

Supplementary Table 2. Molecular functions enriched for low TMB. Preranked GSEA results using the correlation levels of individual genes with TMB. Similarly shown with Supplementary Table 1.

Gene Ontology terms (MSigDB, c5)	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
GO_CATION_CHANNEL_COMPLEX	165	-0.54	-2.57	0	0	0
GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	55	-0.64	-2.53	0	0	0
GO_SYNAPTIC_MEMBRANE	260	-0.5	-2.49	0	0	0
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	40	-0.66	-2.46	0	0	0
GO_MODULATION_OF_SYNAPTIC_TRANSMISSION	298	-0.48	-2.45	0	0	0
GO_POSTSYNAPSE	374	-0.47	-2.45	0	0	0
GO_EXCITATORY_SYNAPSE	196	-0.5	-2.42	0	0	0
GO_SYNAPTIC_SIGNALING	423	-0.46	-2.42	0	0	0
GO_MAIN_AXON	57	-0.61	-2.4	0	0	0
GO_NEURONAL_POSTSYNAPTIC_DENSITY	53	-0.61	-2.4	0	0	0
GO_POSTSYNAPTIC_MEMBRANE	204	-0.49	-2.39	0	0	0
GO_PRESYNAPTIC_ACTIVE_ZONE	29	-0.7	-2.38	0	0	0
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_Glutamatergic	50	-0.61	-2.38	0	0	0
GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	133	-0.52	-2.38	0	0	0
GO_PRESYNAPSE	280	-0.47	-2.38	0	0	0
GO_POTASSIUM_CHANNEL_COMPLEX	90	-0.55	-2.37	0	0	0.001
GO_PRESYNAPTIC_MEMBRANE	55	-0.59	-2.37	0	0	0.001
GO_ACTION_POTENTIAL	94	-0.54	-2.36	0	0	0.001
GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	189	-0.48	-2.34	0	0	0.002
GO_Glutamate_receptor_signaling_pathway	41	-0.63	-2.34	0	0	0.002
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	42	-0.63	-2.34	0	0	0.002
GO_CALCIUM_CHANNEL_COMPLEX	60	-0.58	-2.33	0	0	0.002
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	39	-0.64	-2.32	0	0	0.002
GO_EXOCYTOTIC_VESICLE_MEMBRANE	56	-0.58	-2.3	0	0	0.004
GO_GATED_CHANNEL_ACTIVITY	322	-0.45	-2.3	0	0	0.004
GO_TRANSPORTER_COMPLEX	318	-0.45	-2.29	0	0	0.005
GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	188	-0.47	-2.27	0	0	0.008
GO_CATION_CHANNEL_ACTIVITY	295	-0.44	-2.27	0	0	0.009
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	230	-0.46	-2.26	0	0	0.009
GO_PRESYNAPTIC_PROCESS_INVOLVED_IN_SYNAPTIC_TRANSMISSION	115	-0.5	-2.26	0	0	0.009
GO_DENDRITE	445	-0.43	-2.25	0	0	0.01
GO_NEURONAL_CELL_BODY_MEMBRANE	20	-0.72	-2.25	0	0	0.01
GO_REGULATION_OF_DOPAMINE_SECRETION	22	-0.7	-2.24	0	0	0.01
GO_AXON_PART	216	-0.46	-2.23	0	0	0.011
GO_AXON	412	-0.43	-2.23	0	0	0.011
GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	62	-0.55	-2.23	0	0	0.011
GO_NEUROTRANSMITTER_TRANSPORT	154	-0.48	-2.22	0	0	0.013
GO_MEMBRANE_DEPOLARIZATION	61	-0.55	-2.22	0	0	0.014
GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	27	-0.66	-2.21	0	0	0.014
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	123	-0.49	-2.2	0	0	0.014
GO_Glutamate_receptor_activity	27	-0.66	-2.2	0	0	0.014
GO_POTASSIUM_CHANNEL_ACTIVITY	119	-0.49	-2.2	0	0	0.017
GO_PERIKARYON	107	-0.49	-2.19	0	0	0.017
GO_NEURON_MATURATION	30	-0.63	-2.19	0	0	0.017
GO_TRANSMITTER_GATED_CHANNEL_ACTIVITY	26	-0.65	-2.18	0	0	0.018
GO_SYNAPSE_ORGANIZATION	145	-0.47	-2.18	0	0	0.018
GO_POTASSIUM_ION_TRANSPORT	153	-0.46	-2.18	0	0	0.018
GO_Ionotropic_Glutamate_receptor_complex	46	-0.59	-2.18	0	0	0.018
GO_ADULT_BEHAVIOR	132	-0.48	-2.17	0	0	0.018
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	139	-0.47	-2.17	0	0	0.018
GO_REGULATION_OF_NEUROTRANSMITTER_SECRETION	49	-0.56	-2.17	0	0	0.02
GO_AMPA_Glutamate_receptor_complex	26	-0.66	-2.16	0	0	0.023
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	110	-0.48	-2.16	0	0	0.023
GO_SITE_OF_POLARIZED_GROWTH	149	-0.46	-2.16	0	0	0.024
GO_LOCOMOTORY_BEHAVIOR	180	-0.45	-2.16	0	0	0.026
GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	20	-0.69	-2.16	0	0	0.026
GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	29	-0.64	-2.15	0	0	0.027
GO_CILIARY_TIP	42	-0.58	-2.15	0	0	0.027
GO_NEURON_PROJECTION_TERMINUS	127	-0.47	-2.14	0	0	0.032
GO_Ionotropic_Glutamate_receptor_signaling_pathway	24	-0.65	-2.13	0	0	0.037
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	60	-0.53	-2.13	0	0	0.037
GO_REGULATION_OF_MEMBRANE_POTENTIAL	343	-0.41	-2.13	0	0	0.037
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAergic	29	-0.62	-2.13	0	0	0.038
GO_TRANSMISSION_OF_NERVE_IMPULSE	54	-0.54	-2.12	0	0.001	0.053
GO_NEURON_PROJECTION_MEMBRANE	36	-0.59	-2.12	0	0.001	0.057
GO_T_TUBULE	45	-0.57	-2.12	0	0.001	0.057
GO_REGULATION_OF_AMINE_TRANSPORT	71	-0.5	-2.1	0	0.001	0.081
GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	83	-0.49	-2.09	0	0.001	0.094
GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	25	-0.65	-2.07	0	0.001	0.123
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	30	-0.61	-2.07	0	0.001	0.123
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	88	-0.48	-2.07	0	0.001	0.128
GO_REGULATION_OF_SYNAPSE_ORGANIZATION	112	-0.46	-2.06	0	0.001	0.135
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	70	-0.5	-2.06	0	0.001	0.136
GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	30	-0.59	-2.06	0.002	0.001	0.139
GO_PRIMARY_CILIUM	195	-0.42	-2.06	0	0.001	0.14
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	61	-0.51	-2.06	0	0.001	0.142
GO_PROTEIN_LOCALIZATION_TO_CILIUM	25	-0.62	-2.06	0	0.001	0.151
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	21	-0.65	-2.06	0	0.001	0.153
GO_REGULATION_OF_ALPHA_AMINO_3_HYDROXY_5_METHYL_4_ISOAXAZOLE_PROPIONATE_SELECTIVE_Glutamate_receptor_activity	19	-0.67	-2.05	0	0.002	0.156
GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	25	-0.64	-2.05	0	0.002	0.158
GO_CILIUM_MORPHOGENESIS	190	-0.43	-2.05	0	0.002	0.186

GO_REGULATION_OF_CATECHOLAMINE_SECRETION	43	-0.54	-2.04	0	0.002	0.208
GO_REGULATION_OF_SYNAPSE_ASSEMBLY	78	-0.49	-2.04	0	0.002	0.212
GO_CARDIAC_CONDUCTION	82	-0.48	-2.03	0	0.002	0.218
GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	37	-0.56	-2.03	0	0.002	0.229
GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS	232	-0.41	-2.03	0	0.002	0.233
GO_COGNITION	249	-0.4	-2.03	0	0.002	0.234
GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	25	-0.61	-2.03	0	0.002	0.235
GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	74	-0.48	-2.02	0	0.002	0.253
GO_TRANSLATION_REPRESSOR_ACTIVITY	20	-0.66	-2.02	0	0.002	0.258
GO_REGULATION_OF_TRANSPORTER_ACTIVITY	197	-0.42	-2.02	0	0.002	0.259
GO_INTRACILIARY_TRANSPORT_PARTICLE	29	-0.6	-2.02	0	0.002	0.266
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	153	-0.43	-2.02	0	0.002	0.266
GO_REGULATION_OF_HEART_CONTRACTION	221	-0.41	-2.02	0	0.002	0.274
GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	457	-0.38	-2.01	0	0.002	0.294
GO_NEURON_SPINE	117	-0.44	-2.01	0	0.003	0.307
GO_TERMINAL_BOUTON	63	-0.49	-2.01	0	0.003	0.31
GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	15	-0.69	-2	0	0.003	0.317
GO_EXTRACELLULAR_Glutamate_Gated_Ion_Channel_Activity	20	-0.64	-2	0	0.003	0.336
GO_CILIAM_ORGANIZATION	173	-0.42	-1.99	0	0.003	0.355
GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	48	-0.53	-1.99	0	0.003	0.355
GO_LIGAND_GATED_CHANNEL_ACTIVITY	141	-0.44	-1.99	0	0.003	0.361
GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	68	-0.49	-1.99	0	0.003	0.362
GO_EXOCYTOTIC_VESICLE	140	-0.43	-1.99	0	0.003	0.365
GO_CAMP_BINDING	23	-0.6	-1.98	0.002	0.003	0.399
GO_CILIARY_PLASM	75	-0.47	-1.98	0	0.003	0.402
GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	75	-0.48	-1.98	0	0.003	0.402
GO_NONMOTILE_PRIMARY_CILIUM_ASSEMBLY	22	-0.63	-1.98	0	0.003	0.406
GO_CELL_BODY	488	-0.37	-1.98	0	0.003	0.422
GO_LEARNING	131	-0.43	-1.98	0	0.004	0.429
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	17	-0.67	-1.98	0	0.003	0.429
GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	36	-0.55	-1.98	0	0.004	0.434
GO_GABA_RECEPTOR_BINDING	15	-0.7	-1.97	0	0.004	0.441
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	70	-0.48	-1.97	0	0.004	0.445
GO_CELLULAR_RESPONSE_TO_GLUcAGON_STIMULUS	38	-0.55	-1.97	0	0.004	0.448
GO_SYNAPTIC_VESICLE_CYCLE	88	-0.45	-1.97	0	0.004	0.482
GO_RECEPTOR_CLUSTERING	41	-0.53	-1.97	0	0.004	0.482
GO_SARCOLEMMA	125	-0.43	-1.96	0	0.004	0.498
GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	50	-0.5	-1.96	0	0.004	0.498
GO_NEUROMUSCULAR_PROCESS	96	-0.45	-1.96	0	0.004	0.512
GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	48	-0.52	-1.96	0	0.004	0.513
GO_NEURON_NEURON_SYNAPTIC_TRANSMISSION	56	-0.5	-1.96	0	0.004	0.513
GO_SINGLE_ORGANISM_BEHAVIOR	381	-0.38	-1.96	0	0.004	0.519
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	157	-0.41	-1.96	0	0.004	0.524
GO_AXONEME_ASSEMBLY	40	-0.53	-1.95	0	0.004	0.538
GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	34	-0.54	-1.95	0.002	0.004	0.547
GO_REGULATION_OF_LYASE_ACTIVITY	86	-0.45	-1.95	0	0.005	0.563
GO_STARTLE_RESPONSE	25	-0.59	-1.95	0	0.005	0.573
GO_CALCIIUM_ION_REGULATED_EXOCYTOSIS	80	-0.47	-1.94	0	0.005	0.582
GO_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	127	-0.43	-1.94	0	0.005	0.583
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	88	-0.45	-1.94	0	0.005	0.583
GO_CILIARY_PART	286	-0.38	-1.94	0	0.005	0.623
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	422	-0.37	-1.93	0	0.005	0.63
GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	17	-0.65	-1.93	0	0.005	0.643
GO_NONMOTILE_PRIMARY_CILIUM	130	-0.42	-1.93	0	0.005	0.646
GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	22	-0.61	-1.93	0	0.005	0.649
GO_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	145	-0.41	-1.93	0	0.005	0.655
GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	227	-0.39	-1.93	0	0.006	0.658
GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	400	-0.37	-1.92	0	0.006	0.686
GO_ADULT_LOCOMOTORY_BEHAVIOR	79	-0.45	-1.92	0	0.006	0.695
GO_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	68	-0.47	-1.92	0	0.006	0.705
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	69	-0.47	-1.91	0	0.006	0.714
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	61	-0.47	-1.91	0	0.006	0.715
GO_DENDRITE_DEVELOPMENT	78	-0.46	-1.91	0	0.007	0.747
GO_REGULATION_OF_N_METHYL_D_ASPARTATE_SELECTIVE_Glutamate_Receptor_Activity	15	-0.66	-1.91	0	0.007	0.747
GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	32	-0.55	-1.9	0.002	0.007	0.763
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	19	-0.61	-1.9	0.002	0.007	0.771
GO_WALKING_BEHAVIOR	31	-0.55	-1.9	0	0.007	0.773
GO_CILIARY_TRANSITION_ZONE	23	-0.59	-1.9	0	0.007	0.779
GO_STRIATED_MUSCLE_ADAPTATION	23	-0.58	-1.9	0.004	0.007	0.788
GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	61	-0.47	-1.89	0	0.008	0.804
GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	46	-0.5	-1.89	0	0.008	0.807
GO_LONG_TERM_SYNAPTIC_POTENTIATION	39	-0.53	-1.89	0	0.008	0.811
GO_SIGNAL_RELEASE	170	-0.4	-1.89	0	0.008	0.829
GO_REGULATION_OF_RESPIRATORY_SYSTEM_PROCESS	16	-0.65	-1.89	0	0.008	0.833
GO_SYNAPTIC_VESICLE_LOCALIZATION	104	-0.42	-1.88	0	0.008	0.849
GO_CYCLIC_NUCLEOTIDE_BINDING	36	-0.52	-1.88	0	0.009	0.854
GO_SYNTAXIN_BINDING	91	-0.43	-1.88	0.002	0.009	0.857
GO_DENDRITIC_SHAFT	36	-0.53	-1.88	0	0.009	0.865
GO_CHANNEL_REGULATOR_ACTIVITY	129	-0.41	-1.88	0	0.009	0.871
GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	363	-0.36	-1.88	0	0.009	0.874
GO_REGULATION_OF_NEUROTRANSMITTER_UPTAKE	15	-0.65	-1.88	0.002	0.009	0.876
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	301	-0.37	-1.87	0	0.009	0.877
GO_NEURON_RECOGNITION	33	-0.54	-1.87	0	0.009	0.88

GO_SYNAPTIC_TRANSMISSION_Glutamatergic	22	-0.59	-1.87	0	0.009	0.88
GO_CILium	440	-0.35	-1.87	0	0.009	0.888
GO_NEURON_CELL_CELL_Adhesion	16	-0.64	-1.87	0.004	0.009	0.89
GO_REGULATION_OF_Blood_Circulation	295	-0.37	-1.87	0	0.009	0.891
GO_NODE_OF_RANVIER	15	-0.65	-1.87	0	0.009	0.891
GO_EXPLORATION_BEHAVIOR	24	-0.57	-1.87	0	0.009	0.895
GO_EXCITATORY_EXTRACELLULAR_Ligand_Gated_Ion_Channel_Act	55	-0.47	-1.87	0	0.009	0.895
GO_PHOSPHOLIPID_DEPHOSPHORYLATION	34	-0.53	-1.87	0.002	0.009	0.903
GO_REGULATION_OF_CAMP_Metabolic_Process	129	-0.4	-1.87	0	0.009	0.903
GO_PROTEIN_KINASE_A_BINDING	40	-0.51	-1.86	0	0.009	0.907
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	414	-0.35	-1.86	0	0.01	0.911
GO_DENDRITE_MEMBRANE	20	-0.6	-1.86	0.002	0.01	0.912
GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	15	-0.65	-1.86	0	0.01	0.913
GO_GLYCOPROTEIN_COMPLEX	21	-0.59	-1.86	0.002	0.01	0.917
GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	26	-0.56	-1.86	0	0.01	0.93
GO_1_PHOSPHATIDYLINOSITOL_BINDING	19	-0.6	-1.85	0.006	0.011	0.943
GO_SODIUM_CHANNEL_ACTIVITY	37	-0.52	-1.85	0	0.011	0.944
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	36	-0.5	-1.85	0.003	0.011	0.946
GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	20	-0.59	-1.85	0	0.011	0.947
GO_DENDRITE_MORPHOGENESIS	41	-0.51	-1.85	0	0.011	0.949
GO_REGULATION_OF_CARDIAC_CONDUCTION	66	-0.45	-1.84	0	0.011	0.951
GO_REGULATION_OF_SYNAPTIC_VESICLE_EXOCYTOSIS	19	-0.6	-1.84	0.004	0.011	0.953
GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	23	-0.58	-1.84	0.004	0.011	0.955
GO_CYCLIC_NUCLEOTIDE_Metabolic_Process	56	-0.46	-1.84	0	0.012	0.959
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	21	-0.58	-1.82	0.004	0.013	0.977
GO_REGULATION_OF_HEART_RATE	86	-0.43	-1.82	0	0.014	0.981
GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	30	-0.54	-1.82	0	0.014	0.981
GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	19	-0.59	-1.82	0.002	0.014	0.981
GO_RESPONSE_TO_GLUcAGON	48	-0.47	-1.82	0.003	0.015	0.985
GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	75	-0.43	-1.82	0	0.015	0.985
GO_NEURON_PROJECTION_MORPHOGENESIS	398	-0.35	-1.81	0	0.015	0.986
GO_CILium_MOVEMENT	33	-0.52	-1.81	0	0.015	0.987
GO_ION_CHANNEL_BINDING	111	-0.41	-1.81	0	0.015	0.99
GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	63	-0.44	-1.81	0	0.016	0.991
GO_CAMP_MEDIATED_SIGNALING	37	-0.49	-1.8	0	0.016	0.991
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	38	-0.49	-1.8	0.002	0.016	0.993
GO_NEUROPEPTIDE_RECEPTOR_ACTIVITY	44	-0.48	-1.8	0.002	0.017	0.993
GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	23	-0.56	-1.8	0	0.017	0.993
GO_SYNTAXIN_1_BINDING	18	-0.6	-1.8	0.009	0.017	0.993
GO_Glutamate_Secretion	28	-0.53	-1.8	0.004	0.017	0.993
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	164	-0.38	-1.79	0	0.019	0.995
GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	84	-0.41	-1.78	0	0.019	0.995
GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLEDTO_CYCLIC_NUCLEOTIDE_SECOND_MESSENGER	172	-0.38	-1.78	0.002	0.019	0.995
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	204	-0.37	-1.78	0	0.019	0.996
GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	39	-0.48	-1.78	0.004	0.02	0.996
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_Metabolic_Process	155	-0.37	-1.77	0.002	0.021	0.998
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	29	-0.52	-1.77	0.004	0.022	0.998
GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	30	-0.52	-1.77	0.002	0.022	0.998
GO_MUSCLE_SYSTEM_PROCESS	281	-0.35	-1.77	0	0.022	0.998
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_THE_RELEASE_OF_SEQUESTERED_CALCIUM_ION	19	-0.57	-1.77	0.005	0.022	0.998
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_SARCOPLASMIC_RETICULUM	25	-0.55	-1.77	0.005	0.022	0.998
GO_GAMMA_AMINOBUtyRIC_ACID_SIGNALING_PATHWAY	23	-0.55	-1.76	0.006	0.022	0.998
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	429	-0.34	-1.76	0	0.022	0.998
GO_CARDIAC_MUSCLE_CELL_CONTRACTION	29	-0.51	-1.76	0.002	0.022	0.999
GO_AXON_EXTENSION	36	-0.48	-1.76	0.004	0.023	0.999
GO_REGULATION_OF_DENDRITE_DEVELOPMENT	118	-0.39	-1.76	0	0.022	0.999
GO_I_BAND	120	-0.38	-1.76	0	0.023	1
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL_SIGNALING	71	-0.43	-1.76	0	0.023	1
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_Glutamatergic	18	-0.59	-1.75	0.007	0.024	1
GO_NEUROPEPTIDE_SIGNALING_PATHWAY	98	-0.4	-1.75	0	0.024	1
GO_CAMP_Metabolic_Process	34	-0.5	-1.75	0.005	0.024	1
GO_BETA_AMYLOID_BINDING	34	-0.5	-1.75	0.004	0.024	1
GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	207	-0.36	-1.75	0	0.024	1
GO_MUSCLE_CONTRACTION	232	-0.35	-1.75	0	0.024	1
GO_CGMP_Metabolic_Process	23	-0.54	-1.75	0.01	0.024	1
GO_MELANOCYTE_DIFFERENTIATION	19	-0.57	-1.75	0.005	0.024	1
GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	54	-0.45	-1.73	0.002	0.027	1
GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	25	-0.53	-1.73	0.004	0.028	1
GO_REGULATION_OF_RESPONSE_TO_FOOD	19	-0.58	-1.73	0.005	0.027	1
GO_ENSHEATHMENT_OF_NEURONS	91	-0.4	-1.73	0	0.028	1
GO_NEUROTRANSMITTER_UPTAKE	15	-0.6	-1.73	0.013	0.028	1
GO_NEGATIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_Metabolic_Process	42	-0.47	-1.73	0.002	0.028	1
GO_REGULATION_OF_ARF_PROTEIN_SIGNAL_TRANSDUCTION	16	-0.6	-1.73	0.002	0.028	1
GO_WW_DOMAIN_BINDING	31	-0.51	-1.73	0.008	0.028	1
GO_Glutamate_Receptor_Binding	36	-0.48	-1.73	0.007	0.028	1
GO_REGULATION_OF_MICROTUBULE_BASED_MOVEMENT	18	-0.57	-1.72	0.016	0.03	1
GO_REGULATION_OF_AXONOGENESIS	166	-0.36	-1.72	0	0.03	1
GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	37	-0.48	-1.72	0.01	0.031	1
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	157	-0.36	-1.71	0	0.032	1

GO_SODIUM_CHANNEL_COMPLEX	17	-0.57	-1.71	0.015	0.033	1
GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	15	-0.59	-1.71	0.007	0.033	1
GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	45	-0.45	-1.71	0.007	0.034	1
GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	166	-0.36	-1.71	0	0.034	1
GO_FOREBRAIN_CELL_MIGRATION	61	-0.42	-1.7	0.002	0.035	1
GO_REGULATION_OF_AMINO_ACID_TRANSPORT	25	-0.52	-1.7	0.008	0.035	1
GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	24	-0.52	-1.7	0.011	0.036	1
GO_LONG_TERM_MEMORY	28	-0.5	-1.7	0.007	0.036	1
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	28	-0.5	-1.7	0.011	0.036	1
GO_MEMORY	98	-0.39	-1.69	0	0.039	1
GO_AXONAL_FASCICULATION	20	-0.55	-1.69	0.011	0.039	1
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_BINDING	28	-0.5	-1.69	0.021	0.04	1
GO_RENAL_WATER_HOMEOSTASIS	34	-0.48	-1.69	0.004	0.039	1
GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	30	-0.48	-1.68	0.005	0.04	1
GO_MOTILE_CILIUM	101	-0.38	-1.68	0	0.04	1
GO_CYTOSOLIC_TRANSPORT	210	-0.34	-1.68	0	0.04	1
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	297	-0.33	-1.68	0	0.04	1
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	45	-0.45	-1.68	0.006	0.041	1
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	26	-0.51	-1.68	0.009	0.042	1
GO_SNARE_BINDING	124	-0.37	-1.68	0	0.042	1
GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	62	-0.41	-1.68	0	0.042	1
GO_CAMERA_TYPE_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	15	-0.57	-1.67	0.01	0.042	1
GO_MUSCLE_HYPERTROPHY	28	-0.49	-1.67	0.014	0.044	1
GO_SARCOPLASM	67	-0.41	-1.67	0.002	0.044	1
GO_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	17	-0.57	-1.67	0.018	0.044	1
GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	24	-0.51	-1.67	0.014	0.044	1
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	89	-0.39	-1.67	0	0.044	1
GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	78	-0.4	-1.67	0.002	0.044	1
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	31	-0.48	-1.67	0.015	0.045	1
GO_CEREBELLAR_CORTEX_FORMATION	21	-0.53	-1.66	0.015	0.045	1
GO_CALCIUM_ION_TRANSPORT	220	-0.34	-1.66	0	0.046	1
GO_REGULATION_OF_BEHAVIOR	65	-0.41	-1.66	0.003	0.046	1
GO_REGULATION_OF_METAL_ION_TRANSPORT	322	-0.32	-1.66	0	0.047	1
GO_RESPONSE_TO_AUDITORY_STIMULUS	23	-0.51	-1.66	0.025	0.048	1
GO_REGULATION_OF_PROTEIN_KINASE_A_SIGNALING	17	-0.56	-1.66	0.023	0.048	1
GO_AXONAL_GROWTH_CONE	20	-0.53	-1.65	0.009	0.049	1
GO_SYNAPSE_ASSEMBLY	69	-0.41	-1.65	0.002	0.049	1
GO_POTASSIUM_ION_IMPORT	28	-0.49	-1.65	0.009	0.051	1
GO_REGULATION_OF_MITOCHONDRIAL_FISSION	17	-0.55	-1.64	0.022	0.053	1
GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	56	-0.41	-1.64	0.005	0.054	1
GO_ALPHA_ACTININ_BINDING	21	-0.52	-1.64	0.022	0.055	1
GO_GABA_RECEPTOR_ACTIVITY	22	-0.52	-1.64	0.013	0.055	1
GO_TRANSPORT_VESICLE_MEMBRANE	149	-0.35	-1.64	0	0.056	1
GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	32	-0.47	-1.63	0.019	0.057	1
GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	293	-0.32	-1.63	0	0.057	1
GO_ALKALI_METAL_ION_BINDING	21	-0.52	-1.63	0.011	0.058	1
GO_VENTRAL_SPINAL_CORD_INTERNEURON_DIFFERENTIATION	17	-0.54	-1.63	0.031	0.059	1
GO_SMOOTHENED_SIGNALING_PATHWAY	70	-0.39	-1.63	0.012	0.059	1
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_ION_SIGNALING	23	-0.51	-1.62	0.016	0.062	1
GO_RETROGRADE_TRANSPORT_VESICLE_RECYCLING_WITHIN_GOLGI	23	-0.5	-1.62	0.009	0.063	1
GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	16	-0.56	-1.62	0.021	0.063	1
GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	77	-0.38	-1.62	0.007	0.064	1
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	26	-0.48	-1.61	0.014	0.065	1
GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	131	-0.35	-1.61	0.002	0.065	1
GO_PHOTORECEPTOR_CONNECTING_CILIUM	30	-0.47	-1.61	0.018	0.065	1
GO_CALMODULIN_BINDING	177	-0.34	-1.61	0	0.065	1
GO_NEURONAL_ACTION_POTENTIAL	28	-0.48	-1.61	0.012	0.065	1
GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	23	-0.51	-1.61	0.02	0.066	1
GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	34	-0.45	-1.61	0.014	0.066	1
GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	18	-0.53	-1.61	0.024	0.066	1
GO_PHOTORECEPTOR_CELL_DIFFERENTIATION	50	-0.42	-1.61	0.006	0.067	1
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COACTIVATOR_ACTIVITY	36	-0.45	-1.61	0.014	0.068	1
GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	89	-0.37	-1.6	0.002	0.068	1
GO_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	36	-0.45	-1.6	0.004	0.068	1
GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	18	-0.53	-1.6	0.019	0.069	1
GO_TELENCEPHALON_GLIAL_CELL_MIGRATION	19	-0.53	-1.6	0.014	0.069	1
GO_EPITHELIAL_CILIUM_MOVEMENT	17	-0.53	-1.6	0.029	0.07	1
GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	21	-0.51	-1.6	0.021	0.07	1
GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	225	-0.33	-1.6	0	0.07	1
GO_REGULATION_OF_CILIUM_ASSEMBLY	48	-0.42	-1.6	0.012	0.07	1
GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	37	-0.44	-1.6	0.012	0.071	1
GO_SIALYLATION	21	-0.51	-1.6	0.025	0.071	1
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	89	-0.37	-1.59	0.003	0.072	1
GO_NEURON_MIGRATION	109	-0.35	-1.59	0.003	0.073	1
GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	34	-0.45	-1.59	0.021	0.073	1
GO_CILIARY_MEMBRANE	77	-0.39	-1.59	0.007	0.074	1
GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	73	-0.38	-1.59	0.005	0.075	1
GO_RESPONSE_TO_MONOAMINE	35	-0.45	-1.59	0.021	0.075	1
GO_GABA_RECEPTOR_COMPLEX	18	-0.53	-1.59	0.026	0.076	1
GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	429	-0.3	-1.58	0	0.079	1
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	133	-0.34	-1.58	0.003	0.08	1
GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	360	-0.3	-1.58	0	0.08	1

GO_RENAL_SYSTEM_PROCESS	99	-0.36	-1.58	0.002	0.08	1
GO_CATECHOLAMINE_BINDING	16	-0.53	-1.57	0.024	0.081	1
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	211	-0.32	-1.57	0	0.081	1
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	27	-0.47	-1.57	0.03	0.082	1
GO_NEGATIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	16	-0.54	-1.57	0.025	0.082	1
GO_FERROUS_IRON_BINDING	22	-0.49	-1.57	0.042	0.083	1
GO_PHOTORECEPTOR_CELL_MAINTENANCE	35	-0.44	-1.57	0.028	0.083	1
GO_INTRACILIARY_TRANSPORT_PARTICLE_BINDING	19	-0.52	-1.57	0.027	0.084	1
GO_INSULIN_RECEPTOR_BINDING	32	-0.45	-1.57	0.015	0.084	1
GO_SCF_UBIQUITIN_LIGASE_COMPLEX	34	-0.44	-1.57	0.016	0.084	1
GO_NEUROTROPHIN_SIGNALING_PATHWAY	23	-0.49	-1.57	0.028	0.084	1
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	109	-0.35	-1.57	0.003	0.085	1
GO_NEURAL_RETINA_DEVELOPMENT	50	-0.41	-1.57	0.01	0.084	1
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	41	-0.43	-1.57	0.012	0.084	1
GO_SENSORY_PERCEPTION_OF_PAIN	75	-0.37	-1.56	0.005	0.084	1
GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	26	-0.48	-1.56	0.018	0.085	1
GO_MEMBRANE_BIOGENESIS	30	-0.45	-1.56	0.028	0.085	1
GO_CALCIIUM_MEDIATED_SIGNALING_USING_INTRACELLULAR_CALCIIUM_SOURCE	16	-0.54	-1.56	0.041	0.085	1
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	15	-0.53	-1.56	0.034	0.085	1
GO_METENCEPHALON_DEVELOPMENT	99	-0.35	-1.56	0.002	0.085	1
GO_NEUROPEPTIDE_HORMONE_ACTIVITY	29	-0.46	-1.56	0.021	0.085	1
GO_CELL_PROJECTION_ASSEMBLY	248	-0.31	-1.56	0.002	0.088	1
GO_MYOFIBRIL_ASSEMBLY	48	-0.41	-1.56	0.014	0.089	1
GO_DENDRITE_CYTOPLASM	16	-0.53	-1.55	0.028	0.089	1
GO_POSITIVE_REGULATION_OF_AXONOGENESIS	68	-0.38	-1.55	0.009	0.089	1
GO_MULTI_ORGANISM_BEHAVIOR	75	-0.37	-1.55	0.003	0.089	1
GO_PDZ_DOMAIN_BINDING	90	-0.36	-1.55	0.008	0.09	1
GO_PEPTIDE_HORMONE_BINDING	36	-0.43	-1.55	0.021	0.09	1
GO_POSITIVE_REGULATION_OF_BEHAVIOR	26	-0.48	-1.55	0.024	0.091	1
GO_FOREBRAIN_NEURON_DEVELOPMENT	34	-0.43	-1.55	0.02	0.091	1
GO_REGULATION_OF_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	18	-0.51	-1.55	0.052	0.092	1
GO_PHOTORECEPTOR_CELL_DEVELOPMENT	39	-0.42	-1.55	0.022	0.092	1
GO_NUCLEUS_LOCALIZATION	20	-0.5	-1.55	0.026	0.092	1
GO_ACROSOME_REACTION	17	-0.51	-1.55	0.042	0.092	1
GO_DEVELOPMENTAL_CELL_GROWTH	76	-0.36	-1.54	0.011	0.095	1
GO_MUSCLE_MYOSIN_COMPLEX	19	-0.5	-1.54	0.038	0.096	1
GO_ORGANELLE_MEMBRANE_FUSION	95	-0.35	-1.54	0.005	0.096	1
GO_NEUROMUSCULAR_JUNCTION	54	-0.39	-1.54	0.019	0.097	1
GO_SPINAL_CORD_PATTERNING	24	-0.47	-1.54	0.037	0.098	1
GO_REGULATION_OF_CIRCADIAN_SLEEP_WAKE_CYCLE	25	-0.48	-1.54	0.026	0.098	1
GO_REGULATION_OF_Glutamate_Secretion	15	-0.54	-1.54	0.039	0.097	1
GO_CALCIIUM_MEDIATED_SIGNALING	88	-0.36	-1.54	0.008	0.098	1
GO_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	116	-0.34	-1.53	0.003	0.099	1
GO_CILIARY_BASAL_BODY	76	-0.37	-1.53	0.017	0.1	1
GO_TRANSLATION_REGULATOR_ACTIVITY	35	-0.43	-1.53	0.02	0.102	1
GO_APICAL_DENDRITE	15	-0.54	-1.53	0.036	0.101	1
GO_REGULATION_OF_VESICLE_FUSION	60	-0.38	-1.53	0.018	0.102	1
GO_POTASSIUM_ION_BINDING	15	-0.53	-1.53	0.047	0.103	1
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	125	-0.33	-1.53	0.005	0.103	1
GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	46	-0.41	-1.53	0.017	0.103	1
GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	18	-0.5	-1.53	0.018	0.103	1
GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	37	-0.42	-1.52	0.028	0.106	1
GO_SNARE_COMPLEX	53	-0.39	-1.52	0.008	0.11	1
GO_NEGATIVE_REGULATION_OF_CATECHOLAMINE_SECRETION	16	-0.53	-1.52	0.045	0.11	1
GO_ANATOMICAL_STRUCTURE_MATURATION	39	-0.41	-1.52	0.02	0.111	1
GO_CONTRACTILE_FIBER	209	-0.31	-1.51	0.002	0.112	1
GO_MYELIN_ASSEMBLY	17	-0.5	-1.51	0.051	0.113	1
GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	63	-0.37	-1.51	0.026	0.115	1
GO_CALCIIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_Membrane_Cell_Adhesion_Molecules	27	-0.45	-1.51	0.029	0.115	1
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	234	-0.3	-1.51	0	0.114	1
GO_NEGATIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	15	-0.53	-1.51	0.053	0.115	1
GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	25	-0.47	-1.51	0.042	0.115	1
GO_PEROXISOMAL_TRANSPORT	18	-0.5	-1.51	0.055	0.115	1
GO_GANGLIOSIDE_BIOSYNTHETIC_PROCESS	18	-0.49	-1.51	0.051	0.116	1
GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	49	-0.38	-1.5	0.021	0.117	1
GO_CALCIIUM_CHANNEL_REGULATOR_ACTIVITY	37	-0.41	-1.5	0.04	0.117	1
GO_PROTEIN_LOCALIZATION_TO_GOLGI_APPARATUS	32	-0.42	-1.5	0.041	0.117	1
GO_GLIAL_CELL_PROJECTION	15	-0.52	-1.5	0.046	0.117	1
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	29	-0.43	-1.5	0.045	0.117	1
GO_MICROTUBULE_BUNDLE_FORMATION	64	-0.37	-1.5	0.009	0.118	1
GO_INTRASPECIES_INTERACTION_BETWEEN_ORGANISMS	46	-0.4	-1.5	0.027	0.118	1
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	265	-0.3	-1.5	0.005	0.118	1
GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	24	-0.45	-1.5	0.047	0.119	1
GO_PEROXISOME_ORGANIZATION	32	-0.43	-1.5	0.031	0.122	1
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	49	-0.39	-1.49	0.029	0.123	1
GO_CALCIIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	17	-0.5	-1.49	0.052	0.124	1
GO_LYSOSOMAL_TRANSPORT	67	-0.37	-1.49	0.017	0.125	1
GO_HEART_PROCESS	84	-0.35	-1.49	0.013	0.125	1
GO_PROTEIN_KINASE_A_REGULATORY_SUBUNIT_BINDING	16	-0.5	-1.49	0.056	0.125	1

GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PR						
OTEIN_SIGNALING_PATHWAY	25	-0.45	-1.49	0.045	0.125	1
GO_CARDIAC_MYOFIBRIL_ASSEMBLY	16	-0.51	-1.49	0.053	0.125	1
GO_REFLEX	20	-0.49	-1.49	0.044	0.125	1
GO_EXOCYTOSIS	299	-0.29	-1.49	0.001	0.128	1
GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	19	-0.48	-1.49	0.057	0.128	1
GO_SARCOPLASMIC_RETICULUM_MEMBRANE	37	-0.41	-1.48	0.031	0.129	1
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFEREN						
TIATION	335	-0.29	-1.48	0	0.129	1
GO_MUSCLE_FIBER_DEVELOPMENT	47	-0.39	-1.48	0.026	0.128	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KIN						
ASE_ACTIVITY	17	-0.51	-1.48	0.047	0.129	1
GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	100	-0.34	-1.48	0.012	0.132	1
GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	27	-0.44	-1.48	0.05	0.133	1
GO_FEEDING_BEHAVIOR	91	-0.34	-1.48	0.024	0.133	1
GO_CILIARY_BASE	23	-0.46	-1.48	0.049	0.133	1
GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	39	-0.4	-1.48	0.043	0.132	1
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	33	-0.42	-1.48	0.036	0.133	1
GO_DETECTION_OF_ABIOTIC_STIMULUS	115	-0.33	-1.48	0.005	0.133	1
GO_MONOAMINE_TRANSPORT	22	-0.47	-1.48	0.049	0.133	1
GO_DYNEIN_COMPLEX	43	-0.39	-1.47	0.03	0.136	1
GO_REGULATION_OF_VACUOLE_ORGANIZATION	41	-0.4	-1.47	0.042	0.136	1
GO_ADRENAL_GLAND_DEVELOPMENT	23	-0.46	-1.47	0.044	0.136	1
GO_PRIMARY_AMINO_COMPOUND_METABOLIC_PROCESS	15	-0.5	-1.47	0.062	0.136	1
GO_ASSOCIATIVE_LEARNING	73	-0.36	-1.47	0.025	0.137	1
GO_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	42	-0.4	-1.47	0.031	0.137	1
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	154	-0.31	-1.47	0.005	0.139	1
GO_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPOR	97	-0.34	-1.47	0.017	0.139	1
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	66	-0.35	-1.46	0.032	0.142	1
GO_RAC_PROTEIN_SIGNAL_TRANSDUCTION	18	-0.49	-1.46	0.049	0.143	1
GO_IONOTROPIC_GLUTAMATE_RECEPTOR_BINDING	23	-0.46	-1.46	0.06	0.144	1
GO_THYROID_HORMONE_METABOLIC_PROCESS	16	-0.49	-1.46	0.071	0.145	1
GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC						
_PROCESS	17	-0.49	-1.46	0.074	0.145	1
GO_MEMBRANE_ASSEMBLY	25	-0.45	-1.46	0.049	0.145	1
GO_REGULATION_OF_FATTY_ACID_OXIDATION	27	-0.44	-1.46	0.032	0.146	1
GO_REGULATION_OF_CORTICOSTEROID_HORMONE_SECRETION	15	-0.51	-1.46	0.064	0.146	1
GO_REGULATION_OF_NEURON_MIGRATION	29	-0.43	-1.46	0.045	0.147	1
GO_NEURON_PROJECTION_GUIDANCE	204	-0.3	-1.46	0.005	0.147	1
GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_						
MIGRATION	24	-0.45	-1.46	0.045	0.147	1
GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	28	-0.43	-1.45	0.065	0.148	1
GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	260	-0.29	-1.45	0.005	0.148	1
GO_HEART_GROWTH	26	-0.44	-1.45	0.052	0.15	1
GO_CEREBRAL_CORTEX_CELL_MIGRATION	42	-0.38	-1.45	0.037	0.15	1
GO_REGULATION_OF_CYTOSOLIC_CALCIIUM_ION_CONCENTRATION	202	-0.3	-1.45	0	0.15	1
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	42	-0.39	-1.45	0.039	0.149	1
GO_NEURON_PROJECTION_EXTENSION	52	-0.37	-1.45	0.035	0.15	1
GO_REGULATED_EXOCYTOSIS	219	-0.3	-1.45	0.005	0.151	1
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	32	-0.41	-1.45	0.047	0.153	1
GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION	31	-0.42	-1.45	0.054	0.153	1
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	463	-0.27	-1.45	0.001	0.153	1
GO_REGULATION_OF_APPETITE	24	-0.44	-1.45	0.064	0.153	1
GO_SPERM_FLAGELLUM	53	-0.37	-1.45	0.036	0.153	1
GO_REGULATION_OF_SODIUM_ION_TRANSPORT	75	-0.34	-1.45	0.025	0.154	1
GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	211	-0.3	-1.44	0.002	0.156	1
GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	192	-0.3	-1.44	0.002	0.156	1
GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	63	-0.36	-1.44	0.035	0.156	1
GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	66	-0.35	-1.44	0.032	0.159	1
GO_ACTIN_MEDIATED_CELL_CONTRACTION	74	-0.35	-1.44	0.026	0.16	1
GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	32	-0.41	-1.44	0.071	0.16	1
GO_REGULATION_OF_SENSORY_PERCEPTION	36	-0.4	-1.44	0.059	0.16	1
GO_ORGANELLE_FUSION	128	-0.31	-1.44	0.022	0.16	1
GO_A_BAND	34	-0.41	-1.44	0.048	0.16	1
GO_DIPEPTIDASE_ACTIVITY	15	-0.5	-1.44	0.092	0.161	1
GO_REGULATION_OF_CATECHOLAMINE_METABOLIC_PROCESS	17	-0.48	-1.44	0.07	0.161	1
GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENE	21	-0.46	-1.43	0.084	0.162	1
GO_CALCIIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	28	-0.42	-1.43	0.055	0.164	1
GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	19	-0.47	-1.43	0.067	0.164	1
GO_GLIOGENESIS	174	-0.3	-1.43	0.005	0.165	1
GO_PHOSPHOLIPASE_BINDING	18	-0.47	-1.43	0.066	0.165	1
GO_CERAMIDE_BIOSYNTHETIC_PROCESS	37	-0.4	-1.43	0.054	0.165	1
GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	30	-0.41	-1.43	0.042	0.164	1
GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_T						
RANSDUCTION	38	-0.39	-1.43	0.05	0.167	1
GO_PROTEIN_MANNOSYLATION	22	-0.45	-1.43	0.066	0.17	1
GO_HINDBRAIN_MORPHOGENESIS	39	-0.39	-1.42	0.045	0.17	1
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	32	-0.41	-1.42	0.068	0.17	1
GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIIUM_RELEASE_CHA						
NNEL_ACTIVITY	27	-0.42	-1.42	0.055	0.172	1
GO_PIGMENTATION	83	-0.33	-1.42	0.028	0.175	1
GO_SINGLE_ORGANISM_MEMBRANE_FUSION	128	-0.31	-1.42	0.018	0.174	1
GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	79	-0.34	-1.42	0.029	0.178	1
GO_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	35	-0.4	-1.42	0.056	0.179	1
GO_REGULATION_OF_STEROID_HORMONE_SECRETION	20	-0.45	-1.42	0.085	0.178	1
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	287	-0.28	-1.42	0.003	0.178	1
GO_MYOSIN_FILAMENT	22	-0.44	-1.41	0.055	0.18	1

GO_PROTEIN_KINASE_A_CATALYTIC_SUBUNIT_BINDING	15	-0.5	-1.41	0.083	0.181	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	17	-0.48	-1.41	0.078	0.181	1
GO_TRANSPORT_VESICLE	333	-0.27	-1.41	0.002	0.182	1
GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	16	-0.49	-1.41	0.089	0.182	1
GO_CEREBELLAR_CORTEX_MORPHOGENESIS	29	-0.41	-1.41	0.063	0.183	1
GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	57	-0.35	-1.41	0.051	0.183	1
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	32	-0.41	-1.41	0.062	0.183	1
GO_LIGAND_GATED_CALCIUM_CHANNEL_ACTIVITY	16	-0.48	-1.41	0.082	0.184	1
GO_DENDRITIC_SPINE_ORGANIZATION	17	-0.47	-1.41	0.076	0.183	1
GO_SODIUM_ION_TRANSPORT	142	-0.3	-1.41	0.017	0.185	1
GO_SECRETION_BY_CELL	474	-0.26	-1.41	0.001	0.185	1
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	41	-0.39	-1.41	0.051	0.185	1
GO_HINDBRAIN_DEVELOPMENT	135	-0.3	-1.4	0.012	0.186	1
GO_CLATHRIN_BINDING	65	-0.35	-1.4	0.043	0.187	1
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIM	48	-0.37	-1.4	0.046	0.189	1
GO_GLIAL_CELL_DIFFERENTIATION	136	-0.3	-1.4	0.03	0.189	1
GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	18	-0.46	-1.4	0.083	0.188	1
GO_NEGATIVE_REGULATION_OF_BEHAVIOR	17	-0.47	-1.4	0.081	0.188	1
GO_REGULATION_OF_CLATHRIN_MEDIATED_ENDOCYTOSIS	16	-0.49	-1.4	0.097	0.189	1
GO_VESICLE_LOCALIZATION	220	-0.29	-1.4	0.005	0.189	1
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	34	-0.39	-1.4	0.067	0.189	1
GO_AUTOPHAGOSOME	76	-0.34	-1.4	0.038	0.191	1
GO_DEVELOPMENTAL_MATURATION	191	-0.29	-1.4	0.014	0.19	1
GO_DOPAMINE_RECEPTOR_BINDING	17	-0.47	-1.4	0.088	0.191	1
GO_INCLUSION_BODY	68	-0.34	-1.4	0.046	0.191	1
GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	17	-0.46	-1.4	0.092	0.191	1
GO_MEMBRANE_FUSION	157	-0.3	-1.39	0.011	0.194	1
GO_N_GLYCAN_PROCESSING	20	-0.45	-1.39	0.103	0.194	1
GO_ESTABLISHMENT_OF_LOCALIZATION_BY_MOVEMENT_ALONG_MICR OTUBULE	95	-0.32	-1.39	0.034	0.194	1
GO_CGMP_BINDING	16	-0.48	-1.39	0.088	0.195	1
GO_SPECIFICATION_OF_SYMMETRY	114	-0.31	-1.39	0.033	0.195	1
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	208	-0.28	-1.39	0.015	0.196	1
GO_REGULATION_OF_DEVELOPMENTAL_PIGMENTATION	16	-0.48	-1.39	0.104	0.196	1
GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	189	-0.29	-1.39	0.009	0.196	1
GO_PHOTORECEPTOR_OUTER_SEGMENT	69	-0.34	-1.39	0.036	0.198	1
GO_REGULATION_OF_PROTEIN_ACETYLATION	63	-0.35	-1.39	0.035	0.198	1
GO_CYTOSKELETAL_ADAPTOR_ACTIVITY	16	-0.48	-1.39	0.08	0.198	1
GO_PERICENTRIOLAR_MATERIAL	17	-0.47	-1.39	0.091	0.198	1
GO_M_BAND	21	-0.44	-1.39	0.093	0.199	1
GO_REGULATION_OF_HORMONE_SECRETION	258	-0.27	-1.39	0.003	0.2	1
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	47	-0.36	-1.38	0.062	0.201	1
GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_GOLGI	71	-0.34	-1.38	0.039	0.203	1
GO_REGULATION_OF_RECEPTOR_ACTIVITY	117	-0.31	-1.38	0.038	0.203	1
GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	21	-0.44	-1.38	0.095	0.205	1
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	131	-0.3	-1.38	0.018	0.205	1
GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX	23	-0.43	-1.38	0.082	0.206	1
GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	20	-0.45	-1.38	0.086	0.208	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	81	-0.32	-1.38	0.036	0.209	1
GO_REGULATION_OF_PEPTIDE_SECRETION	206	-0.28	-1.38	0.014	0.21	1
GO_RECEPTOR_COMPLEX	326	-0.27	-1.38	0	0.209	1
GO_EYE_PHOTORECEPTOR_CELL_DEVELOPMENT	31	-0.4	-1.38	0.065	0.21	1
GO_HORMONE_BINDING	65	-0.34	-1.37	0.041	0.21	1
GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	61	-0.34	-1.37	0.038	0.212	1
GO_RETINA_LAYER_FORMATION	22	-0.43	-1.37	0.092	0.216	1
GO_REGULATION_OF_MUSCLE_CONTRACTION	147	-0.29	-1.37	0.016	0.216	1
GO_REGULATION_OF_DENDRITE_EXTENSION	19	-0.45	-1.37	0.091	0.216	1
GO_KIDNEY_EPITHELIUM_DEVELOPMENT	125	-0.3	-1.37	0.016	0.221	1
GO_TRANS_GOLGI_NETWORK	186	-0.28	-1.36	0.02	0.223	1
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	80	-0.33	-1.36	0.045	0.223	1
GO_SYNAPTIC_VESICLE_ENDOCYTOSIS	17	-0.46	-1.36	0.117	0.223	1
GO_PHOSPHATIDYLINOSITOL_BINDING	198	-0.28	-1.36	0.017	0.223	1
GO_RESPONSE_TO_FOLIC_ACID	15	-0.49	-1.36	0.102	0.223	1
GO_OLFACTORY_BULB_INTERNEURON_DIFFERENTIATION	15	-0.47	-1.36	0.121	0.223	1
GO_MEMBRANE_REPOLARIZATION	15	-0.48	-1.36	0.125	0.225	1
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	23	-0.41	-1.36	0.108	0.227	1
GO_FEAR_RESPONSE	29	-0.41	-1.36	0.096	0.231	1
GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEI N_CATABOLIC_PROCESS	23	-0.42	-1.36	0.094	0.231	1
GO_BETA_CATENIN_BINDING	84	-0.31	-1.35	0.034	0.233	1
GO_INTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	28	-0.39	-1.35	0.102	0.234	1
GO_CAMP_BIOSYNTHETIC_PROCESS	17	-0.45	-1.35	0.098	0.234	1
GO_VISUAL_BEHAVIOR	50	-0.35	-1.35	0.069	0.234	1
GO_NITRIC_OXIDE_SYNTHASE_BINDING	19	-0.44	-1.35	0.102	0.233	1
GO_DENDRITIC_SPINE_DEVELOPMENT	19	-0.44	-1.35	0.115	0.233	1
GO_STRIATED_MUSCLE_CONTRACTION	98	-0.32	-1.35	0.04	0.234	1
GO_DEVELOPMENTAL_PIGMENTATION	38	-0.37	-1.35	0.082	0.234	1
GO_MUSCLE_ADAPTATION	29	-0.4	-1.35	0.091	0.239	1
GO_ADRENERGIC_RECEPTOR_BINDING	19	-0.44	-1.35	0.118	0.24	1
GO_CATECHOLAMINE_METABOLIC_PROCESS	40	-0.37	-1.35	0.08	0.24	1
GO_RESPONSE_TO_AMPHETAMINE	30	-0.4	-1.35	0.101	0.24	1
GO_DETECTION_OF_MECHANICAL_STIMULUS	41	-0.36	-1.35	0.075	0.24	1
GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	340	-0.26	-1.35	0.008	0.24	1
GO_VENTRICULAR_SYSTEM_DEVELOPMENT	25	-0.41	-1.35	0.105	0.241	1
GO_CELL_PROJECTION_CYTOPLASM	52	-0.34	-1.35	0.064	0.241	1
GO_CIRCULATORY_SYSTEM_PROCESS	364	-0.26	-1.34	0.005	0.243	1
GO_INSULIN_SECRETION	38	-0.37	-1.34	0.079	0.244	1

GO_PEPTIDE_SECRETION	57	-0.34	-1.34	0.073	0.244	1
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	-0.47	-1.34	0.126	0.245	1
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	20	-0.44	-1.34	0.123	0.246	1
GO_SPECTRIN_BINDING	24	-0.42	-1.34	0.111	0.246	1
GO_CYCLASE_ACTIVITY	22	-0.42	-1.34	0.095	0.248	1
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	172	-0.28	-1.34	0.029	0.25	1
GO_CELLULAR_RESPONSE_TO_CAMP	50	-0.35	-1.34	0.069	0.25	1
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	47	-0.35	-1.34	0.059	0.25	1
GO_INTERCALATED_DISC	51	-0.35	-1.34	0.091	0.251	1
GO_OTIC_VESICLE_DEVELOPMENT	15	-0.47	-1.33	0.112	0.252	1
GO_PROTEOGLYCAN_METABOLIC_PROCESS	82	-0.31	-1.33	0.05	0.252	1
GO_CELL_PROJECTION_MEMBRANE	295	-0.26	-1.33	0.007	0.252	1
GO_HIPPOCAMPUS_DEVELOPMENT	72	-0.32	-1.33	0.07	0.256	1
GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	25	-0.41	-1.33	0.102	0.256	1
GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	68	-0.32	-1.33	0.084	0.257	1
GO_DICARBOXYLIC_ACID_TRANSPORT	71	-0.32	-1.33	0.08	0.258	1
GO_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	58	-0.33	-1.33	0.093	0.259	1
GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	120	-0.29	-1.33	0.042	0.259	1
GO_REGULATION_OF_ANION_TRANSPORT	136	-0.29	-1.33	0.046	0.26	1
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	135	-0.29	-1.33	0.03	0.26	1
GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	150	-0.28	-1.33	0.026	0.26	1
GO_REGULATION_OF_FILOPODIUM_ASSEMBLY	38	-0.36	-1.33	0.093	0.26	1
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	53	-0.34	-1.33	0.094	0.261	1
GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	56	-0.34	-1.33	0.081	0.26	1
GO_CORONARY_VASCULATURE_DEVELOPMENT	37	-0.37	-1.32	0.08	0.26	1
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	85	-0.31	-1.32	0.057	0.26	1
GO_NEGATIVE_REGULATION_OF_GLIA_CELL_DIFFERENTIATION	26	-0.39	-1.32	0.112	0.262	1
GO_AUTOPHAGOSOME_MEMBRANE	26	-0.41	-1.32	0.111	0.262	1
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	271	-0.26	-1.32	0.015	0.262	1
GO_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	60	-0.33	-1.32	0.102	0.266	1
GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	300	-0.26	-1.32	0.019	0.265	1
GO_FOREBRAIN_DEVELOPMENT	353	-0.25	-1.32	0.015	0.265	1
GO_REGULATION_OF_VASCULAR_PERMEABILITY	29	-0.38	-1.32	0.105	0.267	1
GO_VASCULOGENESIS	59	-0.33	-1.32	0.073	0.267	1
GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	68	-0.32	-1.32	0.062	0.271	1
GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	126	-0.29	-1.32	0.039	0.271	1
GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	33	-0.37	-1.32	0.095	0.27	1
GO_SPINAL_CORD_DEVELOPMENT	106	-0.3	-1.32	0.049	0.271	1
GO_BICARBONATE_TRANSPORT	44	-0.35	-1.32	0.109	0.27	1
GO_REGULATION_OF_ION_HOMEOSTASIS	201	-0.27	-1.31	0.024	0.272	1
GO_MUSCLE_CELL_DIFFERENTIATION	236	-0.26	-1.31	0.022	0.273	1
GO_CEREBRAL_CORTEX_RADIALY_ORIENTED_CELL_MIGRATION	28	-0.39	-1.31	0.117	0.273	1
GO_RAB_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	30	-0.38	-1.31	0.101	0.273	1
GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	18	-0.43	-1.31	0.134	0.276	1
GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	17	-0.45	-1.31	0.137	0.276	1
GO_DETECTION_OF_LIGHT_STIMULUS	58	-0.33	-1.31	0.094	0.276	1
GO_STRIATUM_DEVELOPMENT	16	-0.44	-1.31	0.139	0.277	1
GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	20	-0.42	-1.31	0.144	0.278	1
GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	320	-0.25	-1.31	0.013	0.281	1
GO_REGULATION_OF_CELL_SIZE	170	-0.27	-1.31	0.045	0.28	1
GO_HEART_DEVELOPMENT	462	-0.24	-1.31	0.01	0.28	1
GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	21	-0.41	-1.31	0.124	0.28	1
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	38	-0.36	-1.31	0.107	0.28	1
GO_RESPONSE_TO_EPINEPHRINE	16	-0.44	-1.3	0.133	0.286	1
GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	33	-0.37	-1.3	0.113	0.288	1
GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	134	-0.28	-1.3	0.052	0.291	1
GO_REGULATION_OF_HEART_GROWTH	41	-0.35	-1.3	0.108	0.292	1
GO_PROTEIN_ADP_RIBOSYLATION	20	-0.42	-1.3	0.147	0.296	1
GO_PIGMENT_CELL_DIFFERENTIATION	28	-0.38	-1.29	0.143	0.297	1
GO_NEUROTRANSMITTER_METABOLIC_PROCESS	25	-0.4	-1.29	0.134	0.297	1
GO_ORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	-0.45	-1.29	0.132	0.298	1
GO_REGULATION_OF_NOREPINEPHRINE_SECRETION	17	-0.44	-1.29	0.145	0.298	1
GO_CATION_CATION_ANTIPORTER_ACTIVITY	23	-0.4	-1.29	0.153	0.3	1
GO_SYNAPTIC_VESICLE_RECYCLING	23	-0.4	-1.29	0.15	0.3	1
GO_PROTEIN_O_LINKED_MANNOSYLATION	16	-0.43	-1.29	0.152	0.303	1
GO_NEGATIVE_REGULATION_OF_AXONOGENESIS	65	-0.32	-1.29	0.089	0.304	1
GO_ACTININ_BINDING	29	-0.38	-1.29	0.118	0.303	1
GO_GMP_METABOLIC_PROCESS	20	-0.42	-1.29	0.179	0.304	1
GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	162	-0.27	-1.29	0.07	0.305	1
GO_SMOOTH_MUSCLE_CONTRACTION	45	-0.34	-1.29	0.111	0.305	1
GO_CHLORIDE_TRANSPORT	99	-0.29	-1.29	0.072	0.305	1
GO_ORGAN_GROWTH	68	-0.32	-1.29	0.099	0.306	1
GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	30	-0.38	-1.29	0.132	0.307	1
GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	24	-0.39	-1.29	0.15	0.307	1
GO_NEPHRON_DEVELOPMENT	115	-0.29	-1.29	0.072	0.306	1
GO_SULFOTRANSFERASE_ACTIVITY	51	-0.34	-1.29	0.106	0.306	1
GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	36	-0.36	-1.28	0.113	0.307	1
GO_ACIDIC_AMINO_ACID_TRANSPORT	21	-0.41	-1.28	0.139	0.307	1
GO_CEREBELLAR_CORTEX_DEVELOPMENT	45	-0.34	-1.28	0.12	0.307	1
GO_CHLORIDE_CHANNEL_COMPLEX	50	-0.33	-1.28	0.115	0.309	1
GO_CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	113	-0.29	-1.28	0.061	0.309	1

GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_CELLULAR_RESPONSE_TO_CHEMICAL_STIMULUS	27	-0.38	-1.28	0.157	0.31	1
GO_LIPID_MODIFICATION	208	-0.26	-1.28	0.039	0.312	1
GO_VASOCONSTRICTION	28	-0.38	-1.28	0.13	0.314	1
GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	15	-0.46	-1.28	0.161	0.315	1
GO_REGULATION_OF_RENAL_SODIUM_EXCRETION	24	-0.39	-1.28	0.14	0.315	1
GO_REGULATION_OF_CIRCADIAN_RHYTHM	103	-0.29	-1.28	0.076	0.316	1
GO_COCHLEA_DEVELOPMENT	39	-0.35	-1.28	0.118	0.319	1
GO_ENDOCARDIAL_CUSHION_FORMATION	15	-0.45	-1.27	0.151	0.321	1
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	227	-0.26	-1.27	0.042	0.322	1
GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	41	-0.35	-1.27	0.131	0.326	1
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	66	-0.31	-1.27	0.117	0.329	1
GO_CELL_GROWTH	129	-0.28	-1.27	0.074	0.329	1
GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	19	-0.42	-1.27	0.152	0.329	1
GO_RNA_POLYMERASE_II_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	27	-0.38	-1.27	0.148	0.334	1
GO_CLATHRIN_MEDIATED_ENDOCYTOSIS	35	-0.36	-1.26	0.136	0.335	1
GO_RESPONSE_TO_STIMULUS_INVOLVED_IN_REGULATION_OF_MUSCLE_ADAPTATION	15	-0.44	-1.26	0.168	0.335	1
GO_PROTEIN_KINASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	32	-0.36	-1.26	0.138	0.336	1
GO_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	22	-0.4	-1.26	0.15	0.336	1
GO_PIGMENT_GRANULE_LOCALIZATION	25	-0.39	-1.26	0.157	0.336	1
GO_NEGATIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	141	-0.27	-1.26	0.058	0.335	1
GO_POSITIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	24	-0.38	-1.26	0.158	0.335	1
GO_BRAIN_MORPHOGENESIS	34	-0.36	-1.26	0.155	0.335	1
GO_REGULATION_OF_EXCRETION	29	-0.36	-1.26	0.132	0.335	1
GO_CELL_CELL_CONTACT_ZONE	64	-0.31	-1.26	0.118	0.334	1
GO_RETROMER_COMPLEX	21	-0.4	-1.26	0.158	0.334	1
GO_REGULATION_OF_BLOOD_PRESSURE	169	-0.27	-1.26	0.057	0.335	1
GO_VACUOLE_FUSION	21	-0.4	-1.26	0.182	0.337	1
GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	79	-0.3	-1.26	0.098	0.337	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	55	-0.32	-1.26	0.124	0.338	1
GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	56	-0.32	-1.26	0.13	0.338	1
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	42	-0.33	-1.26	0.14	0.338	1
GO_RECEPTOR_SIGNALING_PROTEIN_ACTIVITY	172	-0.26	-1.26	0.061	0.338	1
GO_ACYL_COA_DEHYDROGENASE_ACTIVITY	17	-0.43	-1.26	0.178	0.341	1
GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	30	-0.37	-1.26	0.147	0.34	1
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	36	-0.34	-1.26	0.15	0.34	1
GO_LOCALIZATION_WITHIN_MEMBRANE	120	-0.28	-1.26	0.085	0.342	1
GO_MUSCLE_CELL_DEVELOPMENT	128	-0.27	-1.26	0.075	0.342	1
GO_PROTEIN_TARGETING_TO_PLASMA_MEMBRANE	23	-0.39	-1.26	0.17	0.342	1
GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	374	-0.24	-1.26	0.038	0.342	1
GO_ANTIPORTER_ACTIVITY	71	-0.3	-1.25	0.112	0.342	1
GO_CELLULAR_RESPONSE_TO_PEPTIDE	271	-0.25	-1.25	0.044	0.342	1
GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	59	-0.31	-1.25	0.14	0.346	1
GO_ORGAN_MATURATION	18	-0.42	-1.25	0.169	0.348	1
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	497	-0.23	-1.25	0.017	0.348	1
GO_CULLIN_RING_UBIQUITIN_LIGASE_COMPLEX	149	-0.27	-1.25	0.078	0.348	1
GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	361	-0.24	-1.25	0.036	0.35	1
GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	23	-0.38	-1.25	0.19	0.35	1
GO_LYTIC_VACUOLE_ORGANIZATION	50	-0.32	-1.25	0.127	0.35	1
GO_VESICLE_DOCKING	56	-0.31	-1.25	0.132	0.352	1
GO_CATION_AMINO_ACID_SYMPORTER_ACTIVITY	16	-0.43	-1.25	0.167	0.353	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVATION	64	-0.31	-1.25	0.135	0.353	1
GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	74	-0.3	-1.25	0.114	0.353	1
GO_MUSCLE_STRUCTURE_DEVELOPMENT	431	-0.24	-1.25	0.029	0.354	1
GO_PHOSPHOLIPID_BINDING	353	-0.24	-1.24	0.032	0.357	1
GO_AXO_DENDRITIC_TRANSPORT	37	-0.34	-1.24	0.159	0.357	1
GO_REGULATION_OF_URINE_VOLUME	20	-0.41	-1.24	0.182	0.357	1
GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	20	-0.41	-1.24	0.183	0.357	1
GO_MYOSIN_II_COMPLEX	25	-0.38	-1.24	0.162	0.362	1
GO_SPERM_PRINCIPAL_PIECE	17	-0.41	-1.24	0.189	0.362	1
GO_HISTONE_H4_K16_ACETYLATION	17	-0.41	-1.24	0.185	0.361	1
GO_ACTIN_FILAMENT_BASED_MOVEMENT	93	-0.28	-1.24	0.109	0.362	1
GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	31	-0.36	-1.24	0.148	0.364	1
GO_REGULATION_OF_PH	89	-0.28	-1.24	0.126	0.367	1
GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	30	-0.36	-1.24	0.185	0.367	1
GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	130	-0.27	-1.24	0.093	0.367	1
GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	39	-0.34	-1.24	0.161	0.366	1
GO_RESPONSE_TO_PAIN	29	-0.36	-1.23	0.168	0.373	1
GO_COMPACT_MYELIN	15	-0.44	-1.23	0.193	0.372	1
GO_OLIGODENDROCYTE_DIFFERENTIATION	60	-0.31	-1.23	0.139	0.372	1
GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	36	-0.34	-1.23	0.159	0.372	1
GO_DEACETYLASE_ACTIVITY	55	-0.31	-1.23	0.149	0.374	1
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	42	-0.33	-1.23	0.154	0.374	1
GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	36	-0.34	-1.23	0.172	0.373	1
GO_LIMBIC_SYSTEM_DEVELOPMENT	99	-0.28	-1.23	0.114	0.375	1
GO_RECEPTOR_INTERNALIZATION	50	-0.32	-1.23	0.155	0.375	1
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	83	-0.29	-1.23	0.121	0.375	1
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	117	-0.27	-1.23	0.119	0.377	1
GO_DETECTION_OF_VISIBLE_LIGHT	43	-0.33	-1.23	0.166	0.377	1
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	53	-0.31	-1.23	0.147	0.378	1

GO_SH3_DOMAIN_BINDING	116	-0.27	-1.23	0.105	0.379	1
GO_LEADING_EDGE_MEMBRANE	132	-0.27	-1.23	0.092	0.379	1
GO_ACID_SECRETION	66	-0.3	-1.23	0.149	0.379	1
GO_POSITIVE_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	59	-0.3	-1.23	0.151	0.38	1
GO_PHASIC_SMOOTH_MUSCLE_CONTRACTION	16	-0.42	-1.23	0.211	0.38	1
GO_ENDOTHELIUM_DEVELOPMENT	88	-0.29	-1.23	0.128	0.379	1
GO_ATRIOVENTRICULAR_VALVE_MORPHOGENESIS	16	-0.42	-1.23	0.207	0.379	1
GO_RESPONSE_TO_BMP	94	-0.28	-1.23	0.118	0.378	1
GO_INORGANIC_ANION_TRANSPORT	128	-0.27	-1.23	0.102	0.378	1
GO_EATING_BEHAVIOR	30	-0.36	-1.22	0.177	0.382	1
GO_ENERGY_RESERVE_METABOLIC_PROCESS	72	-0.3	-1.22	0.141	0.382	1
GO_INTRACELLULAR_LIPID_TRANSPORT	20	-0.4	-1.22	0.194	0.383	1
GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	29	-0.36	-1.22	0.18	0.384	1
GO_MICROTUBULE_BASED_MOVEMENT	199	-0.25	-1.22	0.084	0.386	1
GO_CLATHRIN_COAT_OF_COATED_PIT	16	-0.42	-1.22	0.214	0.386	1
GO_TELENCEPHALON_DEVELOPMENT	225	-0.25	-1.22	0.075	0.39	1
GO_REGULATION_OF_FEEDING_BEHAVIOR	22	-0.39	-1.22	0.201	0.395	1
GO_RAB_GTPASE_BINDING	119	-0.27	-1.22	0.124	0.397	1
GO_DERMATAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	16	-0.42	-1.21	0.223	0.398	1
GO_RESPONSE_TO_AXON_INJURY	47	-0.32	-1.21	0.166	0.398	1
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	45	-0.32	-1.21	0.17	0.398	1
GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	32	-0.35	-1.21	0.172	0.398	1
GO_CELLULAR_RESPONSE_TO_ZINC_ION	16	-0.41	-1.21	0.195	0.398	1
GO_PHOSPHATIDYLSERINE_BINDING	33	-0.35	-1.21	0.18	0.399	1
GO_ION_GATED_CHANNEL_ACTIVITY	43	-0.33	-1.21	0.174	0.399	1
GO_FOREBRAIN_GENERATION_OF_NEURONS	66	-0.3	-1.21	0.168	0.399	1
GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	27	-0.37	-1.21	0.181	0.4	1
GO_POTASSIUM_ION_HOMEOSTASIS	18	-0.4	-1.21	0.214	0.4	1
GO_AP_TYPE_MEMBRANE_COAT_ADAPTOR_COMPLEX	40	-0.33	-1.21	0.183	0.401	1
GO_MITOCHONDRION_LOCALIZATION	35	-0.33	-1.21	0.178	0.401	1
GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	36	-0.34	-1.21	0.188	0.403	1
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	100	-0.27	-1.21	0.121	0.404	1
GO_DETECTION_OF_LIGHT_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	18	-0.4	-1.21	0.217	0.403	1
GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS	150	-0.26	-1.21	0.115	0.407	1
GO_SNAP_RECEPTOR_ACTIVITY	38	-0.33	-1.21	0.196	0.407	1
GO_GLYCAN_METABOLIC_PROCESS	58	-0.3	-1.21	0.154	0.407	1
GO_SARCOMERE_ORGANIZATION	27	-0.36	-1.21	0.2	0.407	1
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	15	-0.41	-1.21	0.22	0.407	1
GO_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	171	-0.25	-1.2	0.126	0.409	1
GO_CELLULAR_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	95	-0.28	-1.2	0.134	0.409	1
GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	26	-0.36	-1.2	0.222	0.409	1
GO_AXONEME_PART	22	-0.38	-1.2	0.208	0.409	1
GO_METHYLATED_HISTONE_BINDING	49	-0.31	-1.2	0.175	0.409	1
GO_BETA_TUBULIN_BINDING	36	-0.34	-1.2	0.187	0.408	1
GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	22	-0.37	-1.2	0.207	0.412	1
GO_MESONEPHROS_DEVELOPMENT	90	-0.28	-1.2	0.164	0.417	1
GO_CYTOPLASMIC_MICROTUBULE_ORGANIZATION	42	-0.32	-1.2	0.176	0.417	1
GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	69	-0.29	-1.2	0.16	0.417	1
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	31	-0.35	-1.2	0.221	0.417	1
GO_AXON_REGENERATION	23	-0.37	-1.2	0.201	0.417	1
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	93	-0.28	-1.2	0.157	0.417	1
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	17	-0.41	-1.2	0.239	0.419	1
GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	128	-0.26	-1.2	0.138	0.422	1
GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	28	-0.35	-1.2	0.209	0.422	1
GO_ANKYRIN_BINDING	20	-0.39	-1.2	0.237	0.422	1
GO_ENDOTHELIAL_CELL_DIFFERENTIATION	70	-0.29	-1.2	0.155	0.422	1
GO_PEPTIDE_RECEPTOR_ACTIVITY	133	-0.26	-1.19	0.126	0.424	1
GO_SUBPALLIUM_DEVELOPMENT	22	-0.38	-1.19	0.242	0.425	1
GO_SECRETORY GRANULE MEMBRANE	78	-0.28	-1.19	0.146	0.424	1
GO_BICARBONATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	19	-0.38	-1.19	0.227	0.424	1
GO_CERAMIDE_METABOLIC_PROCESS	67	-0.29	-1.19	0.173	0.424	1
GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	122	-0.26	-1.19	0.147	0.423	1
GO_VESICLE_ORGANIZATION	276	-0.24	-1.19	0.089	0.423	1
GO_AMINO_ACID_TRANSPORT	124	-0.26	-1.19	0.125	0.425	1
GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	26	-0.36	-1.19	0.215	0.425	1
GO_COATED_PIT	66	-0.29	-1.19	0.179	0.425	1
GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	103	-0.27	-1.19	0.132	0.426	1
GO_PHOSPHOLIPASE_C_ACTIVITY	31	-0.35	-1.19	0.199	0.426	1
GO_LYMPH_VESSEL_DEVELOPMENT	20	-0.39	-1.19	0.236	0.427	1
GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	50	-0.3	-1.19	0.187	0.428	1
GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	24	-0.36	-1.19	0.22	0.429	1
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_GOLGI	19	-0.39	-1.19	0.226	0.43	1
GO_NEPHRON_EPITHELIUM_DEVELOPMENT	93	-0.28	-1.19	0.173	0.432	1
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COREPRESSOR_ACTIVITY	26	-0.36	-1.19	0.226	0.432	1
GO_PROTEIN_DEACETYLASE_ACTIVITY	43	-0.31	-1.19	0.191	0.432	1
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE	22	-0.38	-1.19	0.241	0.432	1
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	30	-0.34	-1.18	0.223	0.435	1
GO_BLOC_1_COMPLEX	15	-0.42	-1.18	0.255	0.435	1
GO_POSITIVE_REGULATION_OF_PROTEIN_ACETYLTATION	36	-0.33	-1.18	0.208	0.435	1
GO_HEART TRABECULA MORPHOGENESIS	26	-0.35	-1.18	0.207	0.437	1
GO_NEUROPEPTIDE_BINDING	22	-0.38	-1.18	0.235	0.437	1

GO_AGGRESOME	32	-0.34	-1.18	0.221	0.438	1
GO_POSITIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	19	-0.38	-1.18	0.263	0.438	1
GO_GLUCCOCORTICOID_METABOLIC_PROCESS	16	-0.41	-1.18	0.222	0.442	1
GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_BINDING	16	-0.4	-1.18	0.258	0.443	1
GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	66	-0.29	-1.18	0.194	0.444	1
GO_REGULATION_OF_CELLULAR_PH	75	-0.28	-1.18	0.176	0.444	1
GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	179	-0.25	-1.18	0.149	0.446	1
GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	21	-0.38	-1.18	0.242	0.445	1
GO_NEUROMUSCULAR_PROCESS_CONTROLLING_POSTURE	15	-0.42	-1.18	0.264	0.445	1
GO_PROTEIN_TARGETING_TO_LYSOSOME	15	-0.41	-1.18	0.246	0.446	1
GO_ION_ANTIPORTER_ACTIVITY	45	-0.31	-1.18	0.216	0.446	1
GO_NEGATIVE_REGULATION_OF_TRANSPORT	451	-0.22	-1.18	0.084	0.445	1
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	64	-0.29	-1.18	0.201	0.446	1
GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	69	-0.28	-1.17	0.182	0.449	1
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	39	-0.32	-1.17	0.21	0.449	1
GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	48	-0.31	-1.17	0.202	0.448	1
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	50	-0.3	-1.17	0.192	0.45	1
GO_CYTOPLASMIC_REGION	276	-0.23	-1.17	0.118	0.45	1
GO_SMOOTH_ENDOPLASMIC_RETICULUM	33	-0.33	-1.17	0.214	0.45	1
GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	16	-0.41	-1.17	0.281	0.45	1
GO_GLOMERULUS_DEVELOPMENT	49	-0.3	-1.17	0.213	0.451	1
GO_REGULATION_OF_AUTOPHAGY	244	-0.24	-1.17	0.111	0.451	1
GO_AMINO_ACID_IMPORT	15	-0.4	-1.17	0.248	0.452	1
GO_GLIAL_CELL_MIGRATION	36	-0.33	-1.17	0.233	0.451	1
GO_MICROBODY_MEMBRANE	58	-0.29	-1.17	0.199	0.451	1
GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	205	-0.24	-1.17	0.134	0.451	1
GO_SECRETORY_VESICLE	452	-0.22	-1.17	0.071	0.452	1
GO_PLASMA_MEMBRANE_ORGANIZATION	202	-0.24	-1.17	0.133	0.452	1
GO_MYOSIN_V_BINDING	17	-0.39	-1.17	0.245	0.452	1
GO_REGULATION_OF_GLUCCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	16	-0.41	-1.17	0.246	0.452	1
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	25	-0.36	-1.17	0.228	0.453	1
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_BINDING	116	-0.25	-1.17	0.17	0.455	1
GO_BASAL_PLASMA_MEMBRANE	33	-0.33	-1.17	0.22	0.454	1
GO_ANION_CHANNEL_ACTIVITY	91	-0.27	-1.17	0.191	0.454	1
GO_ESTABLISHMENT_OF_MITOCHONDRION_LOCALIZATION	17	-0.39	-1.17	0.264	0.455	1
GO_HEART_VALVE_DEVELOPMENT	34	-0.33	-1.17	0.224	0.457	1
GO_GANGLIOSIDE_METABOLIC_PROCESS	26	-0.35	-1.17	0.244	0.457	1
GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	22	-0.36	-1.17	0.262	0.456	1
GO_REGULATION_OF_HORMONE_LEVELS	472	-0.22	-1.17	0.089	0.456	1
GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_ACCEPTOR	37	-0.33	-1.17	0.229	0.458	1
GO_CARDIAC_SEPTUM_DEVELOPMENT	85	-0.27	-1.16	0.177	0.458	1
GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	50	-0.3	-1.16	0.216	0.459	1
GO_SENSORY_ORGAN_DEVELOPMENT	490	-0.22	-1.16	0.071	0.46	1
GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	17	-0.4	-1.16	0.287	0.463	1
GO_REGULATION_OF_CHROMATIN_BINDING	17	-0.39	-1.16	0.262	0.463	1
GO_RESPONSE_TO_MUSCLE_ACTIVITY	20	-0.37	-1.16	0.247	0.463	1
GO_REGULATION_OF_RECEPTOR_INTERNALIZATION	37	-0.32	-1.16	0.234	0.464	1
GO_HEART_MORPHOGENESIS	211	-0.23	-1.16	0.14	0.465	1
GO_GAS_TRANSPORT	19	-0.38	-1.16	0.267	0.465	1
GO_ENZYME_ACTIVATOR_ACTIVITY	459	-0.22	-1.16	0.099	0.467	1
GO_RESPONSE_TO_NERVE_GROWTH_FACTOR	37	-0.32	-1.16	0.212	0.467	1
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	76	-0.28	-1.16	0.183	0.468	1
GO_SPERM_MOTILITY	48	-0.3	-1.16	0.241	0.47	1
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	27	-0.34	-1.16	0.257	0.473	1
GO_CELL_LEADING_EDGE	346	-0.22	-1.15	0.107	0.476	1
GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	51	-0.3	-1.15	0.224	0.477	1
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	35	-0.32	-1.15	0.244	0.477	1
GO_PHOSPHATIDYLINOSITOL_METABOLIC_PROCESS	193	-0.24	-1.15	0.161	0.477	1
GO_REGULATION_OF_OSSIFICATION	177	-0.24	-1.15	0.148	0.477	1
GO_NEGATIVE_CHEMOTAXIS	39	-0.31	-1.15	0.241	0.477	1
GO_REGULATION_OF_EXOCYTOSIS	182	-0.24	-1.15	0.159	0.477	1
GO_RESPONSE_TO_PH	42	-0.31	-1.15	0.221	0.48	1
GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	50	-0.3	-1.15	0.228	0.482	1
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	77	-0.27	-1.15	0.203	0.481	1
GO_POSITIVE_REGULATION_OF_HEART_GROWTH	26	-0.35	-1.15	0.246	0.482	1
GO_NEGATIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	61	-0.29	-1.15	0.242	0.482	1
GO_REGULATION_OF_ENDOCRINE_PROCESS	47	-0.3	-1.15	0.243	0.483	1
GO_EYE_DEVELOPMENT	323	-0.22	-1.15	0.125	0.484	1
GO_MUSCLE_ORGAN_DEVELOPMENT	277	-0.23	-1.15	0.153	0.484	1
GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	16	-0.39	-1.15	0.274	0.486	1
GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	37	-0.32	-1.15	0.251	0.488	1
GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	38	-0.32	-1.15	0.262	0.489	1
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	48	-0.3	-1.14	0.232	0.491	1
GO_VENTRAL_SPINAL_CORD_DEVELOPMENT	46	-0.3	-1.14	0.239	0.494	1
GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	18	-0.38	-1.14	0.282	0.497	1
GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	48	-0.3	-1.14	0.258	0.498	1
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	65	-0.28	-1.14	0.274	0.498	1
GO_NEURAL_NUCLEUS_DEVELOPMENT	65	-0.28	-1.14	0.217	0.498	1
GO_DRUG_TRANSPORTER_ACTIVITY	21	-0.35	-1.14	0.267	0.497	1
GO_VACUOLAR_ACIDIFICATION	15	-0.39	-1.14	0.286	0.497	1
GO_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	101	-0.26	-1.14	0.206	0.497	1

GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	50	-0.3	-1.14	0.223	0.497	1
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE	26	-0.35	-1.14	0.274	0.497	1
GO_RESPONSE_TO_PEPTIDE	400	-0.22	-1.14	0.135	0.497	1
GO_REGULATION_OF_LIPASE_ACTIVITY	83	-0.27	-1.14	0.219	0.498	1
GO_NEUROPEPTIDE_RECEPTOR_BINDING	28	-0.34	-1.14	0.28	0.501	1
GO_CARBOHYDRATE_HOMEOSTASIS	168	-0.24	-1.14	0.198	0.504	1
GO_NEURON_PROJECTION_REGENERATION	32	-0.33	-1.14	0.268	0.504	1
GO_OUTFLOW_TRACT_MORPHOGENESIS	56	-0.29	-1.14	0.254	0.505	1
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	19	-0.37	-1.14	0.282	0.505	1
GO_ADRENERGIC_RECEPTOR_ACTIVITY	16	-0.39	-1.14	0.282	0.505	1
GO_EXTRACELLULAR_MATRIX_ASSEMBLY	16	-0.4	-1.14	0.272	0.505	1
GO_REGULATION_OF_ALTERNATIVE_MRNA_SPLICING_VIA_SPLICEOSOM	28	-0.33	-1.13	0.24	0.506	1
GO_REGULATION_OF_VASOCONSTRICTION	66	-0.28	-1.13	0.235	0.506	1
GO_CELL_CORTEX_REGION	16	-0.4	-1.13	0.297	0.505	1
GO_REGULATION_OF_GLUCOSE_IMPORT	59	-0.28	-1.13	0.252	0.506	1
GO_GOLGI_TO_VACUOLE_TRANSPORT	27	-0.34	-1.13	0.303	0.508	1
GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	20	-0.37	-1.13	0.274	0.514	1
GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_BINDING	21	-0.36	-1.13	0.291	0.515	1
GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	53	-0.29	-1.13	0.276	0.515	1
GO_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY	17	-0.37	-1.13	0.291	0.515	1
GO_REGULATION_OF_PEPTIDE_TRANSPORT	253	-0.23	-1.13	0.165	0.516	1
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	67	-0.27	-1.13	0.237	0.517	1
GO_FILOPODIUM	94	-0.26	-1.13	0.241	0.52	1
GO_SPINAL_CORD_MOTOR_NEURON_DIFFERENTIATION	34	-0.32	-1.13	0.275	0.523	1
GO_MICROBODY_PART	92	-0.26	-1.13	0.25	0.523	1
GO_REPLACEMENT_OSSIFICATION	26	-0.34	-1.12	0.291	0.524	1
GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	22	-0.36	-1.12	0.315	0.525	1
GO_OLIGODENDROCYTE_DEVELOPMENT	34	-0.32	-1.12	0.258	0.524	1
GO_MRNA_SPLICE_SITE_SELECTION	19	-0.36	-1.12	0.297	0.525	1
GO_PROTEIN_COMPLEX_SCAFFOLD	64	-0.28	-1.12	0.237	0.526	1
GO_TRANSCRIPTION_FACTOR_ACTIVITY_DIRECT_LIGAND_REGULATED_SEQUENCE_SPECIFIC_DNA_BINDING	48	-0.29	-1.12	0.281	0.527	1
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	20	-0.36	-1.12	0.302	0.531	1
GO_WNT_SIGNALING_PATHWAY_CALCIUM_MODULATING_PATHWAY	39	-0.31	-1.12	0.283	0.531	1
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	170	-0.23	-1.12	0.208	0.533	1
GO_POLYSACCHARIDE_METABOLIC_PROCESS	80	-0.27	-1.12	0.248	0.533	1
GO_MYOTUBE_CELL_DEVELOPMENT	30	-0.32	-1.12	0.312	0.534	1
GO_POSITIVE_REGULATION_OF_HEART_RATE	22	-0.36	-1.12	0.319	0.534	1
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	15	-0.39	-1.12	0.325	0.533	1
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COFACTOR_ACTIVITY	91	-0.26	-1.12	0.234	0.533	1
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	63	-0.28	-1.12	0.271	0.533	1
GO_R_SMAD_BINDING	23	-0.34	-1.12	0.32	0.533	1
GO_POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	88	-0.26	-1.12	0.264	0.533	1
GO_SMAD_BINDING	70	-0.27	-1.12	0.273	0.534	1
GO_KINASE_INHIBITOR_ACTIVITY	89	-0.26	-1.12	0.26	0.536	1
GO_HORMONE_TRANSPORT	76	-0.27	-1.12	0.26	0.536	1
GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_BINDING	24	-0.34	-1.12	0.304	0.538	1
GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	29	-0.33	-1.11	0.312	0.539	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	114	-0.25	-1.11	0.246	0.541	1
GO_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	107	-0.25	-1.11	0.235	0.541	1
GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	60	-0.28	-1.11	0.281	0.542	1
GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	117	-0.25	-1.11	0.222	0.542	1
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	39	-0.3	-1.11	0.293	0.545	1
GO_NEGATIVE_REGULATION_OF_OSTEObLAST_DIFFERENTIATION	40	-0.3	-1.11	0.289	0.545	1
GO_ACTIVATION_OF_MAPKK_ACTIVITY	51	-0.29	-1.11	0.293	0.545	1
GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	35	-0.32	-1.11	0.289	0.545	1
GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	155	-0.23	-1.11	0.237	0.547	1
GO_REGULATION_OF_MUSCLE_HYPERTROPHY	34	-0.32	-1.11	0.323	0.547	1
GO_SYNAPTIC_VESICLE_CYTOSKELETAL_TRANSPORT	15	-0.38	-1.11	0.335	0.549	1
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	75	-0.27	-1.11	0.264	0.549	1
GO_POSITIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	49	-0.29	-1.11	0.276	0.549	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	36	-0.3	-1.11	0.31	0.549	1
GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	121	-0.25	-1.11	0.267	0.551	1
GO_LONG_TERM_SYNAPTIC_DEPRESSION	15	-0.38	-1.11	0.331	0.552	1
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANETRANSPORT	21	-0.35	-1.11	0.329	0.552	1
GO_GOLGI_TO_ENDOSOME_TRANSPORT	19	-0.37	-1.11	0.322	0.552	1
GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	72	-0.27	-1.11	0.276	0.552	1
GO_GOLGI_TO_PLASMA_MEMBRANE_TRANSPORT	41	-0.3	-1.11	0.31	0.552	1
GO_FATTY_ACYL_COA_BINDING	30	-0.32	-1.11	0.332	0.552	1
GO_NARROW_PORE_CHANNEL_ACTIVITY	17	-0.38	-1.1	0.32	0.552	1
GO_REGULATION_OF_ENERGY_HOMEOSTASIS	17	-0.37	-1.1	0.321	0.552	1
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	18	-0.37	-1.1	0.325	0.558	1
GO_GENETIC_IMPRINTING	20	-0.36	-1.1	0.308	0.56	1
GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	456	-0.21	-1.1	0.192	0.562	1
GO_SYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	21	-0.35	-1.1	0.324	0.565	1
GO_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	191	-0.23	-1.1	0.241	0.564	1
GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	83	-0.26	-1.1	0.262	0.566	1
GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	22	-0.35	-1.1	0.333	0.571	1
GO_MYOBlast_FUSION	20	-0.35	-1.1	0.327	0.571	1
GO_OXYGEN_TRANSPORT	15	-0.39	-1.1	0.339	0.571	1
GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	22	-0.35	-1.09	0.318	0.573	1
GO_REGULATION_OF_VASODILATION	48	-0.29	-1.09	0.295	0.574	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	106	-0.24	-1.09	0.285	0.575	1

GO_MEMBRANE_DOCKING	68	-0.26	-1.09	0.293	0.578	1
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSP	94	-0.25	-1.09	0.287	0.578	1
GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	19	-0.35	-1.09	0.346	0.577	1
GO_POLYSACCHARIDE_CATABOLIC_PROCESS	24	-0.33	-1.09	0.335	0.578	1
GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	17	-0.36	-1.09	0.344	0.582	1
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	466	-0.21	-1.09	0.208	0.584	1
GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	32	-0.31	-1.09	0.313	0.584	1
GO_DEPHOSPHORYLATION	280	-0.22	-1.09	0.227	0.586	1
GO_POSITIVE_REGULATION_OF_ACTIN_NUCLEATION	15	-0.37	-1.09	0.357	0.589	1
GO_DOPAMINE_METABOLIC_PROCESS	25	-0.33	-1.09	0.323	0.589	1
GO_CELL_CORTEX	227	-0.22	-1.08	0.246	0.593	1
GO_SPERMATID_DIFFERENTIATION	124	-0.24	-1.08	0.286	0.593	1
GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	29	-0.33	-1.08	0.347	0.593	1
GO_MICROBODY	132	-0.24	-1.08	0.301	0.6	1
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	92	-0.25	-1.08	0.295	0.6	1
GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	19	-0.36	-1.08	0.352	0.6	1
GO_SPERM_PART	134	-0.23	-1.08	0.283	0.601	1
GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	151	-0.23	-1.08	0.276	0.6	1
GO_DETECTION_OF_TEMPERATURE_STIMULUS	17	-0.36	-1.08	0.372	0.6	1
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION	18	-0.36	-1.08	0.331	0.601	1
GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_ME						
MBRANE	97	-0.25	-1.08	0.313	0.606	1
GO_GLIAL_CELL_DEVELOPMENT	76	-0.26	-1.08	0.312	0.605	1
GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	54	-0.27	-1.08	0.313	0.606	1
GO_EMBRYONIC_HEMOPOIESIS	20	-0.34	-1.08	0.36	0.606	1
GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	23	-0.34	-1.08	0.366	0.607	1
GO_CELL_RECOGNITION	128	-0.23	-1.08	0.311	0.607	1
GO_BASAL_PART_OF_CELL	51	-0.28	-1.08	0.346	0.607	1
GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	20	-0.35	-1.08	0.331	0.607	1
GO_CORTICAL_CYTOSKELETON	80	-0.25	-1.08	0.316	0.608	1
GO_NUCLEOTIDE_KINASE_ACTIVITY	22	-0.34	-1.08	0.341	0.608	1
GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	19	-0.35	-1.08	0.352	0.607	1
GO_REGULATION_OF_ORGANELLE_ASSEMBLY	143	-0.23	-1.08	0.289	0.608	1
GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	15	-0.37	-1.07	0.375	0.608	1
GO_POLYOL_METABOLIC_PROCESS	95	-0.25	-1.07	0.329	0.608	1
GO_REGULATION_OF_COLLATERAL_SPROUTING	17	-0.37	-1.07	0.383	0.608	1
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBR	90	-0.25	-1.07	0.317	0.608	1
GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	19	-0.35	-1.07	0.355	0.608	1
GO_RENAL_TUBULE_DEVELOPMENT	78	-0.26	-1.07	0.326	0.608	1
GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRIN						
SIC_APOPTOTIC_SIGNALING_PATHWAY	21	-0.34	-1.07	0.367	0.611	1
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	29	-0.31	-1.07	0.343	0.615	1
GO_RELAXATION_OF_MUSCLE	20	-0.35	-1.07	0.379	0.614	1
GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	24	-0.33	-1.07	0.364	0.614	1
GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	18	-0.37	-1.07	0.36	0.614	1
GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVI	16	-0.37	-1.07	0.375	0.613	1
GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	23	-0.33	-1.07	0.356	0.613	1
GO_FILOPODIUM_MEMBRANE	18	-0.36	-1.07	0.346	0.613	1
GO_MYOTUBE_DIFFERENTIATION	57	-0.27	-1.07	0.333	0.613	1
GO_PHAGOSOME_ACIDIFICATION	27	-0.32	-1.07	0.33	0.615	1
GO_CELL_SUBSTRATE_ADHESION	161	-0.22	-1.07	0.306	0.616	1
GO_PALLIUM_DEVELOPMENT	151	-0.23	-1.07	0.311	0.616	1
GO_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	47	-0.28	-1.07	0.327	0.616	1
GO_POSITIVE_REGULATION_OF_AUTOPHAGY	74	-0.25	-1.07	0.347	0.615	1
GO_L_AMINO_ACID_TRANSPORT	58	-0.27	-1.07	0.356	0.618	1
GO_E_BOX_BINDING	34	-0.3	-1.07	0.375	0.617	1
GO_ACETYLCHOLINE_RECEPTOR_ACTIVITY	30	-0.31	-1.07	0.348	0.619	1
GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	16	-0.37	-1.07	0.366	0.621	1
GO_REGULATION_OF_CELL_GROWTH	386	-0.2	-1.07	0.27	0.62	1
GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	104	-0.24	-1.07	0.321	0.621	1
GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	20	-0.34	-1.06	0.386	0.622	1
GO_CELL_MATRIX_ADHESION	118	-0.24	-1.06	0.311	0.622	1
GO_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	34	-0.3	-1.06	0.353	0.622	1
GO_HISTONE_DEACETYLASE_COMPLEX	61	-0.27	-1.06	0.346	0.622	1
GO_COSTAMERE	19	-0.35	-1.06	0.365	0.621	1
GO_SCHWANN_CELL_DEVELOPMENT	26	-0.32	-1.06	0.377	0.621	1
GO_CLATHRIN_VESICLE_COAT	23	-0.33	-1.06	0.352	0.621	1
GO_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	56	-0.27	-1.06	0.351	0.62	1
GO_PERIPHERAL_NERVOUS_SYSTEM_AXON_ENSHEATHMENT	22	-0.34	-1.06	0.362	0.62	1
GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	169	-0.22	-1.06	0.296	0.619	1
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	22	-0.34	-1.06	0.352	0.619	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KIN						
ASE_SIGNALING_PATHWAY	189	-0.22	-1.06	0.314	0.62	1
GO_SERTOLI_CELL_DEVELOPMENT	15	-0.37	-1.06	0.364	0.623	1
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	140	-0.23	-1.06	0.32	0.624	1
GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	21	-0.34	-1.06	0.374	0.624	1
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	138	-0.23	-1.06	0.325	0.624	1
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_						
DIFFERENTIATION	161	-0.23	-1.06	0.328	0.624	1
GO ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	55	-0.27	-1.06	0.348	0.625	1
GO_RESPONSE_TO_AMINE	48	-0.28	-1.06	0.34	0.626	1
GO_REGULATION_OF_NEURON_DEATH	251	-0.21	-1.06	0.317	0.628	1
GO_CYTOPLASMIC_DYNEIN_COMPLEX	15	-0.37	-1.06	0.388	0.63	1
GO_14_3_3_PROTEIN_BINDING	19	-0.35	-1.06	0.409	0.63	1
GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	112	-0.24	-1.06	0.349	0.631	1
GO_RESPONSE_TO_COCAINE	46	-0.28	-1.06	0.349	0.63	1
GO_REGULATION_OF_DEPHOSPHORYLATION	147	-0.23	-1.06	0.322	0.63	1

GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	69	-0.26	-1.06	0.366	0.63	1
GO_ATPASE_BINDING	75	-0.25	-1.06	0.344	0.63	1
GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	70	-0.25	-1.06	0.348	0.63	1
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	17	-0.36	-1.06	0.39	0.63	1
GO_ACYLGLYCEROL_HOMEOSTASIS	29	-0.31	-1.06	0.371	0.631	1
GO_EMBRYONIC_HEART_TUBE_MORPHOGENESIS	61	-0.26	-1.05	0.361	0.632	1
GO_INNERVATION	23	-0.34	-1.05	0.367	0.632	1
GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	44	-0.28	-1.05	0.379	0.632	1
GO_NEURAL_TUBE_PATTERNING	34	-0.3	-1.05	0.373	0.633	1
GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	27	-0.31	-1.05	0.383	0.635	1
GO_RESPONSE_TO_NICOTINE	51	-0.27	-1.05	0.371	0.638	1
GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	15	-0.36	-1.05	0.384	0.64	1
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	49	-0.27	-1.05	0.362	0.641	1
GO_CLATHRIN_COATED_VESICLE_MEMBRANE	79	-0.25	-1.05	0.355	0.646	1
GO_ACTIN_FILAMENT_BASED_PROCESS	445	-0.2	-1.05	0.297	0.645	1
GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	57	-0.26	-1.05	0.395	0.644	1
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	44	-0.28	-1.05	0.353	0.646	1
GO_NEGATIVE_REGULATION_OF_STAT_CASCADE	44	-0.28	-1.05	0.369	0.646	1
GO_CHANNEL_INHIBITOR_ACTIVITY	37	-0.29	-1.05	0.386	0.647	1
GO_POSITIVE_REGULATION_OF_GROWTH	234	-0.21	-1.05	0.346	0.646	1
GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	76	-0.25	-1.05	0.356	0.646	1
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	83	-0.25	-1.05	0.368	0.65	1
GO_PHAGOSOME_MATURATION	38	-0.29	-1.04	0.383	0.653	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	17	-0.34	-1.04	0.391	0.655	1
GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	53	-0.27	-1.04	0.39	0.657	1
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	111	-0.23	-1.04	0.376	0.657	1
GO_CELL_MATURATION	129	-0.23	-1.04	0.367	0.662	1
GO_BAF_TYPE_COMPLEX	23	-0.33	-1.04	0.418	0.663	1
GO_PHOTOTRANSDUCTION	42	-0.28	-1.04	0.414	0.662	1
GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	112	-0.23	-1.04	0.364	0.663	1
GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	42	-0.28	-1.04	0.383	0.663	1
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	24	-0.32	-1.04	0.373	0.664	1
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	50	-0.27	-1.04	0.396	0.664	1
GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	18	-0.34	-1.04	0.397	0.665	1
GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	16	-0.36	-1.04	0.409	0.664	1
GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	345	-0.2	-1.04	0.343	0.666	1
GO_POSITIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	24	-0.32	-1.04	0.404	0.667	1
GO_CELL_CYCLE_ARREST	150	-0.22	-1.04	0.361	0.669	1
GO_NEURAL_CRESCENT_CELL_DIFFERENTIATION	75	-0.25	-1.03	0.377	0.672	1
GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	62	-0.26	-1.03	0.389	0.673	1
GO_FATTY_ACID_BETA_OXIDATION	49	-0.27	-1.03	0.405	0.679	1
GO_CELL_CORTEX_PART	110	-0.23	-1.03	0.388	0.679	1
GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	18	-0.34	-1.03	0.409	0.679	1
GO_RESPONSE_TO_ELECTRICAL_STIMULUS	43	-0.28	-1.03	0.407	0.679	1
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	17	-0.34	-1.03	0.409	0.679	1
GO_MODIFIED_AMINO_ACID_BINDING	64	-0.25	-1.03	0.408	0.679	1
GO_CELLULAR_RESPONSE_TO_PH	19	-0.34	-1.03	0.407	0.679	1
GO_CHOLESTEROL_EFFLUX	26	-0.31	-1.03	0.409	0.678	1
GO_PROTEIN_TYROSINE_KINASE_BINDING	54	-0.26	-1.03	0.434	0.681	1
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	260	-0.2	-1.03	0.376	0.68	1
GO_ATRIAL_SEPTUM_DEVELOPMENT	18	-0.34	-1.03	0.41	0.684	1
GO_PROTEIN_STABILIZATION	130	-0.23	-1.03	0.398	0.684	1
GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	35	-0.29	-1.03	0.423	0.684	1
GO_CARDIAC_CHAMBER_DEVELOPMENT	144	-0.22	-1.03	0.388	0.684	1
GO_GOLGI_VESICLE_TRANSPORT	313	-0.2	-1.03	0.381	0.684	1
GO_REGULATION_OF_MUSCLE_ADAPTATION	60	-0.26	-1.03	0.402	0.684	1
GO_GASTRULATION_WITH_MOUTH_FORMING_SECOND	28	-0.3	-1.03	0.428	0.684	1
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	74	-0.24	-1.03	0.403	0.684	1
GO_ADHERENS_JUNCTION_ASSEMBLY	34	-0.3	-1.02	0.421	0.688	1
GO_IMPORT_INTO_CELL	36	-0.28	-1.02	0.392	0.687	1
GO_PHOTORECEPTOR_OUTER_SEGMENT_MEMBRANE	15	-0.36	-1.02	0.42	0.687	1
GO_RESPONSE_TO_INSULIN	203	-0.21	-1.02	0.394	0.696	1
GO_PROLINE_RICH_REGION_BINDING	19	-0.34	-1.02	0.418	0.698	1
GO_LYSOSOME_LOCALIZATION	21	-0.33	-1.02	0.437	0.699	1
GO_HYDROGEN_EXPORTING_ATPASE_ACTIVITY	27	-0.3	-1.02	0.442	0.7	1
GO_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	25	-0.31	-1.02	0.431	0.7	1
GO_INOSITOL_LIPID_MEDIATED_SIGNALING	123	-0.22	-1.02	0.414	0.699	1
GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	64	-0.25	-1.02	0.402	0.699	1
GO_VACUOLAR_TRANSPORT	243	-0.2	-1.02	0.412	0.7	1
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	106	-0.23	-1.02	0.424	0.699	1
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	53	-0.26	-1.02	0.435	0.703	1
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	246	-0.2	-1.02	0.411	0.705	1
GO_ATP_HYDROLYSIS_COUPLED_TRANSMEMBRANE_TRANSPORT	36	-0.28	-1.02	0.433	0.705	1
GO_EARLY_ENDOSOME_MEMBRANE	106	-0.23	-1.02	0.422	0.704	1
GO_GABAERGIC_NEURON_DIFFERENTIATION	15	-0.35	-1.02	0.417	0.705	1
GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	15	-0.36	-1.01	0.459	0.71	1
GO_NEGATIVE_REGULATION_OF_DEPHOSPHORYLATION	70	-0.25	-1.01	0.433	0.71	1
GO_RESPONSE_TO_ACETYLCHOLINE	18	-0.35	-1.01	0.436	0.71	1
GO_RETINAL_GANGLION_CELL_AXON_GUIDANCE	18	-0.33	-1.01	0.428	0.71	1
GO_REGULATION_OF_PROTEIN_HOMOOLOGOMERIZATION	16	-0.35	-1.01	0.444	0.71	1
GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	74	-0.24	-1.01	0.433	0.709	1
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	20	-0.32	-1.01	0.448	0.709	1
GO_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	57	-0.26	-1.01	0.43	0.713	1
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	26	-0.31	-1.01	0.45	0.713	1

GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	78	-0.24	-1.01	0.43	0.715	1
GO_ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	163	-0.21	-1.01	0.427	0.715	1
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	30	-0.29	-1.01	0.441	0.715	1
GO_ORGANELLE_SUBCOMPARTMENT	301	-0.2	-1.01	0.41	0.715	1
GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	58	-0.25	-1.01	0.423	0.717	1
GO_SULFUR_COMPOUND_BINDING	231	-0.2	-1.01	0.429	0.716	1
GO_NEGATIVE_REGULATION_OF_SECRETION	196	-0.21	-1.01	0.433	0.72	1
GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	18	-0.33	-1.01	0.444	0.722	1
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	30	-0.29	-1.01	0.455	0.722	1
GO_MYOSIN_COMPLEX	67	-0.24	-1.01	0.446	0.723	1
GO_UBIQUITIN_LIGASE_COMPLEX	260	-0.2	-1.01	0.442	0.723	1
GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	115	-0.22	-1.01	0.434	0.723	1
GO_HISTONE_H4_ACETYLATION	46	-0.27	-1	0.445	0.725	1
GO_POLYPEPTIDE_N_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	19	-0.33	-1	0.441	0.725	1
GO_ANTEROGRADE_AXONAL_TRANSPORT	26	-0.3	-1	0.477	0.726	1
GO_NEGATIVE_REGULATION_OF_CELL_GROWTH	170	-0.21	-1	0.449	0.725	1
GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	114	-0.22	-1	0.452	0.726	1
GO_LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_BINDING	23	-0.31	-1	0.437	0.728	1
GO_RESPONSE_TO_AMINO_ACID	108	-0.22	-1	0.454	0.728	1
GO_CGMP_BIOSYNTHETIC_PROCESS	15	-0.35	-1	0.454	0.728	1
GO_REGULATION_OF_CELL_PROJECTION_ASSEMBLY	147	-0.21	-1	0.451	0.728	1
GO_ANION_TRANSMEMBRANE_TRANSPORT	251	-0.2	-1	0.457	0.728	1
GO_HMG_BOX_DOMAIN_BINDING	18	-0.34	-1	0.438	0.731	1
GO_ANCHORED_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_Membrane	19	-0.32	-1	0.457	0.733	1
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_TRANSPORT_INTO_CYT	19	-0.33	-1	0.451	0.733	1
GO_ORGANIC_ACID_TRANSPORT	260	-0.2	-1	0.448	0.734	1
GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	248	-0.2	-1	0.48	0.734	1
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	100	-0.23	-1	0.446	0.734	1
GO_REGULATION_OF_AXON_GUIDANCE	39	-0.27	-1	0.457	0.734	1
GO_LIPID_PHOSPHORYLATION	99	-0.23	-1	0.463	0.734	1
GO_POST_EMBRYONIC_DEVELOPMENT	88	-0.23	-1	0.45	0.736	1
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	84	-0.23	-1	0.461	0.735	1
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	396	-0.19	-1	0.464	0.735	1
GO_CARBOXYPEPTIDASE_ACTIVITY	41	-0.27	-0.99	0.47	0.74	1
GO_ATPASE_COUPLED_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	71	-0.24	-0.99	0.464	0.74	1
GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	39	-0.27	-0.99	0.47	0.743	1
GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	40	-0.27	-0.99	0.465	0.743	1
GO_STABILIZATION_OF_MEMBRANE_POTENTIAL	16	-0.34	-0.99	0.464	0.744	1
GO_CELLULAR_RESPONSE_TO_ESTROGEN_STIMULUS	40	-0.27	-0.99	0.466	0.744	1
GO_RECEPTOR_METABOLIC_PROCESS	81	-0.23	-0.99	0.493	0.743	1
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	23	-0.31	-0.99	0.479	0.744	1
GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	24	-0.31	-0.99	0.471	0.745	1
GO_POSITIVE_REGULATION_OF_CREB_TRANSCRIPTION_FACTOR_ACTIVATION	15	-0.34	-0.99	0.472	0.744	1
GO_COPULATION	17	-0.33	-0.99	0.479	0.745	1
GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	144	-0.21	-0.99	0.482	0.745	1
GO_CENTRIOLAR_SATELLITE	24	-0.31	-0.99	0.474	0.746	1
GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	51	-0.25	-0.99	0.459	0.747	1
GO_EAR_DEVELOPMENT	194	-0.21	-0.99	0.49	0.746	1
GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	34	-0.28	-0.99	0.47	0.75	1
GO_NEGATIVE_REGULATION_OF_OSSIFICATION	68	-0.24	-0.99	0.497	0.752	1
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	166	-0.21	-0.99	0.481	0.753	1
GO_DORSAL_VENTRAL_PATTERN_FORMATION	91	-0.23	-0.99	0.496	0.753	1
GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	33	-0.28	-0.99	0.505	0.753	1
GO_CARDIAC_VENTRICLE_DEVELOPMENT	106	-0.22	-0.99	0.498	0.752	1
GO_UBIQUITIN_LIKE_PROTEIN_TRANSFERASE_ACTIVITY	409	-0.19	-0.99	0.507	0.753	1
GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	36	-0.28	-0.99	0.464	0.752	1
GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	44	-0.26	-0.99	0.481	0.752	1
GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	35	-0.27	-0.99	0.471	0.752	1
GO_CLATHRIN_COAT	46	-0.26	-0.99	0.478	0.753	1
GO_ACTIN_BASED_CELL_PROJECTION	179	-0.21	-0.99	0.497	0.753	1
GO_REPRODUCTIVE_BEHAVIOR	30	-0.29	-0.98	0.467	0.753	1
GO_MOTOR_NEURON_AXON_GUIDANCE	27	-0.3	-0.98	0.487	0.753	1
GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	418	-0.19	-0.98	0.51	0.753	1
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	144	-0.21	-0.98	0.507	0.756	1
GO_RESPONSE_TO_AMMONIUM_ION	51	-0.25	-0.98	0.476	0.756	1
GO_FIBRIL_ORGANIZATION	18	-0.33	-0.98	0.468	0.758	1
GO_LEFT_RIGHT_PATTERN_FORMATION	20	-0.32	-0.98	0.469	0.758	1
GO_COFACTOR_TRANSPORTER_ACTIVITY	21	-0.31	-0.98	0.468	0.759	1
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	97	-0.22	-0.98	0.496	0.76	1
GO_POLYSACCHARIDE_BINDING	22	-0.31	-0.98	0.502	0.761	1
GO_REVERSE_CHOLESTEROL_TRANSPORT	17	-0.33	-0.98	0.499	0.762	1
GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	86	-0.23	-0.98	0.488	0.761	1
GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	174	-0.21	-0.98	0.516	0.763	1
GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	331	-0.19	-0.98	0.545	0.764	1
GO_PLASMA_MEMBRANE_RAFT	86	-0.23	-0.98	0.513	0.764	1
GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	19	-0.31	-0.98	0.472	0.767	1
GO_METALLO_SULFUR_CLUSTER_ASSEMBLY	17	-0.33	-0.98	0.489	0.768	1
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	308	-0.19	-0.98	0.52	0.77	1
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	103	-0.22	-0.97	0.514	0.772	1

GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	70	-0.24	-0.97	0.504	0.771	1
GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	33	-0.28	-0.97	0.496	0.771	1
GO_LYTIC_VACUOLE_MEMBRANE	265	-0.19	-0.97	0.532	0.772	1
GO_TRANS_GOLGI_NETWORK_MEMBRANE	78	-0.23	-0.97	0.488	0.775	1
GO_NAD_ADP_RIBOSYLTRANSFERASE_ACTIVITY	26	-0.29	-0.97	0.466	0.775	1
GO_ADIPOSE_TISSUE_DEVELOPMENT	32	-0.28	-0.97	0.5	0.776	1
GO_SERTOLI_CELL_DIFFERENTIATION	20	-0.31	-0.97	0.493	0.779	1
GO_CELLULAR_RESPONSE_TO ESTRADIOL_STIMULUS	30	-0.28	-0.97	0.488	0.78	1
GO_KIDNEY_MORPHOGENESIS	82	-0.23	-0.97	0.539	0.781	1
GO_AMMONIUM_ION_METABOLIC_PROCESS	168	-0.2	-0.97	0.557	0.78	1
GO_CELL_SUBSTRATE_ADHERENS_JUNCTION_ASSEMBLY	24	-0.3	-0.97	0.51	0.781	1
GO_VACUOLE_ORGANIZATION	159	-0.2	-0.97	0.536	0.782	1
GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	47	-0.26	-0.97	0.494	0.783	1
GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	292	-0.19	-0.97	0.546	0.783	1
GO_REGULATION_OF_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEPENDENT_DECAY	15	-0.34	-0.97	0.477	0.782	1
GO_CALCIIUM_DEPENDENT_PROTEIN_BINDING	61	-0.24	-0.97	0.528	0.783	1
GO_AMMONIUM_TRANSPORT	57	-0.24	-0.97	0.5	0.783	1
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	33	-0.28	-0.97	0.51	0.783	1
GO_UROGENITAL_SYSTEM_DEVELOPMENT	297	-0.19	-0.97	0.559	0.783	1
GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	41	-0.26	-0.97	0.495	0.784	1
GO_EYE_MORPHOGENESIS	136	-0.21	-0.97	0.547	0.786	1
GO_METHIONINE_METABOLIC_PROCESS	18	-0.32	-0.97	0.495	0.786	1
GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIIUM_ION	16	-0.33	-0.96	0.516	0.786	1
GO_ALCOHOL_BINDING	99	-0.22	-0.96	0.537	0.788	1
GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	19	-0.31	-0.96	0.491	0.791	1
GO_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	36	-0.26	-0.96	0.504	0.791	1
GO_RESPONSE_TO_CALCIIUM_ION	115	-0.21	-0.96	0.548	0.791	1
GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	24	-0.3	-0.96	0.511	0.794	1
GO_BITTER_TASTE_RECEPTOR_ACTIVITY	24	-0.29	-0.96	0.516	0.794	1
GO_CYCLIN_BINDING	19	-0.32	-0.96	0.508	0.795	1
GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	47	-0.26	-0.96	0.52	0.795	1
GO_CIS_GOLGI_NETWORK	40	-0.26	-0.96	0.518	0.796	1
GO_HISTONE_H3_DEACETYLATION	22	-0.29	-0.96	0.491	0.796	1
GO_POSITIVE_REGULATION_OF_VASODILATION	32	-0.27	-0.96	0.499	0.797	1
GO_REGULATION_OF_CALCIIUM_ION_IMPORT	102	-0.22	-0.96	0.535	0.797	1
GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	49	-0.25	-0.96	0.549	0.8	1
GO_CARDIAC_CELL_DEVELOPMENT	49	-0.25	-0.96	0.534	0.8	1
GO_ADHERENS_JUNCTION_ORGANIZATION	71	-0.23	-0.96	0.531	0.802	1
GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	205	-0.19	-0.96	0.557	0.803	1
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	132	-0.21	-0.96	0.567	0.804	1
GO_O_METHYLTRANSFERASE_ACTIVITY	18	-0.31	-0.96	0.53	0.804	1
GO_NUCLEOBASE_CONTAINING_COMPOUND_KINASE_ACTIVITY	45	-0.25	-0.95	0.531	0.807	1
GO_SWI_SNF_COMPLEX	15	-0.34	-0.95	0.503	0.807	1
GO_ACTOMYOSIN	58	-0.24	-0.95	0.551	0.809	1
GO_CATION_TRANSPORTING_ATPASE_ACTIVITY	59	-0.24	-0.95	0.548	0.809	1
GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	20	-0.3	-0.95	0.53	0.811	1
GO_PEPTIDE_TRANSPORT	70	-0.23	-0.95	0.557	0.81	1
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	34	-0.27	-0.95	0.512	0.812	1
GO_REGULATION_OF_TOR_SIGNALING	63	-0.24	-0.95	0.538	0.815	1
GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	90	-0.22	-0.95	0.562	0.817	1
GO_CELLULAR_PIGMENTATION	46	-0.25	-0.95	0.545	0.818	1
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	62	-0.24	-0.95	0.569	0.819	1
GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	278	-0.19	-0.95	0.626	0.819	1
GO_PHOTOPERIODISM	24	-0.29	-0.95	0.526	0.818	1
GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	29	-0.27	-0.95	0.545	0.818	1
GO_PHOSPHATIDYLETHANOLAMINE_METABOLIC_PROCESS	18	-0.31	-0.95	0.535	0.818	1
GO_REGULATION_OF_CHOLESTEROL_METABOLIC_PROCESS	22	-0.29	-0.95	0.516	0.818	1
GO_PROTEIN_C_TERMINUS_BINDING	184	-0.19	-0.95	0.594	0.819	1
GO_POSITIVE_REGULATION_OF_TOR_SIGNALING	26	-0.29	-0.95	0.511	0.82	1
GO_MATING	37	-0.26	-0.95	0.565	0.82	1
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	134	-0.21	-0.95	0.572	0.82	1
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	51	-0.24	-0.95	0.569	0.82	1
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	174	-0.2	-0.94	0.585	0.82	1
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	30	-0.27	-0.94	0.552	0.822	1
GO_ENDOTHELIAL_CELL_PROLIFERATION	24	-0.29	-0.94	0.557	0.823	1
GO_GERM_CELL_DEVELOPMENT	206	-0.19	-0.94	0.614	0.822	1
GO_BLOC_COMPLEX	20	-0.3	-0.94	0.541	0.823	1
GO_BODY_MORPHOGENESIS	44	-0.25	-0.94	0.54	0.823	1
GO_CALCIIUM_ION_IMPORT	63	-0.23	-0.94	0.574	0.824	1
GO_NEGATIVE_REGULATION_OF_RECEPTOR_ACTIVITY	29	-0.27	-0.94	0.55	0.829	1
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	40	-0.25	-0.94	0.545	0.828	1
GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	43	-0.25	-0.94	0.55	0.829	1
GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	295	-0.18	-0.94	0.648	0.831	1
GO_PCG_PROTEIN_COMPLEX	43	-0.25	-0.94	0.563	0.831	1
GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	21	-0.3	-0.94	0.545	0.831	1
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	43	-0.25	-0.94	0.543	0.834	1
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	167	-0.2	-0.94	0.619	0.834	1
GO_DEVELOPMENTAL_INDUCTION	27	-0.28	-0.94	0.553	0.835	1
GO_GTPASE_BINDING	291	-0.18	-0.94	0.645	0.837	1
GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	19	-0.31	-0.94	0.557	0.836	1
GO_MONOCYTE_DIFFERENTIATION	16	-0.32	-0.94	0.575	0.836	1
GO_NEGATIVE_REGULATION_OF_GROWTH	236	-0.19	-0.93	0.642	0.838	1

GO_CAMERA_TYPE_EYE_MORPHOGENESIS	101	-0.21	-0.93	0.588	0.843	1
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	39	-0.26	-0.93	0.59	0.846	1
GO_PHOSPHATASE_REGULATOR_ACTIVITY	80	-0.22	-0.93	0.599	0.847	1
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	66	-0.23	-0.93	0.578	0.848	1
GO_PROTEIN_AUTOUBIQUITINATION	47	-0.24	-0.93	0.592	0.848	1
GO_CALCIIUM_DEPENDENT_PHOSPHOLIPID_BINDING	55	-0.24	-0.93	0.58	0.849	1
GO_NEGATIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	21	-0.29	-0.93	0.563	0.854	1
GO_ATPASE_ACTIVATOR_ACTIVITY	17	-0.31	-0.93	0.556	0.855	1
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	37	-0.26	-0.93	0.585	0.855	1
GO_TEMPERATURE_HOMEOSTASIS	26	-0.28	-0.93	0.572	0.855	1
GO_SAGA_TYPE_COMPLEX	34	-0.26	-0.93	0.586	0.857	1
GO_HYDRO_LYASE_ACTIVITY	49	-0.24	-0.93	0.59	0.857	1
GO_ECTODERMAL_PLACODE_DEVELOPMENT	15	-0.33	-0.92	0.535	0.857	1
GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	38	-0.25	-0.92	0.571	0.859	1
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY	16	-0.31	-0.92	0.568	0.858	1
GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	28	-0.28	-0.92	0.592	0.858	1
GO_SEX_DETERMINATION	22	-0.29	-0.92	0.572	0.858	1
GO_DORSAL_SPINAL_CORD_DEVELOPMENT	21	-0.3	-0.92	0.568	0.858	1
GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	117	-0.21	-0.92	0.65	0.858	1
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	32	-0.26	-0.92	0.606	0.858	1
GO_REGULATION_OF_HOMEOSTATIC_PROCESS	438	-0.17	-0.92	0.724	0.859	1
GO_SCHWANN_CELL_DIFFERENTIATION	31	-0.27	-0.92	0.585	0.866	1
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFOR						
MING_GROWTH_FACTOR_BETA_STIMULUS	24	-0.28	-0.92	0.585	0.867	1
GO_FERTILIZATION	144	-0.2	-0.92	0.629	0.867	1
GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	40	-0.25	-0.92	0.583	0.868	1
GO_NUCLEAR_OUTER_MEMBRANE	23	-0.29	-0.92	0.581	0.868	1
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT						
_PEPTIDE_BONDS_IN_LINEAR_AMIDES	84	-0.21	-0.92	0.639	0.867	1
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	33	-0.26	-0.92	0.603	0.868	1
GO_MYOSIN_BINDING	59	-0.23	-0.92	0.608	0.869	1
GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	67	-0.22	-0.92	0.625	0.868	1
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	27	-0.28	-0.92	0.581	0.87	1
GO_RESPONSE_TO_SALT	16	-0.31	-0.92	0.602	0.87	1
GO_ADAPTATION_OF_SIGNALING_PATHWAY	21	-0.3	-0.92	0.566	0.87	1
GO_POSITIVE_REGULATION_OF_RECEPTOR_ACTIVITY	45	-0.24	-0.91	0.601	0.873	1
GO_ATPASE_COMPLEX	24	-0.28	-0.91	0.594	0.874	1
GO_AUTOPHAGOSOME_ORGANIZATION	40	-0.25	-0.91	0.615	0.875	1
GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	20	-0.29	-0.91	0.565	0.875	1
GO_CARDIOCYTE_DIFFERENTIATION	96	-0.21	-0.91	0.644	0.875	1
GO_HEPARAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	28	-0.27	-0.91	0.582	0.875	1
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	38	-0.25	-0.91	0.617	0.875	1
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	41	-0.24	-0.91	0.612	0.875	1
GO_GLYCOSPHINGOLIPID_METABOLIC_PROCESS	69	-0.22	-0.91	0.637	0.875	1
GO_RHYTHMIC_BEHAVIOR	19	-0.3	-0.91	0.589	0.876	1
GO_PEPTIDYL_TYROSINE_MODIFICATION	184	-0.19	-0.91	0.701	0.877	1
GO_PEPTIDE_HORMONE_PROCESSING	32	-0.26	-0.91	0.631	0.879	1
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	68	-0.22	-0.91	0.632	0.88	1
GO_MESONEPHRIC_TUBULE_MORPHOGENESIS	53	-0.23	-0.91	0.614	0.88	1
GO_FATTY_ACID_TRANSPORT	56	-0.23	-0.91	0.632	0.88	1
GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	20	-0.29	-0.91	0.587	0.883	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	27	-0.27	-0.91	0.623	0.883	1
GO_CELLULAR_IRON_ION_HOMEOSTASIS	44	-0.24	-0.91	0.627	0.882	1
GO_FATTY_ACID_LIGASE_ACTIVITY	16	-0.3	-0.91	0.599	0.883	1
GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	137	-0.2	-0.91	0.701	0.883	1
GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	55	-0.23	-0.91	0.639	0.883	1
GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	22	-0.29	-0.91	0.582	0.883	1
GO_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	19	-0.3	-0.91	0.602	0.883	1
GO_PHOSPHOLIPID_METABOLIC_PROCESS	362	-0.17	-0.91	0.759	0.883	1
GO_CLATHRIN_ADAPTOR_COMPLEX	27	-0.27	-0.91	0.609	0.883	1
GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	479	-0.17	-0.9	0.814	0.884	1
GO_PROTEIN_DEPHOSPHORYLATION	188	-0.19	-0.9	0.706	0.885	1
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	233	-0.18	-0.9	0.718	0.884	1
GO_MACROMOLECULE_DEACYLATION	66	-0.22	-0.9	0.629	0.884	1
GO_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	74	-0.22	-0.9	0.654	0.884	1
GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	51	-0.23	-0.9	0.608	0.884	1
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	41	-0.24	-0.9	0.635	0.883	1
GO_POSITIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATI	17	-0.3	-0.9	0.595	0.883	1
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	28	-0.27	-0.9	0.595	0.883	1
GO_NUCLEOSIDE_DIPHOSPHATE_KINASE_ACTIVITY	15	-0.32	-0.9	0.581	0.883	1
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	42	-0.24	-0.9	0.633	0.882	1
GO_POSITIVE_REGULATION_OF_CELL_GROWTH	144	-0.19	-0.9	0.703	0.883	1
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_T						
RANSPORTER_ACTIVITY	16	-0.31	-0.9	0.587	0.883	1
GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	106	-0.2	-0.9	0.691	0.882	1
GO_EPHRIN_RECEPTOR_ACTIVITY	19	-0.3	-0.9	0.618	0.885	1
GO_TRANSCRIPTION_COREPRESSOR_ACTIVITY	212	-0.19	-0.9	0.749	0.884	1
GO_DEVELOPMENTAL_GROWTH	328	-0.17	-0.9	0.77	0.884	1
GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	349	-0.17	-0.9	0.791	0.885	1
GO_CELLULAR_PROCESS_INVOLVED_IN_REPRODUCTION_IN_MULTICEL						
LULAR_ORGANISM	249	-0.18	-0.9	0.729	0.885	1
GO_PROTEIN_SERINE_THREONINE_KINASE_INHIBITOR_ACTIVITY	30	-0.26	-0.9	0.634	0.885	1
GO_ASTROCYTE_DIFFERENTIATION	39	-0.25	-0.9	0.634	0.885	1
GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	58	-0.22	-0.9	0.662	0.889	1
GO_PROTEIN_KINASE_COMPLEX	88	-0.2	-0.9	0.673	0.888	1
GO_POSITIVE_REGULATION_OF_OSSIFICATION	84	-0.21	-0.9	0.661	0.889	1
GO_ORGANIC_ANION_TRANSPORT	385	-0.17	-0.9	0.793	0.89	1

GO_COFACTOR_TRANSPORT	26	-0.27	-0.9	0.591	0.891	1
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	18	-0.3	-0.9	0.592	0.891	1
GO_LAMELLIPODIUM	170	-0.19	-0.9	0.704	0.891	1
GO_ASYMMETRIC_PROTEIN_LOCALIZATION	19	-0.29	-0.89	0.592	0.893	1
GO_REGULATION_OF_CELLULAR_RESPIRATION	21	-0.28	-0.89	0.611	0.897	1
GO_ACETYLCHOLINE_BINDING	24	-0.27	-0.89	0.617	0.897	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	-0.28	-0.89	0.613	0.896	1
GO_RECYCLING_ENDOSOME	126	-0.2	-0.89	0.736	0.896	1
GO_NEGATIVE_REGULATION_OF_CIRCADIAN_RHYTHM	17	-0.29	-0.89	0.61	0.898	1
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	105	-0.2	-0.89	0.678	0.901	1
GO_VENTRICULAR_SEPTUM_DEVELOPMENT	54	-0.23	-0.89	0.668	0.901	1
GO_POSITIVE_REGULATION_OF_PROTEIN_BINDING	73	-0.22	-0.89	0.686	0.901	1
GO_AMMONIUM_ION_BINDING	70	-0.22	-0.89	0.668	0.903	1
GO_REGULATION_OF_HEAT_GENERATION	15	-0.31	-0.89	0.629	0.903	1
GO_MANNOSIDASE_ACTIVITY	15	-0.3	-0.89	0.61	0.906	1
GO_REGULATION_OF_PROTEIN_POLYMERIZATION	169	-0.19	-0.89	0.713	0.906	1
GO_NEGATIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	32	-0.26	-0.89	0.64	0.908	1
GO_CELLULAR_GLUCOSE_HOMEOSTASIS	75	-0.21	-0.89	0.682	0.908	1
GO_AXON_CYTOPLASM	33	-0.25	-0.89	0.643	0.908	1
GO_NEPHRIC_DUCT_DEVELOPMENT	15	-0.31	-0.89	0.611	0.909	1
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	495	-0.17	-0.88	0.855	0.909	1
GO_PROTEIN_PALMITOYLATION	23	-0.27	-0.88	0.633	0.909	1
GO_PHOTORECEPTOR_DISC_MEMBRANE	18	-0.29	-0.88	0.643	0.91	1
GO_CLATHRIN_COATED_VESICLE	155	-0.19	-0.88	0.753	0.912	1
GO_GLYCEROLIPID_METABOLIC_PROCESS	352	-0.17	-0.88	0.837	0.911	1
GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	16	-0.3	-0.88	0.612	0.911	1
GO_MRNA_3_UTR_BINDING	48	-0.23	-0.88	0.645	0.912	1
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	38	-0.25	-0.88	0.662	0.912	1
GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	74	-0.21	-0.88	0.685	0.912	1
GO_RESPONSE_TO_CAMP	104	-0.2	-0.88	0.712	0.912	1
GO_MECHANORECEPTOR_DIFFERENTIATION	50	-0.23	-0.88	0.676	0.912	1
GO_LATE_ENDOSOME	202	-0.18	-0.88	0.772	0.913	1
GO_GLYCOPROTEIN_METABOLIC_PROCESS	344	-0.17	-0.88	0.837	0.913	1
GO_REGULATION_OF_VACUOLAR_TRANSPORT	29	-0.26	-0.88	0.637	0.913	1
GO_APOLIPOPROTEIN_BINDING	15	-0.31	-0.88	0.642	0.913	1
GO_ENTEROENDOCRINE_CELL_DIFFERENTIATION	19	-0.29	-0.88	0.647	0.913	1
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	47	-0.23	-0.88	0.669	0.915	1
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	26	-0.26	-0.88	0.644	0.916	1
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	22	-0.28	-0.88	0.636	0.918	1
GO_CYTOPLASMIC_SEQUESTERING_OF_TRANSCRIPTION_FACTOR	18	-0.29	-0.88	0.631	0.919	1
GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	24	-0.27	-0.88	0.642	0.92	1
GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	19	-0.29	-0.87	0.683	0.92	1
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	84	-0.21	-0.87	0.729	0.92	1
GO_MUSCLE_CELL_FATE_COMMITMENT	15	-0.31	-0.87	0.635	0.92	1
GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K4_SPECIFIC	18	-0.28	-0.87	0.661	0.92	1
GO_MUSCLE_TISSUE_DEVELOPMENT	275	-0.17	-0.87	0.846	0.92	1
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	48	-0.23	-0.87	0.646	0.92	1
GO_RECEPTOR_SIGNALING_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	92	-0.2	-0.87	0.723	0.92	1
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	86	-0.2	-0.87	0.741	0.922	1
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	58	-0.22	-0.87	0.693	0.921	1
GO_POLYOL_CATABOLIC_PROCESS	18	-0.3	-0.87	0.645	0.921	1
GO_REGULATION_OF_NFAT_PROTEIN_IMPORT_INTO_NUCLEUS	17	-0.3	-0.87	0.659	0.92	1
GO_RHYTHMIC_PROCESS	298	-0.17	-0.87	0.838	0.921	1
GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	104	-0.2	-0.87	0.733	0.924	1
GO_GLYCEROLIPID_BIOSYNTHETIC_PROCESS	208	-0.18	-0.87	0.784	0.925	1
GO_ACTIN_BINDING	388	-0.17	-0.87	0.875	0.925	1
GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	31	-0.25	-0.87	0.655	0.924	1
GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	31	-0.25	-0.87	0.658	0.924	1
GO_VOLTAGE_GATED_ANION_CHANNEL_ACTIVITY	17	-0.3	-0.87	0.668	0.923	1
GO_MICROTUBULE_NUCLEATION	18	-0.28	-0.87	0.667	0.923	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	98	-0.2	-0.87	0.73	0.923	1
GO_NADH_DEHYDROGENASE_COMPLEX	42	-0.23	-0.87	0.671	0.923	1
GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	31	-0.25	-0.87	0.67	0.922	1
GO_REGULATION_OF_GLIOGENESIS	88	-0.2	-0.87	0.724	0.922	1
GO_REGULATION_OF_MYELINATION	33	-0.25	-0.87	0.658	0.922	1
GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	140	-0.19	-0.87	0.774	0.921	1
GO_STEROL_TRANSPORTER_ACTIVITY	18	-0.28	-0.87	0.652	0.922	1
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	18	-0.28	-0.87	0.66	0.922	1
GO_NEGATIVE_REGULATION_OF_ENDOCYTOSIS	39	-0.24	-0.87	0.718	0.923	1
GO_PLATELET_DEGRANULATION	105	-0.2	-0.87	0.749	0.922	1
GO_PH_REDUCTION	39	-0.24	-0.87	0.696	0.923	1
GO_ORGANIC_ACID_CATABOLIC_PROCESS	202	-0.18	-0.87	0.816	0.925	1
GO_PATTERN_SPECIFICATION_PROCESS	415	-0.17	-0.87	0.858	0.925	1
GO_RESPONSE_TO_GROWTH_FACTOR	473	-0.16	-0.86	0.907	0.925	1
GO_REGULATION_OF_ATPASE_ACTIVITY	58	-0.22	-0.86	0.73	0.926	1
GO_CIRCADIAN_RHYTHM	137	-0.19	-0.86	0.791	0.925	1
GO_PHOSPHOLIPID_CATABOLIC_PROCESS	29	-0.25	-0.86	0.678	0.927	1
GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS	16	-0.3	-0.86	0.659	0.928	1
GO_CONNECTIVE_TISSUE_DEVELOPMENT	194	-0.18	-0.86	0.805	0.927	1
GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	25	-0.26	-0.86	0.673	0.926	1
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	20	-0.28	-0.86	0.696	0.929	1
GO_MEGAKARYOCYTE_DEVELOPMENT	16	-0.3	-0.86	0.664	0.929	1

GO_EMBRYONIC_PATTERN_SPECIFICATION	58	-0.21	-0.86	0.735	0.929	1
GO_RESPONSE_TO_ALKALOID	137	-0.18	-0.86	0.795	0.93	1
GO_MACROMOLECULAR_COMPLEX_REMODELING	24	-0.27	-0.86	0.664	0.93	1
GO_ENDOPLASMIC_RETICULUM_CALCIIUM_ION_HOMEOSTASIS	20	-0.27	-0.86	0.673	0.931	1
GO_MESENCHYME_MORPHOGENESIS	38	-0.24	-0.86	0.68	0.93	1
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	27	-0.26	-0.86	0.668	0.931	1
GO_NOTCH_BINDING	18	-0.28	-0.86	0.677	0.931	1
GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	35	-0.24	-0.86	0.711	0.933	1
GO_MULTIVESICULAR_BODY	37	-0.23	-0.86	0.697	0.932	1
GO_CHEMOREPELLENT_ACTIVITY	27	-0.25	-0.86	0.685	0.932	1
GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	15	-0.3	-0.86	0.677	0.932	1
GO_STEROL_BINDING	43	-0.23	-0.86	0.721	0.932	1
GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	18	-0.28	-0.86	0.656	0.932	1
GO_REGULATION_OF_ORGAN_GROWTH	72	-0.21	-0.86	0.719	0.932	1
GO_MUSCLE_CELL_PROLIFERATION	19	-0.28	-0.86	0.681	0.932	1
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	18	-0.28	-0.86	0.676	0.931	1
GO_METANEPHROS_DEVELOPMENT	81	-0.2	-0.86	0.768	0.932	1
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	26	-0.26	-0.86	0.685	0.931	1
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	30	-0.24	-0.86	0.695	0.931	1
GO_NEGATIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	124	-0.19	-0.85	0.803	0.932	1
GO_RESPONSE_TO_MERCURY_ION	15	-0.3	-0.85	0.673	0.932	1
GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	36	-0.24	-0.85	0.729	0.932	1
GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	29	-0.25	-0.85	0.695	0.934	1
GO_TELOMERIC_DNA_BINDING	28	-0.25	-0.85	0.704	0.934	1
GO_STRUCTURAL_CONSTITUENT_OF_EYE_LENS	20	-0.28	-0.85	0.682	0.935	1
GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	30	-0.25	-0.85	0.685	0.936	1
GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	40	-0.23	-0.85	0.722	0.937	1
GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	75	-0.2	-0.85	0.761	0.937	1
GO_PHOSPHOLIPASE_ACTIVITY	93	-0.2	-0.85	0.782	0.938	1
GO_HEPARAN_SULFATE_SULFOTRANSFERASE_ACTIVITY	15	-0.29	-0.85	0.652	0.937	1
GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	67	-0.21	-0.85	0.735	0.938	1
GO_EARLY_ENDOSOME	292	-0.17	-0.85	0.911	0.939	1
GO_EMBRYONIC_AXIS_SPECIFICATION	33	-0.24	-0.85	0.734	0.938	1
GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	47	-0.22	-0.85	0.748	0.94	1
GO_MANNOSYLATION	34	-0.23	-0.85	0.714	0.94	1
GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	24	-0.26	-0.85	0.694	0.941	1
GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	19	-0.28	-0.85	0.653	0.943	1
GO_COATED_MEMBRANE	87	-0.2	-0.84	0.778	0.942	1
GO_ORGAN_FORMATION	34	-0.24	-0.84	0.709	0.944	1
GO_POLYAMINE_METABOLIC_PROCESS	15	-0.3	-0.84	0.678	0.943	1
GO_AU_RICH_ELEMENT_BINDING	23	-0.26	-0.84	0.7	0.943	1
GO_PROTEIN_INSERTION_INTO_MEMBRANE	22	-0.26	-0.84	0.682	0.943	1
GO_REGULATION_OF_PLATELET_AGGREGATION	17	-0.28	-0.84	0.671	0.942	1
GO_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	53	-0.22	-0.84	0.755	0.942	1
GO_STEREOCILUM_BUNDLE	41	-0.23	-0.84	0.745	0.941	1
GO_ENDOSOMAL_PART	415	-0.16	-0.84	0.931	0.942	1
GO_PHOTORECEPTOR_INNER_SEGMENT	36	-0.24	-0.84	0.715	0.942	1
GO_SPHINGOLIPID_METABOLIC_PROCESS	130	-0.18	-0.84	0.81	0.942	1
GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	19	-0.27	-0.84	0.662	0.943	1
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	94	-0.19	-0.84	0.806	0.943	1
GO_PROTEIN_KINASE_B_SIGNALING	34	-0.23	-0.84	0.72	0.943	1
GO_SIGNALING_ADAPTOR_ACTIVITY	74	-0.2	-0.84	0.761	0.942	1
GO_PROTEIN_DEGLYCOSYLATION	21	-0.26	-0.84	0.694	0.942	1
GO_SECRETORY_GRANULE_LUMEN	81	-0.2	-0.84	0.775	0.941	1
GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	17	-0.28	-0.84	0.681	0.942	1
GO_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	15	-0.29	-0.84	0.689	0.942	1
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	93	-0.19	-0.84	0.819	0.944	1
GO_MESENCHYME_DEVELOPMENT	188	-0.17	-0.84	0.876	0.944	1
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	23	-0.26	-0.84	0.715	0.948	1
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	119	-0.18	-0.84	0.837	0.948	1
GO_NEGATIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	26	-0.25	-0.84	0.737	0.948	1
GO_VESICLE_COATING	73	-0.2	-0.84	0.795	0.948	1
GO_IRON_ION_HOMEOSTASIS	67	-0.2	-0.84	0.787	0.948	1
GO_HORMONE_ACTIVITY	115	-0.19	-0.83	0.839	0.949	1
GO_FAT_CELL_DIFFERENTIATION	104	-0.19	-0.83	0.807	0.949	1
GO_GLYCEROLIPID_CATABOLIC_PROCESS	36	-0.23	-0.83	0.759	0.948	1
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	36	-0.23	-0.83	0.729	0.948	1
GO_KINASE_ACTIVATOR_ACTIVITY	61	-0.21	-0.83	0.771	0.949	1
GO_ANION_ANION_ANTIPORTER_ACTIVITY	22	-0.26	-0.83	0.726	0.95	1
GO_TYPE_I_INTERFERON_RECEPTOR_BINDING	17	-0.28	-0.83	0.699	0.951	1
GO_NERVE_DEVELOPMENT	68	-0.2	-0.83	0.781	0.951	1
GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	44	-0.22	-0.83	0.758	0.951	1
GO_REGULATION_OF_ACTION_POTENTIAL	38	-0.23	-0.83	0.774	0.953	1
GO_REGULATION_OF GRANULOCYTE DIFFERENTIATION	16	-0.29	-0.83	0.718	0.953	1
GO_PLATELET_DENSE_GRANULE	20	-0.27	-0.83	0.694	0.952	1
GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	49	-0.22	-0.83	0.764	0.954	1
GO_DRUG_TRANSMEMBRANE_TRANSPORT	19	-0.27	-0.83	0.7	0.954	1
GO_REGULATION_OF_ENDOCYTOSIS	198	-0.17	-0.83	0.898	0.954	1
GO_REGULATION_OF_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	15	-0.29	-0.83	0.692	0.954	1
GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	62	-0.2	-0.83	0.776	0.955	1
GO_EPITHELIAL_CELL_FATE_COMMITMENT	15	-0.29	-0.83	0.711	0.955	1
GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	122	-0.18	-0.83	0.838	0.955	1

GO_ARTERY_DEVELOPMENT	75	-0.2	-0.83	0.799	0.956	1
GO_LIPID_TRANSLOCATION	21	-0.26	-0.82	0.713	0.959	1
GO_GLUCAN_BIOSYNTHETIC_PROCESS	25	-0.25	-0.82	0.724	0.961	1
GO_SECRETORY_GRANULE	345	-0.16	-0.82	0.96	0.961	1
GO_N_ACETYLGALACTOSAMINE_METABOLIC_PROCESS	16	-0.28	-0.82	0.726	0.964	1
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	50	-0.21	-0.82	0.779	0.964	1
GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	18	-0.27	-0.82	0.716	0.963	1
GO_POSITIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	35	-0.23	-0.82	0.755	0.969	1
GO_RESPONSE_TO_CORTICOSTERONE	26	-0.24	-0.82	0.767	0.97	1
GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	19	-0.27	-0.82	0.707	0.969	1
GO_NEGATIVE_REGULATION_OF_MACROAUTOPHAGY	22	-0.25	-0.81	0.727	0.97	1
GO_DEFINITIVE_HEMOPOIESIS	17	-0.27	-0.81	0.721	0.969	1
GO_PROTEIN_LIPID_COMPLEX_BINDING	24	-0.25	-0.81	0.722	0.97	1
GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	36	-0.22	-0.81	0.777	0.973	1
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	33	-0.23	-0.81	0.755	0.973	1
GO_CALCIIUM_ION_IMPORT_INTO_CYTOSOL	42	-0.22	-0.81	0.79	0.974	1
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	16	-0.28	-0.81	0.703	0.975	1
GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	26	-0.24	-0.81	0.759	0.975	1
GO_CELL_VOLUME_HOMEOSTASIS	28	-0.24	-0.81	0.749	0.976	1
GO_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	17	-0.27	-0.81	0.739	0.976	1
GO_MONOCARBOXYLIC_ACID_TRANSPORT	123	-0.18	-0.81	0.887	0.976	1
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	31	-0.23	-0.81	0.769	0.976	1
GO_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	48	-0.21	-0.81	0.811	0.976	1
GO_AMINO_ACID_BINDING	106	-0.18	-0.81	0.875	0.977	1
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	15	-0.28	-0.81	0.718	0.977	1
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION_OF_STAT_PROTEIN	21	-0.26	-0.81	0.732	0.976	1
GO_NOTCH_SIGNALING_PATHWAY	114	-0.18	-0.81	0.868	0.976	1
GO_NATURAL_KILLER_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	24	-0.25	-0.81	0.78	0.976	1
GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	87	-0.19	-0.8	0.847	0.978	1
GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	41	-0.22	-0.8	0.826	0.978	1
GO_KINASE_REGULATOR_ACTIVITY	184	-0.17	-0.8	0.934	0.978	1
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	95	-0.19	-0.8	0.875	0.977	1
GO_ACTIN_FILAMENT_POLYMERIZATION	23	-0.25	-0.8	0.745	0.977	1
GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	105	-0.18	-0.8	0.867	0.977	1
GO_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	73	-0.19	-0.8	0.849	0.977	1
GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSPORT	16	-0.28	-0.8	0.76	0.976	1
GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	60	-0.2	-0.8	0.829	0.978	1
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	96	-0.19	-0.8	0.849	0.978	1
GO_SECONDARY_METABOLIC_PROCESS	47	-0.21	-0.8	0.842	0.979	1
GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	16	-0.28	-0.8	0.748	0.982	1
GO_PANCREAS_DEVELOPMENT	72	-0.19	-0.8	0.85	0.982	1
GO_NUCLEOSIDE_BIPHOSPHATE_BIOSYNTHETIC_PROCESS	17	-0.27	-0.8	0.773	0.983	1
GO_LIPID_HOMEOSTASIS	107	-0.18	-0.8	0.911	0.983	1
GO_CARBOHYDRATE_TRANSPORTER_ACTIVITY	43	-0.21	-0.8	0.823	0.983	1
GO_DRUG_TRANSPORT	25	-0.24	-0.8	0.785	0.983	1
GO_CATION_TRANSPORTING_ATPASE_COMPLEX	16	-0.27	-0.8	0.74	0.983	1
GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	-0.24	-0.79	0.77	0.983	1
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	263	-0.16	-0.79	0.962	0.983	1
GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	34	-0.22	-0.79	0.803	0.983	1
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	274	-0.16	-0.79	0.971	0.984	1
GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	45	-0.21	-0.79	0.842	0.984	1
GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_MULTIVESICULAR_BODY_SORTING_PATHWAY	18	-0.27	-0.79	0.75	0.984	1
GO_STEROID_BINDING	91	-0.18	-0.79	0.866	0.984	1
GO_SIGNAL_PEPTIDE_PROCESSING	24	-0.25	-0.79	0.773	0.984	1
GO_GALACTOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	-0.24	-0.79	0.799	0.984	1
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	23	-0.24	-0.79	0.796	0.984	1
GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	25	-0.24	-0.79	0.774	0.984	1
GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	36	-0.22	-0.79	0.809	0.984	1
GO_SULFATION	16	-0.27	-0.79	0.768	0.984	1
GO_MESENCHYMAL_CELL_DIFFERENTIATION	134	-0.17	-0.79	0.918	0.984	1
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	228	-0.16	-0.79	0.976	0.984	1
GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	233	-0.16	-0.79	0.964	0.983	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_ACETYLATION	20	-0.25	-0.79	0.778	0.984	1
GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	42	-0.21	-0.79	0.834	0.984	1
GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	21	-0.25	-0.79	0.786	0.984	1
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	35	-0.22	-0.79	0.833	0.984	1
GO_RESPONSE_TO_MAGNESIUM_ION	23	-0.25	-0.79	0.819	0.984	1
GO_OLFACTORY_LOBE_DEVELOPMENT	36	-0.21	-0.79	0.804	0.984	1
GO_DEMETHYLASE_ACTIVITY	34	-0.22	-0.79	0.815	0.984	1
GO_SINGLE_FERTILIZATION	109	-0.18	-0.79	0.891	0.984	1
GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	155	-0.17	-0.78	0.938	0.985	1
GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	62	-0.2	-0.78	0.866	0.986	1
GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	15	-0.27	-0.78	0.752	0.986	1
GO_ENDOTHELIAL_CELL_DEVELOPMENT	44	-0.21	-0.78	0.843	0.987	1
GO_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	25	-0.24	-0.78	0.805	0.986	1
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	36	-0.22	-0.78	0.809	0.987	1
GO_BINDING_BRIDGING	173	-0.16	-0.78	0.949	0.987	1
GO_NEURAL_CRESCENT_CELL_MIGRATION	51	-0.2	-0.78	0.853	0.986	1

GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	23	-0.24	-0.78	0.793	0.987	1
GO_EXTRACELLULAR_MATRIX	417	-0.15	-0.78	0.994	0.987	1
GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	52	-0.2	-0.78	0.86	0.99	1
GO_COENZYME_A_METABOLIC_PROCESS	17	-0.26	-0.78	0.793	0.99	1
GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	59	-0.19	-0.77	0.876	0.992	1
GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	25	-0.23	-0.77	0.828	0.993	1
GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	126	-0.17	-0.77	0.941	0.998	1
GO TRABECULA MORPHOGENESIS	39	-0.21	-0.77	0.861	0.997	1
GO_PLATELET_ALPHA_GRANULE	74	-0.18	-0.77	0.894	0.997	1
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	24	-0.24	-0.77	0.801	0.998	1
GO_REGULATION_OF_PROTEIN_DEACETYLATION	34	-0.22	-0.77	0.831	0.998	1
GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	16	-0.27	-0.77	0.806	0.998	1
GO_MAINTENANCE_OF_LOCATION_IN_CELL	93	-0.18	-0.77	0.897	1	1
GO_POSITIVE_REGULATION_OF_EXOCYTOSIS	82	-0.18	-0.76	0.915	1	1
GO_CELL_PROLIFERATION_IN_FOREBRAIN	27	-0.23	-0.76	0.812	1	1
GO_ENDOCRINE_PROCESS	44	-0.21	-0.76	0.833	1	1
GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	43	-0.2	-0.76	0.837	1	1
GO_GAMMA_TUBULIN_COMPLEX	16	-0.26	-0.76	0.79	1	1
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN	17	-0.26	-0.76	0.81	1	1
GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	74	-0.18	-0.76	0.901	1	1
GO_RESPONSE_TO_ISCHEMIA	28	-0.22	-0.76	0.842	1	1
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	16	-0.26	-0.76	0.826	1	1
GO_ETHANOLAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	84	-0.18	-0.76	0.94	1	1
GO_CADHERIN_BINDING	28	-0.22	-0.75	0.845	1	1
GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	21	-0.24	-0.75	0.836	1	1
GO_TRIVALENT_INORGANIC_CATION_TRANSPORT	38	-0.21	-0.75	0.887	1	1
GO_NEGATIVE_REGULATION_OF_MRNA_METABOLIC_PROCESS	28	-0.22	-0.75	0.859	1	1
GO_HYDROGEN_TRANSPORT	134	-0.16	-0.75	0.973	1	1
GO_PROTEIN_SECRETION	115	-0.17	-0.75	0.952	1	1
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_EPITHELIAL_CELL_APICAL_BASAL_POLARITY	29	-0.22	-0.75	0.82	1	1
GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	36	-0.21	-0.75	0.88	1	1
GO_RESPONSE_TO_DIETARY_EXCESS	21	-0.24	-0.75	0.841	1	1
GO_CELL_FATE_DETERMINATION	43	-0.2	-0.75	0.871	1	1
GO_SYMPORTER_ACTIVITY	141	-0.16	-0.75	0.961	1	1
GO_STEROID_CATABOLIC_PROCESS	24	-0.23	-0.75	0.834	1	1
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	29	-0.22	-0.75	0.845	1	1
GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	60	-0.19	-0.75	0.894	1	1
GO_NEGATIVE_REGULATION_OF_HISTONE_ACETYLATION	15	-0.26	-0.75	0.815	1	1
GO_REGULATION_OF_CGMP_BIOSYNTHETIC_PROCESS	22	-0.24	-0.75	0.845	1	1
GO_CELLULAR_COMPONENT_MAINTENANCE	17	-0.25	-0.75	0.836	1	1
GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	29	-0.22	-0.75	0.838	1	1
GO_ANION_CATION_SYMPORTER_ACTIVITY	53	-0.19	-0.75	0.896	1	1
GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	27	-0.23	-0.75	0.853	1	1
GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	42	-0.2	-0.74	0.87	1	1
GO_MICROBODY_LUMEN	44	-0.2	-0.74	0.886	1	1
GO_CHONDROCYTE_DIFFERENTIATION	60	-0.19	-0.74	0.909	1	1
GO_GROWTH_FACTOR_ACTIVITY	159	-0.16	-0.74	0.972	1	1
GO_REGULATION_OF_CELL_FATE_COMMITMENT	26	-0.22	-0.74	0.869	1	1
GO_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHONDRION	96	-0.17	-0.74	0.956	1	1
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	16	-0.25	-0.74	0.835	1	1
GO_RESPONSE_TO_PROSTAGLANDIN_E	25	-0.23	-0.74	0.853	1	1
GO_ACTIN_MONOMER_BINDING	24	-0.23	-0.74	0.858	1	1
GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	29	-0.22	-0.74	0.863	1	1
GO_WATER_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	-0.26	-0.74	0.834	1	1
GO_NEGATIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	15	-0.26	-0.74	0.835	1	1
GO_PALATE_DEVELOPMENT	84	-0.17	-0.74	0.925	1	1
GO_QUATERNARY_AMMONIUM_GROUP_BINDING	49	-0.19	-0.74	0.909	1	1
GO_ORGANIC_CATION_TRANSPORT	20	-0.24	-0.74	0.839	1	1
GO_LATE_ENDOSOME_MEMBRANE	97	-0.17	-0.74	0.945	1	1
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	113	-0.16	-0.74	0.963	1	1
GO_RESPONSE_TO_ACIDIC_PH	21	-0.23	-0.74	0.872	1	1
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	50	-0.19	-0.73	0.898	1	1
GO_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	64	-0.18	-0.73	0.913	1	1
GO_HISTONE_ACETYLTRANSFERASE_BINDING	28	-0.22	-0.73	0.893	1	1
GO_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	16	-0.25	-0.73	0.818	1	1
GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	165	-0.16	-0.73	0.987	1	1
GO_COP9_SIGNALOSOME	34	-0.2	-0.73	0.892	1	1
GO_AUDITORY_RECEPTOR_CELL_DEVELOPMENT	17	-0.25	-0.73	0.834	1	1
GO_STEROL_TRANSPORT	50	-0.19	-0.73	0.918	1	1
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	15	-0.26	-0.73	0.841	1	1
GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	39	-0.2	-0.73	0.885	1	1
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	54	-0.19	-0.73	0.908	1	1
GO_REGULATION_OF_HISTONE_DEACETYLATION	24	-0.23	-0.73	0.861	1	1
GO_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	59	-0.18	-0.73	0.933	1	1
GO_ACTIN_CYTOSKELETON_REORGANIZATION	55	-0.18	-0.73	0.909	1	1
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	15	-0.26	-0.73	0.86	1	1
GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	43	-0.19	-0.73	0.919	1	1
GO_ERYTHROCYTE_DEVELOPMENT	24	-0.22	-0.72	0.876	1	1
GO_2_OXOGLUTARATE_METABOLIC_PROCESS	20	-0.23	-0.72	0.834	1	1
GO_REGULATION_OF_ACTIN_NUCLEATION	26	-0.21	-0.72	0.875	1	1

GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	19	-0.24	-0.72	0.848	1	1
GO_LENS_FIBER_CELL_DIFFERENTIATION	25	-0.22	-0.72	0.881	1	1
GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	341	-0.14	-0.72	0.999	1	1
GO_PLASMA_MEMBRANE_FUSION	26	-0.22	-0.72	0.891	1	1
GO_MATING_BEHAVIOR	23	-0.23	-0.72	0.883	1	1
GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	170	-0.15	-0.72	0.999	1	1
GO_RESPIRATORY_GASEOUS_EXCHANGE	48	-0.19	-0.72	0.915	1	1
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	15	-0.25	-0.72	0.839	1	1
GO_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	35	-0.2	-0.72	0.914	1	1
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	216	-0.15	-0.72	0.992	1	1
GO_AMINE_BIOSYNTHETIC_PROCESS	21	-0.23	-0.72	0.848	1	1
GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	15	-0.25	-0.72	0.865	1	1
GO_ACTIN_FILAMENT	70	-0.17	-0.72	0.951	1	1
GO_CHD_TYPE_COMPLEX	17	-0.24	-0.72	0.854	1	1
GO_GLYOXALATE_METABOLIC_PROCESS	27	-0.21	-0.72	0.882	1	1
GO_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION	16	-0.25	-0.72	0.856	1	1
GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	43	-0.19	-0.71	0.894	1	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	105	-0.16	-0.71	0.968	1	1
GO_ENDOCYTIC_VESICLE_MEMBRANE	149	-0.15	-0.71	0.984	1	1
GO_L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	54	-0.18	-0.71	0.941	1	1
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	26	-0.22	-0.71	0.884	1	1
GO_SODIUM_ION_HOMEOSTASIS	29	-0.21	-0.71	0.885	1	1
GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	17	-0.24	-0.71	0.844	1	1
GO_LIPID_OXIDATION	68	-0.17	-0.71	0.941	1	1
GO_CELL_AGGREGATION	21	-0.23	-0.71	0.889	1	1
GO_RESPONSE_TO_LEPTIN	20	-0.23	-0.71	0.899	1	1
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	23	-0.22	-0.71	0.878	1	1
GO_POSITIVE_REGULATION_OF_NEUROBLAST_PROLIFERATION	21	-0.22	-0.71	0.87	1	1
GO_METANEPHRIC_NEPHRON_DEVELOPMENT	32	-0.2	-0.71	0.918	1	1
GO_TASTE_RECEPTOR_ACTIVITY	29	-0.21	-0.71	0.909	1	1
GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	33	-0.2	-0.71	0.908	1	1
GO_EMBRYONIC_DIGIT_MORPHOGENESIS	60	-0.18	-0.71	0.95	1	1
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A_CHEMICAL_SIGNAL	45	-0.19	-0.71	0.952	1	1
GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	23	-0.22	-0.7	0.888	1	1
GO_FATTY_ACID_CATABOLIC_PROCESS	71	-0.17	-0.7	0.966	1	1
GO_CELL_FATE_SPECIFICATION	71	-0.17	-0.7	0.973	1	1
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	36	-0.19	-0.7	0.92	1	1
GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_PHOSPHORYLATIVE_MECHANISM	33	-0.2	-0.7	0.915	1	1
GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	29	-0.21	-0.7	0.89	1	1
GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	25	-0.21	-0.7	0.885	1	1
GO_PARAXIAL_MESODERM_DEVELOPMENT	16	-0.24	-0.7	0.895	1	1
GO_POSITIVE_REGULATION_OF_PROTEIN_DEACETYLATION	18	-0.23	-0.7	0.899	1	1
GO_SULFUR_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	27	-0.21	-0.69	0.901	1	1
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	83	-0.16	-0.69	0.969	1	1
GO_OLFACTORY_RECEPTOR_ACTIVITY	369	-0.13	-0.69	0.999	1	1
GO_LAMELLIPODIUM_ORGANIZATION	36	-0.19	-0.69	0.913	1	1
GO_SUBSTANTIA_NIGRA_DEVELOPMENT	44	-0.18	-0.69	0.945	1	1
GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	29	-0.21	-0.69	0.905	1	1
GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	15	-0.24	-0.69	0.892	1	1
GO_ACID_THIOL_LIGASE_ACTIVITY	20	-0.22	-0.69	0.894	1	1
GO_REGULATION_OF_SMAD_PROTEIN_IMPORT_INTO_NUCLEUS	16	-0.24	-0.69	0.884	1	1
GO_CHEMOSENSORY_BEHAVIOR	15	-0.24	-0.69	0.901	1	1
GO_BRUSH_BORDER_MEMBRANE	55	-0.17	-0.69	0.964	1	1
GO_SEROTONIN_RECEPTOR_ACTIVITY	18	-0.23	-0.69	0.881	1	1
GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	17	-0.23	-0.69	0.887	1	1
GO_INORGANIC_ANION_EXCHANGER_ACTIVITY	21	-0.22	-0.68	0.919	1	1
GO_VESICLE_COAT	45	-0.18	-0.68	0.956	1	1
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	45	-0.18	-0.68	0.947	1	1
GO_AORTA_DEVELOPMENT	41	-0.19	-0.68	0.93	1	1
GO_REGULATION_OF_LIPID_TRANSPORT	93	-0.16	-0.68	0.981	1	1
GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	30	-0.2	-0.68	0.921	1	1
GO_HISTONE_DEUBIQUITINATION	21	-0.21	-0.68	0.895	1	1
GO_DORSAL_VENTRAL_AXIS_SPECIFICATION	20	-0.22	-0.68	0.903	1	1
GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	27	-0.2	-0.68	0.935	1	1
GO_REGULATION_OF_MESODERM_DEVELOPMENT	15	-0.23	-0.68	0.872	1	1
GO_REGULATION_OF_NEUROBLAST_PROLIFERATION	28	-0.2	-0.68	0.91	1	1
GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	91	-0.16	-0.67	0.999	1	1
GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	17	-0.23	-0.67	0.916	1	1
GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	25	-0.21	-0.67	0.934	1	1
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE_MEMBRANE	15	-0.23	-0.67	0.916	1	1
GO_BONE_CELL_DEVELOPMENT	22	-0.21	-0.67	0.905	1	1
GO_HORMONE_BIOSYNTHETIC_PROCESS	49	-0.17	-0.67	0.963	1	1
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	30	-0.2	-0.67	0.932	1	1
GO_WNT_ACTIVATED_RECEPTOR_ACTIVITY	22	-0.21	-0.67	0.922	1	1
GO_PHOSPHATASE_INHIBITOR_ACTIVITY	31	-0.19	-0.67	0.928	1	1
GO_LEUKOTRIENE_BIOSYNTHETIC_PROCESS	20	-0.22	-0.67	0.913	1	1
GO_JAK_STAT_CASCADE_INVOLVED_IN_GROWTH_HORMONE_SIGNALING_PATHWAY	15	-0.23	-0.67	0.906	1	1
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	28	-0.2	-0.67	0.916	1	1
GO_POSITIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	17	-0.22	-0.67	0.914	1	1
GO_NUCLEAR_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	22	-0.21	-0.67	0.914	1	1
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	103	-0.15	-0.67	0.994	1	1
GO_NOTCH_RECEPTOR_PROCESSING	16	-0.23	-0.67	0.903	1	1
GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	23	-0.21	-0.66	0.941	1	1

GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	21	-0.21	-0.66	0.915	1	1
GO_AXIS_SPECIFICATION	90	-0.15	-0.66	0.995	1	1
GO_NEPHRON_TUBULE_FORMATION	18	-0.22	-0.66	0.93	1	1
GO_PSEUDOPODIUM	17	-0.22	-0.66	0.906	1	1
GO_PROTEIN_DEALKYLATION	29	-0.19	-0.66	0.952	1	1
GO_TRACHEA_DEVELOPMENT	20	-0.21	-0.66	0.929	1	1
GO_SPERM_CAPACITATION	17	-0.22	-0.66	0.906	1	1
GO_POSITIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	15	-0.23	-0.66	0.909	1	1
GO_CARDIAC_ATRIUM_DEVELOPMENT	31	-0.19	-0.66	0.95	1	1
GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	42	-0.18	-0.66	0.961	1	1
GO_B_CELL_PROLIFERATION	38	-0.18	-0.66	0.95	1	1
GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	40	-0.18	-0.66	0.963	1	1
GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANSPORT	16	-0.23	-0.65	0.912	1	1
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	211	-0.13	-0.65	1	1	1
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	50	-0.17	-0.65	0.969	1	1
GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	113	-0.14	-0.65	0.995	1	1
GO_REGULATION_OF_CALCINEURIN_NFAT_SIGNALING_CASCADE	17	-0.22	-0.65	0.926	1	1
GO_GOLGI_ASSOCIATED_VESICLE	82	-0.15	-0.64	0.989	1	1
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCCOSE_STIMULUS	27	-0.19	-0.64	0.946	1	1
GO_THYROID_GLAND_DEVELOPMENT	25	-0.19	-0.64	0.956	1	1
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	35	-0.18	-0.64	0.972	1	1
GO_CELLULAR_ANION_HOMEOSTASIS	15	-0.22	-0.64	0.917	1	1
GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	65	-0.15	-0.63	0.985	1	1
GO_SEMAPHORIN_RECEPTOR_BINDING	22	-0.2	-0.63	0.944	1	1
GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_Membrane	24	-0.2	-0.63	0.954	1	1
GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	29	-0.19	-0.63	0.961	1	1
GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	79	-0.15	-0.63	0.997	1	1
GO_HISTONE_H3_K4_METHYLATION	32	-0.18	-0.63	0.955	1	1
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	17	-0.21	-0.63	0.959	1	1
GO_REGULATION_OF_RECEPTOR_RECYCLING	19	-0.21	-0.63	0.952	1	1
GO_RECEPTOR_SIGNALING_COMPLEX_SCAFFOLD_ACTIVITY	23	-0.19	-0.63	0.957	1	1
GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	62	-0.15	-0.62	0.986	1	1
GO_CELLULAR_RESPONSE_TO_STEROL	15	-0.22	-0.62	0.944	1	1
GO_SOMITE_DEVELOPMENT	77	-0.15	-0.62	1	1	1
GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	20	-0.2	-0.62	0.965	1	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	22	-0.19	-0.62	0.955	1	1
GO_RESPONSE_TO_THYROID_HORMONE	22	-0.19	-0.61	0.951	1	1
GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	18	-0.2	-0.61	0.952	1	1
GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	45	-0.16	-0.61	0.979	1	1
GO_PHOSPHOTRANSFERASE_ACTIVITY_FOR_OTHER_SUBSTITUTED_PHOSPHATE_GROUPS	19	-0.2	-0.61	0.959	1	1
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	27	-0.18	-0.61	0.969	1	1
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_ON_TRANSPORTING_DOMAIN	21	-0.19	-0.6	0.964	1	1
GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	29	-0.17	-0.6	0.972	1	1
GO_NEUTRAL_LIPID_METABOLIC_PROCESS	83	-0.14	-0.6	0.995	1	1
GO_SEGMENT_SPECIFICATION	17	-0.2	-0.6	0.957	1	1
GO_PARASYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	17	-0.2	-0.59	0.972	1	1
GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	18	-0.2	-0.59	0.97	1	1
GO_NEUROTRANSMITTER_BINDING	30	-0.17	-0.59	0.977	1	1
GO_METANEPHRIC_NEPHRON_MORPHOGENESIS	21	-0.19	-0.59	0.962	1	1
GO_RNA_POLYMERASE_II_CORE_BINDING	19	-0.19	-0.59	0.961	1	1
GO_MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	20	-0.19	-0.58	0.972	1	1
GO_RESPONSE_TO_MUSCLE_STRETCH	19	-0.19	-0.58	0.976	1	1
GO_SULFUR_AMINO_ACID_BIOSYNTHETIC_PROCESS	19	-0.19	-0.58	0.971	1	1
GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	21	-0.18	-0.58	0.977	1	1
GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	24	-0.18	-0.57	0.977	1	1
GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVATOR_ACTIVITY	19	-0.18	-0.56	0.983	1	1
GO_C21_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	15	-0.19	-0.56	0.967	1	1
GO_PIGMENT_GRANULE_ORGANIZATION	23	-0.17	-0.56	0.991	1	1
GO_AMINO_SUGAR_METABOLIC_PROCESS	40	-0.15	-0.55	0.998	1	1
GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	33	-0.16	-0.55	0.995	1	1
GO_CARDIAC_SEPTUM_MORPHOGENESIS	49	-0.14	-0.55	0.993	1	1
GO_PERICARDIUM_DEVELOPMENT	18	-0.18	-0.55	0.973	1	1
GO_SULFURIC_ESTER_HYDROLASE_ACTIVITY	17	-0.19	-0.55	0.98	1	1
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	25	-0.17	-0.54	0.989	1	1
GO_NEGATIVE_REGULATION_OF_AXON_EXTENSION	38	-0.15	-0.54	1	1	1
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	23	-0.17	-0.54	0.987	1	1
GO_RAC_GTPASE_BINDING	37	-0.15	-0.54	0.996	1	1
GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	19	-0.17	-0.53	0.989	1	1
GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	21	-0.17	-0.53	0.993	1	1
GO_REGULATION_OF_CELL_PROLIFERATION_INVOLVED_IN_HEART_MORPHOGENESIS	15	-0.18	-0.53	0.993	1	1
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	102	-0.12	-0.53	1	1	1
GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	30	-0.15	-0.52	0.996	1	1
GO_EXTRINSIC_COMPONENT_OF_ORGANELLE_Membrane	23	-0.16	-0.52	0.995	1	1
GO_RESPONSE_TO_IMMobilIZATION_STRESS	22	-0.16	-0.52	0.987	1	1
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	74	-0.13	-0.52	1	1	1
GO_MRNA_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	15	-0.18	-0.51	0.991	1	1

GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPARTMENTS	20	-0.16	-0.49	0.989	1	1
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	19	-0.16	-0.49	0.991	1	1
GO_PHOSPHATIDYLCHOLINE_BINDING	19	-0.16	-0.49	0.998	1	1
GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	28	-0.15	-0.49	0.997	1	1
GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	23	-0.15	-0.48	0.998	1	1
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	27	-0.14	-0.48	0.993	1	1
GO_FILOPODIUM_ASSEMBLY	17	-0.16	-0.48	0.995	1	1
GO_ARTERY_MORPHOGENESIS	51	-0.12	-0.48	1	1	1
GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	463	-0.09	-0.46	1	1	1
GO_PROTEIN_KINASE_C_ACTIVITY	16	-0.15	-0.45	1	1	1
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	55	-0.11	-0.44	1	0.999	1