDING	17	0.608	1.525	0.084	0.113
GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	78	0.376	1.524	0.018	0.113
GO_MAST_CELL_ACTIVATION	21	0.543	1.524	0.079	0.113
GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	32	0.422	1.523	0.043	0.114
GO_MYOFILAMENT	23	0.496	1.523	0.076	0.114
GO_REGULATION_OF_MUSCLE_ADAPTATION	61	0.399	1.522	0.035	0.114
GO_NEGATIVE_REGULATION_OF_CELL	19	0.534	1.521	0.063	0.115

_JUNCTION_ASSEMBLY					
GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	28	0.456	1.521	0.027	0.115
GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	19	0.535	1.521	0.055	0.115
GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	50	0.401	1.520	0.035	0.115
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	38	0.471	1.519	0.043	0.116
GO_REGULATION_OF_PROTEIN_KINASE_A_SIGNALING	17	0.526	1.519	0.062	0.116
GO_STAT_CASCADE	47	0.458	1.519	0.058	0.116
GO_CELL_CORTEX_PART	110	0.369	1.518	0.025	0.117
GO_T_CELL_DIFFERENTIATION	123	0.436	1.517	0.087	0.116
GO_REGULATION_OF_ENERGY_HOMEOSTASIS	17	0.536	1.517	0.062	0.117
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	16	0.521	1.517	0.072	0.117
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	323	0.322	1.516	0.010	0.117
GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	16	0.520	1.516	0.052	0.117
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	20	0.565	1.516	0.082	0.117
GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	29	0.473	1.515	0.074	0.118
GO_IMMUNOGLOBULIN_BINDING	20	0.585	1.515	0.079	0.118
GO_RESPONSE_TO_MAGNESIUM_ION	23	0.477	1.515	0.031	0.118
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	31	0.470	1.515	0.064	0.118
GO_SARCOPLASMIC_RETICULUM_MEMBRANE	36	0.455	1.515	0.065	0.118
GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	15	0.575	1.514	0.047	0.118
GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	27	0.472	1.514	0.039	0.118
GO_POSITIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	52	0.396	1.514	0.029	0.118
GO_EPITHELIAL_CELL_PROLIFERATION	86	0.378	1.514	0.026	0.118
GO_POSITIVE_REGULATION_OF_NEUT	26	0.502	1.514	0.069	0.118

ROPHIL_MIGRATION					
GO_RESPONSE_TO_ESTRADIOL	145	0.339	1.513	0.010	0.118
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.486	1.513	0.081	0.118
GO_GLUTAMATE_RECEPTOR_ACTIVITY	27	0.529	1.511	0.072	0.119
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	43	0.421	1.511	0.042	0.119
GO_VENTRICULAR_SEPTUM_DEVELOPMENT	53	0.415	1.511	0.038	0.119
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	29	0.466	1.511	0.043	0.119
GO_REGULATION_OF_THYMOCYTE_AGGREGATION	25	0.453	1.510	0.030	0.119
GO_REGULATION_OF_RECEPTOR_BINDING	17	0.520	1.510	0.050	0.120
GO_ENDOTHELIAL_CELL_MIGRATION	55	0.417	1.510	0.046	0.120
GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	39	0.436	1.509	0.043	0.120
GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	76	0.424	1.509	0.078	0.120
GO_SECONDARY_METABOLIC_PROCESS	48	0.428	1.509	0.049	0.120
GO_REGULATION_OF_HISTONE_DEACETYLATION	24	0.464	1.508	0.052	0.120
GO_REGULATION_OF_ORGAN_MORPHOGENESIS	240	0.332	1.508	0.022	0.120
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	78	0.384	1.508	0.052	0.120
GO_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	41	0.460	1.507	0.059	0.121
GO_COPPER_ION_BINDING	51	0.403	1.507	0.029	0.121
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	313	0.371	1.507	0.050	0.121
GO_ENDODERM_DEVELOPMENT	70	0.399	1.507	0.048	0.121
GO_REPLACEMENT_OSSIFICATION	25	0.508	1.507	0.077	0.121
GO_RESPONSE_TO_ALKALOID	133	0.348	1.507	0.012	0.121
GO_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	33	0.422	1.507	0.041	0.121
GO_POLYSACCHARIDE_METABOLIC_PROCESS	78	0.389	1.507	0.032	0.121
GO_MULTI_ORGANISM_BEHAVIOR	73	0.378	1.506	0.039	0.121
GO_NEGATIVE_REGULATION_OF_WOUND_HEALING	58	0.481	1.506	0.051	0.121

GO_PHOTORECEPTOR_OUTER_SEGMENT	66	0.423	1.506	0.053	0.121
GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	69	0.380	1.505	0.026	0.121
GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	157	0.324	1.505	0.006	0.121
GO_ACTIN_FILAMENT_ORGANIZATION	161	0.345	1.504	0.034	0.121
GO_ACTIN_BASED_CELL_PROJECTION	171	0.322	1.504	0.024	0.121
GO_MYOBLAST_FUSION	19	0.519	1.504	0.063	0.121
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	100	0.410	1.504	0.083	0.122
GO_PHOSPHOLIPASE_C_ACTIVITY	31	0.450	1.504	0.036	0.122
GO_ENDOCYTOSIS	462	0.336	1.503	0.025	0.122
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	22	0.551	1.502	0.107	0.122
GO_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	55	0.425	1.502	0.041	0.122
GO_REGULATION_OF_MESODERM_DEVELOPMENT	15	0.548	1.502	0.035	0.123
GO_TELENCEPHALON_GLIAL_CELL_MIGRATION	18	0.522	1.501	0.052	0.123
GO_POSITIVE_CHEMOTAXIS	35	0.441	1.501	0.041	0.123
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	18	0.513	1.501	0.046	0.123
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_FOLD	15	0.515	1.501	0.052	0.123
GO_MAST_CELL_MEDIATED_IMMUNITY	18	0.545	1.500	0.084	0.123
GO_REGULATION_OF_PLATELET_AGGREGATION	16	0.532	1.500	0.074	0.123
GO_METALLOENDOPEPTIDASE_ACTIVITY	107	0.378	1.499	0.049	0.124
GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	17	0.536	1.499	0.086	0.124
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	41	0.415	1.499	0.043	0.124
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	32	0.435	1.499	0.048	0.124
GO_PROTEIN_TYROSINE_KINASE_BINDING	52	0.387	1.498	0.027	0.124
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	155	0.368	1.498	0.053	0.124
GO_CELL_CHEMOTAXIS	157	0.407	1.497	0.056	0.124
GO_CELL_CORTEX	225	0.335	1.497	0.022	0.124

GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	61	0.388	1.497	0.032	0.124
GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	53	0.432	1.497	0.048	0.125
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	112	0.409	1.497	0.064	0.124
GO_REGULATION_OF_HORMONE_SECRETION	250	0.332	1.495	0.014	0.126
GO_ENDODERMAL_CELL_DIFFERENTIATION	40	0.461	1.495	0.067	0.126
GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	37	0.443	1.494	0.044	0.126
GO_CELLULAR_RESPONSE_TO_OXYGEN_LEVELS	137	0.332	1.494	0.020	0.126
GO_NEGATIVE_REGULATION_OF_BEHAVIOR	16	0.526	1.493	0.052	0.127
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	374	0.299	1.493	0.004	0.127
GO_MRNA_TRANSCRIPTION	21	0.483	1.493	0.048	0.127
GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	41	0.440	1.493	0.041	0.127
GO_REGULATION_OF_ANION_TRANSPORT	133	0.331	1.492	0.012	0.127
GO_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	100	0.413	1.492	0.058	0.127
GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	75	0.431	1.492	0.067	0.127
GO_HUMORAL_IMMUNE_RESPONSE	139	0.403	1.491	0.059	0.128
GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	20	0.500	1.491	0.064	0.128
GO_CHRONIC_INFLAMMATORY_RESPONSE	15	0.542	1.491	0.066	0.128
GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	19	0.540	1.490	0.066	0.128
GO_MYELIN_ASSEMBLY	15	0.523	1.490	0.078	0.128
GO_BETA_CATENIN_BINDING	80	0.395	1.490	0.059	0.128
GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	17	0.538	1.490	0.065	0.128
GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	72	0.379	1.489	0.031	0.128
GO_PEPTIDE_HORMONE_PROCESSING	29	0.496	1.489	0.045	0.128
GO_SPINAL_CORD_MOTOR_NEURON_DIFFERENTIATION	34	0.449	1.488	0.030	0.129
GO_PATTERNING_OF_BLOOD_VESSELS	31	0.484	1.488	0.073	0.129

GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	451	0.311	1.488	0.015	0.129
GO_PROXIMAL_DISTAL_PATTERN_FORMATION	32	0.478	1.488	0.057	0.129
GO_REGULATION_OF_MACROPHAGE_ACTIVATION	25	0.464	1.487	0.038	0.129
GO_NEGATIVE_REGULATION_OF_AXON_EXTENSION	37	0.436	1.487	0.053	0.129
GO_ACTIN_MONOMER_BINDING	25	0.449	1.487	0.052	0.129
GO_MYELOID_LEUKOCYTE_MIGRATION	95	0.419	1.486	0.061	0.130
GO_ADRENERGIC_RECEPTOR_BINDING	18	0.488	1.486	0.068	0.130
GO_EPITHELIAL_CELL_DIFFERENTIATION	464	0.321	1.486	0.027	0.130
GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	96	0.402	1.485	0.080	0.130
GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	29	0.455	1.485	0.054	0.130
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	123	0.395	1.484	0.068	0.131
GO_NEGATIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	58	0.377	1.483	0.033	0.131
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	18	0.529	1.483	0.071	0.131
GO_POSITIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	60	0.410	1.483	0.048	0.132
GO_CELL_VOLUME_HOMEOSTASIS	27	0.432	1.482	0.039	0.132
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	28	0.451	1.482	0.057	0.132
GO_LENS_FIBER_CELL_DIFFERENTIATION	25	0.459	1.482	0.045	0.132
GO_SODIUM_CHANNEL_ACTIVITY	32	0.455	1.481	0.057	0.132
GO_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	35	0.438	1.480	0.051	0.133
GO_RESPONSE_TO_MONOAMINE	34	0.433	1.480	0.042	0.133
GO_POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	74	0.368	1.479	0.026	0.134
GO_GLYCOSPHINGOLIPID_METABOLIC_PROCESS	66	0.383	1.478	0.036	0.134
GO_SPLEEN_DEVELOPMENT	38	0.411	1.477	0.062	0.134
GO_REGULATION_OF_CORTICOSTEROID_HORMONE_SECRETION	15	0.557	1.477	0.065	0.135

GO_SECRETORY_GRANULE_MEMBRANE	76	0.371	1.477	0.023	0.135
GO_MUSCLE_FIBER_DEVELOPMENT	41	0.417	1.477	0.045	0.135
GO_MYOSIN_II_COMPLEX	25	0.501	1.475	0.058	0.136
GO_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	52	0.416	1.475	0.058	0.136
GO_PRESYNAPSE	273	0.346	1.474	0.028	0.136
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	17	0.528	1.474	0.071	0.136
GO_GAP_JUNCTION_CHANNEL_ACTIVITY	16	0.520	1.474	0.086	0.136
GO_EXOCYTIC_VESICLE	139	0.354	1.474	0.056	0.136
GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	37	0.474	1.473	0.111	0.136
GO_EPIDERMIS_MORPHOGENESIS	28	0.480	1.473	0.061	0.136
GO_DETECTION_OF_ABIOTIC_STIMULUS	110	0.394	1.473	0.069	0.136
GO_SALIVARY_GLAND_DEVELOPMENT	31	0.465	1.473	0.073	0.137
GO_B_CELL_PROLIFERATION	24	0.556	1.473	0.095	0.137
GO_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	15	0.520	1.473	0.053	0.136
GO_REGENERATION	155	0.340	1.472	0.032	0.137
GO_RECEPTOR_SIGNALING_COMPLEX_SCAFFOLD_ACTIVITY	23	0.466	1.472	0.050	0.137
GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	55	0.381	1.472	0.037	0.137
GO_ALPHA_BETA_T_CELL_ACTIVATION	52	0.464	1.471	0.104	0.137
GO_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	67	0.426	1.471	0.077	0.138
GO_REGULATION_OF_PROTEIN_TARGETING	285	0.300	1.471	0.010	0.137
GO_ODONTOGENESIS	103	0.375	1.470	0.044	0.138
GO_CARTILAGE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL_BONE_MORPHOGENESIS	19	0.487	1.470	0.074	0.138
GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	29	0.447	1.469	0.063	0.138
GO_EMBRYONIC_HEART_TUBE_MORPHOGENESIS	61	0.389	1.468	0.043	0.139
GO_REGULATION_OF_HEART_MORPHOGENESIS	28	0.437	1.468	0.041	0.139

GO_MYOSIN_COMPLEX	66	0.399	1.468	0.063	0.139
GO_REGULATION_OF_LIPID_STORAGE	39	0.430	1.467	0.095	0.139
GO_APPENDAGE_DEVELOPMENT	165	0.359	1.467	0.046	0.140
GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	162	0.347	1.467	0.038	0.139
GO_PROTEIN_LIPID_COMPLEX_BINDING	24	0.495	1.467	0.074	0.139
GO_REGULATION_OF_COAGULATION	86	0.423	1.466	0.060	0.140
GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	322	0.305	1.465	0.014	0.140
GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	244	0.304	1.465	0.015	0.140
GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	23	0.484	1.465	0.069	0.140
GO_KIDNEY_MESENCHYME_DEVELOPMENT	17	0.524	1.465	0.070	0.140
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	241	0.327	1.465	0.029	0.140
GO_LEUKOCYTE_CHEMOTAXIS	113	0.422	1.464	0.083	0.140
GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	297	0.310	1.464	0.024	0.140
GO_TRANSCRIPTION_FACTOR_ACTIVITY_DIRECT_LIGAND_REGULATED_SEQUENCE_SPECIFIC_DNA_BINDING	46	0.414	1.464	0.065	0.140
GO_MYELOID_CELL_DIFFERENTIATION	181	0.334	1.464	0.044	0.140
GO_CATION_TRANSPORTING_ATPASE_COMPLEX	16	0.505	1.464	0.061	0.141
GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	342	0.302	1.463	0.028	0.141
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	63	0.381	1.463	0.041	0.141
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	24	0.495	1.463	0.077	0.141
GO_SYNCYTIUM_FORMATION	25	0.478	1.463	0.090	0.141
GO_RESPONSE_TO_VITAMIN	98	0.337	1.462	0.020	0.141
GO_VENTRAL_SPINAL_CORD_DEVELOPMENT	46	0.424	1.459	0.055	0.144
GO_REGULATION_OF_PROTEIN_DEACETYLATION	33	0.415	1.459	0.065	0.144
GO_REGULATION_OF_REPRODUCTIVE_PROCESS	125	0.346	1.458	0.031	0.144

GO_POSITIVE_REGULATION_OF_SECRETION	358	0.309	1.458	0.011	0.144
GO_FORMATION_OF_PRIMARY_GERM_LAYER	109	0.369	1.458	0.058	0.144
GO_CELL_CORTEX_REGION	16	0.509	1.457	0.056	0.144
GO_LONG_TERM_MEMORY	28	0.457	1.456	0.070	0.146
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIOTENSIN	22	0.507	1.455	0.078	0.146
GO_CELLULAR_RESPONSE_TO_KETONE	71	0.385	1.455	0.049	0.146
GO_MICROVILLUS	73	0.376	1.454	0.073	0.146
GO_CELL_MATURATION	121	0.314	1.454	0.022	0.146
GO_POSITIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	48	0.401	1.453	0.062	0.147
GO_CERAMIDE_BIOSYNTHETIC_PROCESS	43	0.393	1.453	0.063	0.147
GO_REGULATION_OF_HEMOPOIESIS	300	0.330	1.453	0.059	0.147
GO_RESPONSE_TO_PEPTIDE	392	0.298	1.452	0.016	0.148
GO_ISOPRENOID_BINDING	40	0.436	1.452	0.062	0.148
GO_LEUKOTRIENE_BIOSYNTHETIC_PROCESS	20	0.480	1.452	0.056	0.148
GO_PDZ_DOMAIN_BINDING	88	0.349	1.452	0.048	0.148
GO_APOPTOTIC_PROCESS_INVOLVED_IN_DEVELOPMENT	20	0.477	1.451	0.061	0.148
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	33	0.429	1.451	0.049	0.148
GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	20	0.465	1.451	0.077	0.148
GO_INNER_EAR_MORPHOGENESIS	91	0.370	1.450	0.047	0.148
GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	42	0.402	1.450	0.048	0.148
GO_ORGAN_INDUCTION	16	0.515	1.450	0.083	0.149
GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	181	0.313	1.449	0.029	0.149
GO_MATURE_B_CELL_DIFFERENTIATION	17	0.553	1.449	0.102	0.149
GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	180	0.351	1.449	0.034	0.149
GO_SH3_SH2_ADAPTOR_ACTIVITY	52	0.410	1.449	0.084	0.149
GO_BINDING_BRIDGING	172	0.328	1.449	0.028	0.149
GO_SERINE_HYDROLASE_ACTIVITY	211	0.344	1.448	0.026	0.149
GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	71	0.372	1.448	0.049	0.149

GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	34	0.492	1.447	0.081	0.150
GO_REGULATION_OF_CYTOKINE_SECRETION	138	0.401	1.447	0.084	0.150
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	20	0.496	1.447	0.079	0.150
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	146	0.332	1.446	0.035	0.151
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	27	0.461	1.445	0.094	0.151
GO_PATTERN_SPECIFICATION_PROCESS	405	0.315	1.445	0.028	0.151
GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	20	0.461	1.444	0.083	0.152
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	30	0.409	1.444	0.054	0.152
GO_HYALURONAN_METABOLIC_PROCESS	29	0.461	1.444	0.095	0.152
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	101	0.357	1.443	0.056	0.152
GO_REGULATION_OF_CELL_PROJECTION_ASSEMBLY	142	0.325	1.442	0.033	0.153
GO_RESPONSE_TO_RETINOIC_ACID	102	0.339	1.442	0.038	0.153
GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	23	0.442	1.441	0.057	0.154
GO_LYMPH_NODE_DEVELOPMENT	17	0.518	1.441	0.109	0.154
GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_BLOOD_VOLUME	17	0.499	1.441	0.072	0.154
GO_AMMONIUM_TRANSPORT	55	0.371	1.441	0.040	0.154
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	32	0.407	1.441	0.046	0.154
GO_NEURON_PROJECTION_TERMINUS	124	0.378	1.441	0.044	0.154
GO_REGULATION_OF_CHEMOKINE_PRODUCTION	63	0.428	1.440	0.078	0.154
GO_CELLULAR_RESPONSE_TO_LIPID	439	0.297	1.440	0.028	0.154
GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	36	0.455	1.440	0.089	0.154
GO_EMBRYONIC_EYE_MORPHOGENESIS	33	0.432	1.439	0.075	0.154
GO_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	100	0.344	1.439	0.038	0.154

GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	22	0.449	1.438	0.067	0.155
GO_MYOSIN_BINDING	58	0.360	1.437	0.050	0.156
GO_ALCOHOL_BINDING	98	0.361	1.436	0.038	0.156
GO_REGULATION_OF_CGMP_BIOSYNTHETIC_PROCESS	22	0.461	1.436	0.083	0.156
GO_EMBRYO_IMPLANTATION	37	0.404	1.436	0.072	0.156
GO_MAMMARY_GLAND_EPITHELIAL_CELL_DIFFERENTIATION	16	0.493	1.436	0.076	0.156
GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_BINDING	68	0.358	1.435	0.052	0.157
GO_ACTIN_CYTOSKELETON_REORGANIZATION	54	0.395	1.434	0.068	0.157
GO_NEGATIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	15	0.537	1.434	0.080	0.157
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	17	0.492	1.433	0.092	0.158
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	84	0.376	1.433	0.068	0.158
GO_BONE_REMODELING	35	0.430	1.432	0.076	0.158
GO_AORTA_MORPHOGENESIS	22	0.478	1.432	0.084	0.159
GO_SECRETORY_GRANULE_ORGANIZATION	23	0.430	1.431	0.049	0.159
GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	150	0.313	1.431	0.039	0.159
GO_HYALURONIC_ACID_BINDING	20	0.497	1.431	0.090	0.159
GO_DORSAL_VENTRAL_PATTERN_FORMATION	90	0.363	1.431	0.046	0.159
GO_RESPONSE_TO_CARBOHYDRATE	161	0.327	1.431	0.035	0.159
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	34	0.456	1.430	0.104	0.160
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	95	0.351	1.430	0.048	0.160
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	40	0.403	1.430	0.074	0.159
GO_STEROID_HYDROXYLASE_ACTIVITY	31	0.463	1.429	0.101	0.160
GO_COPULATION	17	0.506	1.429	0.097	0.160
GO_AXONAL_GROWTH_CONE	19	0.479	1.429	0.097	0.160
GO_AXON_PART	208	0.334	1.428	0.044	0.161
GO_CELLULAR_RESPONSE_TO_FATTY_ACID	51	0.383	1.428	0.070	0.161
GO_DRUG_BINDING	106	0.322	1.428	0.018	0.161

GO_REGULATION_OF_P38MAPK_CASCADE	26	0.434	1.428	0.070	0.161
GO_SEX_DETERMINATION	22	0.452	1.427	0.082	0.161
GO_DIENCEPHALON_DEVELOPMENT	76	0.375	1.427	0.046	0.161
GO_EXOCRINE_SYSTEM_DEVELOPMENT	43	0.410	1.426	0.054	0.161
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	124	0.328	1.426	0.051	0.162
GO_POSITIVE_REGULATION_OF_HEART_RATE	22	0.435	1.424	0.072	0.163
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	49	0.410	1.424	0.070	0.163
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	176	0.310	1.423	0.050	0.163
GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	64	0.361	1.423	0.051	0.163
GO_B_CELL_DIFFERENTIATION	74	0.411	1.422	0.084	0.164
GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	317	0.309	1.422	0.054	0.164
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	35	0.557	1.422	0.181	0.164
GO_RESPONSE_TO_FOLIC_ACID	15	0.495	1.422	0.099	0.164
GO_REGULATION_OF_ARF_PROTEIN_SIGNAL_TRANSDUCTION	15	0.524	1.421	0.082	0.165
GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	33	0.442	1.420	0.067	0.165
GO_CORTICAL_ACTIN_CYTOSKELETON	58	0.378	1.420	0.078	0.165
GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT	460	0.284	1.420	0.021	0.166
GO_SCAFFOLD_PROTEIN_BINDING	45	0.392	1.418	0.069	0.167
GO_ASTROCYTE_DEVELOPMENT	19	0.495	1.418	0.092	0.167
GO_NEGATIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	15	0.525	1.418	0.070	0.167
GO_NARROW_PORE_CHANNEL_ACTIVITY	16	0.504	1.417	0.096	0.167
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	90	0.341	1.417	0.055	0.167
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	72	0.378	1.417	0.089	0.167
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_	57	0.441	1.416	0.145	0.168

CYTOKINE_PRODUCTION					
GO_CATION_CATION_ANTIPORTER_ACTIVITY	24	0.442	1.414	0.067	0.169
GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	22	0.440	1.414	0.069	0.169
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	84	0.356	1.414	0.068	0.170
GO_FILAMENTOUS_ACTIN	19	0.474	1.413	0.115	0.170
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	36	0.469	1.413	0.125	0.170
GO_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	228	0.304	1.413	0.042	0.170
GO_CATECHOLAMINE_BINDING	15	0.508	1.412	0.076	0.170
GO_BIOMINERAL_TISSUE_DEVELOPMENT	72	0.360	1.412	0.047	0.170
GO_RUFFLE	152	0.336	1.412	0.058	0.171
GO_PROTEIN_TRIMERIZATION	38	0.408	1.411	0.107	0.171
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_ABSENCE_OF_LIGAND	46	0.402	1.411	0.081	0.171
GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	40	0.444	1.411	0.103	0.171
GO_GLUTAMATE_RECEPTOR_BINDING	37	0.395	1.410	0.091	0.171
GO_GENITALIA_DEVELOPMENT	42	0.394	1.410	0.073	0.172
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	19	0.472	1.409	0.094	0.172
GO_INTRASPECIES_INTERACTION_BETWEEN_ORGANISMS	45	0.391	1.409	0.080	0.172
GO_POSITIVE_REGULATION_OF_BINDING	125	0.316	1.409	0.024	0.172
GO_ENDOCYTIC_VESICLE	251	0.325	1.409	0.057	0.173
GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	20	0.466	1.408	0.089	0.173
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	29	0.457	1.408	0.119	0.173
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	21	0.535	1.408	0.156	0.173
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	279	0.379	1.408	0.131	0.173
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	27	0.445	1.408	0.109	0.173
GO_CRANIAL_NERVE_DEVELOPMENT	42	0.388	1.407	0.087	0.174

GO_RECEPTOR_ACTIVATOR_ACTIVITY	32	0.388	1.406	0.040	0.174
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	19	0.476	1.406	0.077	0.174
GO_MYELOID_LEUKOCYTE_ACTIVATION	95	0.411	1.405	0.145	0.174
GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	71	0.351	1.405	0.047	0.174
GO_ENZYME_INHIBITOR_ACTIVITY	356	0.313	1.405	0.042	0.174
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	32	0.389	1.405	0.071	0.174
GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	15	0.514	1.404	0.109	0.175
GO_LYMPHOCYTE_MIGRATION	48	0.493	1.403	0.133	0.175
GO_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	36	0.387	1.403	0.070	0.176
GO_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	16	0.488	1.403	0.102	0.176
GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	23	0.456	1.403	0.093	0.176
GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	16	0.502	1.403	0.090	0.176
GO_CALCIUM_DEPENDENT_PROTEIN_BINDING	58	0.364	1.402	0.063	0.176
GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	16	0.500	1.402	0.084	0.176
GO_DENDRITE_CYTOPLASM	16	0.490	1.402	0.083	0.176
GO_PITUITARY_GLAND_DEVELOPMENT	42	0.398	1.402	0.061	0.176
GO_LAMELLIPODIUM_ORGANIZATION	34	0.392	1.402	0.089	0.176
GO_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	56	0.425	1.401	0.095	0.176
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	22	0.445	1.401	0.100	0.176
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	394	0.280	1.401	0.023	0.176
GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	17	0.474	1.400	0.102	0.177
GO_CELLULAR_GLUCOSE_HOMEOSTASIS	71	0.359	1.399	0.071	0.177
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	35	0.419	1.399	0.095	0.177

GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	203	0.346	1.399	0.080	0.177
GO_GABAERGIC_NEURON_DIFFERENTIATION	15	0.531	1.399	0.097	0.177
GO_RESPONSE_TO_EPINEPHRINE	16	0.499	1.399	0.094	0.178
GO_POSITIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	51	0.377	1.399	0.081	0.177
GO_ERK1_AND_ERK2_CASCADE	22	0.431	1.398	0.095	0.178
GO_LEUKOCYTE_PROLIFERATION	73	0.424	1.397	0.142	0.178
GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	46	0.391	1.397	0.075	0.178
GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	20	0.470	1.397	0.120	0.178
GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	256	0.296	1.397	0.043	0.178
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	289	0.366	1.397	0.142	0.178
GO_MECHANORECEPTOR_DIFFERENTIATION	49	0.365	1.397	0.055	0.178
GO_RESPONSE_TO_ACETYLCHOLINE	17	0.474	1.396	0.081	0.179
GO_STARTLE_RESPONSE	24	0.451	1.396	0.118	0.179
GO_REGULATION_OF_GLIOGENESIS	88	0.335	1.396	0.037	0.179
GO_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	166	0.308	1.394	0.052	0.180
GO_THYMOCYTE_AGGREGATION	45	0.424	1.394	0.119	0.180
GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	17	0.485	1.393	0.067	0.180
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	196	0.344	1.393	0.099	0.181
GO_OXYGEN_BINDING	44	0.422	1.393	0.115	0.181
GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	143	0.306	1.393	0.039	0.181
GO_POSITIVE_REGULATION_OF_BEHAVIOR	23	0.468	1.392	0.074	0.181
GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	26	0.453	1.392	0.106	0.181
GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	41	0.378	1.391	0.101	0.182
GO_RESPONSE_TO_AUDITORY_STIMULUS	23	0.453	1.391	0.088	0.182
GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	27	0.429	1.391	0.104	0.182
GO_REGULATION_OF_ODONTOGENESI	24	0.450	1.391	0.073	0.182

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GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	42	0.386	1.390	0.085	0.183
GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	23	0.536	1.390	0.109	0.183
GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	92	0.354	1.390	0.083	0.183
GO_LEUKOTRIENE_METABOLIC_PROCESS	30	0.424	1.389	0.100	0.183
GO_REGULATION_OF_FIBROBLAST_PROLIFERATION	80	0.339	1.389	0.076	0.183
GO_CELLULAR_RESPONSE_TO_OSMOTIC_STRESS	20	0.458	1.388	0.116	0.183
GO_PARASYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	16	0.507	1.388	0.099	0.184
GO_REGULATION_OF_CELL_CELL_ADHESION	359	0.342	1.388	0.137	0.184
GO_PROTEIN_KINASE_A_BINDING	41	0.374	1.387	0.081	0.184
GO_REGULATION_OF_T_CELL_MIGRATION	24	0.466	1.387	0.128	0.184
GO_METALLOPEPTIDASE_ACTIVITY	177	0.305	1.387	0.050	0.184
GO_CELLULAR_RESPONSE_TO_PEPTIDE	265	0.294	1.387	0.044	0.184
GO_PHARYNGEAL_SYSTEM_DEVELOPMENT	16	0.500	1.386	0.101	0.184
GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	92	0.364	1.386	0.103	0.184
GO_ADRENAL_GLAND_DEVELOPMENT	23	0.445	1.386	0.091	0.184
GO_GAMMA_AMINOBUTYRIC_ACID_SIGNALING_PATHWAY	23	0.468	1.386	0.112	0.184
GO_DETECTION_OF_TEMPERATURE_STIMULUS	16	0.484	1.386	0.094	0.184
GO_NEURON_FATE_COMMITMENT	66	0.388	1.385	0.084	0.185
GO_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	40	0.390	1.385	0.088	0.184
GO_REGULATION_OF_VACUOLAR_TRANSPORT	29	0.424	1.385	0.115	0.185
GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	94	0.373	1.385	0.129	0.185
GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	20	0.422	1.385	0.089	0.185
GO_POSITIVE_REGULATION_OF_POTA	37	0.413	1.385	0.103	0.185

SSIUM_ION_TRANSPORT					
GO_REGULATION_OF_MAST_CELL_ACTIVATION	38	0.439	1.383	0.143	0.186
GO_RESPONSE_TO_INORGANIC_SUBSTANCE	467	0.276	1.383	0.017	0.186
GO_SIGNAL_RELEASE	165	0.338	1.382	0.093	0.187
GO_CELL_PROLIFERATION_IN_FOREBRAIN	27	0.424	1.382	0.116	0.187
GO_APOPTOTIC_CELL_CLEARANCE	27	0.447	1.381	0.107	0.187
GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	94	0.370	1.380	0.121	0.188
GO_COCHLEA_MORPHOGENESIS	21	0.453	1.379	0.108	0.189
GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	40	0.386	1.379	0.071	0.189
GO_REGIONALIZATION	304	0.308	1.379	0.062	0.189
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	211	0.299	1.379	0.041	0.189
GO_ENDOCRINE_SYSTEM_DEVELOPMENT	123	0.333	1.379	0.046	0.189
GO_CYTOPLASMIC_REGION	270	0.295	1.379	0.044	0.189
GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	53	0.364	1.378	0.083	0.190
GO_SEROTONIN_RECEPTOR_ACTIVITY	18	0.514	1.378	0.114	0.190
GO_POSITIVE_REGULATION_OF_PROTEIN_SECRETION	202	0.322	1.377	0.059	0.190
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	445	0.276	1.376	0.021	0.190
GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	48	0.354	1.376	0.074	0.190
GO_CEREBRAL_CORTEX_RADIALLY_ORIENTED_CELL_MIGRATION	27	0.425	1.376	0.095	0.191
GO_GRANULOCYTE_MIGRATION	71	0.408	1.376	0.128	0.191
GO_LEUKOCYTE_CELL_CELL_ADHESION	238	0.375	1.376	0.139	0.191
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	26	0.465	1.375	0.149	0.191
GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	16	0.482	1.375	0.107	0.191
GO_PRIMARY_CILIUM	191	0.327	1.373	0.103	0.193
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	66	0.454	1.373	0.137	0.193
GO_POSITIVE_REGULATION_OF_PROTEIN_DEACETYLATION	18	0.452	1.372	0.106	0.193

GO_REGULATION_OF_HORMONE_LEVELS	458	0.295	1.372	0.044	0.193
GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	126	0.323	1.372	0.049	0.193
GO_PHAGOCYTOSIS	158	0.352	1.372	0.114	0.193
GO_WNT_SIGNALING_PATHWAY_CALCIUM_MODULATING_PATHWAY	34	0.384	1.371	0.095	0.194
GO_GLUCOCORTICOID_METABOLIC_PROCESS	16	0.493	1.370	0.101	0.194
GO_NEURON_FATE_SPECIFICATION	31	0.445	1.369	0.097	0.196
GO_MEMBRANE_RAFT_ORGANIZATION	17	0.476	1.368	0.112	0.196
GO_PROTEASE_BINDING	98	0.351	1.367	0.100	0.197
GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	73	0.331	1.367	0.086	0.197
GO_GAP_JUNCTION	30	0.433	1.367	0.116	0.197
GO_STEROID_BINDING	89	0.359	1.367	0.063	0.197
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	49	0.374	1.366	0.103	0.197
GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	43	0.391	1.366	0.106	0.197
GO_RUFFLE_MEMBRANE	78	0.335	1.366	0.082	0.197
GO_RESPONSE_TO_MUSCLE_ACTIVITY	17	0.441	1.366	0.109	0.197
GO_NEPHRON_TUBULE_FORMATION	18	0.482	1.365	0.113	0.198
GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	15	0.522	1.364	0.142	0.199
GO_SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	89	0.394	1.364	0.105	0.199
GO_MAMMARY_GLAND_DUCT_MORPHOGENESIS	28	0.416	1.364	0.119	0.199
GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	25	0.423	1.363	0.103	0.199
GO_POTASSIUM_ION_HOMEOSTASIS	18	0.471	1.363	0.114	0.199
GO_REGULATION_OF_INTERLEUKIN_8_SECRETION	18	0.485	1.363	0.129	0.199
GO_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	28	0.414	1.363	0.103	0.199
GO_RESPONSE_TO_ACIDIC_PH	17	0.463	1.363	0.111	0.199
GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	50	0.380	1.362	0.110	0.200
GO_REGULATION_OF_INTERLEUKIN_1	31	0.450	1.361	0.134	0.200

_SECRETION					
GO_NUCLEAR_OUTER_MEMBRANE	19	0.418	1.361	0.108	0.201
GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	20	0.463	1.361	0.108	0.200
GO_RECEPTOR_SIGNALING_PROTEIN_ACTIVITY	165	0.307	1.361	0.065	0.200
GO_HEPARAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	28	0.436	1.361	0.140	0.200
GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	20	0.451	1.360	0.126	0.201
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_BIPOLAR_CELL_POLARITY	34	0.368	1.359	0.082	0.201
GO_RESPONSE_TO_BACTERIUM	464	0.319	1.359	0.088	0.202
GO_NUCLEUS_LOCALIZATION	20	0.431	1.359	0.112	0.202
GO_TERMINAL_BOUTON	63	0.386	1.358	0.090	0.202
GO_ADULT_LOCOMOTORY_BEHAVIOR	79	0.365	1.358	0.107	0.202
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	22	0.450	1.358	0.125	0.202
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	46	0.420	1.357	0.146	0.203
GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	28	0.406	1.357	0.091	0.203
GO_SCHWANN_CELL_DIFFERENTIATION	30	0.421	1.357	0.114	0.203
GO_POSITIVE_REGULATION_OF_PROTEIN_IMPORT	101	0.318	1.357	0.065	0.203
GO_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	92	0.334	1.357	0.073	0.203
GO_NEUROMUSCULAR_PROCESS_CONTROLLING_POSTURE	15	0.469	1.356	0.114	0.203
GO_SOMATIC_STEM_CELL_POPULATION_MAINTENANCE	66	0.341	1.355	0.088	0.204
GO_STRUCTURAL_CONSTITUENT_OF_EYE_LENS	19	0.497	1.355	0.118	0.204
GO_ENERGY_RESERVE_METABOLIC_PROCESS	70	0.356	1.355	0.093	0.204
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	43	0.376	1.354	0.102	0.204
GO_STABILIZATION_OF_MEMBRANE_POTENTIAL	15	0.497	1.354	0.105	0.204
GO_IONOTROPIC_GLUTAMATE_RECEPTOR_COMPLEX	47	0.396	1.354	0.120	0.204
GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	53	0.349	1.353	0.100	0.205

GO_LIPID_TRANSLOCATION	21	0.463	1.353	0.127	0.205
GO_CAMP_BINDING	21	0.464	1.353	0.133	0.205
GO_MUSCLE_MYOSIN_COMPLEX	19	0.508	1.353	0.138	0.205
GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	28	0.435	1.353	0.150	0.205
GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	158	0.304	1.353	0.064	0.205
GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	64	0.345	1.352	0.063	0.205
GO_EPIBOLY	20	0.460	1.351	0.127	0.206
GO_FLUID_TRANSPORT	26	0.414	1.351	0.112	0.206
GO_MYOSIN_FILAMENT	22	0.491	1.350	0.138	0.207
GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	75	0.377	1.350	0.127	0.206
GO_CANONICAL_WNT_SIGNALING_PATHWAY	92	0.338	1.350	0.113	0.206
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	37	0.402	1.350	0.135	0.207
GO_SYNAPTIC_VESICLE_CYCLE	85	0.352	1.349	0.097	0.207
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	64	0.358	1.349	0.122	0.207
GO_INSULIN_RECEPTOR_BINDING	31	0.409	1.349	0.104	0.208
GO_ENDOTHELIAL_CELL_PROLIFERATION	23	0.432	1.348	0.117	0.208
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	92	0.379	1.347	0.123	0.209
GO_REGULATION_OF_PEPTIDE_TRANSPORT	244	0.291	1.347	0.033	0.209
GO_EMBRYONIC_CRANIAL_SKELETON_MORPHOGENESIS	46	0.386	1.347	0.104	0.209
GO_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS	53	0.364	1.346	0.100	0.210
GO_NEGATIVE_REGULATION_OF_MEIOTIC_CELL_CYCLE	18	0.426	1.345	0.096	0.211
GO_NEURAL_TUBE_DEVELOPMENT	145	0.305	1.345	0.087	0.210
GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	18	0.457	1.344	0.144	0.211
GO_LYSOSOME_LOCALIZATION	23	0.432	1.344	0.139	0.211
GO_NEGATIVE_REGULATION_OF_I_KA	49	0.376	1.344	0.093	0.211

PPAB_KINASE_NF_KAPPAB_SIGNALING					
GO_MODIFIED_AMINO_ACID_BINDING	62	0.328	1.344	0.058	0.211
GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	49	0.412	1.343	0.131	0.211
GO_NEGATIVE_REGULATION_OF_ENDOCYTOSIS	37	0.396	1.342	0.116	0.212
GO_RESPONSE_TO_NUTRIENT	189	0.288	1.342	0.037	0.212
GO_BRANCHING_INVOLVED_IN_SALIVARY_GLAND_MORPHOGENESIS	16	0.530	1.342	0.151	0.212
GO_SOMATIC_STEM_CELL_DIVISION	22	0.444	1.342	0.131	0.212
GO_TISSUE_HOMEOSTASIS	158	0.293	1.342	0.049	0.212
GO_ENZYME_ACTIVATOR_ACTIVITY	451	0.271	1.341	0.057	0.213
GO_POST_EMBRYONIC_DEVELOPMENT	86	0.328	1.341	0.086	0.213
GO_LEUKOCYTE_ACTIVATION	391	0.354	1.341	0.159	0.213
GO_POTASSIUM_ION_IMPORT	29	0.416	1.341	0.127	0.213
GO_LONG_TERM_SYNAPTIC_DEPRESSION	15	0.440	1.340	0.128	0.213
GO_REGULATION_OF_PEPTIDE_SECRETION	198	0.297	1.340	0.060	0.213
GO_PROTEIN_HOMOOLIGOMERIZATION	242	0.272	1.339	0.021	0.214
GO_ALKALI_METAL_ION_BINDING	20	0.444	1.339	0.128	0.214
GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	23	0.434	1.338	0.115	0.215
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	30	0.413	1.337	0.150	0.215
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	231	0.355	1.337	0.169	0.215
GO_CLATHRIN_BINDING	62	0.357	1.337	0.103	0.215
GO_TRANSCRIPTIONAL_ACTIVATOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDING	24	0.404	1.337	0.126	0.215
GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	83	0.325	1.337	0.090	0.215
GO_PHOSPHOLIPID_BINDING	342	0.277	1.337	0.044	0.215
GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	25	0.417	1.336	0.128	0.216
GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	79	0.322	1.336	0.069	0.216
GO_FAT_CELL_DIFFERENTIATION	101	0.326	1.336	0.093	0.215

GO_TRANSLATION_REPRESSOR_ACTIVITY	20	0.459	1.336	0.150	0.216
GO_POSITIVE_REGULATION_OF_GROWTH	227	0.282	1.336	0.063	0.216
GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	36	0.384	1.335	0.102	0.217
GO_AGING	259	0.283	1.335	0.046	0.217
GO_SODIUM_ION_HOMEOSTASIS	30	0.429	1.334	0.112	0.217
GO_POSITIVE_REGULATION_OF_COAGULATION	24	0.461	1.334	0.158	0.218
GO_DOPAMINERGIC_NEURON_DIFFERENTIATION	27	0.415	1.333	0.118	0.218
GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	187	0.305	1.333	0.079	0.218
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	15	0.504	1.332	0.178	0.218
GO_RESPONSE_TO_METAL_ION	324	0.273	1.332	0.028	0.218
GO_TETRAPYRROLE_BINDING	128	0.321	1.332	0.099	0.218
GO_POSITIVE_REGULATION_OF_NEUROBLAST_PROLIFERATION	20	0.428	1.332	0.126	0.219
GO_CELLULAR_DEFENSE_RESPONSE	56	0.438	1.332	0.195	0.218
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	44	0.431	1.332	0.180	0.218
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	129	0.330	1.331	0.133	0.219
GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	27	0.443	1.331	0.117	0.219
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	268	0.288	1.331	0.071	0.219
GO_STEM_CELL_PROLIFERATION	60	0.367	1.329	0.092	0.221
GO_NEGATIVE_REGULATION_OF_COAGULATION	48	0.455	1.329	0.157	0.221
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	15	0.474	1.328	0.148	0.221
GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	120	0.338	1.328	0.134	0.221
GO_NEGATIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	126	0.294	1.328	0.087	0.221
GO_AZOLE_TRANSPORT	15	0.459	1.327	0.131	0.222
GO_ION_GATED_CHANNEL_ACTIVITY	40	0.381	1.326	0.113	0.223
GO_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	214	0.287	1.324	0.064	0.224

GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	19	0.437	1.324	0.123	0.224
GO_CARBOHYDRATE_HOMEOSTASIS	158	0.303	1.324	0.075	0.224
GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	349	0.288	1.323	0.076	0.225
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	169	0.294	1.323	0.101	0.225
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	81	0.314	1.323	0.065	0.225
GO_IONOTROPIC_GLUTAMATE_RECEPTOR_BINDING	23	0.400	1.323	0.124	0.225
GO_RETINOIC_ACID_METABOLIC_PROCESS	21	0.462	1.323	0.154	0.225
GO_GASTRULATION	147	0.310	1.322	0.100	0.226
GO_HINDBRAIN_DEVELOPMENT	136	0.326	1.321	0.101	0.226
GO_SEGMENT_SPECIFICATION	16	0.459	1.320	0.127	0.227
GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	149	0.289	1.320	0.058	0.227
GO_POSITIVE_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	16	0.509	1.320	0.162	0.227
GO_CRANIAL_NERVE_MORPHOGENESIS	23	0.424	1.320	0.143	0.227
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	37	0.418	1.319	0.174	0.228
GO_ACTIVATION_OF_JUN_KINASE_ACTIVITY	32	0.411	1.317	0.154	0.230
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	66	0.340	1.317	0.111	0.230
GO_APICAL_JUNCTION_COMPLEX	119	0.319	1.317	0.129	0.230
GO_WNT_SIGNALING_PATHWAY	336	0.277	1.316	0.085	0.230
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	133	0.380	1.316	0.183	0.230
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	199	0.359	1.314	0.189	0.232
GO_BONE_MINERALIZATION	38	0.364	1.314	0.092	0.232
GO_NEURAL_TUBE_PATTERNING	32	0.393	1.314	0.123	0.232
GO_MULTICELLULAR_ORGANISMAL_WATER_HOMEOSTASIS	57	0.399	1.313	0.152	0.233
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	30	0.446	1.312	0.165	0.234
GO_GUANYL_NUCLEOTIDE_BINDING	357	0.266	1.311	0.071	0.235

GO_REGULATION_OF_ORGAN_GROWTH	71	0.323	1.311	0.082	0.235
GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	19	0.466	1.310	0.124	0.236
GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	17	0.440	1.310	0.130	0.235
GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_BINDING	47	0.338	1.309	0.101	0.236
GO_NEURON_NEURON_SYNAPTIC_TRANSMISSION	54	0.374	1.309	0.133	0.236
GO_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	43	0.380	1.308	0.123	0.237
GO_RESPONSE_TO_ETHANOL	136	0.296	1.307	0.070	0.238
GO_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	189	0.299	1.307	0.112	0.238
GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	21	0.447	1.306	0.149	0.238
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	23	0.441	1.306	0.165	0.239
GO_ATPASE_COMPLEX	24	0.395	1.305	0.134	0.240
GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	269	0.265	1.304	0.046	0.240
GO_MAP_KINASE_KINASE_KINASE_ACTIVITY	18	0.446	1.304	0.162	0.240
GO_POSITIVE_REGULATION_OF_WOUND_HEALING	46	0.389	1.303	0.136	0.241
GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	51	0.366	1.301	0.133	0.243
GO_FORELIMB_MORPHOGENESIS	39	0.385	1.301	0.119	0.243
GO_NEUROPEPTIDE_RECEPTOR_BINDING	27	0.422	1.301	0.121	0.243
GO_PEPTIDE_SECRETION	56	0.373	1.300	0.129	0.243
GO_PEPTIDASE_REGULATOR_ACTIVITY	202	0.316	1.298	0.114	0.245
GO_HEPARAN_SULFATE_SULFOTRANSFERASE_ACTIVITY	15	0.470	1.298	0.175	0.246
GO_NEURAL_RETINA_DEVELOPMENT	49	0.351	1.298	0.115	0.246
GO_RESPONSE_TO_PLATELET_DERIVED_GROWTH_FACTOR	18	0.446	1.298	0.190	0.246
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	0.451	1.298	0.174	0.246
GO_SIGNALING_PATTERN_RECOGNITI	17	0.516	1.298	0.229	0.245

ON_RECEPTOR_ACTIVITY					
GO_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	15	0.445	1.297	0.169	0.246
GO_RESPONSE_TO_EXOGENOUS_DSRNA	32	0.390	1.297	0.155	0.246
GO_METALLOEXOPEPTIDASE_ACTIVITY	48	0.340	1.297	0.094	0.246
GO_CYTOKINE_PRODUCTION	116	0.352	1.297	0.163	0.246
GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	60	0.340	1.296	0.107	0.246
GO_GAS_TRANSPORT	17	0.471	1.296	0.166	0.246
GO_HINDBRAIN_MORPHOGENESIS	39	0.365	1.296	0.143	0.246
GO_PANCREAS_DEVELOPMENT	72	0.341	1.296	0.135	0.246
GO_SERTOLI_CELL_DIFFERENTIATION	18	0.450	1.295	0.148	0.247
GO_LIPID_STORAGE	26	0.408	1.295	0.168	0.247
GO_POSITIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	204	0.266	1.295	0.049	0.247
GO_LYTIC_VACUOLE	496	0.293	1.294	0.135	0.248
GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	15	0.454	1.293	0.158	0.249
GO_RESPONSE_TO_THYROID_HORMONE	21	0.402	1.293	0.152	0.248
GO_SEX_DIFFERENTIATION	253	0.272	1.293	0.061	0.248
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	82	0.326	1.293	0.113	0.248
GO_MYOTUBE_CELL_DEVELOPMENT	24	0.409	1.293	0.133	0.249
GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	25	0.421	1.293	0.178	0.249
GO_CELLULAR_RESPONSE_TO_CAMP	49	0.354	1.292	0.120	0.249
GO_CELL_CELL_JUNCTION_ASSEMBLY	72	0.331	1.291	0.120	0.250
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_6	22	0.417	1.291	0.169	0.250
GO_OSTEOBLAST_DIFFERENTIATION	123	0.309	1.290	0.134	0.250
GO_COMPLEMENT_BINDING	19	0.455	1.289	0.152	0.252
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	51	0.409	1.289	0.206	0.252
GO_RECEPTOR_REGULATOR_ACTIVITY	45	0.343	1.289	0.125	0.252
GO_RESPONSE_TO_IMMOBILIZATION_STRESS	22	0.416	1.288	0.141	0.252
GO_RESPONSE_TO_CAFFEINE	17	0.427	1.288	0.167	0.253
GO_TRANSCRIPTIONAL_REPRESSOR_A	164	0.283	1.287	0.106	0.253

CTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_REGULATORY_REGION_SEQUENCE_SPECIFIC_BINDING					
GO_REGULATION_OF_KERATINOCYTE_PROLIFERATION	26	0.427	1.286	0.150	0.254
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	26	0.395	1.286	0.160	0.254
GO_RESPONSE_TO_CORTICOSTERONE	26	0.402	1.285	0.156	0.254
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	163	0.291	1.285	0.105	0.254
GO_NEUROTRANSMITTER_TRANSPORT	148	0.319	1.285	0.145	0.254
GO_PEPTIDASE_INHIBITOR_ACTIVITY	167	0.330	1.285	0.129	0.255
GO_REGULATION_OF_B_CELL_PROLIFERATION	55	0.392	1.284	0.199	0.255
GO_PHOSPHATIDYLINOSITOL_METABOLIC_PROCESS	189	0.273	1.284	0.082	0.255
GO_REGULATION_OF_MESONEPHROS_DEVELOPMENT	26	0.409	1.284	0.137	0.255
GO_ACROSOME_REACTION	16	0.456	1.284	0.175	0.255
GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	33	0.396	1.284	0.180	0.255
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	46	0.394	1.284	0.219	0.255
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_EPITHELIAL_CELL_APICAL_BASAL_POLARITY	27	0.361	1.284	0.143	0.255
GO_RESPONSE_TO_ELECTRICAL_STIMULUS	42	0.357	1.283	0.147	0.256
GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	33	0.389	1.282	0.168	0.256
GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DIFFERENTIATION	106	0.302	1.282	0.093	0.256
GO_POSITIVE_REGULATION_OF_AUTOPHAGY	74	0.322	1.282	0.132	0.257
GO_AMPA_GLUTAMATE_RECEPTOR_COMPLEX	27	0.422	1.281	0.163	0.257
GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	30	0.379	1.280	0.144	0.258
GO_B_CELL_HOMEOSTASIS	21	0.462	1.279	0.212	0.259
GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	39	0.366	1.278	0.143	0.259
GO_RESPONSE_TO_INTERLEUKIN_1	110	0.326	1.278	0.154	0.259

GO_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	189	0.298	1.278	0.122	0.260
GO_REGULATION_OF_SYNAPTIC_VESICLE_EXOCYTOSIS	19	0.437	1.278	0.194	0.260
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN	142	0.289	1.277	0.125	0.260
GO_STEM_CELL_DIVISION	29	0.397	1.277	0.203	0.261
GO_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	25	0.390	1.276	0.161	0.262
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	17	0.442	1.276	0.174	0.262
GO_AUTOPHAGOSOME_MEMBRANE	27	0.370	1.275	0.179	0.262
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	66	0.356	1.274	0.164	0.263
GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	18	0.443	1.274	0.180	0.263
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE	63	0.352	1.274	0.205	0.263
GO_DETECTION_OF_LIGHT_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	17	0.478	1.274	0.205	0.263
GO_REGULATION_OF_PROTEIN_BINDING	167	0.277	1.273	0.091	0.263
GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	228	0.293	1.273	0.154	0.263
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	130	0.312	1.273	0.138	0.263
GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	42	0.394	1.273	0.169	0.263
GO_T_CELL_PROLIFERATION	34	0.412	1.272	0.210	0.264
GO_RESPONSE_TO_DRUG	426	0.252	1.272	0.067	0.265
GO_PROTEIN_COMPLEX_SCAFFOLD	64	0.309	1.271	0.120	0.265
GO_LYMPHOCYTE_ACTIVATION	322	0.345	1.271	0.213	0.265
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	193	0.282	1.271	0.124	0.265
GO_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	23	0.472	1.271	0.215	0.265
GO_POSITIVE_REGULATION_OF_HEART_GROWTH	26	0.385	1.270	0.162	0.265
GO_HIPPO_SIGNALING	27	0.422	1.270	0.208	0.266

GO_GLUCAN_BIOSYNTHETIC_PROCESS	25	0.406	1.270	0.198	0.266
GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	26	0.393	1.270	0.172	0.266
GO_POSITIVE_REGULATION_OF_STEM_CELL_PROLIFERATION	60	0.337	1.269	0.150	0.266
GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	45	0.342	1.269	0.149	0.266
GO_NOTCH_SIGNALING_PATHWAY	111	0.291	1.268	0.108	0.267
GO_FEMALE_SEX_DIFFERENTIATION	113	0.290	1.268	0.091	0.267
GO_LEUKOCYTE_HOMEOSTASIS	60	0.359	1.267	0.174	0.267
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	358	0.309	1.267	0.204	0.268
GO_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	118	0.292	1.267	0.125	0.268
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	84	0.338	1.266	0.181	0.269
GO_PALLIUM_DEVELOPMENT	150	0.290	1.264	0.132	0.270
GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	65	0.382	1.262	0.223	0.272
GO_CCR_CHEMOKINE_RECEPTOR_BINDING	34	0.448	1.262	0.207	0.273
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	37	0.409	1.261	0.232	0.273
GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	33	0.348	1.261	0.162	0.273
GO_REGULATION_OF_MEMBRANE_LIPID_DISTRIBUTION	37	0.345	1.261	0.162	0.274
GO_PIGMENTATION	80	0.294	1.260	0.125	0.274
GO_ODONTOGENESIS_OF_DENTIN_CONTAINING_TOOTH	74	0.328	1.260	0.145	0.274
GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	30	0.399	1.260	0.185	0.274
GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	428	0.250	1.260	0.057	0.274
GO_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	354	0.247	1.260	0.078	0.274
GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	49	0.353	1.260	0.169	0.274
GO_STEROL_BINDING	42	0.370	1.260	0.166	0.274
GO_LAMELLIPODIUM_ASSEMBLY	28	0.369	1.258	0.150	0.275
GO_AMMONIUM_ION_BINDING	69	0.332	1.258	0.145	0.275
GO_REGULATION_OF_B_CELL_ACTIVATION	100	0.367	1.257	0.234	0.276

GO_NEUROPILIN_BINDING	15	0.449	1.255	0.195	0.278
GO_ACTIVATION_OF_GTPASE_ACTIVITY	73	0.325	1.255	0.184	0.278
GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	35	0.378	1.255	0.152	0.278
GO_MACROPHAGE_DIFFERENTIATION	19	0.414	1.255	0.194	0.278
GO_LOCALIZATION_WITHIN_MEMBRANE	120	0.290	1.255	0.140	0.278
GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS	219	0.297	1.255	0.197	0.278
GO_PRESYNAPTIC_PROCESS_INVOLVED_IN_SYNAPTIC_TRANSMISSION	109	0.321	1.254	0.174	0.278
GO_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	351	0.255	1.254	0.085	0.279
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	31	0.398	1.254	0.214	0.279
GO_POSITIVE_REGULATION_OF_PROTEIN_BINDING	73	0.303	1.253	0.121	0.279
GO_CELLULAR_RESPONSE_TO_ALCOHOL	111	0.291	1.252	0.109	0.280
GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	29	0.355	1.252	0.166	0.280
GO_POSITIVE_REGULATION_OF_DNA_BINDING	41	0.332	1.252	0.163	0.281
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	60	0.349	1.251	0.177	0.281
GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	42	0.315	1.251	0.129	0.282
GO_RESPONSE_TO_INTERLEUKIN_6	26	0.395	1.250	0.176	0.282
GO_MORPHOGENESIS_OF_EMBRYONIC_EPITHELIUM	133	0.290	1.250	0.138	0.282
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	33	0.402	1.250	0.201	0.282
GO_RESPONSE_TO_LIPOPROTEIN_PARTICLE	20	0.413	1.249	0.184	0.282
GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	0.418	1.249	0.190	0.282
GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	414	0.262	1.248	0.116	0.283
GO_EXOCYTIC_VESICLE_MEMBRANE	55	0.377	1.248	0.195	0.284
GO_MAINTENANCE_OF_LOCATION	135	0.285	1.247	0.120	0.284
GO_GLUTATHIONE_PEROXIDASE_ACTI	17	0.462	1.247	0.240	0.284

VITY					
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	23	0.411	1.247	0.220	0.284
GO_RAS_PROTEIN_SIGNAL_TRANSDUCTION	140	0.282	1.246	0.179	0.285
GO_INTERLEUKIN_1_PRODUCTION	15	0.504	1.246	0.245	0.285
GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	16	0.455	1.246	0.207	0.285
GO_REGULATION_OF_STEROID_HORMONE_SECRETION	20	0.444	1.246	0.198	0.285
GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS	104	0.307	1.245	0.151	0.286
GO_MOTOR_NEURON_AXON_GUIDANCE	27	0.414	1.245	0.183	0.286
GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	20	0.443	1.245	0.204	0.286
GO_LIPOPROTEIN_PARTICLE_RECEPTOR_ACTIVITY	16	0.441	1.244	0.221	0.286
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	123	0.354	1.244	0.254	0.286
GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	82	0.318	1.244	0.164	0.286
GO_REGULATION_OF_INTERLEUKIN_13_PRODUCTION	16	0.429	1.243	0.192	0.287
GO_REGULATION_OF_FEEDING_BEHAVIOR	20	0.421	1.242	0.192	0.288
GO_14_3_3_PROTEIN_BINDING	19	0.411	1.242	0.213	0.288
GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	95	0.281	1.242	0.146	0.287
GO_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	18	0.465	1.242	0.258	0.288
GO_PYRIMIDINE_NUCLEOSIDE_CATABOLIC_PROCESS	20	0.432	1.242	0.220	0.288
GO_INACTIVATION_OF_MAPK_ACTIVITY	26	0.370	1.242	0.197	0.288
GO_DEFENSE_RESPONSE_TO_FUNGUS	37	0.433	1.241	0.196	0.288
GO_LYMPHOCYTE_CHEMOTAXIS	37	0.450	1.241	0.229	0.288
GO_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	47	0.397	1.241	0.273	0.288
GO_CHLORIDE_CHANNEL_COMPLEX	49	0.339	1.241	0.168	0.288
GO_REGULATION_OF_ALPHA_BETA_T_	67	0.380	1.240	0.241	0.288

CELL_ACTIVATION					
GO_BONE_RESORPTION	21	0.413	1.240	0.215	0.289
GO_MATING	36	0.352	1.239	0.146	0.290
GO_RUFFLE_ORGANIZATION	20	0.396	1.239	0.198	0.290
GO_ADAPTIVE_IMMUNE_RESPONSE	237	0.372	1.239	0.281	0.290
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_BINDING	111	0.289	1.238	0.134	0.290
GO_NONMOTILE_PRIMARY_CILIUM	127	0.308	1.238	0.189	0.290
GO_MUSCLE_CELL_PROLIFERATION	17	0.443	1.238	0.235	0.290
GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	56	0.327	1.238	0.152	0.290
GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	18	0.443	1.237	0.197	0.290
GO_WATER_HOMEOSTASIS	68	0.355	1.237	0.190	0.291
GO_NEGATIVE_REGULATION_OF_LIPID_TRANSPORT	26	0.437	1.237	0.210	0.291
GO_REGULATION_OF_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	17	0.429	1.236	0.228	0.291
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	43	0.335	1.236	0.175	0.292
GO_BLOOD_MICROPARTICLE	114	0.401	1.235	0.182	0.293
GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	33	0.342	1.235	0.180	0.293
GO_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	93	0.367	1.232	0.250	0.296
GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_BINDING	19	0.411	1.231	0.206	0.297
GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	39	0.314	1.231	0.156	0.297
GO_PROTEIN_SECRETION	110	0.297	1.230	0.166	0.297
GO_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	58	0.358	1.230	0.191	0.297
GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	17	0.412	1.230	0.203	0.297
GO_SOMITOGENESIS	60	0.310	1.230	0.145	0.297
GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	32	0.372	1.230	0.184	0.297
GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	41	0.336	1.229	0.183	0.298
GO_WW_DOMAIN_BINDING	30	0.365	1.228	0.219	0.299
GO_NEGATIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	157	0.291	1.228	0.175	0.299

GO_PSEUDOPODIUM	16	0.442	1.228	0.233	0.299
GO_TRACHEA_DEVELOPMENT	20	0.405	1.228	0.186	0.299
GO_CHLORIDE_TRANSPORT	98	0.297	1.228	0.187	0.299
GO_COATED_PIT	65	0.304	1.227	0.170	0.299
GO_RESPONSE_TO_STARVATION	147	0.278	1.227	0.153	0.299
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	26	0.390	1.227	0.212	0.300
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	345	0.244	1.226	0.096	0.300
GO_NITRIC_OXIDE_SYNTHASE_BINDING	19	0.411	1.226	0.219	0.300
GO_REGULATION_OF_NEURON_DEATH	242	0.258	1.226	0.128	0.300
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	17	0.398	1.226	0.167	0.300
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	40	0.345	1.226	0.204	0.300
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	118	0.349	1.225	0.250	0.301
GO_PROTEIN_KINASE_C_BINDING	47	0.334	1.225	0.192	0.301
GO_DENDRITIC_CELL_MIGRATION	21	0.463	1.225	0.271	0.301
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	24	0.388	1.225	0.203	0.301
GO_REGULATION_OF_INTERLEUKIN_6_BIOSYNTHETIC_PROCESS	16	0.437	1.225	0.208	0.301
GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	17	0.415	1.225	0.221	0.301
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	44	0.368	1.224	0.214	0.301
GO_CELLULAR_RESPONSE_TO_ZINC_ION	16	0.481	1.223	0.261	0.302
GO_REPRODUCTIVE_SYSTEM_DEVELOPMENT	396	0.245	1.223	0.094	0.303
GO_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	16	0.439	1.223	0.243	0.302
GO_PLATELET_MORPHOGENESIS	18	0.411	1.222	0.203	0.303
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	38	0.406	1.221	0.268	0.304
GO_GLAND_DEVELOPMENT	389	0.248	1.220	0.088	0.305
GO_GLUCAN_METABOLIC_PROCESS	57	0.332	1.220	0.220	0.305
GO_FERROUS_IRON_BINDING	22	0.393	1.220	0.227	0.305
GO_PROLINE_RICH_REGION_BINDING	18	0.401	1.220	0.230	0.305
GO_REGULATION_OF_IMMUNE_EFFEC	406	0.284	1.219	0.222	0.306

TOR_PROCESS					
GO_ASTROCYTE_DIFFERENTIATION	38	0.350	1.219	0.185	0.305
GO_B_CELL_ACTIVATION	116	0.348	1.219	0.228	0.306
GO_POSITIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	18	0.431	1.219	0.242	0.306
GO_RESPONSE_TO_HYDROGEN_PEROXIDE	107	0.299	1.219	0.189	0.306
GO_NEUROPEPTIDE_BINDING	21	0.431	1.218	0.210	0.306
GO_REGULATION_OF_DENDRITE_DEVELOPMENT	116	0.288	1.216	0.167	0.308
GO_PIGMENT_GRANULE_ORGANIZATION	20	0.383	1.216	0.202	0.309
GO_POSITIVE_REGULATION_OF_MESONEPHROS_DEVELOPMENT	22	0.410	1.215	0.211	0.309
GO_VESICLE_MEMBRANE	490	0.253	1.214	0.151	0.310
GO_CYTOPLASMIC_SEQUESTERING_OF_PROTEIN	40	0.347	1.213	0.221	0.311
GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	113	0.281	1.213	0.143	0.311
GO_AUTOPHAGOSOME	76	0.309	1.212	0.196	0.313
GO_MALE_GENITALIA_DEVELOPMENT	21	0.392	1.212	0.215	0.312
GO_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	40	0.325	1.212	0.197	0.312
GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	33	0.350	1.211	0.204	0.313
GO_MACROMITOPHAGY	128	0.252	1.211	0.129	0.312
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	27	0.397	1.211	0.226	0.312
GO_MALE_SEX_DIFFERENTIATION	143	0.261	1.211	0.146	0.313
GO_SPINAL_CORD_PATTERNING	24	0.432	1.211	0.230	0.313
GO_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	233	0.284	1.210	0.170	0.314
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	47	0.376	1.210	0.257	0.313
GO_PROSTANOID_BIOSYNTHETIC_PROCESS	18	0.402	1.209	0.218	0.314
GO_NEGATIVE_REGULATION_OF_ANOIKIS	17	0.414	1.208	0.224	0.316
GO_POSITIVE_REGULATION_OF_CELL_GROWTH	141	0.264	1.208	0.162	0.316
GO_CELLULAR_RESPONSE_TO_STARVATION	110	0.282	1.207	0.188	0.316
GO_PROSTATE_GLAND_DEVELOPMEN	41	0.352	1.207	0.218	0.317

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GO_CELL_PROJECTION_ASSEMBLY	241	0.263	1.206	0.195	0.317
GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	79	0.307	1.206	0.201	0.317
GO_LEUKOCYTE_DEGRANULATION	30	0.391	1.206	0.243	0.317
GO_TUBE_FORMATION	129	0.282	1.206	0.184	0.317
GO_INTRINSIC_COMPONENT_OF_THE_CYTOPLASMIC_SIDE_OF_THE_PLASMA_MEMBRANE	15	0.438	1.205	0.245	0.317
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	57	0.393	1.205	0.265	0.317
GO_PHOTORECEPTOR_CELL_DIFFERENTIATION	48	0.333	1.205	0.209	0.318
GO_RHYTHMIC_PROCESS	286	0.249	1.205	0.140	0.318
GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	130	0.281	1.204	0.178	0.318
GO_TONGUE_DEVELOPMENT	19	0.405	1.203	0.223	0.320
GO_RETINOL_DEHYDROGENASE_ACTIVITY	18	0.453	1.203	0.254	0.320
GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	45	0.309	1.202	0.182	0.320
GO_GDP_BINDING	48	0.353	1.201	0.267	0.322
GO_MESODERMAL_CELL_DIFFERENTIATION	26	0.366	1.201	0.226	0.322
GO_REGULATION_OF_BONE_RESORPTION	31	0.354	1.200	0.220	0.322
GO_PROTEIN_AUTOPHOSPHORYLATION	188	0.273	1.200	0.207	0.322
GO_POSITIVE_REGULATION_OF_GLIOGENESIS	45	0.307	1.200	0.187	0.322
GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	42	0.383	1.199	0.266	0.323
GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	39	0.379	1.199	0.264	0.323
GO_LYTIC_VACUOLE_ORGANIZATION	50	0.323	1.198	0.237	0.324
GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	57	0.321	1.198	0.237	0.324
GO_RESPONSE_TO_OXIDATIVE_STRESS	340	0.250	1.198	0.161	0.324
GO_HORMONE_TRANSPORT	75	0.317	1.198	0.180	0.324
GO_LYMPHOCYTE_COSTIMULATION	73	0.386	1.197	0.292	0.324
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	33	0.382	1.197	0.258	0.325
GO_RESPONSE_TO_TEMPERATURE_STI	142	0.264	1.196	0.173	0.325

MULUS					
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	0.423	1.196	0.296	0.325
GO_CALCIUM_ION_REGULATED_EXOCYTOSIS	74	0.312	1.195	0.214	0.326
GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	21	0.431	1.195	0.296	0.326
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	27	0.413	1.195	0.282	0.326
GO_CILIARY_TIP	42	0.352	1.194	0.245	0.327
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	60	0.336	1.194	0.253	0.327
GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	376	0.254	1.194	0.155	0.327
GO_REGULATION_OF_ACTIN_FILAMENT_LENGTH	146	0.274	1.192	0.203	0.329
GO_POSITIVE_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	222	0.263	1.192	0.167	0.329
GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	61	0.297	1.192	0.193	0.329
GO_LYMPHOCYTE_HOMEOSTASIS	50	0.345	1.191	0.246	0.330
GO_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	17	0.422	1.191	0.251	0.330
GO_PHOSPHOLIPASE_ACTIVITY	91	0.279	1.190	0.188	0.331
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	41	0.366	1.190	0.260	0.330
GO_POSITIVE_REGULATION_OF_PROTEIN_ACETYLATION	35	0.330	1.190	0.213	0.330
GO_DORSAL_SPINAL_CORD_DEVELOPMENT	20	0.423	1.190	0.240	0.331
GO_PROSTANOID_METABOLIC_PROCESS	26	0.374	1.189	0.236	0.332
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	15	0.408	1.189	0.251	0.332
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	77	0.287	1.188	0.188	0.332
GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	22	0.378	1.188	0.230	0.333
GO_DENDRITIC_CELL_CHEMOTAXIS	16	0.482	1.188	0.309	0.332
GO_CYTOKINE_PRODUCTION_INVOLV	17	0.421	1.187	0.258	0.333

ED_IN_IMMUNE_RESPONSE					
GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	15	0.412	1.187	0.254	0.333
GO_SCF_UBIQUITIN_LIGASE_COMPLEX	32	0.351	1.187	0.234	0.333
GO_PHAGOCYTIC_VESICLE	84	0.330	1.187	0.265	0.333
GO_DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	206	0.251	1.186	0.142	0.334
GO_THYMUS_DEVELOPMENT	46	0.314	1.186	0.218	0.334
GO_REGULATION_OF_HYDROGEN_PEROXIDE_INDUCED_CELL_DEATH	17	0.406	1.185	0.255	0.334
GO_PROTEIN_KINASE_C_ACTIVITY	16	0.397	1.185	0.276	0.334
GO_FATTY_ACID_BINDING	29	0.383	1.185	0.262	0.334
GO_CEREBRAL_CORTEX_DEVELOPMENT	103	0.283	1.185	0.200	0.334
GO_REGULATION_OF_BINDING	279	0.242	1.185	0.138	0.335
GO_EYE_PHOTORECEPTOR_CELL_DEVELOPMENT	29	0.361	1.184	0.252	0.335
GO_GLUTAMATE_SECRETION	27	0.360	1.184	0.260	0.335
GO_NEGATIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	16	0.395	1.183	0.245	0.336
GO_PROTEIN_SELF_ASSOCIATION	43	0.304	1.183	0.206	0.336
GO_SODIUM_ION_TRANSPORT	135	0.287	1.183	0.208	0.336
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	150	0.280	1.183	0.213	0.336
GO_DETOXIFICATION	71	0.319	1.182	0.227	0.336
GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	16	0.425	1.182	0.267	0.336
GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	16	0.401	1.182	0.246	0.336
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	18	0.422	1.182	0.288	0.336
GO_RESPONSE_TO_ATP	30	0.353	1.181	0.231	0.337
GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	17	0.419	1.181	0.281	0.337
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	33	0.351	1.181	0.254	0.337
GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	56	0.301	1.181	0.200	0.337
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	52	0.306	1.179	0.195	0.339
GO_RAB_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	27	0.369	1.179	0.258	0.339

GO_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	51	0.370	1.177	0.290	0.341
GO_RESPONSE_TO_NITRIC_OXIDE	21	0.382	1.177	0.261	0.341
GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	46	0.339	1.177	0.233	0.342
GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	121	0.278	1.174	0.213	0.345
GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	42	0.366	1.173	0.249	0.345
GO_SUPEROXIDE_METABOLIC_PROCESS	32	0.352	1.172	0.238	0.347
GO_EMBRYONIC_FORELIMB_MORPHOGENESIS	31	0.357	1.172	0.244	0.347
GO_RAC_PROTEIN_SIGNAL_TRANSDUCTION	18	0.392	1.172	0.305	0.347
GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	24	0.409	1.171	0.303	0.348
GO_CEREBELLAR_CORTEX_MORPHOGENESIS	30	0.355	1.170	0.239	0.348
GO_PROTEIN_OLIGOMERIZATION	420	0.226	1.170	0.155	0.348
GO_CYTOSKELETAL_ADAPTOR_ACTIVITY	16	0.393	1.170	0.238	0.348
GO_NEURAL_NUCLEUS_DEVELOPMENT	66	0.303	1.170	0.208	0.348
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	19	0.389	1.170	0.271	0.348
GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	71	0.290	1.169	0.240	0.350
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	55	0.297	1.169	0.223	0.350
GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	176	0.277	1.168	0.258	0.350
GO_WATER_TRANSPORT	19	0.396	1.168	0.252	0.350
GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS	209	0.244	1.168	0.167	0.350
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	47	0.326	1.167	0.250	0.351
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	17	0.399	1.167	0.262	0.351
GO_GTPASE_ACTIVITY	233	0.257	1.167	0.230	0.351
GO_APICAL_PART_OF_CELL	346	0.249	1.167	0.191	0.351
GO_ACID_SECRETION	65	0.303	1.166	0.245	0.352

GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	16	0.431	1.164	0.286	0.354
GO_REGULATION_OF_CELL_MATURATION	18	0.366	1.164	0.259	0.354
GO_MAMMARY_GLAND_DEVELOPMENT	115	0.270	1.164	0.211	0.354
GO_SYNAPTIC_VESICLE_LOCALIZATION	99	0.285	1.163	0.250	0.354
GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.382	1.163	0.307	0.355
GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	150	0.261	1.162	0.218	0.356
GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	88	0.288	1.162	0.232	0.356
GO_ACETYLCHOLINE_RECEPTOR_ACTIVITY	30	0.379	1.161	0.276	0.356
GO_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	35	0.343	1.161	0.259	0.356
GO_EMBRYONIC_DIGIT_MORPHOGENESIS	59	0.316	1.161	0.251	0.357
GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	126	0.321	1.161	0.285	0.357
GO_RESPONSE_TO_AMPHETAMINE	30	0.343	1.161	0.255	0.357
GO_CELLULAR_RESPONSE_TO_ALKALOID	32	0.330	1.159	0.240	0.359
GO_ATPASE_BINDING	73	0.279	1.158	0.244	0.360
GO_PEPTIDASE_ACTIVATOR_ACTIVITY	36	0.317	1.157	0.272	0.361
GO_IRON_ION_BINDING	147	0.264	1.157	0.202	0.361
GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	44	0.312	1.156	0.265	0.361
GO_MIDBRAIN_DEVELOPMENT	88	0.276	1.156	0.239	0.362
GO_XENOPHAGY	101	0.259	1.153	0.234	0.366
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	38	0.325	1.152	0.250	0.367
GO_REGULATION_OF_ACROSOME_REACTION	17	0.416	1.152	0.290	0.367
GO_POSITIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	28	0.355	1.152	0.283	0.367
GO_RESPONSE_TO_NERVE_GROWTH_FACTOR	37	0.348	1.151	0.260	0.367
GO_NEGATIVE_REGULATION_OF_LIPASE_ACTIVITY	15	0.467	1.151	0.289	0.367
GO_DETECTION_OF_LIGHT_STIMULUS	54	0.337	1.150	0.279	0.368

GO_MICROVILLUS_MEMBRANE	19	0.393	1.150	0.284	0.368
GO_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	93	0.326	1.150	0.287	0.368
GO_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	21	0.392	1.148	0.289	0.370
GO_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	16	0.438	1.148	0.310	0.371
GO_REGULATION_OF_CELL_KILLING	62	0.362	1.145	0.320	0.375
GO_CELLULAR_RESPONSE_TO_DRUG	66	0.284	1.145	0.244	0.375
GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	25	0.351	1.144	0.290	0.376
GO_MAINTENANCE_OF_LOCATION_IN_CELL	94	0.273	1.143	0.225	0.376
GO_POSITIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	17	0.415	1.142	0.312	0.377
GO_MYELOID_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	41	0.357	1.142	0.304	0.377
GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM	27	0.368	1.142	0.307	0.377
GO_SEGMENTATION	87	0.272	1.142	0.235	0.377
GO_PEPTIDE_CROSS_LINKING	43	0.489	1.140	0.363	0.379
GO_APICAL_PLASMA_MEMBRANE	281	0.251	1.139	0.229	0.380
GO_REGULATION_OF_VESICLE_FUSION	59	0.311	1.139	0.295	0.380
GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	21	0.362	1.139	0.254	0.380
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	41	0.347	1.139	0.327	0.380
GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	19	0.422	1.139	0.325	0.381
GO_RESPONSE_TO_GROWTH_HORMONE	30	0.357	1.138	0.287	0.381
GO_DETECTION_OF_VISIBLE_LIGHT	40	0.365	1.138	0.314	0.381
GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	34	0.322	1.135	0.290	0.384
GO_MESODERM_DEVELOPMENT	113	0.276	1.135	0.242	0.385
GO_APICOLATERAL_PLASMA_MEMBRANE	15	0.406	1.134	0.260	0.386
GO_JAK_STAT_CASCADE_INVOLVED_IN_GROWTH_HORMONE_SIGNALING_PATHWAY	15	0.452	1.133	0.299	0.386
GO_REGULATION_OF_RUFFLE_ASSEMBLY	20	0.359	1.133	0.311	0.386
GO_PEPTIDE_TRANSPORT	70	0.297	1.133	0.246	0.386

GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	65	0.324	1.132	0.292	0.388
GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	28	0.360	1.131	0.307	0.389
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_VIA_MHC_CLASS_IB	15	0.428	1.131	0.335	0.389
GO_REGULATION_OF_VACUOLE_ORGANIZATION	40	0.313	1.131	0.292	0.389
GO_EATING_BEHAVIOR	30	0.342	1.131	0.269	0.389
GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	29	0.333	1.130	0.279	0.390
GO_RESPONSE_TO_UV_B	16	0.380	1.129	0.325	0.390
GO_NEUROBLAST_PROLIFERATION	29	0.352	1.127	0.293	0.393
GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	102	0.265	1.127	0.265	0.393
GO_WALKING_BEHAVIOR	31	0.344	1.127	0.291	0.394
GO_CHONDROCYTE_DEVELOPMENT	21	0.388	1.126	0.335	0.394
GO_SOMITE_DEVELOPMENT	75	0.281	1.125	0.264	0.395
GO_MONOCYTE_CHEMOTAXIS	40	0.376	1.125	0.342	0.395
GO_PROTEIN_LOCALIZATION_TO_CILIUM	25	0.363	1.125	0.335	0.395
GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DEVELOPMENT	46	0.302	1.125	0.258	0.395
GO_RETINOIC_ACID_BINDING	23	0.378	1.125	0.302	0.395
GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	40	0.310	1.125	0.292	0.395
GO_LIPID_LOCALIZATION	253	0.253	1.124	0.245	0.395
GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	26	0.365	1.124	0.298	0.395
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	94	0.348	1.124	0.359	0.395
GO_PHOSPHATIDYLINOSITOL_BINDING	191	0.248	1.123	0.256	0.396
GO_VIRUS_RECEPTOR_ACTIVITY	65	0.294	1.123	0.290	0.397
GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	54	0.294	1.123	0.275	0.397
GO_NEURAL_PRECURSOR_CELL_PROLIFERATION	70	0.292	1.122	0.278	0.397
GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	86	0.261	1.122	0.245	0.397
GO_DEVELOPMENTAL_INDUCTION	27	0.343	1.122	0.296	0.397
GO_REGULATION_OF_GRANULOCYTE_MACROPHAGE_COLONY_STIMULATING_FACTOR_PRODUCTION	15	0.427	1.122	0.350	0.397

GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	47	0.290	1.121	0.271	0.398
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	63	0.365	1.121	0.363	0.398
GO_RESPONSE_TO_HEAT	86	0.276	1.121	0.271	0.398
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	235	0.225	1.120	0.227	0.398
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	31	0.325	1.120	0.309	0.398
GO_ESTABLISHMENT_OF_EPITHELIAL_CELL_POLARITY	22	0.355	1.120	0.332	0.399
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	33	0.368	1.117	0.351	0.403
GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	30	0.362	1.116	0.341	0.404
GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	23	0.348	1.115	0.306	0.405
GO_PROTEIN_TYROSINE_KINASE_ACTIVATOR_ACTIVITY	15	0.376	1.115	0.303	0.405
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	20	0.374	1.114	0.301	0.406
GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	34	0.322	1.113	0.290	0.407
GO_DEFENSE_RESPONSE_TO_BACTERIUM	183	0.292	1.112	0.285	0.408
GO_SPHINGOLIPID_METABOLIC_PROCESS	130	0.259	1.112	0.282	0.408
GO_CYTOKINE_METABOLIC_PROCESS	17	0.384	1.112	0.314	0.409
GO_RESPONSE_TO_COCAINE	45	0.308	1.111	0.308	0.409
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	85	0.319	1.110	0.329	0.410
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	71	0.335	1.110	0.353	0.410
GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	17	0.377	1.110	0.319	0.410
GO_ERYTHROCYTE_DEVELOPMENT	21	0.328	1.110	0.304	0.410
GO_CLATHRIN_COATED_VESICLE_MEMBRANE	78	0.294	1.110	0.332	0.410
GO_CELLULAR_COMPONENT_MAINTENANCE	18	0.371	1.110	0.317	0.410
GO_CYTOPLASMIC_SEQUESTERING_OF_TRANSCRIPTION_FACTOR	19	0.377	1.110	0.335	0.410

GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	44	0.313	1.109	0.319	0.410
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	25	0.375	1.108	0.323	0.411
GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	46	0.290	1.108	0.301	0.412
GO_PHOSPHATASE_REGULATOR_ACTIVITY	82	0.264	1.108	0.271	0.412
GO_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	31	0.352	1.108	0.314	0.412
GO_REGULATION_OF_LIPID_TRANSPORT	92	0.280	1.106	0.279	0.415
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT1_PROTEIN	16	0.394	1.105	0.313	0.415
GO_BODY_FLUID_SECRETION	68	0.260	1.105	0.253	0.416
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_BINDING	29	0.373	1.104	0.349	0.416
GO_LIPID_TRANSPORTER_ACTIVITY	102	0.266	1.101	0.294	0.420
GO_CALCIUM_DEPENDENT_PHOSPHOLIPID_BINDING	53	0.302	1.101	0.323	0.420
GO_KINASE_REGULATOR_ACTIVITY	180	0.226	1.101	0.274	0.420
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	20	0.393	1.100	0.341	0.421
GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	20	0.367	1.100	0.344	0.421
GO_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	25	0.366	1.099	0.327	0.421
GO_NOSE_DEVELOPMENT	15	0.410	1.099	0.355	0.422
GO_GLYCOPROTEIN_METABOLIC_PROCESS	332	0.240	1.099	0.290	0.421
GO_B_CELL_MEDIATED_IMMUNITY	68	0.322	1.099	0.361	0.421
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	151	0.311	1.099	0.366	0.422
GO_ION_ANTIPORTER_ACTIVITY	46	0.305	1.098	0.321	0.422
GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	24	0.351	1.098	0.345	0.423
GO_DEVELOPMENTAL_PROGRAMMED	26	0.341	1.097	0.305	0.423

_CELL_DEATH					
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	37	0.301	1.097	0.324	0.424
GO_PERICARDIUM_DEVELOPMENT	17	0.362	1.096	0.345	0.424
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	81	0.277	1.096	0.335	0.424
GO_CORE_PROMOTER_PROXIMAL_REGION_DNA_BINDING	357	0.230	1.096	0.279	0.425
GO_REGULATION_OF_COLLATERAL_SPROUTING	18	0.374	1.095	0.337	0.425
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	27	0.316	1.095	0.308	0.425
GO_REGULATION_OF_PROTEIN_POLYMERIZATION	163	0.239	1.095	0.300	0.425
GO_REGULATION_OF_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	15	0.384	1.095	0.326	0.425
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	22	0.397	1.095	0.385	0.425
GO_HORMONE_METABOLIC_PROCESS	158	0.262	1.094	0.300	0.425
GO_MESODERM_MORPHOGENESIS	65	0.291	1.094	0.324	0.426
GO_NEGATIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	26	0.353	1.094	0.353	0.426
GO_REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION	21	0.334	1.094	0.354	0.426
GO_LIPID_MODIFICATION	197	0.238	1.093	0.289	0.426
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	20	0.363	1.093	0.347	0.426
GO_INTRACELLULAR_LIPID_TRANSPORT	20	0.358	1.092	0.340	0.427
GO_MONOAMINE_TRANSPORT	21	0.369	1.092	0.325	0.428
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	18	0.376	1.091	0.351	0.428
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	158	0.285	1.091	0.329	0.428
GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	33	0.304	1.091	0.306	0.429
GO_EXOPEPTIDASE_ACTIVITY	98	0.253	1.091	0.297	0.428
GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	21	0.331	1.090	0.333	0.429
GO_LIMBIC_SYSTEM_DEVELOPMENT	98	0.270	1.090	0.311	0.430
GO_POSITIVE_REGULATION_OF_LYMP	26	0.381	1.090	0.351	0.429

HOCYTE_MIGRATION					
GO_RESPONSE_TO_ACTIVITY	66	0.266	1.090	0.303	0.429
GO_ERYTHROCYTE_HOMEOSTASIS	69	0.257	1.089	0.305	0.430
GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	63	0.285	1.088	0.312	0.431
GO_GTP_DEPENDENT_PROTEIN_BINDING	17	0.363	1.088	0.343	0.431
GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	39	0.332	1.087	0.349	0.432
GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	19	0.362	1.087	0.350	0.432
GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	18	0.377	1.085	0.359	0.434
GO_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	36	0.300	1.085	0.334	0.435
GO_REGULATION_OF_FATTY_ACID_TRANSPORT	26	0.321	1.085	0.345	0.434
GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	482	0.214	1.085	0.265	0.435
GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	60	0.271	1.085	0.323	0.435
GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY	24	0.330	1.084	0.339	0.435
GO_LABYRINTHINE_LAYER_DEVELOPMENT	43	0.304	1.084	0.329	0.435
GO_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	186	0.236	1.084	0.289	0.435
GO_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	15	0.370	1.084	0.346	0.435
GO_RESPONSE_TO_MINERALOCORTICOID	34	0.315	1.083	0.342	0.436
GO_METENCEPHALON_DEVELOPMENT	100	0.281	1.083	0.329	0.436
GO_RESPONSE_TO_FUNGUS	49	0.351	1.082	0.356	0.437
GO_DECIDUALIZATION	20	0.353	1.081	0.358	0.439
GO_AMIDE_BINDING	251	0.220	1.080	0.282	0.439
GO_FATTY_ACID_DERIVATIVE_TRANSPORT	20	0.342	1.079	0.332	0.441
GO_MONOCARBOXYLIC_ACID_BINDING	63	0.306	1.078	0.354	0.441
GO_NEGATIVE_REGULATION_OF_ORG	22	0.311	1.078	0.329	0.441

ANELLE_ASSEMBLY					
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	150	0.293	1.077	0.376	0.444
GO_DENDRITIC_SPINE_ORGANIZATION	17	0.356	1.076	0.362	0.444
GO_TRANSCRIPTION_COREPRESSOR_ACTIVITY	213	0.226	1.076	0.294	0.444
GO_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	18	0.427	1.076	0.404	0.445
GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	15	0.391	1.075	0.388	0.445
GO_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_BINDING	15	0.368	1.075	0.361	0.445
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	18	0.345	1.073	0.347	0.448
GO_R_SMAD_BINDING	21	0.337	1.073	0.344	0.448
GO_MYELOID_CELL_HOMEOSTASIS	84	0.254	1.071	0.342	0.450
GO_REGULATION_OF_SUPEROXIDE_METABOLIC_PROCESS	22	0.347	1.071	0.366	0.450
GO_ENDOSOME_LUMEN	24	0.368	1.071	0.356	0.450
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	15	0.452	1.070	0.416	0.450
GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	24	0.322	1.070	0.366	0.450
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	134	0.246	1.070	0.332	0.451
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	129	0.241	1.069	0.314	0.451
GO_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	47	0.304	1.069	0.375	0.452
GO_MATERNAL_PLACENTA_DEVELOPMENT	30	0.313	1.069	0.366	0.452
GO_MACROLIDE_BINDING	18	0.354	1.068	0.413	0.452
GO_HORMONE_ACTIVITY	102	0.296	1.068	0.341	0.452
GO_REGULATION_OF_ICOSANOID_SECRETION	20	0.339	1.067	0.356	0.453
GO_PEPTIDYL_SERINE_MODIFICATION	146	0.235	1.067	0.317	0.454
GO_PORE_COMPLEX	17	0.392	1.065	0.381	0.456
GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	23	0.338	1.064	0.375	0.458
GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	18	0.357	1.064	0.362	0.457
GO_POSITIVE_REGULATION_OF_EPIDE	19	0.351	1.063	0.354	0.458

RMAL_CELL_DIFFERENTIATION					
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	103	0.245	1.063	0.327	0.459
GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	251	0.215	1.063	0.322	0.459
GO_CELL_CYCLE_ARREST	142	0.236	1.063	0.365	0.459
GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	22	0.322	1.061	0.380	0.460
GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	15	0.474	1.061	0.440	0.461
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	50	0.317	1.060	0.376	0.462
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	24	0.375	1.059	0.370	0.463
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	125	0.260	1.059	0.384	0.463
GO_HIPPOCAMPUS_DEVELOPMENT	72	0.267	1.057	0.360	0.465
GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	31	0.330	1.057	0.358	0.466
GO_REPRODUCTIVE_BEHAVIOR	28	0.305	1.056	0.352	0.466
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	20	0.339	1.056	0.372	0.466
GO_SULFATION	16	0.384	1.055	0.385	0.468
GO_REGULATION_OF_PEPTIDASE_ACTIVITY	376	0.227	1.054	0.316	0.470
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	31	0.309	1.053	0.360	0.470
GO_DOPAMINE_METABOLIC_PROCESS	24	0.323	1.053	0.377	0.471
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	34	0.373	1.053	0.433	0.471
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	425	0.267	1.052	0.369	0.471
GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	303	0.217	1.051	0.367	0.473
GO_EARLY_ENDOSOME	277	0.226	1.050	0.341	0.474
GO_LIPOPOLYSACCHARIDE_BINDING	20	0.367	1.050	0.382	0.474
GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	24	0.305	1.049	0.380	0.475
GO_INTERMEDIATE_FILAMENT_ORGANIZATION	20	0.370	1.049	0.393	0.475

GO_HYPEROSMOTIC_RESPONSE	19	0.340	1.045	0.391	0.480
GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	15	0.378	1.044	0.427	0.482
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	130	0.228	1.044	0.377	0.482
GO_NOTOCHORD_DEVELOPMENT	18	0.360	1.044	0.418	0.482
GO_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	52	0.305	1.043	0.397	0.483
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	29	0.304	1.043	0.400	0.483
GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	371	0.241	1.041	0.379	0.485
GO_RESPONSE_TO_ISCHEMIA	28	0.311	1.041	0.403	0.485
GO_MACROAUTOPHAGY	260	0.210	1.040	0.376	0.487
GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	154	0.227	1.038	0.371	0.489
GO_BASOLATERAL_PLASMA_MEMBRANE	208	0.226	1.038	0.360	0.489
GO_QUINONE_BINDING	15	0.362	1.038	0.415	0.489
GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	97	0.260	1.037	0.391	0.491
GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	328	0.218	1.037	0.374	0.490
GO_RESPONSE_TO_OSMOTIC_STRESS	62	0.259	1.037	0.386	0.490
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	32	0.293	1.036	0.426	0.491
GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	344	0.198	1.036	0.348	0.490
GO_DOPAMINE_RECEPTOR_BINDING	17	0.336	1.036	0.386	0.491
GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	39	0.289	1.034	0.382	0.493
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	25	0.366	1.034	0.404	0.493
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	48	0.279	1.034	0.407	0.494
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	109	0.301	1.032	0.432	0.497
GO_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	97	0.262	1.031	0.421	0.497
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	52	0.273	1.030	0.429	0.498

GO_PHAGOCYTIC_VESICLE_MEMBRANE	56	0.297	1.030	0.432	0.499
GO_NEGATIVE_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	128	0.226	1.030	0.393	0.499
GO_REGULATION_OF_ATPASE_ACTIVITY	61	0.255	1.028	0.401	0.500
GO_HINDLIMB_MORPHOGENESIS	37	0.321	1.028	0.424	0.500
GO_REGULATION_OF_CLATHRIN_MEDIATED_ENDOCYTOSIS	16	0.349	1.027	0.428	0.502
GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	33	0.286	1.027	0.400	0.502
GO_PROTEIN_BINDING_INVOLVED_IN_CELL_ADHESION	17	0.366	1.027	0.424	0.502
GO_BENZENE_CONTAINING_COMPOUND_METABOLIC_PROCESS	22	0.339	1.027	0.397	0.502
GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	32	0.305	1.026	0.390	0.503
GO_TERPENOID_METABOLIC_PROCESS	102	0.269	1.024	0.401	0.505
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	27	0.319	1.023	0.413	0.506
GO_RESPONSE_TO_PROTOZOAN	20	0.372	1.023	0.426	0.507
GO_OSTEOBLAST_DEVELOPMENT	18	0.352	1.023	0.435	0.507
GO_NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	28	0.310	1.023	0.415	0.507
GO_MAMMARY_GLAND_LOBULE_DEVELOPMENT	17	0.333	1.021	0.410	0.509
GO_T_CELL_LINEAGE_COMMITMENT	15	0.394	1.021	0.407	0.509
GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	18	0.338	1.021	0.435	0.509
GO_ADIPOSE_TISSUE_DEVELOPMENT	30	0.308	1.021	0.416	0.509
GO_REGULATION_OF_T_CELL_PROLIFERATION	142	0.286	1.021	0.426	0.509
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	36	0.336	1.020	0.430	0.509
GO_APOPTOTIC_PROCESS_INVOLVED_IN_MORPHOGENESIS	16	0.359	1.020	0.438	0.509
GO_EPITHELIAL_CELL_FATE_COMMITMENT	15	0.396	1.020	0.445	0.509
GO_REGULATION_OF_PROTEIN_ACETYLATION	62	0.252	1.019	0.409	0.511
GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESP	49	0.264	1.018	0.427	0.512

ONSE_TO_GLUCOSE_STIMULUS					
GO_ESTABLISHMENT_OF_CELL_POLARITY	85	0.260	1.017	0.424	0.513
GO_NITRIC_OXIDE_METABOLIC_PROCESS	15	0.349	1.017	0.430	0.514
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	20	0.398	1.017	0.443	0.513
GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	114	0.237	1.017	0.436	0.513
GO_AMIDE_TRANSPORT	93	0.249	1.016	0.432	0.514
GO_REGULATION_OF_AUTOPHAGY	242	0.209	1.015	0.448	0.515
GO_ESTABLISHMENT_OF_TISSUE_POLARITY	17	0.348	1.015	0.427	0.515
GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS	145	0.232	1.015	0.426	0.515
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	29	0.322	1.013	0.416	0.518
GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	16	0.354	1.013	0.443	0.518
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	46	0.278	1.013	0.436	0.518
GO_CHEMOKINE_ACTIVITY	45	0.332	1.012	0.428	0.520
GO_GLANDULAR_EPITHELIAL_CELL_DIFFERENTIATION	38	0.313	1.011	0.451	0.521
GO_ACETYLCHOLINE_BINDING	24	0.350	1.010	0.441	0.522
GO_ANION_CHANNEL_ACTIVITY	90	0.244	1.009	0.398	0.522
GO_EMBRYONIC_PLACENTA_MORPHOGENESIS	22	0.320	1.009	0.424	0.522
GO_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	102	0.238	1.009	0.438	0.522
GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	29	0.325	1.009	0.436	0.523
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	110	0.259	1.008	0.419	0.523
GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	87	0.243	1.008	0.396	0.524
GO_ORGANELLE_MEMBRANE_FUSION	91	0.240	1.007	0.435	0.525
GO_RHO_GTPASE_BINDING	76	0.250	1.007	0.442	0.525
GO_AMINE_METABOLIC_PROCESS	127	0.225	1.005	0.447	0.527
GO_CILIARY_PART	279	0.221	1.003	0.429	0.530
GO_REGULATION_OF_DEPHOSPHORYLATION	145	0.214	1.003	0.436	0.531
GO_SYNTAXIN_1_BINDING	18	0.351	1.001	0.442	0.534

GO_CELLULAR_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	94	0.240	0.999	0.463	0.536
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	15	0.399	0.999	0.453	0.536
GO_PHAGOSOME_MATURATION	37	0.300	0.998	0.455	0.537
GO_EMBRYONIC_HINDLIMB_MORPHOGENESIS	29	0.324	0.998	0.464	0.537
GO_RESPONSE_TO_HYDROPEROXIDE	15	0.363	0.998	0.454	0.537
GO_FEEDING_BEHAVIOR	88	0.262	0.998	0.441	0.536
GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	101	0.224	0.998	0.459	0.537
GO_DENDRITIC_SPINE_DEVELOPMENT	19	0.324	0.996	0.470	0.538
GO_CLATHRIN_COATED_VESICLE	154	0.239	0.996	0.446	0.539
GO_N_GLYCAN_PROCESSING	19	0.336	0.996	0.442	0.539
GO_NEURAL_TUBE_FORMATION	94	0.236	0.996	0.464	0.539
GO_REGULATION_OF_CHROMATIN_BINDING	16	0.334	0.994	0.469	0.541
GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	135	0.236	0.994	0.424	0.541
GO_DRUG_METABOLIC_PROCESS	38	0.320	0.994	0.460	0.542
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	70	0.285	0.993	0.446	0.542
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	52	0.325	0.993	0.492	0.542
GO_CILIUM	422	0.218	0.993	0.463	0.542
GO_NATURAL_KILLER_CELL_ACTIVATION	41	0.326	0.992	0.469	0.543
GO_POSITIVE_REGULATION_OF_ACTIN_NUCLEATION	16	0.346	0.992	0.482	0.544
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	130	0.245	0.991	0.445	0.544
GO_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	22	0.288	0.990	0.488	0.545
GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	61	0.267	0.990	0.476	0.546
GO_RECEPTOR_SIGNALING_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	85	0.241	0.990	0.458	0.546
GO_SKIN_EPIDERMIS_DEVELOPMENT	69	0.260	0.989	0.470	0.546
GO_REGULATION_OF_EXOCYTOSIS	182	0.222	0.989	0.458	0.547
GO_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	17	0.335	0.989	0.468	0.547
GO_MITOGEN_ACTIVATED_PROTEIN_K	18	0.304	0.986	0.483	0.551

INASE_KINASE_KINASE_BINDING					
GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	103	0.225	0.986	0.451	0.551
GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	58	0.251	0.986	0.479	0.551
GO_PROTEIN_HETERODIMERIZATION_ACTIVITY	442	0.201	0.986	0.439	0.551
GO_LEUKOCYTE_MEDIATED_IMMUNITY	157	0.262	0.986	0.442	0.551
GO_CERAMIDE_METABOLIC_PROCESS	72	0.239	0.985	0.480	0.551
GO_FATTY_ACID_METABOLIC_PROCESS	282	0.220	0.984	0.469	0.552
GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	19	0.340	0.984	0.479	0.553
GO_LIPOSACCHARIDE_METABOLIC_PROCESS	109	0.233	0.983	0.449	0.554
GO_MULTIVESICULAR_BODY	38	0.292	0.982	0.473	0.556
GO_ENDOPEPTIDASE_ACTIVITY	399	0.203	0.981	0.497	0.556
GO_CYTOKINE_SECRETION	38	0.313	0.981	0.477	0.556
GO_NEGATIVE_REGULATION_OF_CELL_KILLING	18	0.364	0.981	0.484	0.556
GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	16	0.347	0.978	0.472	0.560
GO_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	58	0.252	0.977	0.493	0.561
GO_REGULATION_OF_ANOIKIS	24	0.296	0.977	0.472	0.562
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	45	0.288	0.977	0.460	0.561
GO_ENTEROENDOCRINE_CELL_DIFFERENTIATION	19	0.368	0.976	0.507	0.562
GO_POSITIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	82	0.235	0.975	0.474	0.564
GO_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	40	0.287	0.975	0.473	0.564
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	26	0.305	0.975	0.503	0.564
GO_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	44	0.308	0.975	0.461	0.564
GO_1_PHOSPHATIDYLINOSITOL_BINDING	19	0.336	0.974	0.495	0.565
GO_CHEMOKINE_RECEPTOR_BINDING	54	0.304	0.974	0.499	0.565
GO_LIPASE_ACTIVITY	113	0.225	0.974	0.510	0.565

GO_AMMONIUM_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	26	0.303	0.974	0.506	0.565
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	27	0.321	0.973	0.454	0.565
GO_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	33	0.274	0.973	0.491	0.565
GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	119	0.219	0.972	0.482	0.566
GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	82	0.224	0.972	0.494	0.567
GO_OMEGA_PEPTIDASE_ACTIVITY	16	0.320	0.972	0.507	0.567
GO_QUATERNARY_AMMONIUM_GROUP_BINDING	49	0.274	0.971	0.489	0.568
GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	23	0.289	0.971	0.488	0.568
GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	49	0.262	0.970	0.486	0.568
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	37	0.262	0.970	0.508	0.569
GO_MATERNAL_PROCESS_INVOLVED_IN_FEMALE_PREGNANCY	58	0.247	0.968	0.506	0.572
GO_REGULATION_OF_NEURON_MIGRATION	26	0.299	0.967	0.492	0.573
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	61	0.241	0.966	0.496	0.574
GO_PHOTORECEPTOR_DISC_MEMBRANE	18	0.361	0.965	0.514	0.575
GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	26	0.286	0.965	0.512	0.576
GO_POSITIVE_REGULATION_OF_CELL_KILLING	38	0.337	0.964	0.498	0.578
GO_IMMUNE_EFFECTOR_PROCESS	432	0.243	0.963	0.481	0.578
GO_SULFUR_COMPOUND_METABOLIC_PROCESS	343	0.204	0.963	0.503	0.579
GO_INTRACELLULAR_CALCIUM_ACTIVATED_CHLORIDE_CHANNEL_ACTIVITY	16	0.343	0.963	0.525	0.579
GO_NEUROPEPTIDE_HORMONE_ACTIVITY	26	0.323	0.962	0.493	0.579
GO_RESPIRATORY_BURST	15	0.397	0.961	0.514	0.580
GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	20	0.301	0.961	0.500	0.580

GO_RETINA_LAYER_FORMATION	22	0.308	0.961	0.506	0.580
GO_WIDE_PORE_CHANNEL_ACTIVITY	23	0.297	0.961	0.484	0.581
GO_LEFT_RIGHT_PATTERN_FORMATION	21	0.304	0.960	0.498	0.582
GO_BITTER_TASTE_RECEPTOR_ACTIVITY	16	0.411	0.960	0.516	0.582
GO_PHOTORECEPTOR_CELL_DEVELOPMENT	37	0.280	0.959	0.495	0.582
GO_THYROID_HORMONE_METABOLIC_PROCESS	15	0.345	0.959	0.491	0.582
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	26	0.296	0.958	0.507	0.583
GO_REGULATION_OF_CIRCADIAN_RHYTHM	97	0.225	0.958	0.509	0.584
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	23	0.309	0.957	0.531	0.586
GO_MULTICELLULAR_ORGANISM_GROWTH	75	0.224	0.957	0.521	0.585
GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	287	0.192	0.956	0.550	0.585
GO_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	18	0.322	0.956	0.495	0.585
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	116	0.263	0.956	0.475	0.585
GO_MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN_INTERACTION_WITH_HOST	16	0.398	0.955	0.551	0.587
GO_GABA_RECEPTOR_ACTIVITY	22	0.327	0.954	0.508	0.588
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	224	0.207	0.954	0.520	0.588
GO_POSITIVE_REGULATION_OF_NEURON_DEATH	66	0.234	0.953	0.527	0.589
GO_POSITIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	49	0.256	0.953	0.511	0.589
GO_PHOSPHOTYROSINE_BINDING	15	0.356	0.953	0.509	0.589
GO_ETHANOLAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	84	0.235	0.953	0.535	0.589
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	35	0.262	0.953	0.532	0.589
GO_SPERM_PRINCIPAL_PIECE	15	0.326	0.952	0.530	0.590
GO_MOLTING_CYCLE	79	0.250	0.952	0.476	0.590
GO_INTERFERON_GAMMA_PRODUCTION	15	0.373	0.951	0.531	0.592

GO_RNA_POLYMERASE_II_TRANSCRIPTION_COFACTOR_ACTIVITY	89	0.220	0.950	0.542	0.593
GO_STEROID_CATABOLIC_PROCESS	24	0.315	0.949	0.507	0.593
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	54	0.262	0.949	0.524	0.593
GO_INORGANIC_ANION_TRANSPORT	127	0.223	0.949	0.481	0.593
GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	128	0.234	0.948	0.482	0.595
GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	15	0.362	0.948	0.514	0.595
GO_REGULATION_OF_MONOOXYGENASE_ACTIVITY	58	0.242	0.947	0.555	0.596
GO_INSULIN_SECRETION	37	0.299	0.947	0.524	0.596
GO_CORTICAL_CYTOSKELETON_ORGANIZATION	34	0.258	0.947	0.526	0.596
GO_UTERUS_DEVELOPMENT	18	0.316	0.946	0.535	0.596
GO_T_CELL_HOMEOSTASIS	34	0.283	0.946	0.503	0.597
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	184	0.205	0.945	0.501	0.598
GO_REGULATION_OF_RESPONSE_TO_FOOD	17	0.325	0.944	0.552	0.600
GO_POLYSACCHARIDE_CATABOLIC_PROCESS	24	0.301	0.942	0.498	0.603
GO_CELLULAR_RESPONSE_TO_OXIDATIVE_STRESS	179	0.203	0.942	0.560	0.602
GO_REGULATION_OF_MEIOTIC_CELL_CYCLE	39	0.253	0.941	0.533	0.604
GO_CLATHRIN_COAT_OF_COATED_PIT	16	0.322	0.940	0.526	0.605
GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	41	0.257	0.939	0.546	0.607
GO_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	39	0.287	0.938	0.541	0.607
GO_PHOTOTRANSDUCTION	38	0.293	0.938	0.500	0.608
GO_FEAR_RESPONSE	29	0.278	0.938	0.522	0.607
GO_RESPONSE_TO_TOXIC_SUBSTANCE	231	0.199	0.938	0.585	0.608
GO_PHOSPHOLIPID_TRANSPORT	54	0.265	0.937	0.527	0.609
GO_SKIN_DEVELOPMENT	195	0.265	0.937	0.498	0.609
GO_REGULATION_OF_CILIUM_ASSEMBLY	47	0.250	0.937	0.540	0.609
GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	68	0.224	0.935	0.582	0.610
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	29	0.311	0.934	0.524	0.612

GO_PLACENTA_DEVELOPMENT	135	0.214	0.934	0.551	0.612
GO_CILIARY_PLASM	72	0.261	0.934	0.502	0.613
GO_PLASMA_MEMBRANE_FUSION	24	0.284	0.933	0.560	0.614
GO_ACIDIC_AMINO_ACID_TRANSPORT	21	0.286	0.933	0.562	0.614
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	19	0.378	0.932	0.553	0.614
GO_EARLY_ENDOSOME_MEMBRANE	101	0.230	0.932	0.539	0.614
GO_RESPONSE_TO_EPIDERMAL_GROWTH_FACTOR	28	0.273	0.931	0.558	0.615
GO_DICARBOXYLIC_ACID_TRANSPORT	70	0.228	0.930	0.569	0.617
GO_ORGANIC_ACID_BINDING	199	0.204	0.930	0.586	0.617
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	30	0.267	0.930	0.541	0.617
GO_PHAGOCYTIC_CUP	17	0.334	0.930	0.513	0.617
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	26	0.310	0.929	0.545	0.617
GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	22	0.300	0.928	0.546	0.619
GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	46	0.287	0.928	0.542	0.619
GO_TRANSLATION_REGULATOR_ACTIVITY	34	0.272	0.928	0.552	0.619
GO_LABYRINTHINE_LAYER_BLOOD_VESSEL_DEVELOPMENT	18	0.310	0.927	0.554	0.620
GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	24	0.289	0.927	0.562	0.620
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	48	0.285	0.927	0.546	0.620
GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	19	0.300	0.927	0.567	0.620
GO_OSTEOCLAST_DIFFERENTIATION	28	0.292	0.927	0.550	0.620
GO_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	43	0.244	0.927	0.580	0.620
GO_RESPONSE_TO_DEXAMETHASONE	32	0.278	0.926	0.566	0.620
GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM	24	0.370	0.926	0.571	0.620
GO_RESPONSE_TO_SALT	15	0.328	0.926	0.549	0.620
GO_IMMUNOLOGICAL_SYNAPSE	31	0.313	0.925	0.533	0.621
GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	17	0.321	0.925	0.565	0.621
GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	107	0.214	0.924	0.604	0.623

GO_MATING_BEHAVIOR	22	0.284	0.921	0.583	0.628
GO_CADHERIN_BINDING	28	0.278	0.920	0.576	0.628
GO_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	18	0.346	0.920	0.581	0.629
GO_INTERACTION_WITH_HOST	127	0.215	0.919	0.551	0.630
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COREPRESSOR_ACTIVITY	25	0.268	0.916	0.574	0.634
GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	313	0.200	0.915	0.618	0.636
GO_EPOXYGENASE_P450_PATHWAY	18	0.332	0.914	0.549	0.638
GO_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	84	0.217	0.914	0.600	0.637
GO_LATE_ENDOSOME	200	0.208	0.913	0.581	0.638
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	47	0.239	0.913	0.585	0.638
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	0.299	0.912	0.581	0.639
GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	149	0.223	0.912	0.621	0.639
GO_CLATHRIN_VESICLE_COAT	23	0.282	0.912	0.584	0.639
GO_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	17	0.321	0.912	0.543	0.640
GO_FEMALE_GENITALIA_DEVELOPMENT	16	0.308	0.911	0.565	0.640
GO_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	15	0.305	0.910	0.601	0.641
GO_ACUTE_INFLAMMATORY_RESPONSE	70	0.262	0.910	0.569	0.642
GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	43	0.251	0.910	0.590	0.642
GO_INTERLEUKIN_1_RECEPTOR_BINDING	16	0.372	0.909	0.575	0.643
GO_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	84	0.265	0.908	0.551	0.644
GO_HORMONE_BIOSYNTHETIC_PROCESS	47	0.249	0.907	0.592	0.645
GO_AUTOPHAGY	366	0.183	0.907	0.608	0.645
GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION	31	0.269	0.906	0.562	0.646
GO_PRESYNAPTIC_ACTIVE_ZONE	28	0.312	0.906	0.561	0.646
GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	56	0.237	0.905	0.580	0.648
GO_HYPOTHALAMUS_DEVELOPMENT	23	0.289	0.905	0.592	0.648
GO_NEGATIVE_REGULATION_OF_LIPID	75	0.227	0.904	0.618	0.648

_METABOLIC_PROCESS					
GO_MEMBRANE_LIPID_METABOLIC_PROCESS	174	0.202	0.902	0.620	0.652
GO_ENDOLYSOSOME	15	0.338	0.902	0.583	0.652
GO_BRAIN_MORPHOGENESIS	34	0.261	0.901	0.611	0.654
GO_PROTEIN_HETEROOLIGOMERIZATION	109	0.215	0.898	0.601	0.657
GO_LENS_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	17	0.309	0.898	0.582	0.658
GO_GLYCEROLIPID_METABOLIC_PROCESS	343	0.181	0.896	0.699	0.661
GO_VESICLE_ORGANIZATION	265	0.195	0.895	0.614	0.662
GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	111	0.201	0.895	0.671	0.662
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	67	0.275	0.895	0.560	0.662
GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	35	0.243	0.894	0.605	0.663
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	31	0.272	0.894	0.596	0.663
GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	23	0.303	0.894	0.568	0.662
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	16	0.318	0.894	0.598	0.662
GO_LRR_DOMAIN_BINDING	17	0.308	0.894	0.590	0.663
GO_TRANSPORT_VESICLE	322	0.199	0.893	0.650	0.664
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	62	0.231	0.893	0.630	0.664
GO_RECYCLING_ENDOSOME_MEMBRANE	38	0.256	0.893	0.613	0.664
GO_AUDITORY_RECEPTOR_CELL_DEVELOPMENT	18	0.283	0.891	0.607	0.667
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	35	0.298	0.890	0.566	0.667
GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	429	0.208	0.889	0.587	0.669
GO_PROTEIN_KINASE_C_SIGNALING	15	0.311	0.889	0.641	0.668
GO_CELLULAR_RESPONSE_TO_VIRUS	21	0.297	0.889	0.566	0.669
GO_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE	144	0.200	0.889	0.691	0.668
GO_RESPONSE_TO_DIETARY_EXCESS	21	0.272	0.888	0.657	0.670
GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	141	0.193	0.888	0.689	0.670

GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	442	0.186	0.887	0.666	0.671
GO_SPECTRIN_BINDING	25	0.273	0.887	0.618	0.671
GO_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS	63	0.227	0.887	0.650	0.671
GO_REGULATION_OF_APPETITE	21	0.302	0.886	0.606	0.672
GO_ACTIVATION_OF_IMMUNE_RESPONSE	387	0.228	0.885	0.554	0.674
GO_PEPTIDYL_ASPARAGINE_MODIFICATION	39	0.252	0.885	0.597	0.673
GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	47	0.231	0.883	0.659	0.676
GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	18	0.301	0.882	0.612	0.677
GO_PHOSPHOLIPASE_A2_ACTIVITY	30	0.251	0.882	0.645	0.677
GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	23	0.307	0.882	0.601	0.678
GO_IRON_ION_HOMEOSTASIS	64	0.222	0.881	0.646	0.678
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	15	0.345	0.878	0.594	0.684
GO_NEUROTRANSMITTER_METABOLIC_PROCESS	25	0.271	0.875	0.647	0.688
GO_ANTIGEN_BINDING	76	0.274	0.875	0.553	0.688
GO_DETECTION_OF_STIMULUS	331	0.239	0.875	0.579	0.688
GO_INORGANIC_ION_IMPORT_INTO_CELL	15	0.303	0.874	0.642	0.688
GO_2_OXOGLUTARATE_METABOLIC_PROCESS	19	0.299	0.874	0.628	0.688
GO_EMBRYONIC_PLACENTA_DEVELOPMENT	82	0.216	0.874	0.641	0.688
GO_LYSOSOMAL_TRANSPORT	65	0.228	0.872	0.632	0.691
GO_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	107	0.245	0.871	0.609	0.693
GO_ENDOCRINE_PANCREAS_DEVELOPMENT	40	0.267	0.871	0.648	0.693
GO_RESPONSE_TO_AMMONIUM_ION	48	0.228	0.870	0.706	0.693
GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	84	0.222	0.869	0.661	0.695
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	357	0.211	0.869	0.589	0.695
GO_POLYPEPTIDE_N_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	16	0.326	0.868	0.589	0.697
GO_CELLULAR_IRON_ION_HOMEOSTASIS	42	0.242	0.867	0.644	0.698

GO_REGULATION_OF_HORMONE_METABOLIC_PROCESS	26	0.264	0.866	0.663	0.699
GO_THYROID_GLAND_DEVELOPMENT	25	0.270	0.865	0.652	0.701
GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	23	0.283	0.864	0.663	0.702
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	44	0.251	0.863	0.636	0.703
GO_APOLIPOPROTEIN_BINDING	15	0.307	0.863	0.648	0.704
GO_CELLULAR_HORMONE_METABOLIC_PROCESS	101	0.222	0.861	0.653	0.706
GO_PHOSPHATIDYLINOSITOL_ACYL_CHAIN_REMODELING	16	0.304	0.861	0.645	0.706
GO_FILOPODIUM_ASSEMBLY	17	0.292	0.861	0.670	0.706
GO_AMMONIUM_ION_METABOLIC_PROCESS	166	0.191	0.860	0.731	0.708
GO_BRUSH_BORDER_MEMBRANE	55	0.238	0.859	0.651	0.708
GO_FOREBRAIN_REGIONALIZATION	24	0.266	0.859	0.657	0.708
GO_LIPID_PARTICLE	60	0.230	0.858	0.673	0.709
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	26	0.285	0.857	0.655	0.711
GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	20	0.316	0.857	0.604	0.711
GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	472	0.179	0.855	0.735	0.714
GO_MONOCARBOXYLIC_ACID_TRANSPORT	118	0.202	0.853	0.721	0.718
GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	46	0.255	0.850	0.649	0.723
GO_PROTEIN_KINASE_A_CATALYTIC_SUBUNIT_BINDING	15	0.287	0.849	0.653	0.723
GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_BINDING	30	0.252	0.848	0.699	0.725
GO_POSITIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT	31	0.257	0.846	0.658	0.728
GO_CEREBELLAR_CORTEX_FORMATION	22	0.277	0.846	0.669	0.728
GO_FIBROBLAST_GROWTH_FACTOR_BINDING	23	0.260	0.845	0.676	0.729
GO_ANATOMICAL_STRUCTURE_ARRANGEMENT	17	0.277	0.844	0.653	0.730
GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	24	0.254	0.843	0.671	0.731
GO_INNER_EAR_RECEPTOR_STEREOCI	19	0.275	0.840	0.682	0.736

LIUM_ORGANIZATION					
GO_REGULATION_OF_PH	87	0.203	0.839	0.737	0.738
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	31	0.286	0.839	0.644	0.738
GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_PHOSPHORYLATIVE_MECHANISM	33	0.248	0.839	0.719	0.738
GO_ANTIPORTER_ACTIVITY	70	0.215	0.838	0.732	0.738
GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_BINDING	24	0.269	0.837	0.670	0.740
GO_PROTEIN_SERINE_THREONINE_KINASE_INHIBITOR_ACTIVITY	30	0.250	0.837	0.696	0.740
GO_CHOLESTEROL_EFFLUX	26	0.328	0.832	0.678	0.748
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.316	0.832	0.630	0.748
GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	23	0.260	0.832	0.706	0.748
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE	25	0.250	0.830	0.699	0.750
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.304	0.830	0.625	0.750
GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	36	0.236	0.830	0.683	0.750
GO_GOLGI_TO_PLASMA_MEMBRANE_TRANSPORT	41	0.220	0.827	0.730	0.754
GO_FIBRINOLYSIS	21	0.337	0.827	0.724	0.754
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	16	0.319	0.826	0.636	0.755
GO_MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	20	0.277	0.826	0.659	0.755
GO_RESPONSE_TO_COPPER_ION	27	0.245	0.826	0.717	0.755
GO_T_CELL_MEDIATED_IMMUNITY	28	0.270	0.826	0.668	0.755
GO_PHOSPHOLIPID_DEPHOSPHORYLATION	24	0.274	0.825	0.669	0.755
GO_PROTEIN_O_LINKED_GLYCOSYLATION	90	0.207	0.825	0.718	0.756
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY	15	0.298	0.824	0.685	0.757
GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	120	0.192	0.824	0.800	0.757
GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	23	0.278	0.824	0.667	0.757
GO_NEGATIVE_REGULATION_OF_PROT	19	0.259	0.823	0.713	0.758

EIN_TYROSINE_KINASE_ACTIVITY					
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	118	0.205	0.823	0.701	0.758
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	17	0.289	0.823	0.703	0.758
GO_POST_ANAL_TAIL_MORPHOGENESIS	18	0.269	0.822	0.711	0.759
GO_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	44	0.222	0.820	0.773	0.761
GO_FATTY_ACID_TRANSPORT	55	0.212	0.820	0.762	0.761
GO_RESPONSE_TO_ANGIOTENSIN	17	0.273	0.819	0.753	0.762
GO_ACTIN_FILAMENT_POLYMERIZATION	21	0.260	0.818	0.728	0.763
GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	20	0.307	0.818	0.650	0.763
GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	121	0.191	0.818	0.773	0.763
GO_STEROL_TRANSPORT	49	0.256	0.818	0.725	0.763
GO_SERTOLI_CELL_DEVELOPMENT	15	0.295	0.816	0.717	0.766
GO_CEREBELLAR_CORTEX_DEVELOPMENT	46	0.229	0.815	0.778	0.766
GO_REGULATION_OF_DENDRITE_EXTENSION	17	0.277	0.814	0.737	0.768
GO_PROTEIN_HYDROXYLATION	15	0.300	0.814	0.677	0.768
GO_PROTEIN_MATURATION	252	0.175	0.812	0.835	0.770
GO_MEMBRANE_PROTEIN_PROTEOLYSIS	34	0.238	0.809	0.721	0.775
GO_SENSORY_PERCEPTION_OF_TASTE	51	0.258	0.809	0.708	0.775
GO_BRANCHING_INVOLVED_IN_MAMMARY_GLAND_DUCT_MORPHOGENESIS	20	0.267	0.809	0.726	0.775
GO_BILE_ACID_METABOLIC_PROCESS	35	0.242	0.808	0.735	0.777
GO_RESPONSE_TO_LEPTIN	20	0.259	0.807	0.749	0.778
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	83	0.241	0.807	0.657	0.778
GO_TASTE_RECEPTOR_ACTIVITY	20	0.323	0.807	0.634	0.778
GO_ANION_TRANSPORT	487	0.169	0.806	0.870	0.778
GO_REGULATION_OF_STEROL_TRANSPORT	38	0.261	0.806	0.729	0.778
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	480	0.172	0.806	0.834	0.778
GO_EPHRIN_RECEPTOR_BINDING	24	0.252	0.804	0.740	0.781
GO_POSITIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	31	0.226	0.803	0.807	0.782

GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA	30	0.227	0.803	0.719	0.783
GO_INDOLALKYLAMINE_METABOLIC_PROCESS	16	0.278	0.798	0.742	0.790
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	20	0.270	0.796	0.756	0.792
GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	17	0.276	0.796	0.764	0.792
GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	39	0.212	0.795	0.802	0.793
GO_IMPORT_INTO_CELL	36	0.226	0.795	0.781	0.793
GO_AMELOGENESIS	19	0.263	0.793	0.744	0.797
GO_EMBRYONIC_PATTERN_SPECIFICATION	57	0.212	0.792	0.788	0.796
GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	16	0.279	0.792	0.764	0.796
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	45	0.229	0.792	0.720	0.796
GO_DETECTION_OF_CHEMICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION_OF_TASTE	33	0.276	0.792	0.725	0.797
GO_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	69	0.216	0.792	0.734	0.797
GO_STEROL_HOMEOSTASIS	56	0.243	0.792	0.715	0.796
GO_PHOSPHATIDYLETHANOLAMINE_ACYL_CHAIN_REMODELING	23	0.250	0.791	0.775	0.797
GO_RETINOL_METABOLIC_PROCESS	28	0.256	0.789	0.747	0.800
GO_ENDOSOMAL_PART	402	0.174	0.786	0.794	0.804
GO_REGULATION_OF_MYELINATION	29	0.241	0.784	0.766	0.807
GO_ALCOHOL_METABOLIC_PROCESS	341	0.168	0.783	0.880	0.808
GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANSPORT	16	0.273	0.782	0.752	0.809
GO_STEROL_METABOLIC_PROCESS	120	0.194	0.781	0.786	0.810
GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	27	0.223	0.781	0.809	0.811
GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	24	0.257	0.780	0.780	0.812
GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSPORT	22	0.280	0.780	0.715	0.812
GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	40	0.208	0.780	0.805	0.812
GO_MEMBRANE_FUSION	143	0.167	0.779	0.890	0.812

GO_T_CELL_RECEPTOR_COMPLEX	19	0.325	0.779	0.667	0.812
GO_RECEPTOR_CATABOLIC_PROCESS	16	0.264	0.779	0.756	0.812
GO_SYNAPTIC_VESICLE_RECYCLING	23	0.243	0.778	0.769	0.814
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION	18	0.262	0.777	0.753	0.814
GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	30	0.220	0.777	0.784	0.814
GO_ORGANIC_ANION_TRANSPORT	368	0.166	0.776	0.908	0.815
GO_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	33	0.210	0.775	0.821	0.816
GO_TOR_SIGNALING	16	0.256	0.775	0.761	0.816
GO_OTIC_VESICLE_DEVELOPMENT	15	0.279	0.775	0.742	0.816
GO_ORGANIC_ACID_TRANSPORT	251	0.171	0.772	0.894	0.820
GO_AMINO_ACID_TRANSPORT	120	0.181	0.771	0.858	0.821
GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	101	0.210	0.770	0.775	0.823
GO_NOTCH_BINDING	18	0.259	0.767	0.773	0.826
GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	23	0.243	0.766	0.784	0.828
GO_SH2_DOMAIN_BINDING	28	0.239	0.765	0.753	0.829
GO_ORGANELLE_FUSION	121	0.169	0.762	0.920	0.833
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	18	0.253	0.760	0.788	0.835
GO_CELLULAR_PIGMENTATION	43	0.202	0.760	0.827	0.835
GO_MONOSACCHARIDE_BINDING	65	0.198	0.760	0.826	0.835
GO_RESPONSE_TO_INSULIN	199	0.157	0.759	0.943	0.837
GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	61	0.188	0.758	0.855	0.837
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	25	0.231	0.758	0.838	0.837
GO_REGULATION_OF_TOR_SIGNALING	64	0.185	0.757	0.828	0.838
GO_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	35	0.218	0.757	0.847	0.839
GO_TRIGLYCERIDE_CATABOLIC_PROCESS	20	0.296	0.754	0.763	0.841
GO_VACUOLAR_ACIDIFICATION	15	0.275	0.754	0.773	0.841
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	19	0.268	0.754	0.749	0.841
GO_TRANSPORT_VESICLE_MEMBRANE	145	0.189	0.752	0.864	0.844
GO_ANION_TRANSMEMBRANE_TRANS	286	0.165	0.752	0.908	0.844

PORTER_ACTIVITY					
GO_T_CELL_APOPTOTIC_PROCESS	15	0.278	0.750	0.773	0.846
GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	73	0.194	0.749	0.856	0.847
GO_RAB_GTPASE_BINDING	113	0.191	0.748	0.840	0.849
GO_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	22	0.290	0.748	0.716	0.849
GO_ORGANIC_CATION_TRANSPORT	19	0.259	0.747	0.810	0.849
GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	53	0.208	0.747	0.818	0.849
GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	17	0.248	0.744	0.814	0.852
GO_CILIUM_MORPHOGENESIS	183	0.181	0.744	0.794	0.853
GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX	19	0.270	0.743	0.765	0.854
GO_AXONEME_ASSEMBLY	34	0.241	0.741	0.721	0.856
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	286	0.195	0.739	0.757	0.858
GO_PLASMA_LIPOPROTEIN_PARTICLE_CLEARANCE	21	0.322	0.736	0.807	0.862
GO_PHOSPHATIDYLCHOLINE_ACYL_CHAIN_REMODELING	26	0.220	0.735	0.865	0.863
GO_NEUROTRANSMITTER_BINDING	30	0.237	0.735	0.816	0.863
GO_SINGLE_ORGANISM_MEMBRANE_FUSION	118	0.163	0.734	0.927	0.863
GO_BILE_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	0.257	0.734	0.826	0.864
GO_SYNTAXIN_BINDING	88	0.180	0.732	0.914	0.867
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	37	0.221	0.729	0.844	0.869
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	18	0.246	0.728	0.830	0.871
GO_SNARE_BINDING	121	0.168	0.726	0.906	0.873
GO_CELL_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	18	0.244	0.721	0.839	0.880
GO_LUNG_EPITHELIUM_DEVELOPMENT	34	0.205	0.721	0.890	0.879
GO_ERBB_SIGNALING_PATHWAY	77	0.180	0.717	0.891	0.883
GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	41	0.199	0.716	0.910	0.884
GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY	15	0.278	0.715	0.800	0.886
GO_STEROID_METABOLIC_PROCESS	231	0.169	0.714	0.902	0.887

GO_CYTOLYSIS	23	0.258	0.712	0.818	0.889
GO_SOLUTE_PROTON_ANTIPORTER_ACTIVITY	17	0.247	0.710	0.807	0.890
GO_POSITIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	25	0.243	0.708	0.822	0.892
GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	181	0.235	0.707	0.740	0.894
GO_UDP_GLYCOSYLTRANSFERASE_ACTIVITY	127	0.171	0.706	0.922	0.895
GO_RESPONSE_TO_VITAMIN_E	15	0.241	0.705	0.882	0.896
GO_MONOSACCHARIDE_TRANSPORT	53	0.184	0.703	0.920	0.897
GO_VACUOLE_FUSION	22	0.227	0.702	0.858	0.898
GO_PHOTORECEPTOR_CELL_MAINTENANCE	33	0.216	0.702	0.866	0.898
GO_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	59	0.179	0.700	0.927	0.900
GO_REGULATION_OF_PLASMA_LIPOPROTEIN_PARTICLE_LEVELS	45	0.245	0.699	0.816	0.900
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	25	0.304	0.698	0.809	0.902
GO_EPIDERMIS_DEVELOPMENT	236	0.194	0.697	0.779	0.902
GO_PHOTOPERIODISM	23	0.215	0.696	0.904	0.904
GO_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA	117	0.220	0.695	0.711	0.904
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORATION_OF_MOLECULAR_OXYGEN	26	0.210	0.694	0.906	0.905
GO_LYSOPHOSPHOLIPASE_ACTIVITY	19	0.227	0.694	0.895	0.904
GO_AMINO_ACID_IMPORT	15	0.252	0.692	0.861	0.906
GO_DRUG_TRANSPORTER_ACTIVITY	21	0.222	0.690	0.898	0.909
GO_ODORANT_BINDING	18	0.290	0.689	0.829	0.909
GO_GTP_RHO_BINDING	16	0.233	0.688	0.849	0.910
GO_PHOTORECEPTOR_INNER_SEGMENT	35	0.206	0.687	0.857	0.911
GO_LIPID_DIGESTION	21	0.231	0.687	0.897	0.911
GO_REGULATION_OF_CELLULAR_PH	73	0.169	0.686	0.945	0.911
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	29	0.215	0.686	0.831	0.911
GO_ANKYRIN_BINDING	20	0.227	0.683	0.884	0.913
GO_COFACTOR_CATABOLIC_PROCESS	20	0.234	0.681	0.885	0.916
GO_PHOSPHOLIPID_CATABOLIC_PROCESS	29	0.200	0.679	0.928	0.917
GO_PROTEIN_LIPID_COMPLEX	38	0.249	0.678	0.848	0.918

GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	48	0.197	0.678	0.859	0.918
GO_AXIS_SPECIFICATION	89	0.169	0.675	0.947	0.921
GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	59	0.179	0.674	0.943	0.921
GO_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	36	0.191	0.674	0.940	0.921
GO_GLYCEROLIPID_CATABOLIC_PROCESS	36	0.219	0.674	0.882	0.921
GO_LYMPHOCYTE_APOPTOTIC_PROCESS	18	0.238	0.674	0.853	0.920
GO_INTERMEDIATE_FILAMENT_CYTOSKELETON	174	0.190	0.674	0.904	0.920
GO_PROTEIN_DEGLYCOSYLATION	21	0.238	0.673	0.839	0.920
GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	20	0.217	0.673	0.901	0.920
GO_DIGESTION	126	0.186	0.673	0.942	0.920
GO_OLFACTORY_RECEPTOR_ACTIVITY	102	0.274	0.672	0.739	0.921
GO_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	28	0.195	0.670	0.909	0.922
GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	170	0.155	0.670	0.976	0.922
GO_ISOPRENOID_METABOLIC_PROCESS	122	0.171	0.668	0.949	0.923
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	0.244	0.668	0.871	0.923
GO_CALCIUM_INDEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	20	0.224	0.668	0.909	0.923
GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	77	0.162	0.667	0.952	0.924
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_CELLULAR_RESPONSE_TO_CHEMICAL_STIMULUS	25	0.214	0.666	0.869	0.924
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	25	0.201	0.664	0.897	0.926
GO_MODIFIED_AMINO_ACID_TRANSPORT	26	0.197	0.660	0.902	0.929
GO_MONOVALENT_INORGANIC_ANIO	19	0.219	0.660	0.916	0.929

N_HOMEOSTASIS					
GO_CILIARY_TRANSITION_ZONE	23	0.221	0.658	0.854	0.931
GO_RESPONSE_TO_ZINC_ION	55	0.180	0.657	0.942	0.931
GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	16	0.218	0.656	0.909	0.931
GO_ACROSOMAL_VESICLE	82	0.157	0.650	0.968	0.936
GO_ESTROGEN_METABOLIC_PROCESS	23	0.212	0.647	0.942	0.939
GO_NEGATIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	27	0.199	0.646	0.925	0.939
GO_NONMOTILE_PRIMARY_CILIUM_ASSEMBLY	22	0.213	0.642	0.881	0.942
GO_INTERMEDIATE_FILAMENT	134	0.202	0.642	0.911	0.942
GO_GRANULOCYTE_ACTIVATION	19	0.229	0.640	0.882	0.944
GO_ANION_TRANSMEMBRANE_TRANSPORT	245	0.143	0.633	0.994	0.949
GO_REGULATION_OF_HAIR_CYCLE	22	0.196	0.629	0.941	0.951
GO_REGULATION_OF_PROTEIN_SUMOYLATION	21	0.203	0.628	0.930	0.952
GO_REGULATION_OF_WATER_LOSS_VIA_SKIN	18	0.281	0.628	0.838	0.952
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE	28	0.199	0.625	0.913	0.954
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	226	0.143	0.624	0.992	0.954
GO_SYMPORTER_ACTIVITY	141	0.151	0.624	0.983	0.954
GO_LIPID_HOMEOSTASIS	104	0.167	0.623	0.954	0.954
GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	0.211	0.622	0.931	0.954
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	137	0.148	0.619	0.983	0.956
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	15	0.230	0.618	0.931	0.956
GO_POSITIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	34	0.175	0.616	0.973	0.958
GO_ALDEHYDE_DEHYDROGENASE_NAD_ACTIVITY	19	0.211	0.615	0.912	0.958
GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	71	0.159	0.615	0.984	0.958
GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	24	0.210	0.614	0.967	0.958
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	31	0.198	0.614	0.932	0.958
GO_REVERSE_CHOLESTEROL_TRANSPORT	17	0.286	0.612	0.888	0.958

GO_RESPONSE_TO_LITHIUM_ION	27	0.190	0.610	0.960	0.959
GO_NOTCH_RECEPTOR_PROCESSING	16	0.219	0.608	0.924	0.961
GO_PHOSPHATIDIC_ACID_METABOLIC_PROCESS	31	0.174	0.607	0.980	0.961
GO_SKELETAL_MUSCLE_CONTRACTION	31	0.179	0.607	0.966	0.961
GO_LEUKOCYTE_APOPTOTIC_PROCESS	22	0.205	0.605	0.937	0.962
GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	26	0.192	0.602	0.975	0.963
GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	20	0.223	0.601	0.892	0.963
GO_ANTIMICROBIAL_HUMORAL_RESPONSE	45	0.189	0.597	0.986	0.965
GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	27	0.189	0.596	0.971	0.966
GO_ANDROGEN_METABOLIC_PROCESS	30	0.178	0.594	0.974	0.966
GO_ACYLGLYCEROL_HOMEOSTASIS	27	0.213	0.593	0.927	0.967
GO_ASYMMETRIC_PROTEIN_LOCALIZATION	18	0.209	0.592	0.926	0.967
GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	17	0.197	0.591	0.956	0.967
GO_GLUCURONOSYLTRANSFERASE_ACTIVITY	31	0.190	0.588	0.956	0.968
GO_NECROPTOTIC_PROCESS	21	0.209	0.588	0.926	0.968
GO_BICARBONATE_TRANSPORT	44	0.168	0.588	0.980	0.968
GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	19	0.196	0.572	0.957	0.976
GO_RESPONSE_TO_INTERFERON_GAMMA	139	0.173	0.562	0.891	0.980
GO_TRIGLYCERIDE_LIPASE_ACTIVITY	19	0.190	0.561	0.966	0.980
GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	31	0.168	0.556	0.988	0.982
GO_RETINA_HOMEOSTASIS	62	0.149	0.556	0.992	0.981
GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	17	0.191	0.554	0.981	0.982
GO_CORNIFIED_ENVELOPE	32	0.285	0.553	0.879	0.982
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	18	0.202	0.550	0.965	0.983
GO_STEROL_TRANSPORTER_ACTIVITY	17	0.216	0.544	0.954	0.984
GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	26	0.179	0.544	0.955	0.984
GO_CATION_AMINO_ACID_SYMPORTE	16	0.193	0.536	0.971	0.987

R_ACTIVITY					
GO_REGULATION_OF_MICROTUBULE_BASED_MOVEMENT	17	0.184	0.533	0.981	0.987
GO_ANION_CATION_SYMPORTER_ACTIVITY	53	0.148	0.533	0.992	0.987
GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	17	0.186	0.531	0.990	0.987
GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	30	0.159	0.528	0.985	0.988
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	67	0.189	0.526	0.872	0.988
GO_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTIVATED_RECEPTOR_ACTIVITY	22	0.168	0.524	0.986	0.988
GO_MHC_PROTEIN_COMPLEX	24	0.233	0.516	0.834	0.990
GO_EPIDERMAL_CELL_DIFFERENTIATION	126	0.160	0.515	0.957	0.990
GO_GABA_RECEPTOR_COMPLEX	18	0.187	0.511	0.960	0.991
GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	36	0.189	0.509	0.965	0.991
GO_SULFUR_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	27	0.155	0.503	0.986	0.992
GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	172	0.117	0.503	0.998	0.991
GO_K63_LINKED_POLYUBIQUITIN_BINDING	17	0.175	0.498	0.981	0.992
GO_CILIUM_MOVEMENT	30	0.175	0.495	0.952	0.992
GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	51	0.134	0.491	0.998	0.993
GO_NEUTROPHIL_MEDIATED_IMMUNITY	21	0.177	0.485	0.996	0.994
GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	24	0.152	0.478	0.992	0.995
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	55	0.133	0.471	1.000	0.995
GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	33	0.143	0.450	0.998	0.998
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	17	0.178	0.444	0.985	0.998
GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	25	0.157	0.439	0.990	0.998
GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	25	0.164	0.431	0.994	0.998

GO_BICARBONATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	19	0.147	0.429	0.998	0.998
GO_MACROMOLECULAR_COMPLEX_REMODELING	24	0.182	0.415	0.990	0.999
GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	21	0.171	0.407	0.990	0.999
GO_LAMELLAR_BODY	20	0.137	0.378	1.000	1.000
GO_KERATINOCYTE_DIFFERENTIATION	86	0.131	0.358	0.998	1.000
GO_TRIGLYCERIDE_RICH_LIPOPROTEIN_PARTICLE	18	0.143	0.294	1.000	1.000

ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SIII. The co-expressed genes of GSTM5 in gastric cancer tumor tissue in The Cancer Genome Atlas cohort. GSTM5, glutathione S-transferase Mu 5.

Gene1	Gene2	Cor	P-value
GSTM5	CYP1B1	0.600	0.006
GSTM5	SELP	0.600	0.006
GSTM5	TLN1	0.600	0.006
GSTM5	DOK6	0.600	0.006
GSTM5	DCLK2	0.600	0.006
GSTM5	ERG	0.600	0.006
GSTM5	SPEG	0.601	0.006
GSTM5	KLF9	0.601	0.006
GSTM5	FOXN3	0.601	0.006
GSTM5	AC092042.3	0.601	0.006
GSTM5	HTR2A	0.601	0.006
GSTM5	CLEC14A	0.601	0.006
GSTM5	TRPC1	0.602	0.006
GSTM5	ABCA8	0.602	0.006
GSTM5	PLN	0.603	0.006
GSTM5	FRRS1L	0.604	0.006
GSTM5	AR	0.604	0.006
GSTM5	PRIMA1	0.604	0.006
GSTM5	METTL24	0.604	0.006
GSTM5	ARMCX1	0.604	0.006
GSTM5	CPED1	0.605	0.005
GSTM5	PDE5A	0.605	0.005
GSTM5	CXorf36	0.605	0.005
GSTM5	JAZF1	0.605	0.005
GSTM5	CYYR1	0.606	0.005
GSTM5	LURAP1	0.607	0.005
GSTM5	ELN	0.607	0.005
GSTM5	ILK	0.607	0.005
GSTM5	OLFML1	0.607	0.005
GSTM5	PPP1R12C	0.607	0.005
GSTM5	CBX6	0.607	0.005
GSTM5	FEZ1	0.608	0.005
GSTM5	HSPB6	0.608	0.005
GSTM5	FERMT2	0.608	0.005
GSTM5	NFIC	0.608	0.005
GSTM5	COL19A1	0.609	0.005
GSTM5	NFIA	0.609	0.005
GSTM5	IFFO1	0.609	0.005
GSTM5	MAGI2	0.609	0.005
GSTM5	MEOX2	0.610	0.005

GSTM5	MSRB3	0.610	0.005
GSTM5	WWTR1	0.610	0.005
GSTM5	EHD2	0.610	0.005
GSTM5	MOB2	0.611	0.005
GSTM5	SLC2A4	0.611	0.005
GSTM5	PBX3	0.611	0.005
GSTM5	FAM13C	0.611	0.005
GSTM5	PLIN4	0.611	0.005
GSTM5	PTGDS	0.612	0.005
GSTM5	SVEP1	0.612	0.005
GSTM5	LAYN	0.612	0.005
GSTM5	PIP5K1C	0.612	0.005
GSTM5	ZEB1	0.613	0.005
GSTM5	KLHL41	0.613	0.005
GSTM5	KCNA5	0.613	0.005
GSTM5	ITGA7	0.613	0.005
GSTM5	ZNF454	0.613	0.005
GSTM5	BEND6	0.613	0.005
GSTM5	TPM2	0.614	0.005
GSTM5	ANGPTL1	0.614	0.005
GSTM5	PLSCR4	0.614	0.005
GSTM5	TXNIP	0.614	0.005
GSTM5	DIRC3	0.614	0.005
GSTM5	CMYA5	0.614	0.005
GSTM5	CAND2	0.615	0.005
GSTM5	SERPINF1	0.615	0.005
GSTM5	ZFPM2	0.615	0.005
GSTM5	SERPING1	0.617	0.005
GSTM5	GPRASP2	0.617	0.005
GSTM5	SYNPO	0.617	0.005
GSTM5	FGF7	0.618	0.005
GSTM5	GRIK5	0.618	0.005
GSTM5	EPM2A	0.618	0.005
GSTM5	HACD4	0.618	0.005
GSTM5	ANXA6	0.618	0.005
GSTM5	CALCOCO1	0.618	0.005
GSTM5	FLNA	0.618	0.005
GSTM5	LTBP1	0.618	0.005
GSTM5	ADH1B	0.619	0.004
GSTM5	FAM212B	0.620	0.004
GSTM5	SCRG1	0.620	0.004
GSTM5	PDZRN3	0.620	0.004
GSTM5	PDLIM7	0.620	0.004
GSTM5	LIX1L	0.620	0.004

GSTM5	CMTM5	0.620	0.004
GSTM5	PRR34	0.621	0.004
GSTM5	RHOB	0.621	0.004
GSTM5	PTGFR	0.622	0.004
GSTM5	MAP1B	0.622	0.004
GSTM5	FAT3	0.622	0.004
GSTM5	C1S	0.623	0.004
GSTM5	SMTN	0.623	0.004
GSTM5	IL17B	0.623	0.004
GSTM5	PRDM6	0.624	0.004
GSTM5	ADHFE1	0.624	0.004
GSTM5	PARVA	0.624	0.004
GSTM5	PKD2	0.625	0.004
GSTM5	GHR	0.625	0.004
GSTM5	SLC9A9	0.626	0.004
GSTM5	PTGIS	0.626	0.004
GSTM5	PGM5	0.627	0.004
GSTM5	CADM3	0.628	0.004
GSTM5	APBB1	0.628	0.004
GSTM5	ZNF385D	0.628	0.004
GSTM5	RBPMS	0.628	0.004
GSTM5	FBLN1	0.628	0.004
GSTM5	COLEC12	0.629	0.004
GSTM5	CPEB1	0.629	0.004
GSTM5	TCEAL3	0.629	0.004
GSTM5	PDZRN4	0.630	0.004
GSTM5	ZNF835	0.630	0.004
GSTM5	OLFML3	0.631	0.004
GSTM5	C16orf45	0.631	0.004
GSTM5	MPDZ	0.631	0.004
GSTM5	FAM229B	0.632	0.004
GSTM5	PRICKLE2	0.633	0.004
GSTM5	MMRN2	0.634	0.004
GSTM5	NXPH3	0.634	0.004
GSTM5	GUCY1A3	0.635	0.004
GSTM5	CHRM2	0.635	0.004
GSTM5	COL14A1	0.635	0.004
GSTM5	S1PR1	0.636	0.003
GSTM5	CSRP1	0.636	0.003
GSTM5	RNF180	0.636	0.003
GSTM5	CCL14	0.637	0.003
GSTM5	JPH2	0.637	0.003
GSTM5	NEGR1	0.638	0.003
GSTM5	CASQ2	0.638	0.003

GSTM5	MAP1A	0.639	0.003
GSTM5	RHOJ	0.639	0.003
GSTM5	EVC	0.639	0.003
GSTM5	IGFBP7	0.640	0.003
GSTM5	PLAC9	0.640	0.003
GSTM5	GNG11	0.641	0.003
GSTM5	SYNC	0.641	0.003
GSTM5	ZNF135	0.642	0.003
GSTM5	KCNMA1	0.642	0.003
GSTM5	FAM129A	0.643	0.003
GSTM5	LMO3	0.643	0.003
GSTM5	NLGN2	0.643	0.003
GSTM5	4-Sep	0.644	0.003
GSTM5	ITPR1	0.644	0.003
GSTM5	RERG	0.645	0.003
GSTM5	KIAA0408	0.645	0.003
GSTM5	OGN	0.646	0.003
GSTM5	ABI3BP	0.646	0.003
GSTM5	EDNRA	0.646	0.003
GSTM5	SLIT2	0.647	0.003
GSTM5	PDZD4	0.647	0.003
GSTM5	SPARCL1	0.647	0.003
GSTM5	ATP1A2	0.647	0.003
GSTM5	GUCY1B3	0.648	0.003
GSTM5	MCAM	0.648	0.003
GSTM5	PDE1A	0.648	0.003
GSTM5	CCDC69	0.648	0.003
GSTM5	ADAMTSL3	0.649	0.003
GSTM5	PLPP7	0.649	0.003
GSTM5	CRISPLD2	0.649	0.003
GSTM5	C11orf96	0.650	0.003
GSTM5	PLPP1	0.651	0.003
GSTM5	ASB2	0.651	0.003
GSTM5	ITGA9	0.652	0.003
GSTM5	LRCH2	0.652	0.003
GSTM5	FAM110D	0.653	0.003
GSTM5	PRELP	0.653	0.003
GSTM5	TCF21	0.653	0.003
GSTM5	NCS1	0.653	0.003
GSTM5	FRZB	0.654	0.003
GSTM5	BNC2	0.654	0.003
GSTM5	DMPK	0.655	0.003
GSTM5	C1QTNF4	0.655	0.003
GSTM5	HOXA4	0.656	0.003

GSTM5	SLIT3	0.656	0.003
GSTM5	TACR2	0.656	0.003
GSTM5	SH3BGRL	0.657	0.003
GSTM5	SYDE1	0.658	0.003
GSTM5	FAM198A	0.658	0.003
GSTM5	MAP3K3	0.659	0.002
GSTM5	STON1	0.659	0.002
GSTM5	RBPMS2	0.659	0.002
GSTM5	EML1	0.659	0.002
GSTM5	HSPB8	0.659	0.002
GSTM5	NPR2	0.660	0.002
GSTM5	RAMP3	0.660	0.002
GSTM5	TMEM240	0.660	0.002
GSTM5	DMGDH	0.662	0.002
GSTM5	LMOD1	0.662	0.002
GSTM5	KCNMB1	0.663	0.002
GSTM5	MEIS1	0.663	0.002
GSTM5	C3orf18	0.663	0.002
GSTM5	NPR1	0.663	0.002
GSTM5	DNAJC18	0.663	0.002
GSTM5	ADAM33	0.664	0.002
GSTM5	CYSLTR1	0.664	0.002
GSTM5	PRKN	0.664	0.002
GSTM5	MYOC	0.665	0.002
GSTM5	ROR2	0.665	0.002
GSTM5	ATP8B2	0.665	0.002
GSTM5	ABCC9	0.668	0.002
GSTM5	SFRP1	0.669	0.002
GSTM5	DCN	0.669	0.002
GSTM5	KCNE4	0.669	0.002
GSTM5	SELENOM	0.669	0.002
GSTM5	MYL9	0.670	0.002
GSTM5	PLEKHO1	0.670	0.002
GSTM5	SETBP1	0.671	0.002
GSTM5	EFEMP2	0.671	0.002
GSTM5	ST3GAL3	0.672	0.002
GSTM5	A2M	0.672	0.002
GSTM5	ATP1B2	0.673	0.002
GSTM5	COL8A2	0.673	0.002
GSTM5	GNAO1	0.674	0.002
GSTM5	LGI4	0.674	0.002
GSTM5	TMEM35A	0.674	0.002
GSTM5	RGMA	0.675	0.002
GSTM5	MAN1C1	0.676	0.002

GSTM5	LHFP	0.676	0.002
GSTM5	RSPO1	0.676	0.002
GSTM5	NACAD	0.676	0.002
GSTM5	RNF150	0.677	0.002
GSTM5	CC2D2A	0.679	0.002
GSTM5	CPXM2	0.679	0.002
GSTM5	FHL1	0.680	0.002
GSTM5	TNS1	0.680	0.002
GSTM5	TMOD1	0.680	0.002
GSTM5	NFATC4	0.681	0.002
GSTM5	WFDC1	0.682	0.002
GSTM5	EMILIN1	0.682	0.002
GSTM5	PDLIM3	0.683	0.002
GSTM5	SSBP2	0.685	0.002
GSTM5	VSTM4	0.685	0.002
GSTM5	LCN6	0.686	0.002
GSTM5	RBMS3	0.686	0.002
GSTM5	MRVI1	0.686	0.002
GSTM5	PPP1R14A	0.687	0.002
GSTM5	CRYAB	0.688	0.002
GSTM5	TAGLN	0.688	0.002
GSTM5	GPRASP1	0.688	0.002
GSTM5	RECK	0.688	0.002
GSTM5	ACTA2	0.688	0.002
GSTM5	KANK2	0.688	0.002
GSTM5	PABPC5	0.691	0.002
GSTM5	BEND5	0.691	0.002
GSTM5	ARHGAP20	0.691	0.002
GSTM5	RCAN2	0.693	0.001
GSTM5	TTC28	0.694	0.001
GSTM5	RAI2	0.694	0.001
GSTM5	C1R	0.694	0.001
GSTM5	FBLN5	0.696	0.001
GSTM5	CHRDL1	0.696	0.001
GSTM5	PDE2A	0.697	0.001
GSTM5	RSPO3	0.697	0.001
GSTM5	PKIG	0.698	0.001
GSTM5	CCDC80	0.698	0.001
GSTM5	NMUR1	0.699	0.001
GSTM5	FAXDC2	0.699	0.001
GSTM5	SSC5D	0.701	0.001
GSTM5	SMOC2	0.702	0.001
GSTM5	ANGPTL7	0.703	0.001
GSTM5	P2RY14	0.703	0.001

GSTM5	ZBTB4	0.703	0.001
GSTM5	TGFB1I1	0.703	0.001
GSTM5	MAP6	0.704	0.001
GSTM5	PYGM	0.704	0.001
GSTM5	MRGPRF	0.705	0.001
GSTM5	MFAP4	0.705	0.001
GSTM5	SOD3	0.706	0.001
GSTM5	SPON1	0.706	0.001
GSTM5	CLIP3	0.707	0.001
GSTM5	POU6F1	0.708	0.001
GSTM5	SCN4B	0.709	0.001
GSTM5	NR2F1	0.709	0.001
GSTM5	MXRA7	0.711	0.001
GSTM5	TMEM47	0.711	0.001
GSTM5	DACT3	0.711	0.001
GSTM5	ARHGEF25	0.712	0.001
GSTM5	BARX1	0.713	0.001
GSTM5	NTN1	0.714	0.001
GSTM5	LIMS2	0.715	0.001
GSTM5	ADARB1	0.715	0.001
GSTM5	C1QTNF2	0.716	0.001
GSTM5	C14orf132	0.716	0.001
GSTM5	ZBTB47	0.717	0.001
GSTM5	C2orf40	0.718	0.001
GSTM5	CAVIN1	0.719	0.001
GSTM5	SGCA	0.720	0.001
GSTM5	ADCY5	0.720	0.001
GSTM5	FOXF1	0.722	0.001
GSTM5	BOC	0.722	0.001
GSTM5	SCN2B	0.724	0.001
GSTM5	MGP	0.724	0.001
GSTM5	LRRN4CL	0.725	0.001
GSTM5	SRPX	0.726	0.001
GSTM5	PODN	0.726	0.001
GSTM5	DAAM2	0.728	0.001
GSTM5	NAP1L3	0.729	0.001
GSTM5	TNS2	0.733	0.001
GSTM5	COPZ2	0.733	0.001
GSTM5	CBX7	0.736	0.001
GSTM5	JAM3	0.738	0.001
GSTM5	FBXL7	0.739	0.001
GSTM5	TCEAL7	0.741	0.001
GSTM5	ST6GALNAC6	0.748	0.001
GSTM5	HSPB2	0.749	0.001

GSTM5	ZCCHC24	0.751	0.001
GSTM5	TMEM100	0.751	0.001
GSTM5	C1QTNF7	0.759	<0.001
GSTM5	PKNOX2	0.761	<0.001
GSTM5	COX7A1	0.768	<0.001
GSTM5	BHMT2	0.768	<0.001
GSTM5	JAM2	0.768	<0.001
GSTM5	FXYD6	0.773	<0.001
GSTM5	TNFSF12	0.773	<0.001
GSTM5	INMT	0.776	<0.001
GSTM5	CNRIP1	0.777	<0.001
GSTM5	ITIH5	0.778	<0.001
GSTM5	AOC3	0.781	<0.001
GSTM5	NDN	0.784	<0.001
GSTM5	ACKR1	0.792	<0.001
GSTM5	MAPK10	0.794	<0.001
GSTM5	GYPC	0.821	<0.001
GSTM5	FXYD1	0.827	<0.001
GSTM5	GSTM5	1.000	<0.001

Table SIV. Gene Ontology term analysis of glutathione S-transferase Mu 5 and its co-expressed genes.

Category	Term	Count	P-value	Genes
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	25	<0.001	LTBP1, IGFBP7, DCN, ABI3BP, MMRN2, OGN, ILK, COL8A2, MYOC, SPON1, MGP, CPXM2, SOD3, FLNA, EMILIN1, PRELP, FBLN1, COL14A1, SERPINF1, SFRP1, FBLN5, TGFB1I1, MFAP4, SSC5D, CLEC14A
GOTERM_BP_DIRECT	GO:1903779~regulation of cardiac conduction	12	<0.001	FXYD1, TRPC1, ABCC9, ATP1B2, PLN, NPR1, NPR2, ATP1A2, FXYD6, CASQ2, ITPR1, DMPK
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	18	<0.001	RECK, ELN, CCDC80, DCN, ABI3BP, EMILIN1, ITGA9, SMOC2, FBLN1, COL14A1, COL19A1, CRISPLD2, FOXF1, FBLN5, ITGA7, JAM2, JAM3, COL8A2
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	21	<0.001	LTBP1, PODN, SPARCL1, ADAMTSL3, ELN, MGP, SLIT2, PRELP, SLIT3, EMILIN1, OGN, SMOC2, FBLN1, COL14A1, COL19A1, SFRP1, CRISPLD2, FBLN5, COL8A2, MYOC, SPON1
GOTERM_MF_DIRECT	GO:0008201~heparin binding	14	<0.001	SELP, FGF7, CCDC80, SLIT2, SOD3, ABI3BP, SLIT3, PRELP, SMOC2, OGN, RSPO1, SFRP1, CRISPLD2, RSPO3
GOTERM_CC_DIRECT	GO:0005576~extracellular region	52	<0.001	NXPH3, TLN1, A2M, LTBP1, FGF7, CXORF36, IGFBP7, TNFSF12, OLFML1, OGN, ST3GAL3, RSPO1, RSPO3, ITIH5, LGI4, GHR, SERPING1, SLIT2, FLNA, SLIT3, PRELP, CHRDL1, PTGDS, SERPINF1, MFAP4, ELN, C1R, DCN, C1S, C1QTNF7, METTL24, ANGPTL7, IL17B, CRISPLD2, COL8A2, VSTM4, SVEP1, EFEMP2, PTGFR, FRZB, NTN1, SOD3, PLAC9, EMILIN1, FBLN1, COL14A1, COL19A1,

				CCL14, SFRP1, FAM198A, LCN6, FBLN5
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	11	<0.001	FXYD1, TLN1, GNAO1, ACTA2, TACR2, CRYAB, LMOD1, TPM2, SGCA, TMOD1, MYL9
GOTERM_CC_DIRECT	GO:0071953~elastic fiber	4	<0.001	FBLN1, FBLN5, ELN, MFAP4
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	22	<0.001	SELP, SVEP1, CYP1B1, ATP1B2, MPDZ, IGFBP7, MCAM, EMILIN1, ITGA9, PGM5, SRPX, S1PR1, COL19A1, ITGA7, RHOB, TGFB1I1, MFAP4, BOC, PARVA, FEZ1, AOC3, SPON1
GOTERM_BP_DIRECT	GO:0030308~negative regulation of cell growth	11	<0.001	RERG, SFRP1, DACT3, CRYAB, FHL1, NPR1, WFDC1, FRZB, APBB1, SLIT2, SLIT3
GOTERM_CC_DIRECT	GO:0030018~Z disc	11	<0.001	PGM5, JPH2, CRYAB, SYNC, PDLIM3, KCNA5, CASQ2, FLNA, SYNPO, PARVA, MYL9
GOTERM_BP_DIRECT	GO:0016337~single organismal cell-cell adhesion	10	<0.001	COL14A1, LIMS2, COL19A1, FOXF1, PIP5K1C, NLGN2, JAM2, COL8A2, NTN1, NEGR1
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	19	<0.001	AR, MAGI2, CYP1B1, PODN, ADARB1, NDN, IGFBP7, ZEB1, FRZB, PLPP1, KANK2, SLIT3, RERG, TNS2, SFRP1, SPEG, PKD2, ROR2, TGFB1I1
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	9	<0.001	POU6F1, EVC, SMTN, TAGLN, SPEG, CRYAB, FHL1, ITGA7, SGCA
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	8	<0.001	FBLN1, COL14A1, COL19A1, EFEMP2, ELN, MGP, COL8A2, PRELP
GOTERM_CC_DIRECT	GO:0005615~extracellular space	42	<0.001	PODN, IGFBP7, DCN, TNFSF12, ABI3BP, MMRN2, OGN, PTGIS, IL17B, C1QTNF4, SCRG1, C1QTNF2, LGI4, ANGPTL1, MYOC, GHR, SPON1, SELP, ACTA2, SPARCL1, CPXM2, NLGN2, SERPING1, FRZB, MCAM, SLIT2, SOD3, SLIT3, PRELP, C2ORF40, SH3BGRL, FBLN1,

				COL14A1, CCL14, SFRP1, PTGDS, SERPINF1, FBLN5, WFDC1, SSC5D, JAM3, CMTM5
GOTERM_MF_DIRECT	GO:0004016~adenylate cyclase activity	5	<0.001	ADCY5, GUCY1A3, NPR1, GUCY1B3, NPR2
GOTERM_BP_DIRECT	GO:0006816~calcium ion transport	8	<0.001	RAMP3, ANXA6, TRPC1, CYSLTR1, NMUR1, PLN, PKD2, ITPR1
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	18	<0.001	TLN1, LIMS2, PDLIM7, FHL1, FERMT2, PIP5K1C, CSRP1, MCAM, FLNA, ANXA6, TNS2, TNS1, PGM5, LAYN, ILK, RHOB, TGFB1I1, PARVA
GOTERM_MF_DIRECT	GO:0004383~guanylate cyclase activity	4	<0.001	GUCY1A3, NPR1, GUCY1B3, NPR2
GOTERM_MF_DIRECT	GO:0048495~Roundabout binding	4	<0.001	OGN, TGFB1I1, SLIT2, SLIT3
GOTERM_CC_DIRECT	GO:0005604~basement membrane	8	<0.001	SMOC2, FBLN1, SERPINF1, EFEMP2, CCDC80, COL8A2, NTN1, MMRN2
GOTERM_CC_DIRECT	GO:0008074~guanylate cyclase complex, soluble	4	<0.001	GUCY1A3, NPR1, GUCY1B3, NPR2
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	25	0.001	LTBP1, NCS1, C1R, C1S, MYL9, ANXA6, SMOC2, FAT3, PKD2, EHD2, SVEP1, SPARCL1, EFEMP2, MGP, MAN1C1, SLIT2, ITPR1, SLIT3, FBLN1, EML1, PLSCR4, FBLN5, CASQ2, SGCA, AOC3
GOTERM_BP_DIRECT	GO:0008015~blood circulation	6	0.001	MEOX2, PLN, ELN, GUCY1A3, SERPING1, GUCY1B3
GOTERM_BP_DIRECT	GO:0034329~cell junction assembly	4	0.001	LIMS2, FERMT2, ILK, FLNA
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	8	0.001	RECK, ADARB1, PODN, CYP1B1, MAGI2, SFRP1, RHOB, SLIT2
GOTERM_BP_DIRECT	GO:0008016~regulation of heart contraction	5	0.002	FXYD1, GNAO1, CHRM2, PLN, DMPK
GOTERM_BP_DIRECT	GO:0051414~response to cortisol	3	0.002	IGFBP7, SLIT2, SLIT3
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	92	0.002	RHOJ, SLC9A9, GYPC, CADM3, TLN1, JPH2, ATP1B2,

				TACR2, ADCY5, GRIK5, NCS1, TNFSF12, FRRS1L, DMPK, EDNRA, ST6GALNAC6, S1PR1, SLC2A4, NMUR1, ILK, GUCY1A3, RHOB, ATP8B2, TMEM100, FAM129A, NEGR1, BOC, GHR, RAMP3, KCNMA1, RECK, AR, MAGI2, ACKR1, MRGPRF, COLEC12, FLNA, SLIT2, TNS2, CHRM2, ROR2, GUCY1B3, CLIP3, JAM2, JAM3, AOC3, PARVA, FXYD1, ABCA8, LIMS2, CYSLTR1, ARHGEF25, FHL1, GNG11, KCNA5, PLPP1, FXYD6, KCNMB1, RGMA, FAT3, PLIN4, PKD2, KLHL41, PRIMA1, EHD2, TRPC1, SELP, VSTM4, GNAO1, KLF9, EPM2A, MAP1B, NPR1, NPR2, ATP1A2, MAPK10, MCAM, PTGFR, ITPR1, ITGA9, ABCC9, TMEM47, PDE2A, SFRP1, PLSCR4, P2RY14, BNC2, ITGA7, SCN4B, APBB1, HTR2A, FEZ1
GOTERM_BP_DIRECT	GO:0006182~cGMP biosynthetic process	4	0.002	GUCY1A3, NPR1, GUCY1B3, NPR2
GOTERM_CC_DIRECT	GO:0001725~stress fiber	6	0.002	PGM5, PDLIM7, FERMT2, ILK, SYNPO, MYL9
GOTERM_MF_DIRECT	GO:0044325~ion channel binding	8	0.002	FXYD1, TRPC1, ABCC9, FHL1, PKD2, SCN4B, FLNA, KCNE4
GOTERM_MF_DIRECT	GO:0005518~collagen binding	6	0.003	ITGA9, PODN, COL14A1, SPARCL1, DCN, ABI3BP
GOTERM_BP_DIRECT	GO:0006939~smooth muscle contraction	4	0.003	EDNRA, SMTN, NMUR1, HTR2A
GOTERM_BP_DIRECT	GO:0010811~positive regulation of cell-substrate adhesion	5	0.003	SMOC2, FOXF1, CCDC80, ABI3BP, EMILIN1
GOTERM_BP_DIRECT	GO:0010976~positive regulation of neuron projection development	7	0.003	RGMA, MAGI2, MOB2, SERPINF1, APBB1, NEGR1, FEZ1

GOTERM_BP_DIRECT	GO:0001525~angiogenesis	11	0.004	CYP1B1, S1PR1, MEOX2, RHOB, TMEM100, TNFSF12, MCAM, COL8A2, MEIS1, JAM3, MMRN2
GOTERM_CC_DIRECT	GO:0030017~sarcomere	5	0.004	ABCC9, ARHGEF25, ILK, LMOD1, TMOD1
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	21	0.004	MAGI2, MOB2, SYNC, MRVI1, NCS1, TNFSF12, KCNA5, SELENOM, FLNA, ANXA6, EML1, PDE2A, SERPINF1, SLC2A4, PTGDS, PLN, CMYA5, TMEM100, MAP6, APBB1, EHD2
GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	6	0.004	EDNRA, ACTA2, GUCY1A3, NPR1, NPR2, ATP1A2
GOTERM_BP_DIRECT	GO:0070527~platelet aggregation	5	0.004	TLN1, ILK, CSRP1, FLNA, MYL9
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	7	0.004	C1QTNF7, COL14A1, COL19A1, C1QTNF2, COLEC12, COL8A2, EMILIN1
GOTERM_CC_DIRECT	GO:0005901~caveola	6	0.005	KCNMA1, PTGIS, KCNA5, ATP1A2, EHD2, HTR2A
GOTERM_BP_DIRECT	GO:0046069~cGMP catabolic process	3	0.005	PDE2A, PDE1A, PDE5A
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	4	0.008	SPARCL1, ELN, DCN, SSC5D
GOTERM_MF_DIRECT	GO:0001968~fibronectin binding	4	0.008	FBLN1, CCDC80, SSC5D, MYOC
GOTERM_CC_DIRECT	GO:1903561~extracellular vesicle	5	0.010	OGN, OLFML3, EFEMP2, ATP1A2, PRELP
GOTERM_BP_DIRECT	GO:0030178~negative regulation of Wnt signaling pathway	5	0.010	BARX1, SFRP1, DACT3, NFATC4, FRZB
GOTERM_BP_DIRECT	GO:0006813~potassium ion transport	6	0.011	KCNMA1, ABCC9, ATP1B2, KCNA5, ATP1A2, KCNMB1
GOTERM_BP_DIRECT	GO:0043267~negative regulation of potassium ion transport	3	0.011	KCNA5, CASQ2, HTR2A
GOTERM_CC_DIRECT	GO:0014069~postsynaptic density	9	0.012	MAGI2, MPDZ, CRYAB, MAP1B, GRIK5, NCS1, CPEB1, ITPR1, SYNPO
GOTERM_CC_DIRECT	GO:0005890~sodium:potassium-exchanging	3	0.014	FXYD1, ATP1B2, ATP1A2

	ATPase complex			
GOTERM_MF_DIRECT	GO:0016849~phosphorus-oxygen lyase activity	3	0.015	ADCY5, NPR1, NPR2
GOTERM_BP_DIRECT	GO:0030007~cellular potassium ion homeostasis	3	0.016	KCNMA1, ATP1B2, ATP1A2
GOTERM_BP_DIRECT	GO:0055119~relaxation of cardiac muscle	3	0.016	PLN, PDE5A, ATP1A2
GOTERM_BP_DIRECT	GO:0009190~cyclic nucleotide biosynthetic process	3	0.016	ADCY5, NPR1, NPR2
GOTERM_BP_DIRECT	GO:0048846~axon extension involved in axon guidance	3	0.016	OGN, SLIT2, SLIT3
GOTERM_BP_DIRECT	GO:0035385~Roundabout signaling pathway	3	0.016	OGN, SLIT2, SLIT3
GOTERM_BP_DIRECT	GO:0007585~respiratory gaseous exchange	4	0.017	EDNRA, CYSLTR1, ELN, PBX3
GOTERM_BP_DIRECT	GO:0086012~membrane depolarization during cardiac muscle cell action potential	3	0.018	SCN2B, SCN4B, ATP1A2
GOTERM_BP_DIRECT	GO:0002087~regulation of respiratory gaseous exchange by neurological system process	3	0.018	NLGN2, ATP1A2, PBX3
GOTERM_BP_DIRECT	GO:0030239~myofibril assembly	3	0.018	LMOD1, KLHL41, TMOD1
GOTERM_CC_DIRECT	GO:0033017~sarcoplasmic reticulum membrane	4	0.019	PLN, KLHL41, CASQ2, DMPK
GOTERM_CC_DIRECT	GO:0005614~interstitial matrix	3	0.019	SMOC2, CCDC80, ABI3BP
GOTERM_MF_DIRECT	GO:0005109~frizzled binding	4	0.020	SFRP1, RSPO3, ROR2, MYOC
GOTERM_MF_DIRECT	GO:0004867~serine-type endopeptidase inhibitor activity	6	0.021	RECK, A2M, SERPINF1, ITIH5, WFDC1, SERPING1
GOTERM_MF_DIRECT	GO:0047555~3',5'-cyclic-GMP phosphodiesterase	3	0.021	PDE2A, PDE1A, PDE5A

	activity			
GOTERM_BP_DIRECT	GO:0006937~regulation of muscle contraction	3	0.021	ANXA6, HSPB6, MYL9
GOTERM_BP_DIRECT	GO:0022011~myelination in peripheral nervous system	3	0.021	ILK, LGI4, MYOC
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	6	0.022	ITGA9, FBLN1, FERMT2, ITGA7, ILK, ADAM33
GOTERM_CC_DIRECT	GO:0005911~cell-cell junction	8	0.026	CADM3, TLN1, TMEM47, PDLIM7, ILK, PKD2, FLNA, SGCA
GOTERM_BP_DIRECT	GO:0007224~smoothened signaling pathway	5	0.026	EVC, FOXF1, CC2D2A, ROR2, BOC
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	12	0.026	RBPMS2, RBPMS, PYGM, PABPC5, ADCY5, RBMS3, GUCY1A3, NPR1, GUCY1B3, CPEB1, ATP1A2, RCAN2
GOTERM_BP_DIRECT	GO:2000649~regulation of sodium ion transmembrane transporter activity	3	0.027	FXYD1, SCN2B, SCN4B
GOTERM_BP_DIRECT	GO:0000226~microtubule cytoskeleton organization	5	0.028	EML1, MAP1A, MAP1B, DCLK2, MAP6
GOTERM_BP_DIRECT	GO:0051209~release of sequestered calcium ion into cytosol	4	0.029	JPH2, PKD2, ITPR1, HTR2A
GOTERM_MF_DIRECT	GO:0030553~cGMP binding	3	0.030	PDE2A, PDE1A, PDE5A
GOTERM_MF_DIRECT	GO:0008307~structural constituent of muscle	4	0.030	SMTN, PDLIM3, TPM2, MYL9
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	9	0.030	PKNOX2, POU6F1, SMTN, PDLIM7, ACTA2, PDLIM3, FLNA, SYNPO, PARVA
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	4	0.030	RECK, FBLN1, PTGIS, IGFBP7
GOTERM_BP_DIRECT	GO:0001869~negative regulation of complement	2	0.032	A2M, SERPING1

	activation, lectin pathway			
GOTERM_BP_DIRECT	GO:0010596~negative regulation of endothelial cell migration	3	0.034	SERPINF1, DCN, SLIT2
GOTERM_BP_DIRECT	GO:0048557~embryonic digestive tract morphogenesis	3	0.034	RBPMS2, TCF21, FOXF1
GOTERM_MF_DIRECT	GO:0008144~drug binding	5	0.035	PDE2A, SFRP1, CHRM2, ATP1A2, HTR2A
GOTERM_BP_DIRECT	GO:0032870~cellular response to hormone stimulus	4	0.036	IGFBP7, SLIT2, GHR, SLIT3
GOTERM_BP_DIRECT	GO:0060048~cardiac muscle contraction	4	0.036	SCN2B, SCN4B, ATP1A2, CASQ2
GOTERM_BP_DIRECT	GO:0010881~regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	0.037	PLN, ATP1A2, CASQ2
GOTERM_MF_DIRECT	GO:0003779~actin binding	10	0.037	KCNMA1, SMTN, TNS1, TAGLN, LMOD1, TPM2, DAAM2, TMOD1, SYNPO, PARVA
GOTERM_CC_DIRECT	GO:0014704~intercalated disc	4	0.039	PGM5, SCN4B, KCNA5, ATP1A2
GOTERM_BP_DIRECT	GO:0031532~actin cytoskeleton reorganization	4	0.040	S1PR1, FGF7, FLNA, PARVA
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	4	0.040	SFRP1, LMO3, FRZB, HTR2A
GOTERM_MF_DIRECT	GO:0005248~voltage-gated sodium channel activity	3	0.041	SCN2B, PKD2, SCN4B
GOTERM_BP_DIRECT	GO:0043113~receptor clustering	3	0.041	MAGI2, GRIK5, FLNA
GOTERM_BP_DIRECT	GO:0071805~potassium ion transmembrane transport	6	0.047	SLC9A9, KCNMA1, PKD2, KCNA5, KCNMB1, KCNE4
GOTERM_MF_DIRECT	GO:0016941~natriuretic peptide receptor	2	0.048	NPR1, NPR2

	activity			
GOTERM_BP_DIRECT	GO:0061364~apoptotic process involved in luteolysis	2	0.048	SLIT2, SLIT3
GOTERM_BP_DIRECT	GO:0021834~chemorepulsion involved in embryonic olfactory bulb interneuron precursor migration	2	0.048	SLIT2, SLIT3
GOTERM_BP_DIRECT	GO:0048871~multicellular organismal homeostasis	2	0.048	TNS2, NDN
GOTERM_BP_DIRECT	GO:0034394~protein localization to cell surface	3	0.049	FGF7, FBLN5, FLNA
GOTERM_BP_DIRECT	GO:0060078~regulation of postsynaptic membrane potential	3	0.049	SCN2B, PKD2, SCN4B
GOTERM_BP_DIRECT	GO:0007519~skeletal muscle tissue development	4	0.050	COL19A1, MEOX2, ELN, DCN
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	4	0.050	TXNIP, GNAO1, CRYAB, KCNA5
GOTERM_CC_DIRECT	GO:0030863~cortical cytoskeleton	3	0.051	GYPC, FLNA, TMOD1
GOTERM_BP_DIRECT	GO:0008344~adult locomotory behavior	4	0.052	LGI4, ATP1A2, PBX3, TMOD1
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.052	GNAO1, SERPINF1, CRYAB, SERPING1, DCN, KCNMB1, HTR2A
GOTERM_MF_DIRECT	GO:0004114~3',5'-cyclic-nucleotide phosphodiesterase activity	3	0.053	PDE2A, PDE1A, PDE5A
GOTERM_CC_DIRECT	GO:0042383~sarcolemma	5	0.054	FXYD1, ABCC9, PGM5, SYNC, SGCA
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	8	0.055	ANXA6, FXYD1, ATP1B2, GRIK5, ATP8B2, ATP1A2, FXYD6, CASQ2
GOTERM_CC_DIRECT	GO:0031430~M band	3	0.056	CRYAB, CMYA5, KLHL41
GOTERM_BP_DIRECT	GO:0007160~cell-matrix adhesion	5	0.058	FBLN5, FERMT2, ITGA7, ILK, JAM3

GOTERM_BP_DIRECT	GO:0007368~determination of left/right symmetry	4	0.060	FOXF1, CC2D2A, PKD2, DAAM2
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	5	0.060	TXNIP, CRYAB, WFDC1, PTGFR, GHR
GOTERM_BP_DIRECT	GO:2000134~negative regulation of G1/S transition of mitotic cell cycle	3	0.061	FHL1, PKD2, KANK2
GOTERM_MF_DIRECT	GO:0005102~receptor binding	11	0.062	NXPH3, CADM3, AR, A2M, RSPO1, RSPO3, C1QTNF2, PKD2, ANGPTL1, KCNA5, TNFSF12
GOTERM_MF_DIRECT	GO:0031852~mu-type opioid receptor binding	2	0.063	GNAO1, FLNA
GOTERM_BP_DIRECT	GO:1903278~positive regulation of sodium ion export from cell	2	0.063	FXYD1, ATP1B2
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	8	0.064	MPDZ, CHRM2, GRIK5, NCS1, NLGN2, CPEB1, APBB1, SYNPO
GOTERM_BP_DIRECT	GO:0007202~activation of phospholipase C activity	3	0.066	EDNRA, NMUR1, HTR2A
GOTERM_MF_DIRECT	GO:0048306~calcium-dependent protein binding	4	0.067	ANXA6, SELP, A2M, CASQ2
GOTERM_MF_DIRECT	GO:0017046~peptide hormone binding	3	0.070	NPR1, NPR2, GHR
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	5	0.071	PTGIS, SFRP1, SLC2A4, CPEB1, KCNMB1
GOTERM_BP_DIRECT	GO:0010107~potassium ion import	3	0.075	ABCC9, ATP1B2, ATP1A2
GOTERM_BP_DIRECT	GO:0018146~keratan sulfate biosynthetic process	3	0.075	OGN, ST3GAL3, PRELP
GOTERM_BP_DIRECT	GO:0001933~negative regulation of protein phosphorylation	4	0.076	FBLN1, WWTR1, FAM129A, SLIT2
GOTERM_BP_DIRECT	GO:0007507~heart development	7	0.077	EDNRA, POU6F1, FOXF1, CC2D2A, PKD2, PDLIM3, NFATC4
GOTERM_MF_	GO:0086006~voltage-	2	0.078	SCN2B, SCN4B

DIRECT	gated sodium channel activity involved in cardiac muscle cell action potential			
GOTERM_BP_DIRECT	GO:0090131~mesenchyme migration	2	0.078	ACTA2, FOXF1
GOTERM_BP_DIRECT	GO:0071504~cellular response to heparin	2	0.078	SFRP1, SLIT2
GOTERM_BP_DIRECT	GO:2000809~positive regulation of synaptic vesicle clustering	2	0.078	MAGI2, NLGN2
GOTERM_BP_DIRECT	GO:0032387~negative regulation of intracellular transport	2	0.078	CRYAB, MAP1B
GOTERM_BP_DIRECT	GO:2001046~positive regulation of integrin-mediated signaling pathway	2	0.078	LIMS2, FLNA
GOTERM_BP_DIRECT	GO:0007195~adenylate cyclase-inhibiting dopamine receptor signaling pathway	2	0.078	ADCY5, FLNA
GOTERM_BP_DIRECT	GO:0070100~negative regulation of chemokine-mediated signaling pathway	2	0.078	SLIT2, SLIT3
GOTERM_CC_DIRECT	GO:0030016~myofibril	3	0.079	ARHGEF25, LMOD1, TMOD1
GOTERM_BP_DIRECT	GO:0048662~negative regulation of smooth muscle cell proliferation	3	0.080	OGN, ILK, NPR1
GOTERM_CC_DIRECT	GO:0031088~platelet dense granule membrane	2	0.081	SELP, ITPR1
GOTERM_CC_DIRECT	GO:0045202~synapse	7	0.083	MAGI2, CHRM2, NLGN2, CPEB1, PRIMA1, APBB1, FRRS1L
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	7	0.084	RSPO1, DACT3, RSPO3, FERMT2, TGFB1I1, FRZB, CALCOCO1
GOTERM_BP_DIRECT	GO:0045773~positive regulation of axon extension	3	0.085	ILK, MAP1B, NTN1

GOTERM_CC_DIRECT	GO:0042734~presynaptic membrane	4	0.085	PDE2A, GRIK5, NLGN2, APBB1
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	18	0.085	RBPMS2, CADM3, CRYAB, WWTR1, SLIT2, FLNA, ANXA6, RBPMS, PDE2A, HSPB6, FBLN5, PRDM6, PKD2, ZBTB4, JAM3, CASQ2, GHR, AOC3
GOTERM_CC_DIRECT	GO:0043197~dendritic spine	5	0.086	CRYAB, MAP1B, ATP1A2, APBB1, SYNPO
GOTERM_BP_DIRECT	GO:0002576~platelet degranulation	5	0.086	SELP, TLN1, A2M, SERPING1, FLNA
GOTERM_MF_DIRECT	GO:0017147~Wnt-protein binding	3	0.089	SFRP1, ROR2, FRZB
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	8	0.089	TCF21, AR, SSBP2, MEOX2, NDN, NFIC, MEIS1, NFIA
GOTERM_MF_DIRECT	GO:0005178~integrin binding	5	0.091	TLN1, FBLN1, FBLN5, ILK, JAM3
GOTERM_BP_DIRECT	GO:0050790~regulation of catalytic activity	4	0.092	RNF180, AR, RCAN2, DMPK
GOTERM_MF_DIRECT	GO:0070492~oligosaccharide binding	2	0.093	GYPC, SELP
GOTERM_BP_DIRECT	GO:0051150~regulation of smooth muscle cell differentiation	2	0.093	FOXF1, ZEB1
GOTERM_BP_DIRECT	GO:0003416~endochondral bone growth	2	0.093	EVC, BNC2
GOTERM_BP_DIRECT	GO:0060426~lung vasculature development	2	0.093	TCF21, FOXF1
GOTERM_BP_DIRECT	GO:0007044~cell-substrate junction assembly	2	0.093	TLN1, TNS1
GOTERM_BP_DIRECT	GO:2000052~positive regulation of non-canonical Wnt signaling pathway	2	0.093	SFRP1, RSPO3
GOTERM_MF_	GO:0008270~zinc ion	26	0.093	LIMS2, ZCCHC24, PDLIM7,

DIRECT	binding			ADAMTSL3, LMO3, FHL1, PDLIM3, ADH1B, ZEB1, ADAM33, NR2F1, AR, BHMT2, PDZRN4, CPXM2, PDZRN3, CSRP1, SOD3, MSRB3, RNF180, RNF150, BNC2, PRICKLE2, ZNF385D, ZFPM2, TGFB1I1
GOTERM_CC_DIRECT	GO:0031941~filamentous actin	3	0.094	FERMT2, PKD2, FLNA
GOTERM_MF_DIRECT	GO:0017080~sodium channel regulator activity	3	0.094	FXYD1, SCN2B, SCN4B
GOTERM_CC_DIRECT	GO:0005884~actin filament	4	0.095	LMOD1, TPM2, FLNA, TMOD1
GOTERM_BP_DIRECT	GO:0007399~nervous system development	9	0.095	BARX1, CHRDL1, SCN2B, NDN, CHRM2, SCRG1, EPM2A, MAP1B, FEZ1
GOTERM_CC_DIRECT	GO:0043198~dendritic shaft	3	0.099	ILK, FLNA, HTR2A