

Table S3. Gene Ontology Term Enrichment Analysis. Using the Molecular Signatures Database (MSigDB) a Gene Ontology enrichment analysis was performed with GeneTrail v3.2 (<https://genetrail.bioinf.uni-sb.de/>). For each specifically enriched GO term (at least two independent proteins per term at a p value of >0.05) the total number of input hits (from the uploaded dataset), the expected number of hits as well as the adjusted p value of enrichment (plus the negative log10 version of this) is shown.

GO Term	Number of hits	Expected score	Adjusted p-value	Negative Log p-value
GO AGING	50	3.52737	1.05127E-35	34.97828573
GO REGULATION OF CELL DEATH	79	18.6561	7.36466E-25	24.1328473
GO RESPONSE TO OXYGEN CONTAINING COMPOUND	76	18.0262	1.05775E-23	22.97561697
GO RESPONSE TO OXIDATIVE STRESS	43	4.90167	7.10949E-23	22.14816155
GO RESPONSE TO ABIOTIC STIMULUS	65	13.7888	3.60039E-22	21.44365045
GO CELLULAR RESPONSE TO DNA DAMAGE STIMULUS	55	9.55138	4.87102E-22	21.31238009
GO POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS	73	18.1179	1.0093E-21	20.99597973
GO CELLULAR RESPONSE TO OXYGEN CONTAINING COMPOUND	61	12.4832	1.78602E-21	20.74811368
GO APOPTOTIC PROCESS	78	21.6796	9.7341E-21	20.0117042
GO NEURON DEATH	37	3.8824	9.7341E-21	20.0117042
GO DNA METABOLIC PROCESS	53	9.53993	1.16535E-20	19.93354362
GO REGULATION OF PROTEIN MODIFICATION PROCESS	75	20.2595	1.57219E-20	19.80349497
GO CELLULAR RESPONSE TO OXIDATIVE STRESS	34	3.2296	3.29551E-20	19.48207737
GO REGULATION OF RESPONSE TO STRESS	67	16.3427	3.46277E-20	19.46057635
GO NEGATIVE REGULATION OF CELL DEATH	55	11.0173	1.27547E-19	18.89432975
GO CELL AGING	24	1.19106	1.72489E-19	18.7632386
GO POSITIVE REGULATION OF BIOSYNTHETIC PROCESS	77	22.3896	1.72489E-19	18.7632386
GO POSITIVE REGULATION OF CELLULAR COMPONENT ORGANIZATION	60	13.4338	1.72489E-19	18.7632386
GO CELLULAR RESPONSE TO NITROGEN COMPOUND	45	7.112	2.3312E-19	18.63242047
GO RESPONSE TO NITROGEN COMPOUND	54	10.9142	3.7816E-19	18.42232441
GO HOMEOSTATIC PROCESS	74	21.3131	8.03674E-19	18.09492008
GO POSITIVE REGULATION OF PROTEIN MODIFICATION PROCESS	59	13.5483	1.13037E-18	17.94677938
GO REGULATION OF CELL POPULATION PROLIFERATION	67	18.0377	3.83693E-18	17.41601612
GO RESPONSE TO INORGANIC SUBSTANCE	41	6.25306	5.18387E-18	17.2853459
GO RESPONSE TO ENDOGENOUS STIMULUS	67	18.324	8.00759E-18	17.09649817
GO NEGATIVE REGULATION OF RESPONSE TO STIMULUS	66	17.8774	1.00838E-17	16.99637578
GO REGULATION OF CELLULAR RESPONSE TO STRESS	45	7.94803	1.05275E-17	16.97767475
GO DNA REPAIR	40	6.13854	1.68656E-17	16.7729982
GO POSITIVE REGULATION OF CELL DEATH	44	7.66172	1.68656E-17	16.7729982
GO REGULATION OF PHOSPHORUS METABOLIC PROCESS	66	18.6218	6.97793E-17	16.15627339
GO NEGATIVE REGULATION OF PROTEIN METABOLIC PROCESS	52	11.7846	2.03335E-16	15.69178786
GO REGULATION OF CATABOLIC PROCESS	50	10.8799	2.18673E-16	15.66020484
GO REGULATION OF CELLULAR CATABOLIC PROCESS	46	9.12764	2.4163E-16	15.61684915
GO RESPONSE TO REACTIVE OXYGEN SPECIES	27	2.49664	3.11725E-16	15.50622837
GO POSITIVE REGULATION OF PHOSPHORUS METABOLIC PROCESS	52	12.0137	3.98929E-16	15.39910439
GO REACTIVE OXYGEN SPECIES METABOLIC PROCESS	24	1.8324	5.66731E-16	15.24662303

GO AMYLOID BETA METABOLIC PROCESS	16	0.4581	7.32308E-16	15.13530622
GO POSITIVE REGULATION OF CATABOLIC PROCESS	34	4.74133	7.95912E-16	15.09913495
GO REGULATION OF INTRACELLULAR SIGNAL TRANSDUCTION	67	20.2824	9.28549E-16	15.03219517
GO CELLULAR RESPONSE TO ENDOGENOUS STIMULUS	58	15.3807	1.06098E-15	14.9742928
GO RESPONSE TO DRUG	50	11.4754	1.4265E-15	14.84572822
GO RESPONSE TO PEPTIDE	36	5.62318	1.9422E-15	14.71170605
GO CHROMOSOME ORGANIZATION	54	13.5483	1.95997E-15	14.70775058
GO POSITIVE REGULATION OF DEVELOPMENTAL PROCESS	57	15.1746	2.438E-15	14.6129663
GO REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	20	1.14525	2.82016E-15	14.54972625
GO REGULATION OF TRANSFERASE ACTIVITY	48	10.7768	2.98908E-15	14.52446246
GO POSITIVE REGULATION OF SIGNALING	66	20.3167	3.47562E-15	14.45896771
GO GROWTH	48	10.9715	5.66367E-15	14.24690206
GO PROTEIN PHOSPHORYLATION	68	21.7941	6.78852E-15	14.1682249
GO NEGATIVE REGULATION OF DEVELOPMENTAL PROCESS	47	10.6165	8.13817E-15	14.08947324
GO RESPONSE TO EXTRACELLULAR STIMULUS	36	5.9553	8.90904E-15	14.05016909
GO CELLULAR RESPONSE TO TOXIC SUBSTANCE	26	2.65698	8.92744E-15	14.04927306
GO NEGATIVE REGULATION OF CELLULAR COMPONENT ORGANIZATION	40	7.73044	1.87151E-14	13.72780785
GO RESPONSE TO OXYGEN LEVELS	31	4.3405	2.3398E-14	13.63082126
GO RESPONSE TO TOXIC SUBSTANCE	35	5.80642	2.62557E-14	13.5807764
GO MITOCHONDRION ORGANIZATION	35	5.85223	3.18059E-14	13.49749231
GO PROCESS UTILIZING AUTOPHAGIC MECHANISM	34	5.47429	3.18059E-14	13.49749231
GO REGULATION OF GROWTH	39	7.58155	5.3581E-14	13.27098919
GO CELLULAR RESPONSE TO PEPTIDE	30	4.18016	6.28238E-14	13.2018758
GO PEPTIDE METABOLIC PROCESS	19	1.20251	7.51537E-14	13.12404963
GO NEURON APOPTOTIC PROCESS	25	2.67988	9.06777E-14	13.0424995
GO POSITIVE REGULATION OF GENE EXPRESSION	66	22.0461	1.40773E-13	12.85148063
GO RESPONSE TO IONIZING RADIATION	21	1.69497	1.4397E-13	12.841728
GO RESPONSE TO RADIATION	32	5.07346	1.65409E-13	12.78144086
GO REGULATION OF TRANSPORT	63	20.4656	2.21128E-13	12.65535626
GO CELLULAR SENESCENCE	16	0.755865	3.17479E-13	12.498285
GO NEGATIVE REGULATION OF SIGNALING	53	15.0371	4.09352E-13	12.38790308
GO NEGATIVE REGULATION OF NEURON DEATH	23	2.33631	4.69863E-13	12.32802875
GO POSITIVE REGULATION OF MOLECULAR FUNCTION	61	19.7556	6.1172E-13	12.21344732
GO NEGATIVE REGULATION OF BIOSYNTHETIC PROCESS	57	17.4765	6.734E-13	12.17172689
GO POSITIVE REGULATION OF MULTICELLULAR ORGANISMAL PROCESS	60	19.4005	1.01404E-12	11.99394491
GO REGULATION OF CELLULAR COMPONENT BIOGENESIS	43	10.25	1.02383E-12	11.98977215
GO CELLULAR RESPONSE TO DRUG	28	4.01983	1.12515E-12	11.94878958
GO REGULATION OF MITOCHONDRION ORGANIZATION	21	1.99273	2.28824E-12	11.64049843
GO AMYLOID PRECURSOR PROTEIN CATABOLIC PROCESS	13	0.423742	2.63889E-12	11.57857871
GO REGULATION OF KINASE ACTIVITY	41	9.643	3.07644E-12	11.51195155
GO REGULATION OF DNA METABOLIC PROCESS	25	3.21815	3.53458E-12	11.45166218
GO REGULATION OF PROTEOLYSIS	37	7.89077	4.1371E-12	11.38330398
GO AMYLOID PRECURSOR PROTEIN METABOLIC PROCESS	14	0.606982	6.28986E-12	11.20135902
GO DOUBLE STRAND BREAK REPAIR	23	2.71424	7.60665E-12	11.11880657
GO REGULATION OF CELLULAR LOCALIZATION	41	9.99803	9.15208E-12	11.03848019

GO NEUROINFLAMMATORY RESPONSE	14	0.64134	1.16137E-11	10.9350294
GO CELLULAR RESPONSE TO IONIZING RADIATION	15	0.813127	1.18403E-11	10.92663729
GO POSITIVE REGULATION OF ORGANELLE ORGANIZATION	34	6.98602	1.86283E-11	10.72982678
GO GLIAL CELL ACTIVATION	13	0.515362	1.91189E-11	10.7185371
GO REGULATION OF CELL AGING	13	0.526815	2.39965E-11	10.6198521
GO RESPONSE TO ORGANIC CYCLIC COMPOUND	41	10.3645	2.66167E-11	10.57484579
GO CELLULAR RESPONSE TO REACTIVE OXYGEN SPECIES	19	1.77514	2.9689E-11	10.52740443
GO REGULATION OF AUTOPHAGY	25	3.58463	2.9689E-11	10.52740443
GO REGULATION OF CELLULAR PROTEIN LOCALIZATION	31	5.88658	3.45592E-11	10.46143632
GO REGULATION OF ORGANELLE ORGANIZATION	48	14.1553	3.57014E-11	10.44731475
GO POSITIVE REGULATION OF TRANSFERASE ACTIVITY	34	7.28379	5.26443E-11	10.27864864
GO NEGATIVE REGULATION OF MULTICELLULAR ORGANISMAL PROCESS	46	13.3651	7.52634E-11	10.12341617
GO AMYLOID BETA FORMATION	11	0.32067	9.41395E-11	10.02622811
GO REGULATION OF BINDING	26	4.18016	1.03213E-10	9.986265599
GO POSITIVE REGULATION OF RNA BIOSYNTHETIC PROCESS	54	18.1866	1.29244E-10	9.888589609
GO RESPONSE TO GAMMA RADIATION	13	0.629887	1.50748E-10	9.821748441
GO POSITIVE REGULATION OF PROTEOLYSIS	25	3.9053	1.60135E-10	9.795513736
GO REGULATION OF PROTEIN LOCALIZATION	41	11.086	1.91211E-10	9.718487127
GO BEHAVIOR	32	6.79133	2.09493E-10	9.678830484
GO NEGATIVE REGULATION OF PHOSPHORYLATION	27	4.7986	3.07884E-10	9.51161288
GO INFLAMMATORY RESPONSE	34	7.87932	3.88262E-10	9.410875113
GO ANATOMICAL STRUCTURE HOMEOSTASIS	27	4.85586	3.91941E-10	9.406779304
GO POSITIVE REGULATION OF CATALYTIC ACTIVITY	49	15.8503	4.50353E-10	9.34644694
GO CELLULAR HOMEOSTASIS	40	10.9257	4.82258E-10	9.316720559
GO REGULATION OF PROTEIN STABILITY	22	3.06927	4.82258E-10	9.316720559
GO RESPONSE TO TEMPERATURE STIMULUS	21	2.7486	5.00981E-10	9.300178745
GO DNA BIOSYNTHETIC PROCESS	19	2.14162	5.17982E-10	9.285685332
GO REGULATION OF NUCLEOBASE CONTAINING COMPOUND METABOLIC PROCESS	29	5.76061	5.36396E-10	9.270514469
GO REGULATION OF RESPONSE TO EXTERNAL STIMULUS	35	8.56647	7.18023E-10	9.143861644
GO LEUKOCYTE ACTIVATION INVOLVED IN INFLAMMATORY RESPONSE	11	0.423742	9.82923E-10	9.007480502
GO REGULATION OF MAPK CASCADE	34	8.2687	1.26106E-09	8.89926425
GO RESPONSE TO ANTIBIOTIC	23	3.60754	1.31742E-09	8.880275748
GO POSITIVE REGULATION OF NEURON DEATH	14	0.996367	1.62774E-09	8.788414964
GO REGULATION OF DEVELOPMENTAL GROWTH	23	3.6648	1.74681E-09	8.757754331
GO PROTEOLYSIS	54	19.6181	1.8914E-09	8.723216615
GO REGULATION OF AMYLOID PRECURSOR PROTEIN CATABOLIC PROCESS	10	0.32067	1.97202E-09	8.705088685
GO REGULATION OF PROTEIN COMPLEX ASSEMBLY	26	4.85586	2.01236E-09	8.696294324
GO POSITIVE REGULATION OF BINDING	18	2.0729	2.51479E-09	8.599498275
GO RESPONSE TO HORMONE	39	11.0631	2.51479E-09	8.599498275
GO REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	19	2.38212	2.57379E-09	8.589426891
GO RESPONSE TO HYDROGEN PEROXIDE	16	1.52318	2.58203E-09	8.588038716
GO CELLULAR RESPONSE TO INORGANIC SUBSTANCE	19	2.43938	3.70739E-09	8.430931726
GO NEGATIVE REGULATION OF CELL POPULATION PROLIFERATION	32	7.68463	3.73485E-09	8.427726836
GO CELLULAR RESPONSE TO RADIATION	18	2.14162	3.92678E-09	8.40596343
GO REGULATION OF PROTEIN CATABOLIC PROCESS	24	4.22597	3.92678E-09	8.40596343

GO DEVELOPMENTAL GROWTH	31	7.24943	4.10584E-09	8.386597979
GO RESPONSE TO X RAY	10	0.355027	4.1499E-09	8.381962368
GO POSITIVE REGULATION OF TRANSPORT	38	10.7997	4.69646E-09	8.328229372
GO DNA RECOMBINATION	21	3.18379	5.46688E-09	8.262260459
GO POSITIVE REGULATION OF KINASE ACTIVITY	29	6.4363	5.72286E-09	8.242386878
GO PROTEIN LOCALIZATION TO ORGANELLE	37	10.376	6.03154E-09	8.219571788
GO POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	11	0.526815	6.12658E-09	8.212781891
GO NEGATIVE REGULATION OF DNA METABOLIC PROCESS	14	1.1338	6.56819E-09	8.182554293
GO REGULATION OF RESPONSE TO OXIDATIVE STRESS	13	0.9162	6.98649E-09	8.155740958
GO REGULATION OF AMYLOID BETA FORMATION	9	0.251955	7.06557E-09	8.150852797
GO NEGATIVE REGULATION OF PROTEIN MODIFICATION PROCESS	29	6.52792	7.54337E-09	8.12243459
GO RESPONSE TO PEPTIDE HORMONE	25	4.7986	7.66345E-09	8.115575672
GO TELOMERE ORGANIZATION	17	1.96983	8.88172E-09	8.051502922
GO NEGATIVE REGULATION OF AMYLOID PRECURSOR PROTEIN CATABOLIC PROCESS	8	0.160335	1.07892E-08	7.967010756
GO NEGATIVE REGULATION OF CATABOLIC PROCESS	21	3.33268	1.11605E-08	7.952316348
GO RESPONSE TO HEAT	17	2.00419	1.11605E-08	7.952316348
GO POSITIVE REGULATION OF INTRACELLULAR SIGNAL TRANSDUCTION	38	11.1891	1.14272E-08	7.942060171
GO APOPTOTIC SIGNALING PATHWAY	29	6.68826	1.24229E-08	7.905777011
GO NEGATIVE REGULATION OF NUCLEOBASE CONTAINING COMPOUND METABOLIC PROCESS	16	1.74078	1.35193E-08	7.869045795
GO REGULATION OF CHROMOSOME ORGANIZATION	22	3.77932	1.55197E-08	7.809116678
GO REGULATION OF NERVOUS SYSTEM DEVELOPMENT	36	10.25	1.55197E-08	7.809116678
GO REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	17	2.06145	1.60745E-08	7.793862527
GO CELLULAR RESPONSE TO HYDROGEN PEROXIDE	13	0.996367	1.61728E-08	7.791214784
GO REGULATION OF CELL DIFFERENTIATION	53	20.4656	2.15232E-08	7.667093159
GO REGULATION OF OXIDATIVE STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	9	0.297765	2.15232E-08	7.667093159
GO NEGATIVE REGULATION OF PHOSPHORUS METABOLIC PROCESS	27	5.96675	2.27139E-08	7.643708291
GO REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	19	2.7715	2.28146E-08	7.641787141
GO POSITIVE REGULATION OF PROTEIN CATABOLIC PROCESS	18	2.43938	2.31602E-08	7.635257695
GO RESPONSE TO AMYLOID BETA	10	0.446647	2.32114E-08	7.634298664
GO MUSCLE CELL PROLIFERATION	17	2.13016	2.4444E-08	7.611827725
GO CELLULAR RESPONSE TO ANTIBIOTIC	15	1.54609	2.46428E-08	7.608309948
GO PEPTIDYL AMINO ACID MODIFICATION	42	13.8804	2.87645E-08	7.541143171
GO DNA GEOMETRIC CHANGE	13	1.06508	3.19507E-08	7.495519623
GO SIGNAL TRANSDUCTION BY PROTEIN PHOSPHORYLATION	36	10.5707	3.2246E-08	7.49152415
GO REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	23	4.3634	3.3042E-08	7.480933673
GO CELLULAR RESPONSE TO ORGANIC CYCLIC COMPOUND	27	6.09273	3.3133E-08	7.47973924
GO CELLULAR RESPONSE TO OXYGEN LEVELS	18	2.5081	3.32828E-08	7.477780145
GO BASE EXCISION REPAIR	10	0.469552	3.3443E-08	7.475694771
GO RESPONSE TO ANTINEOPLASTIC AGENT	13	1.07653	3.46995E-08	7.459676783
GO NEGATIVE REGULATION OF APOPTOTIC SIGNALING PATHWAY	18	2.531	3.748E-08	7.426200418
GO POSITIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	21	3.61899	3.90876E-08	7.407960995
GO POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	15	1.6148	4.02043E-08	7.395727495
GO RESPONSE TO OXYGEN RADICAL	9	0.332122	4.29197E-08	7.367343322
GO NEGATIVE REGULATION OF MOLECULAR FUNCTION	39	12.4145	4.69601E-08	7.328270987
GO REGULATION OF APOPTOTIC SIGNALING PATHWAY	23	4.46647	4.77093E-08	7.321396955

GO RESPONSE TO COPPER ION	10	0.492457	4.77093E-08	7.321396955
GO CELLULAR AMIDE METABOLIC PROCESS	36	10.7768	4.95394E-08	7.305049258
GO REGULATION OF INFLAMMATORY RESPONSE	21	3.69916	5.46031E-08	7.2627827
GO REGULATION OF OXIDATIVE STRESS INDUCED CELL DEATH	11	0.68715	5.62406E-08	7.249950055
GO CELL CELL SIGNALING	49	18.576	5.98472E-08	7.222956164
GO MUSCLE CELL MIGRATION	12	0.904747	6.10455E-08	7.214346345
GO RESPONSE TO LIPID	35	10.3531	6.4411E-08	7.191039958
GO RESPONSE TO METAL ION	22	4.16871	7.31438E-08	7.135822481
GO REGULATION OF CELL DEVELOPMENT	35	10.4103	7.33217E-08	7.134767474
GO CARBOHYDRATE HOMEOSTASIS	18	2.66843	7.60662E-08	7.118808279
GO ASTROCYTE ACTIVATION	8	0.22905	7.60855E-08	7.118698101
GO CELL CYCLE PROCESS	43	15.1402	9.67067E-08	7.014543436
GO NEGATIVE REGULATION OF CELLULAR CATABOLIC PROCESS	18	2.71424	9.67067E-08	7.014543436
GO NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	22	4.24888	9.91249E-08	7.003817238
GO GLIAL CELL DEVELOPMENT	13	1.21396	1.17764E-07	6.928987451
GO REGULATION OF IMMUNE SYSTEM PROCESS	46	17.0986	1.18135E-07	6.927621414
GO NEGATIVE REGULATION OF CELL DIFFERENTIATION	30	7.99384	1.19478E-07	6.922712056
GO NEGATIVE REGULATION OF INTRACELLULAR SIGNAL TRANSDUCTION	25	5.60027	1.19736E-07	6.921775254
GO SMOOTH MUSCLE CELL MIGRATION	11	0.755865	1.26699E-07	6.897226813
GO SUPEROXIDE METABOLIC PROCESS	11	0.755865	1.26699E-07	6.897226813
GO NEGATIVE REGULATION OF MITOCHONDRION ORGANIZATION	10	0.561172	1.29789E-07	6.886762114
GO POSITIVE REGULATION OF DNA METABOLIC PROCESS	15	1.79804	1.37934E-07	6.860328669
GO CELLULAR RESPONSE TO PEPTIDE HORMONE STIMULUS	20	3.53882	1.40045E-07	6.853732392
GO REGULATION OF PROTEIN SERINE THREONINE KINASE ACTIVITY	25	5.66899	1.47195E-07	6.832106942
GO PROTEIN CONTAINING COMPLEX ASSEMBLY	52	21.1184	1.47216E-07	6.832044987
GO REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION	18	2.80586	1.47968E-07	6.829832196
GO SMOOTH MUSCLE CELL PROLIFERATION	14	1.52318	1.53845E-07	6.812916614
GO POSITIVE REGULATION OF CELL DIFFERENTIATION	35	10.7653	1.55184E-07	6.809153058
GO REPLICATIVE SENESCENCE	7	0.148882	1.68665E-07	6.772975029
GO CHEMICAL HOMEOSTASIS	39	13.0902	1.71341E-07	6.766138703
GO REGULATION OF CELL CYCLE	39	13.2391	2.32003E-07	6.634506399
GO POSITIVE REGULATION OF AUTOPHAGY	13	1.30558	2.42671E-07	6.61498212
GO DEFENSE RESPONSE	47	18.2324	2.61856E-07	6.581937471
GO POSITIVE REGULATION OF MITOCHONDRION ORGANIZATION	13	1.31704	2.64818E-07	6.577052499
GO ASTROCYTE DEVELOPMENT	9	0.435195	2.68135E-07	6.571646493
GO REGULATION OF TRANS SYNAPTIC SIGNALING	23	4.95893	2.68135E-07	6.571646493
GO MACROAUTOPHAGY	19	3.30977	2.71114E-07	6.566848055
GO REGULATION OF MACROAUTOPHAGY	15	1.91257	2.78815E-07	6.554683865
GO PROTEIN COMPLEX OLIGOMERIZATION	26	6.36759	2.92249E-07	6.534246966
GO TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHWAY	29	7.87932	3.17137E-07	6.498753086
GO POSITIVE REGULATION OF NUCLEOBASE CONTAINING COMPOUND METABOLIC PROCESS	17	2.61117	3.26492E-07	6.486127456
GO REGULATION OF DNA REPAIR	13	1.35139	3.39334E-07	6.469372623
GO POSITIVE REGULATION OF MAPK CASCADE	25	5.9553	3.48116E-07	6.458276015
GO CIRCULATORY SYSTEM DEVELOPMENT	36	11.7274	3.53179E-07	6.452005127
GO DNA CONFORMATION CHANGE	19	3.38994	3.77984E-07	6.422526583

GO CELLULAR GLUCOSE HOMEOSTASIS	14	1.66061	3.92663E-07	6.40598002
GO POSITIVE REGULATION OF CELL DEVELOPMENT	25	6.00111	3.95977E-07	6.402330039
GO MUSCLE STRUCTURE DEVELOPMENT	27	6.97457	4.04342E-07	6.393251145
GO MACROMOLECULE DEACYLATION	12	1.11089	4.07893E-07	6.389453748
GO RESPONSE TO ACID CHEMICAL	20	3.81368	4.12264E-07	6.384824587
GO POSITIVE REGULATION OF PROTEOLYSIS INVOLVED IN CELLULAR PROTEIN CATABOLIC PROCESS	13	1.38575	4.30227E-07	6.366302338
GO NEGATIVE REGULATION OF NEURON APOPTOTIC PROCESS	14	1.68352	4.49564E-07	6.347208473
GO RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	10	0.664245	4.71055E-07	6.326928382
GO CELL DEATH IN RESPONSE TO OXIDATIVE STRESS	11	0.893295	5.21932E-07	6.282386075
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO OXIDATIVE STRESS	9	0.481005	5.27208E-07	6.278018008
GO STRESS INDUCED PREMATURE SENESCENCE	6	0.09162	5.48528E-07	6.260801199
GO RESPONSE TO LIGHT STIMULUS	19	3.51592	6.27875E-07	6.202126809
GO ENZYME LINKED RECEPTOR PROTEIN SIGNALING PATHWAY	35	11.4525	6.3043E-07	6.200363128
GO OXIDATION REDUCTION PROCESS	34	10.8913	6.38442E-07	6.194878551
GO REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	29	8.17708	6.43011E-07	6.191781598
GO RECOMBINATIONAL REPAIR	13	1.44301	6.44856E-07	6.190537255
GO CELLULAR RESPONSE TO GAMMA RADIATION	8	0.332122	6.76269E-07	6.16988052
GO CELL GROWTH	23	5.26815	7.01861E-07	6.153748889
GO TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	11	0.927652	7.13983E-07	6.146312129
GO POSITIVE REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION	15	2.10726	8.37876E-07	6.076820249
GO NEGATIVE REGULATION OF OXIDATIVE STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	7	0.206145	8.41092E-07	6.075156498
GO REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	14	1.78659	8.51191E-07	6.069972977
GO TELOMERIC D LOOP DISASSEMBLY	6	0.103072	8.60115E-07	6.065443478
GO CELL CYCLE	49	20.3854	8.75956E-07	6.057517708
GO REGULATION OF DEFENSE RESPONSE	29	8.31451	8.793E-07	6.055862927
GO CELLULAR RESPONSE TO HORMONE STIMULUS	28	7.82206	9.45733E-07	6.024231457
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY	18	3.2296	9.55525E-07	6.019757946
GO MACROPHAGE ACTIVATION	11	0.96201	9.69663E-07	6.013379176
GO REGULATION OF NEUROINFLAMMATORY RESPONSE	8	0.355027	1.00103E-06	5.999552907
GO RESPONSE TO ACTIVITY	10	0.73296	1.00103E-06	5.999552907
GO CHROMATIN ORGANIZATION	30	8.91004	1.00499E-06	5.99783826
GO MUSCLE ADAPTATION	12	1.23687	1.09134E-06	5.962039927
GO POSITIVE REGULATION OF NERVOUS SYSTEM DEVELOPMENT	24	5.96675	1.38162E-06	5.859611389
GO RESPONSE TO UV	13	1.55754	1.39115E-06	5.85662604
GO MACROMOLECULE CATABOLIC PROCESS	41	15.5181	1.40686E-06	5.851749118
GO REGULATION OF MICROGLIAL CELL ACTIVATION	7	0.22905	1.43344E-06	5.843620481
GO COGNITION	18	3.35558	1.60219E-06	5.795285983
GO NEGATIVE REGULATION OF DEFENSE RESPONSE	15	2.23324	1.60952E-06	5.793303622
GO MULTICELLULAR ORGANISM AGING	8	0.389385	1.79932E-06	5.744891593
GO RESPONSE TO KETONE	15	2.25614	1.81352E-06	5.741477651
GO TELOMERIC LOOP DISASSEMBLY	6	0.125977	1.94071E-06	5.712039356
GO TOR SIGNALING	12	1.31704	1.99575E-06	5.699893862
GO POSITIVE REGULATION OF CHROMOSOME ORGANIZATION	14	1.93547	2.00663E-06	5.697532699
GO NEGATIVE REGULATION OF CATALYTIC ACTIVITY	29	8.68099	2.02649E-06	5.693255535
GO REGULATION OF CELLULAR COMPONENT MOVEMENT	33	10.9142	2.02925E-06	5.692664445

GO SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	17	3.02346	2.04323E-06	5.689682743
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE	8	0.400837	2.11481E-06	5.674728645
GO POSITIVE REGULATION OF PROTEIN BINDING	11	1.05363	2.11481E-06	5.674728645
GO NEGATIVE REGULATION OF TRANSFERASE ACTIVITY	17	3.04636	2.24187E-06	5.649389575
GO POSITIVE REGULATION OF CELL POPULATION PROLIFERATION	32	10.3989	2.24553E-06	5.648681138
GO RNA DEPENDENT DNA BIOSYNTHETIC PROCESS	10	0.813127	2.24575E-06	5.648638592
GO APOPTOTIC MITOCHONDRIAL CHANGES	12	1.33994	2.2915E-06	5.639880138
GO REGULATION OF TRANSMEMBRANE TRANSPORT	24	6.16144	2.29373E-06	5.639457705
GO AUTOPHAGY OF MITOCHONDRION	10	0.82458	2.50442E-06	5.601292837
GO DNA REPLICATION	17	3.09217	2.69276E-06	5.569802353
GO CELLULAR RESPONSE TO X RAY	6	0.13743	2.72458E-06	5.564700436
GO ORGANELLE DISASSEMBLY	11	1.08799	2.76696E-06	5.557997119
GO GLIAL CELL DIFFERENTIATION	15	2.34776	2.77873E-06	5.55615365
GO REGULATION OF MITOCHONDRIAL FISSION	7	0.263407	2.92556E-06	5.533790991
GO NEGATIVE REGULATION OF RNA BIOSYNTHETIC PROCESS	38	14.1324	3.00952E-06	5.521502766
GO POSITIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	11	1.09944	3.00952E-06	5.521502766
GO REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	12	1.38575	3.11314E-06	5.506801348
GO REGULATION OF INTRACELLULAR TRANSPORT	21	4.85586	3.20477E-06	5.494203133
GO GLIOGENESIS	17	3.14944	3.35364E-06	5.474483559
GO ASTROCYTE DIFFERENTIATION	10	0.858937	3.41723E-06	5.46632579
GO POSITIVE REGULATION OF CELL AGING	6	0.148882	3.80464E-06	5.41968643
GO RESPONSE TO XENOBIOTIC STIMULUS	17	3.18379	3.85024E-06	5.414512198
GO REGULATION OF SYNAPTIC PLASTICITY	14	2.0729	4.07976E-06	5.389365384
GO NEGATIVE REGULATION OF CELL CYCLE	25	6.90586	4.28115E-06	5.368439555
GO REGULATION OF ANATOMICAL STRUCTURE MORPHOGENESIS	34	11.9221	4.36967E-06	5.35955136
GO CELLULAR RESPONSE TO OXYGEN RADICAL	7	0.286312	4.54631E-06	5.342340954
GO CELLULAR RESPONSE TO ABIOTIC STIMULUS	18	3.64189	4.58156E-06	5.338986622
GO REGENERATION	14	2.11871	5.16977E-06	5.286528778
GO LYSOSOMAL TRANSPORT	11	1.17961	5.56996E-06	5.254147924
GO NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	10	0.9162	5.74237E-06	5.240908828
GO PROTEIN REPAIR	5	0.068715	6.03597E-06	5.219252927
GO REGULATION OF DNA BIOSYNTHETIC PROCESS	11	1.19106	6.03597E-06	5.219252927
GO SECRETION	44	18.5416	6.93244E-06	5.159113881
GO NEGATIVE REGULATION OF INFLAMMATORY RESPONSE	12	1.51173	7.10471E-06	5.148453644
GO REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	9	0.698602	7.14149E-06	5.146211168
GO POSITIVE REGULATION OF TRANSCRIPTION BY RNA POLYMERASE II	36	13.4567	7.62275E-06	5.117888323
GO REGULATION OF PROTEIN OLIGOMERIZATION	8	0.492457	7.62275E-06	5.117888323
GO PROTEIN LOCALIZATION TO CHROMOSOME	10	0.950557	7.66307E-06	5.115597207
GO REGULATION OF SMALL MOLECULE METABOLIC PROCESS	18	3.79078	0.000007786	5.108685601
GO PROTEIN LOCALIZATION TO CHROMOSOME TELOMERIC REGION	7	0.32067	0.000008414	5.074997492
GO CELLULAR MACROMOLECULE CATABOLIC PROCESS	35	12.9184	8.64686E-06	5.063141573
GO REGULATION OF LIPID LOCALIZATION	12	1.54609	8.68436E-06	5.061262182
GO NEGATIVE REGULATION OF RESPONSE TO OXIDATIVE STRESS	8	0.50391	8.73074E-06	5.058948945
GO POSITIVE REGULATION OF TRANSMEMBRANE TRANSPORT	14	2.23324	9.01238E-06	5.045160505
GO CENTRAL NERVOUS SYSTEM DEVELOPMENT	32	11.1433	9.06673E-06	5.042549317

GO NEUROGENESIS	43	18.0835	9.08024E-06	5.041902672
GO PROTEIN HOMOOLOGOMERIZATION	18	3.84804	9.37981E-06	5.027805959
GO MODULATION OF AGE RELATED BEHAVIORAL DECLINE	5	0.0801675	9.70176E-06	5.013149473
GO CELLULAR RESPONSE TO EXTRACELLULAR STIMULUS	16	3.02346	9.87946E-06	5.005266793
GO RESPONSE TO CORTICOSTEROID	13	1.90111	9.87946E-06	5.005266793
GO MUSCLE CELL DIFFERENTIATION	18	3.87094	1.00705E-05	4.996948966
GO RESPONSE TO INSULIN	16	3.03491	1.02957E-05	4.987344121
GO RESPONSE TO ALCOHOL	15	2.64553	1.05338E-05	4.977414932
GO MUSCLE TISSUE DEVELOPMENT	19	4.3405	1.08373E-05	4.965078904
GO COVALENT CHROMATIN MODIFICATION	21	5.2796	1.08699E-05	4.963774451
GO MUSCLE CELL APOPTOTIC PROCESS	9	0.744412	1.08972E-05	4.962685078
GO REGULATION OF MEMBRANE POTENTIAL	20	4.8215	1.14209E-05	4.942299671
GO POSITIVE REGULATION OF SYNAPTIC TRANSMISSION	13	1.93547	0.000011691	4.932148339
GO NEGATIVE REGULATION OF CHROMOSOME ORGANIZATION	12	1.60335	1.18727E-05	4.925450506
GO DETERMINATION OF ADULT LIFESPAN	6	0.194692	1.19732E-05	4.921789763
GO REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	15	2.69134	1.26617E-05	4.897507981
GO REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	8	0.538267	1.29127E-05	4.888982939
GO CELLULAR CHEMICAL HOMEOSTASIS	28	9.04747	1.33501E-05	4.874515481
GO NEGATIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	12	1.62625	1.34865E-05	4.870100743
GO RESPONSE TO STEROID HORMONE	19	4.42066	1.37047E-05	4.863130467
GO AMYLOID BETA CLEARANCE	7	0.355027	0.000014122	4.850103793
GO CALMODULIN DEPENDENT KINASE SIGNALING PATHWAY	5	0.09162	1.47153E-05	4.83223088
GO REGULATION OF MITOCHONDRIAL MEMBRANE POTENTIAL	9	0.77877	1.48815E-05	4.827353291
GO CELL CYCLE ARREST	15	2.73715	1.51671E-05	4.81909745
GO GLUCOSE METABOLIC PROCESS	11	1.33994	1.60671E-05	4.794062503
GO RESPONSE TO WOUNDING	25	7.48993	1.61841E-05	4.790911447
GO REGULATION OF MULTICELLULAR ORGANISM GROWTH	9	0.790222	1.64584E-05	4.783612387
GO REGULATION OF RESPONSE TO DRUG	10	1.05363	1.65508E-05	4.781181009
GO REGULATION OF SUPEROXIDE METABOLIC PROCESS	7	0.36648	1.66393E-05	4.778864948
GO PEPTIDYL TYROSINE MODIFICATION	18	4.05418	1.79256E-05	4.746526299
GO SYNAPTIC SIGNALING	26	8.08546	1.80031E-05	4.744652706
GO REGULATION OF UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	12	1.68352	1.83647E-05	4.736016162
GO REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	13	2.03854	1.92418E-05	4.715754304
GO MITOCHONDRIAL FISSION	7	0.377932	1.93968E-05	4.712269912
GO MULTICELLULAR ORGANISM GROWTH	12	1.69497	1.93968E-05	4.712269912
GO NEGATIVE REGULATION OF DNA REPAIR	7	0.377932	1.93968E-05	4.712269912
GO NEGATIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	10	1.07653	1.93968E-05	4.712269912
GO REGULATION OF OXIDOREDUCTASE ACTIVITY	10	1.07653	1.93968E-05	4.712269912
GO REGULATION OF RESPONSE TO REACTIVE OXYGEN SPECIES	7	0.377932	1.93968E-05	4.712269912
GO POSITIVE REGULATION OF UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	10	1.08799	2.10076E-05	4.67762356
GO REGULATION OF PROTEIN BINDING	14	2.43938	2.18212E-05	4.66112137
GO CELLULAR RESPONSE TO STARVATION	12	1.71787	2.18295E-05	4.660956212
GO NEGATIVE REGULATION OF RESPONSE TO EXTERNAL STIMULUS	17	3.67625	2.18295E-05	4.660956212
GO REGULATION OF SYSTEM PROCESS	23	6.59664	2.32125E-05	4.634278083
GO REGULATION OF NEUROTRANSMITTER LEVELS	17	3.69916	2.35783E-05	4.627487511

GO POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	8	0.59553	2.37181E-05	4.624920104
GO POSITIVE REGULATION OF AUTOPHAGY OF MITOCHONDRION	6	0.22905	2.41363E-05	4.617329305
GO REGULATION OF GENE EXPRESSION EPIGENETIC	17	3.71061	2.43607E-05	4.613310236
GO MONOSACCHARIDE METABOLIC PROCESS	12	1.74078	2.44486E-05	4.611746005
GO ORGANONITROGEN COMPOUND CATABOLIC PROCESS	36	14.2698	0.000025509	4.593306566
GO REGULATION OF DNA BINDING	11	1.42011	2.55625E-05	4.592396675
GO REGULATION OF DOUBLE STRAND BREAK REPAIR	9	0.847485	0.000026274	4.580473804
GO POSITIVE REGULATION OF PROTEIN SERINE THREONINE KINASE ACTIVITY	17	3.74497	2.71533E-05	4.566177382
GO RESPONSE TO STARVATION	13	2.14162	3.07299E-05	4.512438853
GO NEGATIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	7	0.41229	3.11293E-05	4.506830645
GO REGULATION OF MAP KINASE ACTIVITY	17	3.79078	3.16416E-05	4.499741564
GO ESTABLISHMENT OF PROTEIN LOCALIZATION TO ORGANELLE	22	6.21871	3.22639E-05	4.491283137
GO NEGATIVE REGULATION OF PROTEOLYSIS	17	3.81368	3.40805E-05	4.467494042
GO ORGANELLE FISSION	20	5.24524	3.56626E-05	4.447786998
GO RESPONSE TO CARBOHYDRATE	14	2.56536	3.66628E-05	4.43577437
GO REGULATION OF MACROPHAGE ACTIVATION	8	0.64134	3.78527E-05	4.421903137
GO REGULATION OF TELOMERE MAINTENANCE	9	0.893295	3.83535E-05	4.416194998
GO REGULATION OF PEPTIDASE ACTIVITY	19	4.78714	3.85199E-05	4.414314849
GO CARBOHYDRATE METABOLIC PROCESS	22	6.29887	3.89042E-05	4.410003511
GO NEGATIVE REGULATION OF LONG TERM SYNAPTIC POTENTIATION	5	0.125977	4.28298E-05	4.368253954
GO REGULATION OF ASPARTIC TYPE PEPTIDASE ACTIVITY	5	0.125977	4.28298E-05	4.368253954
GO PROTEIN CATABOLIC PROCESS	29	10.2729	4.32886E-05	4.36362646
GO REGULATION OF SYNAPSE STRUCTURE OR ACTIVITY	14	2.61117	4.38249E-05	4.358279066
GO INCLUSION BODY ASSEMBLY	6	0.263407	0.000045444	4.342523449
GO REGULATION OF CHOLESTEROL EFFLUX	6	0.263407	0.000045444	4.342523449
GO REGULATION OF CARBOHYDRATE METABOLIC PROCESS	13	2.23324	0.000045835	4.338802764
GO CELLULAR MACROMOLECULE LOCALIZATION	46	21.4734	4.62639E-05	4.334757759
GO LIPID LOCALIZATION	18	4.39776	4.91068E-05	4.308858365
GO CELLULAR RESPONSE TO HEAT	11	1.53463	4.91764E-05	4.308243267
GO POSITIVE REGULATION OF CELLULAR COMPONENT BIOGENESIS	21	5.88658	4.96779E-05	4.303836771
GO NEGATIVE REGULATION OF CELL AGING	6	0.27486	5.53863E-05	4.256597646
GO INSULIN RECEPTOR SIGNALING PATHWAY	11	1.55754	5.57721E-05	4.253583003
GO VACUOLAR TRANSPORT	11	1.55754	5.57721E-05	4.253583003
GO POSITIVE REGULATION OF DEVELOPMENTAL GROWTH	12	1.91257	5.75219E-05	4.240166777
GO REGULATION OF MUSCLE ADAPTATION	9	0.950557	5.89734E-05	4.229343833
GO CELLULAR DETOXIFICATION	10	1.24832	6.03476E-05	4.219339997
GO POSITIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	19	4.95893	6.06917E-05	4.216870698
GO RESPONSE TO ENDOPLASMIC RETICULUM STRESS	15	3.11508	6.07686E-05	4.216320769
GO REGULATION OF CELLULAR RESPONSE TO DRUG	6	0.286312	6.66368E-05	4.176285867
GO REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	10	1.27123	6.96457E-05	4.157105692
GO CELLULAR RESPONSE TO CARBOHYDRATE STIMULUS	11	1.60335	7.12951E-05	4.146940317
GO SMALL MOLECULE METABOLIC PROCESS	42	19.057	7.32024E-05	4.13547468
GO RHYTHMIC PROCESS	15	3.17234	7.44406E-05	4.128190135
GO LONG TERM SYNAPTIC POTENTIATION	9	0.984915	7.54976E-05	4.122066854
GO POSITIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	11	1.6148	7.54976E-05	4.122066854

GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	6	0.297765	0.00007981	4.097942689
GO POSITIVE REGULATION OF CELL CYCLE PROCESS	15	3.19525	8.02187E-05	4.09572438
GO PROTEIN KINASE B SIGNALING	14	2.7715	8.02187E-05	4.09572438
GO REGULATION OF LONG TERM SYNAPTIC POTENTIATION	7	0.492457	8.14187E-05	4.089275836
GO IMPORT INTO CELL	24	7.74189	8.37432E-05	4.077050448
GO REGULATION OF CELLULAR CARBOHYDRATE METABOLIC PROCESS	10	1.30558	8.44014E-05	4.073650349
GO REGULATION OF GENERATION OF PRECURSOR METABOLITES AND ENERGY	11	1.63771	8.44014E-05	4.073650349
GO REGULATION OF GLIOGENESIS	10	1.30558	8.44014E-05	4.073650349
GO NEGATIVE REGULATION OF INTRACELLULAR TRANSPORT	8	0.73296	8.58212E-05	4.066405417
GO REGULATION OF PROTEIN TYROSINE KINASE ACTIVITY	9	1.00782	8.78301E-05	4.056356623
GO MEMORY	10	1.31704	9.01725E-05	4.04492589
GO CELLULAR RESPONSE TO INSULIN STIMULUS	13	2.40502	9.26077E-05	4.033352902
GO NEGATIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	6	0.309217	9.37924E-05	4.027832351
GO PROTEIN LOCALIZATION TO NUCLEUS	14	2.82877	9.80647E-05	4.008487296
GO NEGATIVE REGULATION OF CELL DEVELOPMENT	16	3.71061	9.91568E-05	4.003677497
GO CELLULAR RESPONSE TO MANGANESE ION	5	0.160335	9.98878E-05	4.000487552
GO REGULATION OF ATP BIOSYNTHETIC PROCESS	5	0.160335	9.98878E-05	4.000487552
GO REGULATION OF SIGNALING RECEPTOR ACTIVITY	22	6.73407	0.00010055	3.997617925
GO REGULATION OF NEURON DIFFERENTIATION	23	7.29524	0.000103246	3.986126765
GO LIPID METABOLIC PROCESS	34	13.972	0.000104964	3.978959627
GO MITOCHONDRIAL TRANSPORT	14	2.85167	0.000104964	3.978959627
GO MYELOID LEUKOCYTE ACTIVATION	23	7.30669	0.000104964	3.978959627
GO POSITIVE REGULATION OF PEPTIDASE ACTIVITY	12	2.05	0.000104964	3.978959627
GO CELLULAR RESPONSE TO LIPID	22	6.76843	0.000107358	3.969165588
GO CELLULAR RESPONSE TO COPPER ION	6	0.32067	0.000109343	3.961209015
GO REGULATION OF CELLULAR RESPIRATION	6	0.32067	0.000109343	3.961209015
GO LOCOMOTION	43	20.1335	0.00011077	3.955577844
GO POSITIVE REGULATION OF MACROAUTOPHAGY	8	0.767317	0.000112233	3.949879428
GO CELL ACTIVATION	36	15.3578	0.000114165	3.942467019
GO AMYLOID FIBRIL FORMATION	5	0.171787	0.000127503	3.894479597
GO FORMATION OF EXTRACHROMOSOMAL CIRCULAR DNA	5	0.171787	0.000127503	3.894479597
GO REGULATION OF LIPID METABOLIC PROCESS	17	4.27178	0.000127503	3.894479597
GO POSITIVE REGULATION OF GROWTH	14	2.90893	0.000127815	3.893418176
GO CELLULAR RESPONSE TO EXTERNAL STIMULUS	16	3.80223	0.000128017	3.892732354
GO SIGNAL RELEASE	19	5.26815	0.000128428	3.891340281
GO POSITIVE REGULATION OF MAP KINASE ACTIVITY	14	2.92039	0.00013257	3.877554744
GO PROTEASOMAL PROTEIN CATABOLIC PROCESS	19	5.29105	0.000135838	3.866978721
GO CELL MOTILITY	39	17.5681	0.000143628	3.842760887
GO NEGATIVE REGULATION OF TRANSPORT	19	5.31396	0.000143628	3.842760887
GO REGULATION OF HYDROLASE ACTIVITY	34	14.224	0.000146847	3.833134921
GO POSITIVE REGULATION OF MUSCLE TISSUE DEVELOPMENT	8	0.801675	0.000146995	3.832697437
GO MITOTIC CELL CYCLE	29	11.0517	0.000151265	3.820261548
GO REGULATION OF CELL PROJECTION ORGANIZATION	23	7.50139	0.000153044	3.815183692
GO DETOXIFICATION	10	1.42011	0.000156945	3.804252516
GO POSITIVE REGULATION OF CHOLESTEROL EFFLUX	5	0.18324	0.000160707	3.793965206

GO STRIATED MUSCLE ADAPTATION	7	0.561172	0.000161503	3.791819406
GO POSITIVE REGULATION OF RESPONSE TO EXTERNAL STIMULUS	15	3.43575	0.00016866	3.772987904
GO MUSCLE ORGAN DEVELOPMENT	17	4.38631	0.000172213	3.763934068
GO POSITIVE REGULATION OF CELL CYCLE	17	4.38631	0.000172213	3.763934068
GO SYNAPTIC TRANSMISSION DOPAMINERGIC	6	0.355027	0.000173839	3.759852785
GO EPITHELIAL CELL APOPTOTIC PROCESS	9	1.12234	0.000181488	3.741152085
GO POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	8	0.836032	0.000191054	3.718843865
GO POSITIVE REGULATION OF SMALL MOLECULE METABOLIC PROCESS	9	1.1338	0.000194753	3.710515844
GO REGULATION OF CIRCADIAN RHYTHM	9	1.1338	0.000194753	3.710515844
GO VACUOLE ORGANIZATION	11	1.82095	0.000197381	3.704694655
GO POSITIVE REGULATION OF NEUROINFLAMMATORY RESPONSE	5	0.194692	0.000201046	3.696704563
GO PEPTIDYL SERINE MODIFICATION	15	3.51592	0.000215021	3.667519123
GO REGULATION OF MUSCLE SYSTEM PROCESS	13	2.63407	0.000215021	3.667519123
GO POSITIVE REGULATION OF NEURON PROJECTION DEVELOPMENT	14	3.06927	0.000217605	3.66233113
GO NEGATIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY	9	1.1567	0.000223253	3.651202696
GO REGULATION OF TRANSCRIPTION REGULATORY REGION DNA BINDING	7	0.59553	0.000223253	3.651202696
GO REGULATION OF EPITHELIAL CELL APOPTOTIC PROCESS	8	0.858937	0.000224772	3.64825779
GO CIRCULATORY SYSTEM PROCESS	20	6.04692	0.000228504	3.641106193
GO LOCOMOTORY BEHAVIOR	12	2.24469	0.000230908	3.63656102
GO NEGATIVE REGULATION OF MUSCLE CELL APOPTOTIC PROCESS	6	0.377932	0.000231611	3.635240818
GO POSITIVE REGULATION OF LOCOMOTION	20	6.05837	0.000233262	3.632156005
GO SYNAPTIC VESICLE LOCALIZATION	11	1.86676	0.000240553	3.618789223
GO NOTCH RECEPTOR PROCESSING LIGAND DEPENDENT	4	0.0801675	0.000242538	3.615220208
GO ESTABLISHMENT OF PROTEIN LOCALIZATION TO TELOMERE	5	0.206145	0.000246355	3.608438619
GO NEGATIVE REGULATION OF CELLULAR SENESENCE	5	0.206145	0.000246355	3.608438619
GO NEGATIVE REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	5	0.206145	0.000246355	3.608438619
GO REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	9	1.17961	0.00025297	3.596930979
GO CELLULAR COMPONENT DISASSEMBLY	20	6.10418	0.000255937	3.591866925
GO CYTOKINE PRODUCTION	24	8.41759	0.000285582	3.544269169
GO REGULATION OF LIPID TRANSPORT	9	1.20251	0.000290781	3.536433974
GO NEGATIVE REGULATION OF KINASE ACTIVITY	13	2.72569	0.000293688	3.532113798
GO REGULATION OF MUSCLE ORGAN DEVELOPMENT	10	1.54609	0.0002962	3.528414946
GO POSITIVE REGULATION OF OXIDOREDUCTASE ACTIVITY	7	0.629887	0.000301494	3.520721326
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERASE	5	0.217597	0.000303132	3.518368215
GO CARDIOVASCULAR SYSTEM DEVELOPMENT	23	7.87932	0.000308418	3.510860283
GO VESICLE MEDIATED TRANSPORT IN SYNAPSE	12	2.32486	0.000312399	3.505290365
GO SYNAPSE ORGANIZATION	17	4.62681	0.000315716	3.500703408
GO IMMUNE SYSTEM DEVELOPMENT	28	10.9257	0.000320249	3.494512218
GO PROTEIN STABILIZATION	11	1.93547	0.000321024	3.493462498
GO REGULATION OF PROTEIN TARGETING	8	0.9162	0.000332269	3.478510176
GO RESPONSE TO GROWTH FACTOR	23	7.93658	0.0003413	3.466863712
GO NEURON INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO OXIDATIVE STRESS	4	0.09162	0.000343547	3.46401384
GO PEPTIDYL LYSINE DEACETYLATION	4	0.09162	0.000343547	3.46401384
GO REGULATION OF AMYLOID FIBRIL FORMATION	4	0.09162	0.000343547	3.46401384
GO REGULATION OF ASTROCYTE ACTIVATION	4	0.09162	0.000343547	3.46401384

GO REGULATION OF NUCLEOTIDE BIOSYNTHETIC PROCESS	6	0.41229	0.000343547	3.46401384
GO REGULATION OF HISTONE MODIFICATION	10	1.58044	0.000344359	3.462988562
GO RESPONSE TO ALKALOID	9	1.23687	0.000346556	3.460226578
GO POSITIVE REGULATION OF PROTEIN COMPLEX ASSEMBLY	13	2.78296	0.000350065	3.455851308
GO CELLULAR PROTEIN CATABOLIC PROCESS	24	8.56647	0.000361756	3.441584257
GO REGULATION OF CELL CYCLE PROCESS	24	8.56647	0.000361756	3.441584257
GO RESPONSE TO MITOCHONDRIAL DEPOLARISATION	5	0.22905	0.000361756	3.441584257
GO TEMPERATURE HOMEOSTASIS	11	1.96983	0.000365103	3.437584598
GO NEGATIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	9	1.24832	0.00036702	3.435310269
GO EPITHELIAL CELL PROLIFERATION	16	4.21452	0.000387034	3.412250882
GO ORGANONITROGEN COMPOUND BIOSYNTHETIC PROCESS	41	19.8701	0.000388096	3.411060833
GO REGULATION OF MUSCLE HYPERTROPHY	7	0.664245	0.000394711	3.40372077
GO POSITIVE REGULATION OF CELL PROJECTION ORGANIZATION	16	4.22597	0.000397404	3.400767766
GO ACTIVATION OF PROTEIN KINASE ACTIVITY	15	3.75642	0.000417036	3.379826454
GO EXTRACELLULAR STRUCTURE ORGANIZATION	17	4.76424	0.000434862	3.361648541
GO RESPONSE TO MANGANESE ION	5	0.240502	0.000435779	3.360733702
GO HISTONE PHOSPHORYLATION	6	0.435195	0.000437225	3.359295014
GO RESPONSE TO CATECHOLAMINE	6	0.435195	0.000437225	3.359295014
GO NEGATIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	11	2.01564	0.000438428	3.358101718
GO NEURON PROJECTION ORGANIZATION	8	0.96201	0.000440001	3.356546336
GO REGULATION OF DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	17	4.77569	0.000442792	3.353800234
GO REGULATION OF VESICLE MEDIATED TRANSPORT	19	5.85223	0.00046369	3.33377227
GO DNA STRAND RENATURATION	4	0.103072	0.000469649	3.328226598
GO REGULATION OF ASPARTIC TYPE ENDOPEPTIDASE ACTIVITY INVOLVED IN AMYLOID PRECURSOR PROTEIN CATABOLIC PROCESS	4	0.103072	0.000469649	3.328226598
GO LYTIC VACUOLE ORGANIZATION	7	0.68715	0.000471184	3.326809465
GO POSITIVE REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	8	0.973462	0.000471184	3.326809465
GO REGULATION OF CHROMATIN ORGANIZATION	11	2.03854	0.000477227	3.321274993
GO NEGATIVE REGULATION OF GROWTH	13	2.88603	0.000483372	3.31571851
GO REGULATION OF AUTOPHAGY OF MITOCHONDRION	6	0.446647	0.000489077	3.31062276
GO NEGATIVE REGULATION OF TRANSCRIPTION BY RNA POLYMERASE II	25	9.36814	0.000496406	3.304162978
GO POSITIVE REGULATION OF DNA BINDING	7	0.698602	0.00051354	3.289425723
GO POSITIVE REGULATION OF STEROL TRANSPORT	5	0.251955	0.00051354	3.289425723
GO REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	12	2.47374	0.000519953	3.284035912
GO MUSCLE HYPERTROPHY	8	0.996367	0.000543095	3.265124196
GO NEURON DIFFERENTIATION	34	15.2776	0.00054356	3.26475251
GO REGULATION OF SUPRAMOLECULAR FIBER ORGANIZATION	15	3.85949	0.00054356	3.26475251
GO MULTICELLULAR ORGANISMAL HOMEOSTASIS	18	5.39413	0.000544099	3.264322072
GO REGULATION OF SECRETION	24	8.87569	0.000600672	3.221362612
GO POSITIVE REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	10	1.70642	0.00060147	3.220786029
GO GLUCOSE IMPORT	7	0.721507	0.000611048	3.213924673
GO POSITIVE REGULATION OF CARBOHYDRATE METABOLIC PROCESS	7	0.721507	0.000611048	3.213924673
GO RESPONSE TO CADMIUM ION	7	0.721507	0.000611048	3.213924673
GO CHOLESTEROL EFFLUX	6	0.469552	0.00061595	3.21045454
GO NOTCH RECEPTOR PROCESSING	4	0.114525	0.000627083	3.202674973
GO DENDRITE DEVELOPMENT	12	2.531	0.000630556	3.200276337

GO NEGATIVE REGULATION OF NERVOUS SYSTEM DEVELOPMENT	14	3.43575	0.000630556	3.200276337
GO REGULATION OF WNT SIGNALING PATHWAY	15	3.92821	0.000648735	3.187932671
GO TISSUE REGENERATION	7	0.73296	0.000663875	3.177913686
GO POSITIVE REGULATION OF DNA RECOMBINATION	6	0.481005	0.000688227	3.162268293
GO RESPONSE TO DEXAMETHASONE	6	0.481005	0.000688227	3.162268293
GO REGULATION OF MITOTIC CELL CYCLE	21	7.19217	0.000700238	3.154754325
GO REGULATION OF NEURON PROJECTION DEVELOPMENT	18	5.5201	0.000712281	3.14734864
GO REGULATION OF CELL ACTIVATION	19	6.06982	0.000713961	3.146325511
GO POSITIVE REGULATION OF DNA REPAIR	7	0.744412	0.000720267	3.142506483
GO EXOCYTOSIS	26	10.2385	0.00072301	3.140855696
GO POSITIVE REGULATION OF GLUCOSE TRANSMEMBRANE TRANSPORT	6	0.492457	0.000766881	3.115272022
GO PROTEIN DESTABILIZATION	6	0.492457	0.000766881	3.115272022
GO LIPID STORAGE	7	0.755865	0.000783264	3.106091834
GO CELLULAR RESPONSE TO TOPOLOGICALLY INCORRECT PROTEIN	10	1.77514	0.00079966	3.097094627
GO NEUROTRANSMITTER TRANSPORT	13	3.05782	0.000815261	3.088703333
GO MITOCHONDRIAL DNA METABOLIC PROCESS	4	0.125977	0.000818196	3.087142648
GO NEGATIVE REGULATION OF TELOMERASE ACTIVITY	4	0.125977	0.000818196	3.087142648
GO POSITIVE REGULATION OF ATP BIOSYNTHETIC PROCESS	4	0.125977	0.000818196	3.087142648
GO REGULATION OF MULTI ORGANISM PROCESS	16	4.53519	0.000831955	3.079900164
GO DNA INTEGRITY CHECKPOINT	10	1.78659	0.00083343	3.079130871
GO POSITIVE REGULATION OF GLIOGENESIS	7	0.767317	0.000844435	3.073433774
GO CELLULAR RESPONSE TO KETONE	8	1.07653	0.000859411	3.065799092
GO REGULATION OF CARBOHYDRATE BIOSYNTHETIC PROCESS	8	1.07653	0.000859411	3.065799092
GO RESPONSE TO TOPOLOGICALLY INCORRECT PROTEIN	11	2.21033	0.000901075	3.045239059
GO POSTTRANSCRIPTIONAL REGULATION OF GENE EXPRESSION	20	6.76843	0.000919261	3.036561165
GO CIRCADIAN RHYTHM	11	2.22178	0.000937654	3.027957389
GO NEGATIVE REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	6	0.515362	0.000937654	3.027957389
GO PROTEIN ACETYLATION	11	2.22178	0.000937654	3.027957389
GO REGULATION OF LIPID STORAGE	6	0.515362	0.000937654	3.027957389
GO REGULATION OF STEROL TRANSPORT	6	0.515362	0.000937654	3.027957389
GO SUPRAMOLECULAR FIBER ORGANIZATION	21	7.36396	0.000937654	3.027957389
GO CELL DEATH IN RESPONSE TO HYDROGEN PEROXIDE	5	0.297765	0.000955038	3.019979348
GO NEGATIVE REGULATION OF RESPONSE TO DRUG	5	0.297765	0.000955038	3.019979348
GO POSITIVE REGULATION OF TRANSCRIPTION REGULATORY REGION DNA BINDING	5	0.297765	0.000955038	3.019979348
GO NON RECOMBINATIONAL REPAIR	8	1.09944	0.000969087	3.013637232
GO NEGATIVE REGULATION OF SYNAPTIC TRANSMISSION	7	0.790222	0.000978044	3.009641607
GO REGULATION OF DENDRITIC SPINE DEVELOPMENT	7	0.790222	0.000978044	3.009641607
GO REGULATION OF CALCIUM MEDIATED SIGNALING	8	1.11089	0.00103343	2.985718935
GO DOPAMINE BIOSYNTHETIC PROCESS	4	0.13743	0.00103416	2.985412264
GO MUSCLE ATROPHY	4	0.13743	0.00103416	2.985412264
GO NEGATIVE REGULATION OF BINDING	10	1.84385	0.00103416	2.985412264
GO NEURON DEVELOPMENT	29	12.4489	0.00103416	2.985412264
GO POSITIVE REGULATION OF MICROGLIAL CELL ACTIVATION	4	0.13743	0.00103416	2.985412264
GO ENERGY DERIVATION BY OXIDATION OF ORGANIC COMPOUNDS	13	3.14944	0.00103956	2.98315044
GO NEGATIVE REGULATION OF GENE EXPRESSION EPIGENETIC	9	1.46592	0.00104978	2.978901705

GO POSITIVE REGULATION OF CHROMATIN ORGANIZATION	8	1.12234	0.00109168	2.961904646
GO ESTABLISHMENT OF PROTEIN LOCALIZATION TO CHROMOSOME	5	0.309217	0.00109629	2.960074547
GO PROTEIN MATURATION	13	3.17234	0.00110949	2.954876608
GO CELL SURFACE RECEPTOR SIGNALING PATHWAY INVOLVED IN CELL CELL SIGNALING	20	6.8944	0.00112774	2.947791015
GO HISTONE DEACETYLATION	7	0.813127	0.00112774	2.947791015
GO REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	7	0.813127	0.00112774	2.947791015
GO REGULATION OF PROTEIN ACETYLATION	7	0.813127	0.00112774	2.947791015
GO SELECTIVE AUTOPHAGY	6	0.538267	0.00112774	2.947791015
GO SIGNAL TRANSDUCTION IN RESPONSE TO DNA DAMAGE	9	1.48882	0.00115945	2.935747975
GO ORGANIC HYDROXY COMPOUND TRANSPORT	12	2.73715	0.00119431	2.922882931
GO REGULATION OF ION TRANSMEMBRANE TRANSPORT	17	5.24524	0.00121156	2.916655073
GO REGULATION OF DNA RECOMBINATION	8	1.14525	0.00122648	2.911339529
GO REGULATION OF TELOMERASE ACTIVITY	6	0.54972	0.00124565	2.904603968
GO NEGATIVE REGULATION OF MACROPHAGE DERIVED FOAM CELL DIFFERENTIATION	4	0.148882	0.00130182	2.885449061
GO POSITIVE REGULATION OF INSULIN LIKE GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	4	0.148882	0.00130182	2.885449061
GO LIPID OXIDATION	8	1.1567	0.00130203	2.885379009
GO REGULATION OF GLUCOSE METABOLIC PROCESS	7	0.836032	0.00130794	2.883412178
GO REGULATION OF GLUCOSE TRANSMEMBRANE TRANSPORT	7	0.836032	0.00130794	2.883412178
GO REGULATION OF HORMONE LEVELS	18	5.87513	0.00142118	2.847350913
GO REGULATION OF PEPTIDE SECRETION	17	5.32541	0.00143302	2.843747748
GO POSITIVE REGULATION OF INTRACELLULAR TRANSPORT	11	2.35921	0.0014784	2.830208046
GO PROTEIN LIPID COMPLEX SUBUNIT ORGANIZATION	6	0.572625	0.0015136	2.819988881
GO PROTEIN PROCESSING	11	2.37067	0.00153654	2.813456129
GO POSITIVE REGULATION OF INFLAMMATORY RESPONSE	9	1.55754	0.00157715	2.802127
GO CHEMOKINE BIOSYNTHETIC PROCESS	4	0.160335	0.00162323	2.789619939
GO REGULATION OF AMYLOID BETA CLEARANCE	4	0.160335	0.00162323	2.789619939
GO REGULATION OF AUTOPHAGY OF MITOCHONDRION IN RESPONSE TO MITOCHONDRIAL DEPOLARIZATION	4	0.160335	0.00162323	2.789619939
GO RESPONSE TO LEUCINE	4	0.160335	0.00162323	2.789619939
GO DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	8	1.20251	0.00164824	2.78297955
GO REGULATION OF CELL CYCLE ARREST	8	1.20251	0.00164824	2.78297955
GO BLOOD VESSEL MORPHOGENESIS	19	6.52792	0.00165289	2.781756048
GO CELLULAR RESPONSE TO STEROID HORMONE STIMULUS	12	2.85167	0.00168367	2.773743026
GO INTERACTION WITH SYMBIONT	7	0.881842	0.00174778	2.757513235
GO NEGATIVE REGULATION OF AUTOPHAGY	7	0.881842	0.00174778	2.757513235
GO INTRACELLULAR TRANSPORT	40	20.6832	0.00176553	2.753124898
GO FAT CELL DIFFERENTIATION	11	2.41648	0.00177419	2.750999873
GO REGULATION OF ASTROCYTE DIFFERENTIATION	5	0.355027	0.00186515	2.729286235
GO CELL CYCLE PHASE TRANSITION	19	6.60809	0.0019138	2.71810345
GO CALCIUM MEDIATED SIGNALING	11	2.45083	0.00197661	2.704079012
GO CELL CYCLE CHECKPOINT	11	2.45083	0.00197661	2.704079012
GO INTERSTRAND CROSS LINK REPAIR	6	0.606982	0.00197661	2.704079012
GO MITOCHONDRIAL TRANSCRIPTION	4	0.171787	0.00197661	2.704079012
GO POSITIVE REGULATION OF AMYLOID PRECURSOR PROTEIN CATABOLIC PROCESS	4	0.171787	0.00197661	2.704079012
GO POSITIVE REGULATION OF GLUCONEOGENESIS	4	0.171787	0.00197661	2.704079012
GO POSITIVE REGULATION OF MITOCHONDRIAL FISSION	4	0.171787	0.00197661	2.704079012

GO PROTEIN LOCALIZATION TO MITOCHONDRION	9	1.6148	0.00197661	2.704079012
GO REGULATION OF NEUROTRANSMITTER TRANSPORT	9	1.6148	0.00197661	2.704079012
GO TUMOR NECROSIS FACTOR SUPERFAMILY CYTOKINE PRODUCTION	9	1.6148	0.00197661	2.704079012
GO INTERLEUKIN 1 BETA PRODUCTION	7	0.904747	0.00198214	2.702865674
GO PEPTIDYL LYSINE MODIFICATION	15	4.40921	0.00198214	2.702865674
GO DEVELOPMENTAL CELL GROWTH	11	2.46229	0.00203536	2.691358765
GO REGULATION OF DENDRITE DEVELOPMENT	9	1.62625	0.00206824	2.684399067
GO FATTY ACID METABOLIC PROCESS	12	2.93184	0.00210053	2.677671111
GO TELOMERE CAPPING	6	0.618435	0.00213344	2.670919567
GO MYELOID CELL HOMEOSTASIS	9	1.63771	0.00216332	2.664879235
GO REPRODUCTION	34	16.5374	0.00216332	2.664879235
GO PEPTIDE SECRETION	19	6.69971	0.00221646	2.654340102
GO ION HOMEOSTASIS	23	9.13909	0.00221676	2.654281324
GO CARBOHYDRATE TRANSMEMBRANE TRANSPORT	8	1.27123	0.00227485	2.643047235
GO NEGATIVE REGULATION OF CELL GROWTH	10	2.06145	0.00228127	2.641823311
GO ENDOCYTOSIS	18	6.13854	0.00228882	2.64038836
GO MUSCLE SYSTEM PROCESS	16	5.01619	0.00228882	2.64038836
GO NEGATIVE REGULATION OF HYDROLASE ACTIVITY	16	5.01619	0.00228882	2.64038836
GO POSITIVE REGULATION OF PROTEIN TYROSINE KINASE ACTIVITY	6	0.629887	0.00230738	2.636880876
GO EATING BEHAVIOR	5	0.377932	0.00232791	2.633033814
GO SUPEROXIDE ANION GENERATION	5	0.377932	0.00232791	2.633033814
GO CHAPERONE MEDIATED AUTOPHAGY	4	0.18324	0.00235699	2.62764226
GO NEGATIVE REGULATION OF CELLULAR RESPONSE TO DRUG	4	0.18324	0.00235699	2.62764226
GO POSITIVE REGULATION OF ASTROCYTE DIFFERENTIATION	4	0.18324	0.00235699	2.62764226
GO REGULATION OF BROWN FAT CELL DIFFERENTIATION	4	0.18324	0.00235699	2.62764226
GO REGULATION OF TRANSPORTER ACTIVITY	12	2.97765	0.00235699	2.62764226
GO CHEMOKINE PRODUCTION	7	0.939105	0.0023824	2.62298532
GO REGULATION OF RESPONSE TO ENDOPLASMIC RETICULUM STRESS	7	0.939105	0.0023824	2.62298532
GO REGULATION OF IMMUNE RESPONSE	26	11.1433	0.00239791	2.620167121
GO DNA DEPENDENT DNA REPLICATION	9	1.67206	0.00244356	2.611976993
GO STEROID METABOLIC PROCESS	13	3.48156	0.00245509	2.609932583
GO RECEPTOR METABOLIC PROCESS	10	2.09581	0.00253302	2.596361381
GO REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	7	0.950557	0.0025392	2.595303091
GO STRIATED MUSCLE CELL DIFFERENTIATION	12	3.01201	0.00258141	2.588143012
GO NEGATIVE REGULATION OF OXIDATIVE STRESS INDUCED NEURON INTRINSIC APOPTOTIC SIGNALING PATHWAY	3	0.0572625	0.00263491	2.579234214
GO POSITIVE REGULATION OF ASTROCYTE ACTIVATION	3	0.0572625	0.00263491	2.579234214
GO POSITIVE REGULATION OF MAPKKK CASCADE BY FIBROBLAST GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	3	0.0572625	0.00263491	2.579234214
GO REGULATION OF INTERLEUKIN 1 BIOSYNTHETIC PROCESS	3	0.0572625	0.00263491	2.579234214
GO REGULATION OF SPONTANEOUS SYNAPTIC TRANSMISSION	3	0.0572625	0.00263491	2.579234214
GO RESPONSE TO CAMPTOTHECIN	3	0.0572625	0.00263491	2.579234214
GO RESPONSE TO FLUORIDE	3	0.0572625	0.00263491	2.579234214
GO GENERATION OF PRECURSOR METABOLITES AND ENERGY	17	5.65753	0.00264497	2.577579249
GO REGULATION OF MUSCLE CELL DIFFERENTIATION	9	1.69497	0.00264497	2.577579249
GO CHROMOSOME SEGREGATION	13	3.52737	0.00273088	2.563697383
GO ORGANIC CYCLIC COMPOUND CATABOLIC PROCESS	19	6.83714	0.00273088	2.563697383

GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	27	11.9335	0.00278134	2.555745918
GO NEGATIVE REGULATION OF PROTEIN OLIGOMERIZATION	4	0.194692	0.00278674	2.554903549
GO POSITIVE REGULATION OF SUPEROXIDE ANION GENERATION	4	0.194692	0.00278674	2.554903549
GO REVERSE CHOLESTEROL TRANSPORT	4	0.194692	0.00278674	2.554903549
GO CELLULAR RESPIRATION	10	2.13016	0.00280317	2.552350563
GO CELLULAR LIPID METABOLIC PROCESS	24	9.97513	0.00283431	2.547552651
GO REGULATION OF SYNAPTIC VESICLE TRANSPORT	7	0.973462	0.00283431	2.547552651
GO SECONDARY ALCOHOL METABOLIC PROCESS	7	0.973462	0.00283431	2.547552651
GO ACTIVATION OF MAPK ACTIVITY	9	1.71787	0.00286815	2.542398139
GO POSITIVE REGULATION OF NEURON DIFFERENTIATION	14	4.06564	0.00287624	2.541174878
GO LEUKOCYTE DIFFERENTIATION	17	5.7148	0.00291786	2.53493555
GO REGULATION OF VASCULATURE DEVELOPMENT	13	3.56173	0.00294192	2.531369141
GO REGULATION OF PLASMA LIPOPROTEIN PARTICLE LEVELS	7	0.984915	0.00301353	2.520924481
GO CELL CELL SIGNALING BY WNT	17	5.74915	0.00310248	2.508291009
GO MEMBRANE PROTEIN PROTEOLYSIS	6	0.675697	0.00310248	2.508291009
GO NEGATIVE REGULATION OF RNA CATABOLIC PROCESS	6	0.675697	0.00310248	2.508291009
GO TUBE DEVELOPMENT	26	11.3609	0.00310248	2.508291009
GO POSITIVE REGULATION OF MITOTIC CELL CYCLE	9	1.74078	0.00311088	2.507116741
GO REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY	9	1.74078	0.00311088	2.507116741
GO POSITIVE REGULATION OF SMOOTH MUSCLE CELL MIGRATION	5	0.41229	0.0031641	2.499749799
GO MEMBRANE PROTEIN INTRACELLULAR DOMAIN PROTEOLYSIS	4	0.206145	0.00328756	2.483126312
GO POSITIVE REGULATION OF RESPONSE TO OXIDATIVE STRESS	4	0.206145	0.00328756	2.483126312
GO POSITIVE REGULATION OF LIPID TRANSPORT	6	0.68715	0.00334604	2.475468872
GO CHROMATIN ORGANIZATION INVOLVED IN REGULATION OF TRANSCRIPTION	8	1.3743	0.0034988	2.456080882
GO REGULATION OF ION TRANSPORT	20	7.60446	0.00352583	2.452738631
GO TRANSMEMBRANE TRANSPORT	35	17.7972	0.00360934	2.442572205
GO CHROMOSOME SEPARATION	7	1.01927	0.00360996	2.44249761
GO CANONICAL WNT SIGNALING PATHWAY	13	3.65335	0.00366213	2.436266243
GO REGULATION OF CATION TRANSMEMBRANE TRANSPORT	13	3.65335	0.00366213	2.436266243
GO REGULATION OF FAT CELL DIFFERENTIATION	8	1.38575	0.00366244	2.436229481
GO INTERLEUKIN 1 BIOSYNTHETIC PROCESS	3	0.068715	0.00371719	2.42978524
GO REGULATION OF MITOCHONDRIAL ATP SYNTHESIS COUPLED ELECTRON TRANSPORT	3	0.068715	0.00371719	2.42978524
GO REGULATION OF ENDOCYTOSIS	10	2.22178	0.00374658	2.42636499
GO DEVELOPMENTAL MATURATION	12	3.17234	0.00385711	2.413737975
GO MAINTENANCE OF LOCATION	13	3.67625	0.00385711	2.413737975
GO NEGATIVE REGULATION OF LIPID STORAGE	4	0.217597	0.0038658	2.412760618
GO MONOCARBOXYLIC ACID METABOLIC PROCESS	16	5.31396	0.00397135	2.401061836
GO DENDRITIC SPINE DEVELOPMENT	7	1.04218	0.00404082	2.393530495
GO REGULATION OF ORGAN GROWTH	7	1.04218	0.00404082	2.393530495
GO MYELOID LEUKOCYTE DIFFERENTIATION	10	2.25614	0.00418198	2.378618048
GO PROTEIN ACYLATION	11	2.72569	0.00427753	2.368806936
GO INTERLEUKIN 1 PRODUCTION	7	1.05363	0.00428873	2.367671294
GO NEGATIVE REGULATION OF EPITHELIAL CELL APOPTOTIC PROCESS	5	0.446647	0.0043159	2.364928627
GO NERVOUS SYSTEM PROCESS	32	15.8388	0.00444427	2.352199565
GO CATECHOLAMINE BIOSYNTHETIC PROCESS	4	0.22905	0.00452067	2.344797194

GO MITOTIC G2 DNA DAMAGE CHECKPOINT	4	0.22905	0.00452067	2.344797194
GO REGULATION OF NEUROTRANSMITTER UPTAKE	4	0.22905	0.00452067	2.344797194
GO REGULATION OF PROTEIN HOMOOLOGOMERIZATION	4	0.22905	0.00452067	2.344797194
GO STEROL TRANSPORT	7	1.06508	0.00452302	2.344571492
GO POSITIVE REGULATION OF SUPRAMOLECULAR FIBER ORGANIZATION	10	2.2905	0.0046387	2.333603714
GO ANATOMICAL STRUCTURE MATURATION	9	1.8553	0.0047011	2.327800511
GO BROWN FAT CELL DIFFERENTIATION	5	0.4581	0.00473091	2.325055314
GO POSITIVE REGULATION OF GLIAL CELL DIFFERENTIATION	5	0.4581	0.00473091	2.325055314
GO REGULATION OF PROTEIN DEACETYLATION	5	0.4581	0.00473091	2.325055314
GO REGULATION OF VACUOLE ORGANIZATION	5	0.4581	0.00473091	2.325055314
GO IMMUNE EFFECTOR PROCESS	28	13.1246	0.00496806	2.303813168
GO ORGANIC HYDROXY COMPOUND METABOLIC PROCESS	16	5.43994	0.00500129	2.300917962
GO AMYLOID BETA CLEARANCE BY CELLULAR CATABOLIC PROCESS	3	0.0801675	0.00505302	2.296448983
GO LATE ENDOSOME TO LYSOSOME TRANSPORT	3	0.0801675	0.00505302	2.296448983
GO POSITIVE REGULATION OF CELLULAR RESPIRATION	3	0.0801675	0.00505302	2.296448983
GO POSITIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	8	1.46592	0.00505302	2.296448983
GO SPONTANEOUS SYNAPTIC TRANSMISSION	3	0.0801675	0.00505302	2.296448983
GO LEUKOCYTE PROLIFERATION	12	3.28687	0.00509378	2.292959816
GO HOMEOSTASIS OF NUMBER OF CELLS	11	2.79441	0.00510179	2.292277422
GO REGULATION OF GLIAL CELL DIFFERENTIATION	6	0.755865	0.00512591	2.290229023
GO INFLAMMATORY CELL APOPTOTIC PROCESS	4	0.240502	0.00513288	2.289638889
GO MITOCHONDRIAL GENOME MAINTENANCE	4	0.240502	0.00513288	2.289638889
GO MITOPHAGY	4	0.240502	0.00513288	2.289638889
GO NEGATIVE REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	5	0.469552	0.00513288	2.289638889
GO NEGATIVE REGULATION OF STRIATED MUSCLE CELL APOPTOTIC PROCESS	4	0.240502	0.00513288	2.289638889
GO NEUROTRANSMITTER UPTAKE	5	0.469552	0.00513288	2.289638889
GO POSITIVE REGULATION OF NUCLEOTIDE BIOSYNTHETIC PROCESS	4	0.240502	0.00513288	2.289638889
GO REGULATION OF SUPEROXIDE ANION GENERATION	4	0.240502	0.00513288	2.289638889
GO RESPONSE TO ELECTRICAL STIMULUS	5	0.469552	0.00513288	2.289638889
GO RESPONSE TO HYPEROXIA	4	0.240502	0.00513288	2.289638889
GO RESPONSE TO SALT STRESS	4	0.240502	0.00513288	2.289638889
GO CELLULAR RESPONSE TO ACID CHEMICAL	10	2.33631	0.00521258	2.282947267
GO STEROL METABOLIC PROCESS	7	1.09944	0.00522842	2.281629533
GO NEGATIVE REGULATION OF PROTEIN COMPLEX ASSEMBLY	8	1.48882	0.00546029	2.262784291
GO MEMBRANE PROTEIN ECTODOMAIN PROTEOLYSIS	5	0.481005	0.00562865	2.249595756
GO RESPONSE TO TESTOSTERONE	5	0.481005	0.00562865	2.249595756
GO NEGATIVE REGULATION OF LIPID METABOLIC PROCESS	6	0.77877	0.0058291	2.234398494
GO REGULATION OF POSTSYNAPSE ORGANIZATION	7	1.12234	0.00585334	2.232596249
GO INTERLEUKIN 6 BIOSYNTHETIC PROCESS	4	0.251955	0.00594047	2.226179193
GO NEGATIVE REGULATION OF SMOOTH MUSCLE CELL MIGRATION	4	0.251955	0.00594047	2.226179193
GO HEART DEVELOPMENT	17	6.13854	0.00600124	2.221759005
GO REGULATION OF PROTEIN TARGETING TO MITOCHONDRION	5	0.492457	0.00617611	2.209284978
GO POSITIVE REGULATION OF DENDRITE DEVELOPMENT	6	0.790222	0.00622683	2.205732991
GO SIGNAL RELEASE FROM SYNAPSE	9	1.94692	0.00628557	2.201655333
GO SKELETAL MUSCLE ORGAN DEVELOPMENT	9	1.94692	0.00628557	2.201655333

GO PROTEIN TARGETING TO MITOCHONDRION	7	1.14525	0.00650975	2.18643569
GO POSITIVE REGULATION OF LIPID METABOLIC PROCESS	8	1.53463	0.00652834	2.185197235
GO NEGATIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	3	0.09162	0.00657216	2.182291872
GO POSITIVE REGULATION OF ASPARTIC TYPE PEPTIDASE ACTIVITY	3	0.09162	0.00657216	2.182291872
GO POSITIVE REGULATION OF OXIDATIVE PHOSPHORYLATION	3	0.09162	0.00657216	2.182291872
GO POSITIVE REGULATION OF RESPONSE TO REACTIVE OXYGEN SPECIES	3	0.09162	0.00657216	2.182291872
GO WOUND HEALING	17	6.1958	0.00657216	2.182291872
GO SMALL MOLECULE BIOSYNTHETIC PROCESS	19	7.42122	0.00662499	2.178814773
GO ATP BIOSYNTHETIC PROCESS	5	0.50391	0.00669071	2.174527794
GO GLIAL CELL PROLIFERATION	5	0.50391	0.00669071	2.174527794
GO REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	5	0.50391	0.00669071	2.174527794
GO REGULATION OF INSULIN LIKE GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	4	0.263407	0.00675021	2.170682716
GO TUMOR NECROSIS FACTOR BIOSYNTHETIC PROCESS	4	0.263407	0.00675021	2.170682716
GO REGULATION OF ANATOMICAL STRUCTURE SIZE	16	5.63463	0.00689164	2.161677417
GO NEGATIVE REGULATION OF FAT CELL DIFFERENTIATION	5	0.515362	0.0073185	2.135577923
GO REGULATION OF GLUCONEOGENESIS	5	0.515362	0.0073185	2.135577923
GO ENDOTHELIAL CELL PROLIFERATION	8	1.56899	0.00738261	2.131790073
GO CELLULAR CARBOHYDRATE METABOLIC PROCESS	11	2.94329	0.00739597	2.131004859
GO LEUKOCYTE MEDIATED IMMUNITY	21	8.77261	0.00742081	2.129548688
GO CELL PROJECTION ORGANIZATION	33	17.1329	0.00750649	2.12456309
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	7	1.17961	0.00752155	2.123692653
GO MODULATION BY HOST OF VIRAL PROCESS	4	0.27486	0.00768577	2.114312616
GO RESPONSE TO MUSCLE ACTIVITY	4	0.27486	0.00768577	2.114312616
GO SMOOTH MUSCLE CELL APOPTOTIC PROCESS	4	0.27486	0.00768577	2.114312616
GO VESICLE LOCALIZATION	12	3.47011	0.00768577	2.114312616
GO RESPONSE TO NUTRIENT	10	2.47374	0.00768752	2.114213741
GO NEGATIVE REGULATION OF CYTOKINE PRODUCTION	11	2.9662	0.00779172	2.108366662
GO ANATOMICAL STRUCTURE FORMATION INVOLVED IN MORPHOGENESIS	26	12.174	0.00783375	2.106030292
GO POSITIVE REGULATION OF TRANSPORTER ACTIVITY	7	1.20251	0.00830521	2.080649382
GO REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	7	1.20251	0.00830521	2.080649382
GO POSITIVE REGULATION OF VASCULATURE DEVELOPMENT	9	2.03854	0.00835377	2.078117486
GO HYPEROSMOTIC SALINITY RESPONSE	3	0.103072	0.00836687	2.077436979
GO MITOCHONDRIAL FRAGMENTATION INVOLVED IN APOPTOTIC PROCESS	3	0.103072	0.00836687	2.077436979
GO SINGLE STRAND BREAK REPAIR	3	0.103072	0.00836687	2.077436979
GO SKIN MORPHOGENESIS	3	0.103072	0.00836687	2.077436979
GO UBIQUITIN RECYCLING	3	0.103072	0.00836687	2.077436979
GO MYELOID CELL DIFFERENTIATION	14	4.6039	0.008475	2.071860293
GO NEGATIVE REGULATION OF TOR SIGNALING	5	0.538267	0.00856978	2.067030327
GO REGULATION OF PROTEIN LOCALIZATION TO MEMBRANE	9	2.05	0.00860154	2.065423787
GO EXTRINSIC APOPTOTIC SIGNALING PATHWAY	10	2.51955	0.00863208	2.063884543
GO NEGATIVE REGULATION OF NEURON DIFFERENTIATION	10	2.51955	0.00863208	2.063884543
GO POSITIVE REGULATION OF PROTEIN OLIGOMERIZATION	4	0.286312	0.00863208	2.063884543
GO REGULATION OF DNA REPLICATION	7	1.21396	0.00863208	2.063884543
GO REGULATION OF NEUROTRANSMITTER SECRETION	7	1.21396	0.00863208	2.063884543
GO REGULATION OF OXIDATIVE PHOSPHORYLATION	4	0.286312	0.00863208	2.063884543

GO REGULATION OF LIPID BIOSYNTHETIC PROCESS	9	2.06145	0.00886625	2.052260027
GO CARBOHYDRATE TRANSPORT	8	1.62625	0.0089309	2.049104773
GO CARDIOCYTE DIFFERENTIATION	8	1.62625	0.0089309	2.049104773
GO REGULATION OF FATTY ACID METABOLIC PROCESS	5	0.54972	0.00924797	2.033953588
GO POSITIVE REGULATION OF LIPID BIOSYNTHETIC PROCESS	6	0.87039	0.00948604	2.022915048
GO ADULT BEHAVIOR	8	1.64916	0.00972828	2.011963938
GO NEURON DEATH IN RESPONSE TO OXIDATIVE STRESS	4	0.297765	0.00974449	2.011240886
GO POSITIVE REGULATION OF BEHAVIOR	4	0.297765	0.00974449	2.011240886
GO POSITIVE REGULATION OF RESPONSE TO DRUG	4	0.297765	0.00974449	2.011240886
GO POSITIVE REGULATION OF SECRETION	14	4.68407	0.00980154	2.008705683
GO DNA MODIFICATION	7	1.24832	0.00994812	2.002258985
GO NUCLEOTIDE EXCISION REPAIR	7	1.24832	0.00994812	2.002258985
GO ANIMAL ORGAN REGENERATION	6	0.881842	0.010018	1.999218973
GO CELLULAR RESPONSE TO UV	6	0.881842	0.010018	1.999218973
GO REGULATION OF LEUKOCYTE MIGRATION	9	2.10726	0.010162	1.993020809
GO POSITIVE REGULATION OF PEPTIDE SECRETION	11	3.08072	0.0101737	1.992521073
GO CELLULAR RESPONSE TO POTASSIUM ION	3	0.114525	0.0103172	1.986438151
GO CYTOKINE METABOLIC PROCESS	7	1.25977	0.0103172	1.986438151
GO INFLAMMATORY RESPONSE TO WOUNDING	3	0.114525	0.0103172	1.986438151
GO NEGATIVE REGULATION OF MUSCLE ADAPTATION	3	0.114525	0.0103172	1.986438151
GO NEGATIVE REGULATION OF PROTEIN HOMOOLIGOMERIZATION	3	0.114525	0.0103172	1.986438151
GO NEURON PROJECTION MAINTENANCE	3	0.114525	0.0103172	1.986438151
GO POSITIVE REGULATION OF CHEMOKINE BIOSYNTHETIC PROCESS	3	0.114525	0.0103172	1.986438151
GO POSITIVE REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	3	0.114525	0.0103172	1.986438151
GO POSITIVE REGULATION OF MITOPHAGY	3	0.114525	0.0103172	1.986438151
GO REGULATION OF REMOVAL OF SUPEROXIDE RADICALS	3	0.114525	0.0103172	1.986438151
GO STRIATED MUSCLE ATROPHY	3	0.114525	0.0103172	1.986438151
GO CELLULAR RESPONSE TO BIOTIC STIMULUS	10	2.59972	0.0105746	1.975736051
GO REGULATION OF VASCULAR SMOOTH MUSCLE CELL PROLIFERATION	5	0.572625	0.0106628	1.972128737
GO RNA STABILIZATION	5	0.572625	0.0106628	1.972128737
GO NEGATIVE REGULATION OF MUSCLE HYPERTROPHY	4	0.309217	0.0107832	1.96725234
GO RESPONSE TO AMINO ACID	7	1.27123	0.0107832	1.96725234
GO REGULATION OF CELLULAR RESPONSE TO HEAT	6	0.904747	0.0111329	1.953391692
GO POSITIVE REGULATION OF ION TRANSMEMBRANE TRANSPORT	8	1.69497	0.011191	1.951131104
GO ENDOMEMBRANE SYSTEM ORGANIZATION	14	4.76424	0.0112021	1.950700555
GO REGULATION OF UBIQUITIN PROTEIN TRANSFERASE ACTIVITY	5	0.584077	0.0115182	1.938615385
GO POSITIVE REGULATION OF LIPID LOCALIZATION	6	0.9162	0.0117856	1.928648303
GO PROTEIN LOCALIZATION TO SYNAPSE	6	0.9162	0.0117856	1.928648303
GO CARDIAC MUSCLE CELL DIFFERENTIATION	7	1.29413	0.0118251	1.927195178
GO RESPONSE TO CYTOKINE	27	13.2849	0.0118575	1.926006867
GO CELL MORPHOGENESIS INVOLVED IN NEURON DIFFERENTIATION	17	6.59664	0.0119917	1.921119245
GO ADAPTIVE THERMOGENESIS	8	1.71787	0.011999	1.920854947
GO POSITIVE REGULATION OF HYDROLASE ACTIVITY	20	8.50921	0.011999	1.920854947
GO POSITIVE REGULATION OF MACROPHAGE ACTIVATION	4	0.32067	0.011999	1.920854947
GO POSITIVE REGULATION OF MONOOXYGENASE ACTIVITY	4	0.32067	0.011999	1.920854947

GO RESPONSE TO INCREASED OXYGEN LEVELS	4	0.32067	0.011999	1.920854947
GO SKELETAL MUSCLE ADAPTATION	4	0.32067	0.011999	1.920854947
GO LIPID MODIFICATION	10	2.65698	0.0121651	1.914884317
GO CELLULAR KETONE METABOLIC PROCESS	9	2.17597	0.0121938	1.913860932
GO REGULATION OF STEROID METABOLIC PROCESS	7	1.30558	0.0122717	1.91109527
GO DNA SYNTHESIS INVOLVED IN DNA REPAIR	5	0.59553	0.0122903	1.910437516
GO CATECHOLAMINE UPTAKE INVOLVED IN SYNAPTIC TRANSMISSION	3	0.125977	0.0125225	1.90230896
GO POSITIVE REGULATION OF AMYLOID BETA FORMATION	3	0.125977	0.0125225	1.90230896
GO PROGRAMMED CELL DEATH IN RESPONSE TO REACTIVE OXYGEN SPECIES	3	0.125977	0.0125225	1.90230896
GO REGULATION OF DENDRITIC SPINE MAINTENANCE	3	0.125977	0.0125225	1.90230896
GO REGULATION OF DNA CATABOLIC PROCESS	3	0.125977	0.0125225	1.90230896
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER IN RESPONSE TO OXIDATIVE STRESS	3	0.125977	0.0125225	1.90230896
GO SYNAPTIC VESICLE CYCLE	9	2.18743	0.0125225	1.90230896
GO TUBULIN DEACETYLATION	3	0.125977	0.0125225	1.90230896
GO VIRAL LATENCY	3	0.125977	0.0125225	1.90230896
GO NEGATIVE REGULATION OF CELL CYCLE PROCESS	12	3.73351	0.0131047	1.882572917
GO REGULATION OF MACROPHAGE DERIVED FOAM CELL DIFFERENTIATION	4	0.332122	0.0132984	1.876200608
GO ERYTHROCYTE HOMEOSTASIS	7	1.33994	0.0140047	1.85372619
GO HOMOLOGOUS RECOMBINATION	5	0.618435	0.0141952	1.847858484
GO REGULATION OF MONOOXYGENASE ACTIVITY	5	0.618435	0.0141952	1.847858484
GO REGULATION OF RESPONSE TO WOUNDING	8	1.77514	0.014413	1.841245613
GO TISSUE REMODELING	8	1.77514	0.014413	1.841245613
GO MYOBLAST DIFFERENTIATION	6	0.96201	0.0145147	1.838191936
GO MITOTIC G2 M TRANSITION CHECKPOINT	4	0.343575	0.0147676	1.83069008
GO NEGATIVE REGULATION OF MACROAUTOPHAGY	4	0.343575	0.0147676	1.83069008
GO REGULATION OF FATTY ACID OXIDATION	4	0.343575	0.0147676	1.83069008
GO RESPONSE TO ARSENIC CONTAINING SUBSTANCE	4	0.343575	0.0147676	1.83069008
GO CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	19	8.0282	0.0148647	1.827843851
GO PRESYNAPTIC ENDOCYTOSIS	5	0.629887	0.0151868	1.818533726
GO PHOSPHOLIPID EFFLUX	3	0.13743	0.0152221	1.817525429
GO POSITIVE REGULATION OF INTERLEUKIN 6 BIOSYNTHETIC PROCESS	3	0.13743	0.0152221	1.817525429
GO REGULATION OF LYSOSOMAL LUMEN PH	3	0.13743	0.0152221	1.817525429
GO NEUTRAL LIPID METABOLIC PROCESS	7	1.3743	0.0158454	1.800096793
GO POSITIVE REGULATION OF PROTEIN LOCALIZATION TO MEMBRANE	7	1.3743	0.0158454	1.800096793
GO SYNAPTIC VESICLE EXOCYTOSIS	7	1.3743	0.0158454	1.800096793
GO REGULATION OF STEROID BIOSYNTHETIC PROCESS	6	0.984915	0.0160747	1.793857124
GO ANION HOMEOSTASIS	5	0.64134	0.0161885	1.79079339
GO POSITIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	5	0.64134	0.0161885	1.79079339
GO REGULATION OF CELL CYCLE PHASE TRANSITION	14	4.98184	0.0161885	1.79079339
GO SECOND MESSENGER MEDIATED SIGNALING	14	4.98184	0.0161885	1.79079339
GO G2 DNA DAMAGE CHECKPOINT	4	0.355027	0.0162106	1.79020091
GO POSITIVE REGULATION OF DOUBLE STRAND BREAK REPAIR	4	0.355027	0.0162106	1.79020091
GO REGULATION OF GLIAL CELL PROLIFERATION	4	0.355027	0.0162106	1.79020091
GO VASODILATION	4	0.355027	0.0162106	1.79020091
GO NEGATIVE REGULATION OF PEPTIDASE ACTIVITY	10	2.78296	0.0163741	1.785842562

GO ESTABLISHMENT OF ORGANELLE LOCALIZATION	15	5.61172	0.0170725	1.767702879
GO REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	8	1.8324	0.0170927	1.76718933
GO RESPONSE TO BIOTIC STIMULUS	23	10.8455	0.0172316	1.763674395
GO POSITIVE REGULATION OF BLOOD VESSEL DIAMETER	5	0.652792	0.0172728	1.762637256
GO ACTIVATION OF PROTEIN KINASE B ACTIVITY	4	0.36648	0.0178556	1.748225552
GO CELLULAR RESPONSE TO DEXAMETHASONE STIMULUS	4	0.36648	0.0178556	1.748225552
GO POSITIVE REGULATION OF LEUKOCYTE MIGRATION	7	1.40866	0.0178556	1.748225552
GO PROTEIN LIPID COMPLEX ASSEMBLY	4	0.36648	0.0178556	1.748225552
GO REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	4	0.36648	0.0178556	1.748225552
GO REPLICATION FORK PROCESSING	4	0.36648	0.0178556	1.748225552
GO HYDROGEN PEROXIDE METABOLIC PROCESS	3	0.148882	0.0180246	1.744134364
GO MYELOID LEUKOCYTE MEDIATED IMMUNITY	16	6.26452	0.0180246	1.744134364
GO POSITIVE REGULATION OF EXECUTION PHASE OF APOPTOSIS	3	0.148882	0.0180246	1.744134364
GO REGULATION OF METALLOPEPTIDASE ACTIVITY	3	0.148882	0.0180246	1.744134364
GO NEUROTRANSMITTER BIOSYNTHETIC PROCESS	6	1.01927	0.0185251	1.732239439
GO NEUROTRANSMITTER METABOLIC PROCESS	7	1.42011	0.0185251	1.732239439
GO PEPTIDE HORMONE SECRETION	10	2.84022	0.0186762	1.728711484
GO NEGATIVE REGULATION OF MAPK CASCADE	8	1.86676	0.0188531	1.724617229
GO CARDIAC MUSCLE TISSUE DEVELOPMENT	9	2.34776	0.0191892	1.716943131
GO ACYLGlycerol HOMEOSTASIS	4	0.377932	0.0194188	1.711777611
GO LIVER REGENERATION	4	0.377932	0.0194188	1.711777611
GO LONG TERM MEMORY	4	0.377932	0.0194188	1.711777611
GO MULTICELLULAR ORGANISM REPRODUCTION	21	9.58574	0.0194188	1.711777611
GO NEGATIVE REGULATION OF EXOCYTOSIS	4	0.377932	0.0194188	1.711777611
GO NEGATIVE REGULATION OF GENE SILENCING	4	0.377932	0.0194188	1.711777611
GO POSITIVE REGULATION OF MULTICELLULAR ORGANISM GROWTH	4	0.377932	0.0194188	1.711777611
GO POSITIVE REGULATION OF PROTEIN KINASE B SIGNALING	8	1.87821	0.0194188	1.711777611
GO POSITIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER IN RESPONSE TO STRESS	4	0.377932	0.0194188	1.711777611
GO REGULATION OF PEPTIDYL LYSINE ACETYLTATION	5	0.675697	0.0194188	1.711777611
GO RESPONSE TO MINERALOCORTICOID	4	0.377932	0.0194188	1.711777611
GO RESPONSE TO BACTERIUM	17	6.96312	0.0196875	1.705809429
GO CELL CYCLE G1 S PHASE TRANSITION	10	2.88603	0.0206647	1.684770895
GO POSITIVE REGULATION OF RESPONSE TO WOUNDING	5	0.68715	0.0207331	1.683335758
GO RESPONSE TO ETHANOL	7	1.45447	0.0207331	1.683335758
GO RIBONUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	5	0.68715	0.0207331	1.683335758
GO GLIAL CELL APOPTOTIC PROCESS	3	0.160335	0.0210309	1.677142142
GO LOW DENSITY LIPOPROTEIN PARTICLE REMODELING	3	0.160335	0.0210309	1.677142142
GO MODULATION BY HOST OF VIRAL GENOME REPLICATION	3	0.160335	0.0210309	1.677142142
GO NEGATIVE REGULATION OF POSTTRANSCRIPTIONAL GENE SILENCING	3	0.160335	0.0210309	1.677142142
GO POSITIVE REGULATION OF OXIDATIVE STRESS INDUCED CELL DEATH	3	0.160335	0.0210309	1.677142142
GO POSITIVE REGULATION OF TUMOR NECROSIS FACTOR BIOSYNTHETIC PROCESS	3	0.160335	0.0210309	1.677142142
GO REGULATION OF HELICASE ACTIVITY	3	0.160335	0.0210309	1.677142142
GO REGULATION OF LONG TERM SYNAPTIC DEPRESSION	3	0.160335	0.0210309	1.677142142
GO REGULATION OF AUTOPHAGOSOME ASSEMBLY	4	0.389385	0.0211837	1.673998183
GO CELLULAR RESPONSE TO XENOBIOTIC STIMULUS	8	1.91257	0.0212812	1.672003887

GO NUCLEAR CHROMOSOME SEGREGATION	10	2.90893	0.0215688	1.666174017
GO POSITIVE REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	5	0.698602	0.0219441	1.658682226
GO ANTIBIOTIC METABOLIC PROCESS	6	1.06508	0.0221765	1.654106995
GO POSITIVE REGULATION OF CELL CYCLE PHASE TRANSITION	6	1.06508	0.0221765	1.654106995
GO REGULATION OF ANION TRANSPORT	6	1.06508	0.0221765	1.654106995
GO CELLULAR RESPONSE TO ALKALOID	4	0.400837	0.0231495	1.635458385
GO FOAM CELL DIFFERENTIATION	4	0.400837	0.0231495	1.635458385
GO NEURON CELLULAR HOMEOSTASIS	4	0.400837	0.0231495	1.635458385
GO STRIATED MUSCLE CELL APOPTOTIC PROCESS	4	0.400837	0.0231495	1.635458385
GO MODIFICATION DEPENDENT MACROMOLECULE CATABOLIC PROCESS	17	7.0891	0.0232227	1.634087288
GO AUTOPHAGOSOME ORGANIZATION	6	1.07653	0.0232245	1.634053627
GO FEMALE GAMETE GENERATION	7	1.50028	0.0240522	1.618845194
GO POSITIVE REGULATION OF ENDOCYTOSIS	6	1.08799	0.0244102	1.612428662
GO FATTY ACID HOMEOSTASIS	3	0.171787	0.0245282	1.610334321
GO HIGH DENSITY LIPOPROTEIN PARTICLE ASSEMBLY	3	0.171787	0.0245282	1.610334321
GO RESPONSE TO POTASSIUM ION	3	0.171787	0.0245282	1.610334321
GO RESPONSE TO STIMULUS INVOLVED IN REGULATION OF MUSCLE ADAPTATION	3	0.171787	0.0245282	1.610334321
GO REGULATION OF HEART GROWTH	5	0.721507	0.0247109	1.607111437
GO REGULATION OF CELLULAR KETONE METABOLIC PROCESS	7	1.51173	0.0249047	1.603718685
GO NEGATIVE REGULATION OF MULTI ORGANISM PROCESS	8	1.96983	0.0249939	1.602165972
GO CELLULAR RESPONSE TO CADMIUM ION	4	0.41229	0.0250711	1.600826611
GO INSULIN LIKE GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	4	0.41229	0.0250711	1.600826611
GO NEGATIVE REGULATION OF ENDOTHELIAL CELL PROLIFERATION	4	0.41229	0.0250711	1.600826611
GO REGULATION OF COFACTOR METABOLIC PROCESS	4	0.41229	0.0250711	1.600826611
GO SKELETAL MUSCLE TISSUE REGENERATION	4	0.41229	0.0250711	1.600826611
GO ORGANELLE LOCALIZATION	18	7.8106	0.0252529	1.597688741
GO POSITIVE REGULATION OF COLD INDUCED THERMOGENESIS	6	1.09944	0.0253213	1.596514001
GO INTERSPECIES INTERACTION BETWEEN ORGANISMS	22	10.5363	0.025449	1.594329278
GO CELL MATURATION	8	1.98128	0.0256584	1.590770429
GO REGULATION OF RECEPTOR SIGNALING PATHWAY VIA STAT	7	1.52318	0.0256723	1.590535221
GO REGULATION OF LEUKOCYTE PROLIFERATION	9	2.47374	0.0257035	1.590007736
GO CELLULAR RESPONSE TO CORTICOSTEROID STIMULUS	5	0.73296	0.0260175	1.584734437
GO REGULATION OF STRIATED MUSCLE CELL DIFFERENTIATION	6	1.11089	0.0264727	1.577201762
GO POSITIVE REGULATION OF ION TRANSPORT	10	3.01201	0.0268399	1.571219107
GO TUBE MORPHOGENESIS	20	9.20781	0.0269318	1.569734619
GO POSITIVE REGULATION OF HEART GROWTH	4	0.423742	0.0271976	1.565469418
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	4	0.423742	0.0271976	1.565469418
GO ORGAN GROWTH	8	2.00419	0.0272772	1.564200212
GO AXO DENDRITIC TRANSPORT	5	0.744412	0.0275366	1.560089684
GO COFACTOR CATABOLIC PROCESS	5	0.744412	0.0275366	1.560089684
GO CATECHOLAMINE UPTAKE	3	0.18324	0.0279751	1.553228352
GO CELL CYCLE G2 M PHASE TRANSITION	10	3.03491	0.0279751	1.553228352
GO POSITIVE REGULATION OF GLIAL CELL PROLIFERATION	3	0.18324	0.0279751	1.553228352
GO REGULATION OF CAMP DEPENDENT PROTEIN KINASE ACTIVITY	3	0.18324	0.0279751	1.553228352
GO REGULATION OF INCLUSION BODY ASSEMBLY	3	0.18324	0.0279751	1.553228352

GO REGULATION OF MITOPHAGY	3	0.18324	0.0279751	1.553228352
GO REGULATION OF NUCLEAR CELL CYCLE DNA REPLICATION	3	0.18324	0.0279751	1.553228352
GO RESPONSE TO EPINEPHRINE	3	0.18324	0.0279751	1.553228352
GO REGULATION OF RESPONSE TO BIOTIC STIMULUS	7	1.55754	0.0284496	1.545923835
GO REGULATION OF TUBE SIZE	7	1.55754	0.0284496	1.545923835
GO REGULATION OF INFLAMMATORY RESPONSE TO WOUNDING	2	0.0343575	0.0286711	1.542555645
GO POSITIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	5	0.755865	0.0289971	1.537645434
GO NEGATIVE REGULATION OF INSULIN SECRETION	4	0.435195	0.0292257	1.534235078
GO POSITIVE REGULATION OF SIGNALING RECEPTOR ACTIVITY	4	0.435195	0.0292257	1.534235078
GO REGULATION OF PROTEIN LOCALIZATION TO CELL SURFACE	4	0.435195	0.0292257	1.534235078
GO RESPONSE TO FOOD	4	0.435195	0.0292257	1.534235078
GO INTERLEUKIN 6 PRODUCTION	7	1.56899	0.0293827	1.531908299
GO REGULATION OF PEPTIDYL SERINE PHOSPHORYLATION	7	1.56899	0.0293827	1.531908299
GO T CELL PROLIFERATION	8	2.03854	0.0296236	1.528362165
GO NEGATIVE REGULATION OF LOCOMOTION	11	3.61899	0.0298494	1.525064394
GO NEGATIVE REGULATION OF PROTEIN BINDING	6	1.14525	0.0298494	1.525064394
GO MULTI ORGANISM REPRODUCTIVE PROCESS	23	11.4181	0.0301315	1.520979248
GO POSITIVE REGULATION OF TYROSINE PHOSPHORYLATION OF STAT PROTEIN	5	0.767317	0.0304466	1.516461198
GO REGULATION OF BEHAVIOR	5	0.767317	0.0304466	1.516461198
GO REGULATION OF CELLULAR RESPONSE TO INSULIN STIMULUS	5	0.767317	0.0304466	1.516461198
GO SYNAPTIC VESICLE RECYCLING	5	0.767317	0.0304466	1.516461198
GO NEGATIVE REGULATION OF CELL MOTILITY	10	3.08072	0.0305393	1.515140922
GO POSITIVE REGULATION OF NEUROTRANSMITTER TRANSPORT	4	0.446647	0.0315271	1.501315976
GO TORC1 SIGNALING	4	0.446647	0.0315271	1.501315976
GO HORMONE TRANSPORT	11	3.65335	0.0317897	1.497713571
GO MYOBLAST PROLIFERATION	3	0.194692	0.0317982	1.497597463
GO POSITIVE REGULATION OF CIRCADIAN RHYTHM	3	0.194692	0.0317982	1.497597463
GO REGULATION OF CELL GROWTH INVOLVED IN CARDIAC MUSCLE CELL DEVELOPMENT	3	0.194692	0.0317982	1.497597463
GO REGULATION OF TRANSMISSION OF NERVE IMPULSE	3	0.194692	0.0317982	1.497597463
GO CELLULAR PROTEIN CONTAINING COMPLEX ASSEMBLY	24	12.2084	0.0322137	1.49195939
GO FEEDING BEHAVIOR	6	1.16815	0.0323768	1.489766077
GO REGULATION OF STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	9	2.58826	0.0331738	1.479204778
GO PROTEIN IMPORT	8	2.08435	0.0332743	1.477891072
GO NEGATIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	6	1.17961	0.0338445	1.470511898
GO MACROPHAGE DIFFERENTIATION	4	0.4581	0.0340031	1.468481487
GO DEVELOPMENTAL GROWTH INVOLVED IN MORPHOGENESIS	9	2.59972	0.0340229	1.468228671
GO LEARNING	7	1.62625	0.0348889	1.457312723
GO REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORT	7	1.62625	0.0348889	1.457312723
GO CATION TRANSMEMBRANE TRANSPORT	20	9.45976	0.0350719	1.455040706
GO SEXUAL REPRODUCTION	20	9.48267	0.0360249	1.443397216
GO HEAD DEVELOPMENT	19	8.79552	0.0360484	1.443114007
GO CELLULAR RESPONSE TO ARSENIC CONTAINING SUBSTANCE	3	0.206145	0.0360754	1.442788845
GO HISTONE H3 DEACETYLATION	3	0.206145	0.0360754	1.442788845
GO NEGATIVE REGULATION OF VASCULAR SMOOTH MUSCLE CELL PROLIFERATION	3	0.206145	0.0360754	1.442788845
GO REGULATION OF DEFENSE RESPONSE TO BACTERIUM	3	0.206145	0.0360754	1.442788845

GO RESOLUTION OF MEIOTIC RECOMBINATION INTERMEDIATES	3	0.206145	0.0360754	1.442788845
GO RESPONSE TO UV B	3	0.206145	0.0360754	1.442788845
GO STRESS GRANULE ASSEMBLY	3	0.206145	0.0360754	1.442788845
GO TRANSCYTOSIS	3	0.206145	0.0360754	1.442788845
GO MEIOTIC CELL CYCLE PROCESS	8	2.11871	0.036129	1.442144059
GO NEGATIVE REGULATION OF LIPID LOCALIZATION	4	0.469552	0.036349	1.439507533
GO POSITIVE REGULATION OF DENDRITIC SPINE DEVELOPMENT	4	0.469552	0.036349	1.439507533
GO TRIGLYCERIDE METABOLIC PROCESS	4	0.469552	0.036349	1.439507533
GO LEUKOCYTE APOPTOTIC PROCESS	6	1.20251	0.0363556	1.439428684
GO MITOTIC DNA INTEGRITY CHECKPOINT	6	1.20251	0.0363556	1.439428684
GO POSITIVE REGULATION OF PEPTIDYL SERINE PHOSPHORYLATION	6	1.20251	0.0363556	1.439428684
GO NEGATIVE REGULATION OF CELL ACTIVATION	8	2.13016	0.037072	1.430953984
GO RESPONSE TO AXON INJURY	5	0.813127	0.0373823	1.427333982
GO FOREBRAIN DEVELOPMENT	12	4.3405	0.0380365	1.419799452
GO ADIPOSE TISSUE DEVELOPMENT	4	0.481005	0.039121	1.407590052
GO CELLULAR RESPONSE TO GLUCOSE STARVATION	4	0.481005	0.039121	1.407590052
GO DNA DEPENDENT DNA REPLICATION MAINTENANCE OF FIDELITY	4	0.481005	0.039121	1.407590052
GO NUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	5	0.82458	0.0394259	1.404218384
GO MYOFIBROBLAST DIFFERENTIATION	2	0.04581	0.0401628	1.396176017
GO NEGATIVE REGULATION OF METALLOENDOPEPTIDASE ACTIVITY	2	0.04581	0.0401628	1.396176017
GO POSITIVE REGULATION OF DNA CATABOLIC PROCESS	2	0.04581	0.0401628	1.396176017
GO REGULATION OF MYOFIBROBLAST DIFFERENTIATION	2	0.04581	0.0401628	1.396176017
GO REGULATION OF SUPEROXIDE DISMUTASE ACTIVITY	2	0.04581	0.0401628	1.396176017
GO NOTCH SIGNALING PATHWAY	8	2.16452	0.0403526	1.394128478
GO DENDRITIC SPINE MAINTENANCE	3	0.217597	0.0404048	1.393567039
GO NEGATIVE REGULATION OF CHEMOKINE PRODUCTION	3	0.217597	0.0404048	1.393567039
GO NEGATIVE REGULATION OF OXIDATIVE STRESS INDUCED NEURON DEATH	3	0.217597	0.0404048	1.393567039
GO NEGATIVE REGULATION OF TISSUE REMODELING	3	0.217597	0.0404048	1.393567039
GO POSITIVE REGULATION OF MACROPHAGE MIGRATION	3	0.217597	0.0404048	1.393567039
GO REGULATION OF RESPONSE TO FOOD	3	0.217597	0.0404048	1.393567039
GO MODIFICATION OF MORPHOLOGY OR PHYSIOLOGY OF OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	6	1.23687	0.0407758	1.38959751
GO RAS PROTEIN SIGNAL TRANSDUCTION	13	4.99329	0.0407758	1.38959751
GO REGULATION OF SYNAPSE ASSEMBLY	6	1.23687	0.0407758	1.38959751
GO NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	9	2.69134	0.0409954	1.387264872
GO NEGATIVE REGULATION OF DNA RECOMBINATION	4	0.492457	0.0415486	1.381443605
GO PHENOL CONTAINING COMPOUND BIOSYNTHETIC PROCESS	4	0.492457	0.0415486	1.381443605
GO RESPONSE TO ISCHEMIA	4	0.492457	0.0415486	1.381443605
GO RHYTHMIC BEHAVIOR	4	0.492457	0.0415486	1.381443605
GO PLACENTA DEVELOPMENT	7	1.69497	0.0417729	1.379105374
GO REGULATION OF GENE SILENCING	7	1.69497	0.0417729	1.379105374
GO RESPONSE TO MOLECULE OF BACTERIAL ORIGIN	11	3.82513	0.0425149	1.371458838
GO POSITIVE REGULATION OF CYTOKINE PRODUCTION	13	5.0391	0.0436462	1.360053562
GO REGULATION OF PROTEIN LOCALIZATION TO CELL PERIPHERY	6	1.25977	0.0441132	1.355431437
GO NEGATIVE REGULATION OF RESPONSE TO ENDOPLASMIC RETICULUM STRESS	4	0.50391	0.0445932	1.350731362
GO NEGATIVE REGULATION OF STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	4	0.50391	0.0445932	1.350731362

GO POSITIVE REGULATION OF CARDIAC MUSCLE TISSUE DEVELOPMENT	4	0.50391	0.0445932	1.350731362
GO CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	18	8.32597	0.0449725	1.34705297
GO DRUG METABOLIC PROCESS	11	3.85949	0.0451427	1.345412469
GO NEGATIVE REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	3	0.22905	0.0451427	1.345412469
GO NEGATIVE REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	3	0.22905	0.0451427	1.345412469
GO REGULATION OF PRODUCTION OF SMALL RNA INVOLVED IN GENE SILENCING BY RNA	3	0.22905	0.0451427	1.345412469
GO SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	15	6.33323	0.0451427	1.345412469
GO PERIPHERAL NERVOUS SYSTEM DEVELOPMENT	5	0.858937	0.0451455	1.345385533
GO REGULATION OF IMMUNE EFFECTOR PROCESS	12	4.45502	0.0451455	1.345385533
GO BLOOD VESSEL ENDOTHELIAL CELL MIGRATION	6	1.28268	0.0475513	1.322837605
GO NEGATIVE REGULATION OF PEPTIDE HORMONE SECRETION	4	0.515362	0.0476426	1.322004546
GO REGULATION OF ERYTHROCYTE DIFFERENTIATION	4	0.515362	0.0476426	1.322004546
GO CELL PART MORPHOGENESIS	17	7.70753	0.0481234	1.317643697
GO RECEPTOR SIGNALING PATHWAY VIA STAT	7	1.75223	0.0491014	1.308906125
GO CELLULAR COMPONENT MORPHOGENESIS	24	12.7008	0.0498446	1.302381885
GO ADULT LOCOMOTORY BEHAVIOR	5	0.881842	0.0499658	1.301327155