

Supplemental Material

Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver

Afshin Beheshti^{1*}, Kaushik Chakravarty^{2*}, Homer Fogle¹, Hossein Fazelinia³, Willian A. da Silveira⁴, Valery Boyko¹, San-Huei Lai Polo¹, Amanda M. Saravia-Butler⁵, Gary Hardiman⁴, Deanne Taylor², Jonathan M. Galazka⁶, and Sylvain V. Costes⁶

*These authors are co-first authors

¹Wyle Labs, Space Biosciences Division, NASA Ames Research Center, Moffett Field, CA

²twoXAR Inc. Mountain View, CA³Department of Biomedical and Health Informatics, The Children's Hospital of Philadelphia, Philadelphia, USA; Center for Mitochondrial and Epigenomic Medicine, The Children's Hospital of Philadelphia, USA.

⁴Institute for Global Food Security, Queens University Belfast, UK

⁵Logyx LLC, Space Biosciences Division, NASA Ames Research Center, Moffett Field, CA

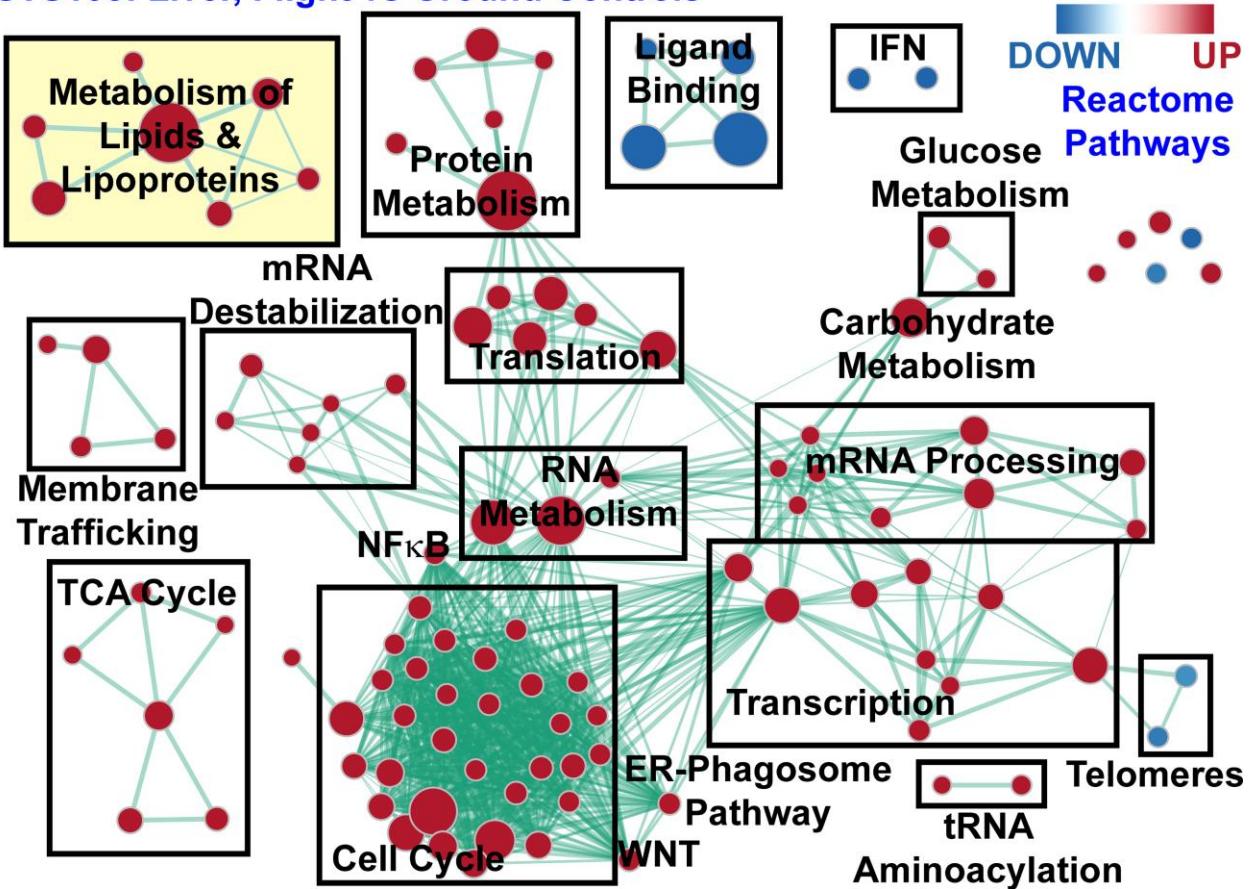
⁶NASA Ames Research Center, Moffett Field, CA

Corresponding Authors:

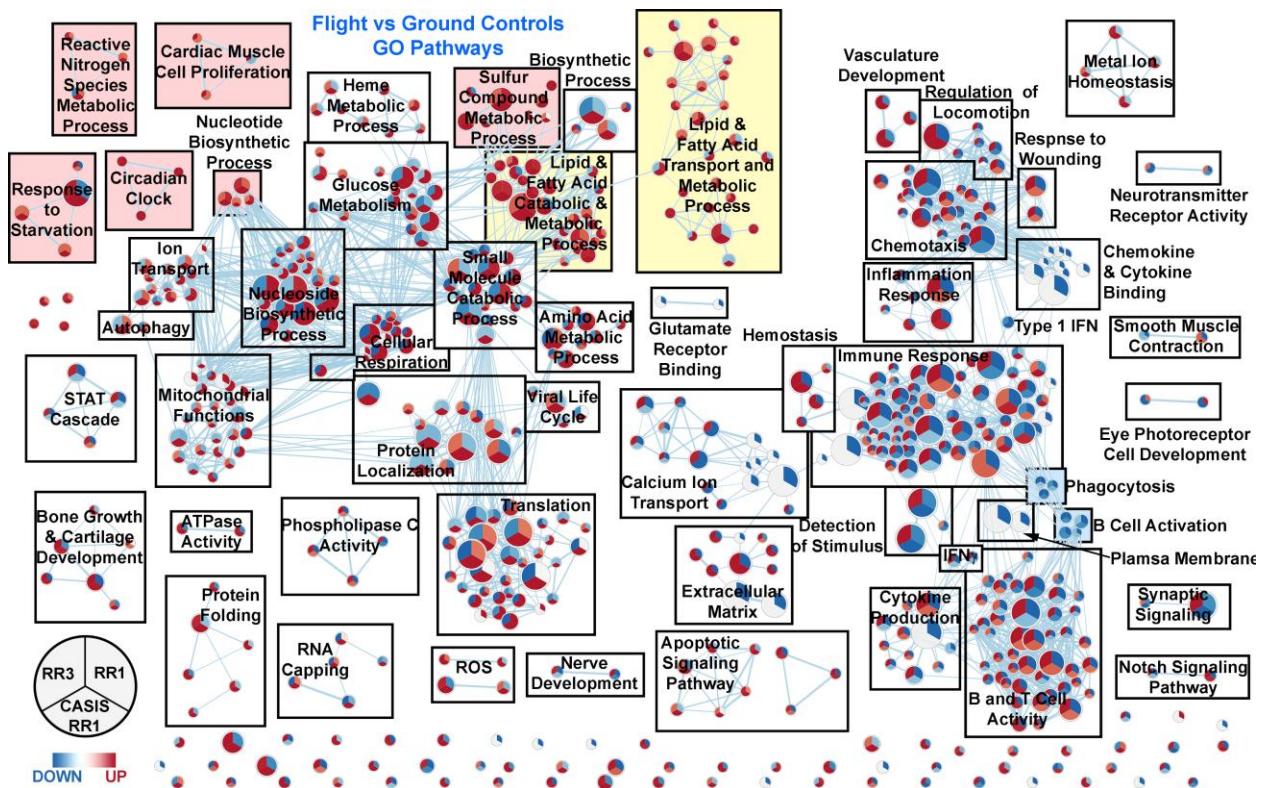
Afshin Beheshti, and Sylvain Costes

afshin.beheshti@nasa.gov, and sylvain.v.costes@nasa.gov

STS135: Liver, Flight vs Ground Controls



Supplemental Figure 1. Pathway analysis for livers from mice on the STS-135 mission.
 Gene Set Enrichment Analysis (GSEA) with Reactome pathways on liver's from STS-135 GeneLab dataset displayed as a network through a Cytoscape plugin, EnrichmentMap. Lipid related pathways are shown with a yellow background. Each node represents one gene set and the size of the node indicates the number of genes involved with the predictions. The color of the node indicates if the gene set is downregulated (blue) or upregulated (red). The shade of the color indicates degree of regulation. The thickness of the edge (green lines) represents the number of genes associated with the overlap of the gene sets (or nodes) that the edge connects. Clusters were named according to common function in each grouping.



Supplemental Figure 2. Pathway analysis for livers from mice on the RR1 and RR3 mission.
 Gene Set Enrichment Analysis (GSEA) with Gene Ontology (GO) pathways on liver's from RR1 and RR3 GeneLab dataset displayed as a network through a Cytoscape plugin, EnrichmentMap. Red nodes indicate upregulation of the pathway and blue nodes represent downregulation. Lipid related pathways are shown with a yellow background. Light red background for nodes in network represents common pathways being upregulated between RR1 and RR3, while light blue background represents common pathways being downregulated between RR1 and RR3. Each node represents one gene set and the size of the node indicates the number of genes involved with the predictions. Each node contains 3 wedges for each condition and the color of each wedge indicates if the gene set is downregulated (blue) or upregulated (red). The shade of the color indicates degree of regulation. The thickness of the edge (blue lines) represents the number of genes associated with the overlap of the gene sets (or nodes) that the edge connects. Clusters were named according to common function in each grouping.

Supplemental Table 1. Gene Set Enrichment Analysis on the Gene Ontology (GO) terms for the STS-135 transcriptomic data set for Flight samples vs Habitat Ground Controls. Size = the number genes for the predicted GO term, and ES = Enrichment Score, NES = Normalized Enrichment Score.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
RIBOSOME BIOGENESIS	248	0.67	3.06	0.0000	0.0000
RIBONUCLEOPROTEIN COMPLEX BIOGENESIS	352	0.63	2.94	0.0000	0.0000
NCRNA PROCESSING	313	0.63	2.93	0.0000	0.0000
RRNA METABOLIC PROCESS	204	0.66	2.90	0.0000	0.0000
MITOCHONDRIAL MATRIX	352	0.60	2.80	0.0000	0.0000
NCRNA METABOLIC PROCESS	445	0.59	2.79	0.0000	0.0000
TRNA METABOLIC PROCESS	152	0.64	2.72	0.0000	0.0000
PRERIBOSOME	46	0.73	2.60	0.0000	0.0000
TRNA PROCESSING	96	0.65	2.58	0.0000	0.0000
COFACTOR BIOSYNTHETIC PROCESS	145	0.60	2.55	0.0000	0.0000
NUCLEOLAR PART	58	0.70	2.54	0.0000	0.0000
RNA MODIFICATION	94	0.63	2.53	0.0000	0.0000
TRANSLATIONAL TERMINATION	84	0.65	2.51	0.0000	0.0000
MITOCHONDRIAL TRANSLATION	96	0.64	2.48	0.0000	0.0000
ORGANELLAR RIBOSOME	65	0.66	2.47	0.0000	0.0000
COFACTOR METABOLIC PROCESS	289	0.54	2.46	0.0000	0.0000
ORGANELLE INNER MEMBRANE	451	0.52	2.45	0.0000	0.0000
AMIDE BIOSYNTHETIC PROCESS	431	0.52	2.45	0.0000	0.0000
MICROBODY	123	0.58	2.41	0.0000	0.0000
MITOCHONDRION ORGANIZATION	489	0.50	2.40	0.0000	0.0000
RIBONUCLEOPROTEIN COMPLEX SUBUNIT ORGANIZATION	162	0.56	2.38	0.0000	0.0000
RIBONUCLEOPROTEIN COMPLEX BINDING	88	0.61	2.38	0.0000	0.0000
RNA METHYLATION	37	0.72	2.37	0.0000	0.0000
MICROBODY PART	85	0.61	2.36	0.0000	0.0000
CELLULAR PROTEIN COMPLEX DISASSEMBLY	111	0.57	2.36	0.0000	0.0000
TRANSLATIONAL ELONGATION	100	0.59	2.36	0.0000	0.0000
LIPID OXIDATION	61	0.63	2.35	0.0000	0.0000
TRANSLATION INITIATION FACTOR ACTIVITY	46	0.67	2.35	0.0000	0.0000
ORGANELLAR LARGE RIBOSOMAL SUBUNIT	28	0.73	2.35	0.0000	0.0000
PEPTIDE METABOLIC PROCESS	483	0.49	2.34	0.0000	0.0000
MITOCHONDRIAL MEMBRANE PART	142	0.55	2.34	0.0000	0.0000

RIBOSOMAL SMALL SUBUNIT BIOGENESIS	41	0.68	2.34	0.0000	0.0000
TRANSLATION FACTOR ACTIVITY RNA BINDING	80	0.60	2.33	0.0000	0.0000
RNA METHYLTRANSFERASE ACTIVITY	30	0.74	2.33	0.0000	0.0000
RNA SPLICING VIA TRANSESTERIFICATION REACTIONS	216	0.53	2.33	0.0000	0.0000
TRNA MODIFICATION	49	0.66	2.33	0.0000	0.0000
FATTY ACID CATABOLIC PROCESS	60	0.63	2.32	0.0000	0.0000
INTRINSIC COMPONENT OF MITOCHONDRIAL MEMBRANE	41	0.67	2.32	0.0000	0.0000
DNA TEMPLATED TRANSCRIPTION ELONGATION	84	0.60	2.32	0.0000	0.0000
MITOCHONDRIAL PROTEIN COMPLEX	111	0.57	2.32	0.0000	0.0000
COENZYME BIOSYNTHETIC PROCESS	111	0.57	2.31	0.0000	0.0000
COENZYME METABOLIC PROCESS	235	0.52	2.31	0.0000	0.0000
CATALYTIC STEP 2 SPliceosome	73	0.60	2.31	0.0000	0.0000
MATURATION OF 5S rRNA	25	0.74	2.29	0.0000	0.0000
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX ASSEMBLY	60	0.62	2.29	0.0000	0.0000
VESICLE COATING	65	0.60	2.28	0.0000	0.0000
MEMBRANE BUDDING	101	0.57	2.28	0.0000	0.0000
RESPONSE TO TYPE I INTERFERON	48	-0.67	-2.61	0.0000	0.0000
LYMPHOCYTE MIGRATION	35	-0.68	-2.41	0.0000	0.0000
RIBOSOMAL LARGE SUBUNIT BIOGENESIS	38	0.67	2.27	0.0000	0.0000
PROTEIN LOCALIZATION TO MITOCHONDRIUM	58	0.60	2.24	0.0000	0.0000
FATTY ACID BETA OXIDATION	43	0.65	2.24	0.0000	0.0000
MATURATION OF SSU rRNA	31	0.70	2.25	0.0000	0.0000
REGULATION OF RECEPTOR BIOSYNTHETIC PROCESS	20	0.78	2.25	0.0000	0.0000
RNA SPLICING	285	0.50	2.25	0.0000	0.0000
SMALL SUBUNIT PROCESSOME	26	0.74	2.26	0.0000	0.0000
STRUCTURAL CONSTITUENT OF RIBOSOME	178	0.52	2.26	0.0000	0.0000
GOLGI ORGANIZATION	78	0.59	2.27	0.0000	0.0000
mRNA METABOLIC PROCESS	494	0.47	2.27	0.0000	0.0000
INNER MITOCHONDRIAL MEMBRANE PROTEIN COMPLEX	84	0.57	2.23	0.0000	0.0001
RIBOSOME	184	0.51	2.23	0.0000	0.0001
ASPARTATE FAMILY AMINO ACID METABOLIC PROCESS	52	0.61	2.23	0.0000	0.0001

SNORNA BINDING	23	0.73	2.23	0.0000	0.0001
RIBOSOMAL SUBUNIT	131	0.53	2.22	0.0000	0.0001
MRNA PROCESSING	343	0.48	2.22	0.0000	0.0001
CELLULAR RESPIRATION	126	0.53	2.22	0.0000	0.0001
ER TO GOLGI VESICLE MEDIATED TRANSPORT	144	0.52	2.22	0.0000	0.0001
LARGE RIBOSOMAL SUBUNIT	77	0.58	2.20	0.0000	0.0001
SINGLE ORGANISM MEMBRANE BUDDING	64	0.59	2.21	0.0000	0.0001
RNA 3 END PROCESSING	76	0.57	2.21	0.0000	0.0001
MULTIVESICULAR BODY ORGANIZATION	27	0.70	2.21	0.0000	0.0001
RIBONUCLEOPROTEIN COMPLEX LOCALIZATION	92	0.56	2.19	0.0000	0.0001
AMINO ACID ACTIVATION	46	0.62	2.19	0.0000	0.0001
EXOSOME RNASE COMPLEX	18	0.79	2.20	0.0000	0.0001
RNA LOCALIZATION	144	0.52	2.20	0.0000	0.0001
TRANSCRIPTION ELONGATION FROM RNA POLYMERASE II PROMOTER	70	0.59	2.20	0.0000	0.0001
MACROMOLECULAR COMPLEX DISASSEMBLY	166	0.51	2.20	0.0000	0.0001
90S PRERIBOSOME	18	0.78	2.18	0.0000	0.0002
TRNA AMINOACYLATION	46	0.62	2.18	0.0000	0.0002
INTRA GOLGI VESICLE MEDIATED TRANSPORT	33	0.67	2.19	0.0000	0.0002
UBIQUITIN LIGASE COMPLEX	235	0.48	2.17	0.0000	0.0002
SPliceosomal complex	137	0.53	2.17	0.0000	0.0002
TRANSLATIONAL INITIATION	122	0.52	2.15	0.0000	0.0002
TRNA BINDING	38	0.63	2.15	0.0000	0.0002
PEROXISOME ORGANIZATION	28	0.67	2.15	0.0000	0.0002
THIOESTER METABOLIC PROCESS	76	0.55	2.15	0.0000	0.0002
VERY LONG CHAIN FATTY ACID METABOLIC PROCESS	24	0.71	2.17	0.0000	0.0002
S ADENOSYL METHIONINE DEPENDENT METHYLTRANSFERASE ACTIVITY	105	0.53	2.15	0.0000	0.0002
AEROBIC RESPIRATION	47	0.61	2.15	0.0000	0.0002
CARBOXYLIC ACID CATABOLIC PROCESS	178	0.50	2.15	0.0000	0.0002
RIBOSOME ASSEMBLY	46	0.62	2.17	0.0000	0.0002
ORGANIC ACID CATABOLIC PROCESS	178	0.50	2.15	0.0000	0.0002
MICROBODY MEMBRANE	54	0.60	2.16	0.0000	0.0002
RNA PHOSPHODIESTER BOND HYDROLYSIS	97	0.54	2.16	0.0000	0.0002
LIPID PARTICLE	53	0.60	2.14	0.0000	0.0002

INTRINSIC COMPONENT OF MITOCHONDRIAL OUTER MEMBRANE	19	0.75	2.14	0.0000	0.0002
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX I ASSEMBLY	46	0.60	2.13	0.0000	0.0003
RNA HELICASE ACTIVITY	59	0.58	2.13	0.0000	0.0003
MATURATION OF SSU RRNA FROM TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA	24	0.70	2.13	0.0000	0.0003
ENERGY DERIVATION BY OXIDATION OF ORGANIC COMPOUNDS	187	0.49	2.12	0.0000	0.0004
PRENYLTRANSFERASE ACTIVITY	15	0.79	2.12	0.0000	0.0004
VESICLE TARGETING	68	0.57	2.12	0.0000	0.0004
PROTEIN TRANSPORTER ACTIVITY	95	0.53	2.13	0.0000	0.0004
TRANSFERASE ACTIVITY TRANSFERRING ONE CARBON GROUPS	164	0.49	2.12	0.0000	0.0004
GOLGI VESICLE TRANSPORT	269	0.47	2.12	0.0000	0.0004
COA HYDROLASE ACTIVITY	19	0.74	2.12	0.0000	0.0004
PROTEIN TARGETING TO MITOCHONDRIUM	42	0.62	2.12	0.0000	0.0004
ACYL COA METABOLIC PROCESS	76	0.55	2.12	0.0000	0.0004
TRNA METHYLTRANSFERASE ACTIVITY	15	0.77	2.11	0.0000	0.0004
NADH DEHYDROGENASE COMPLEX ASSEMBLY	46	0.60	2.11	0.0000	0.0004
CYTOPLASMIC TRANSLATION	34	0.63	2.11	0.0000	0.0004
TRNA METHYLATION	18	0.74	2.10	0.0000	0.0006
PROTEIN POLYUBIQUITINATION	219	0.47	2.09	0.0000	0.0006
PRERIBOSOME LARGE SUBUNIT PRECURSOR	16	0.77	2.09	0.0000	0.0007
TRANSFERASE ACTIVITY TRANSFERRING ACYL GROUPS OTHER THAN AMINO ACYL GROUPS	172	0.48	2.09	0.0000	0.0007
CULLIN RING UBIQUITIN LIGASE COMPLEX	132	0.50	2.09	0.0000	0.0007
MONOCARBOXYLIC ACID CATABOLIC PROCESS	79	0.54	2.09	0.0000	0.0007
AUTOPHAGOSOME ORGANIZATION	29	0.65	2.09	0.0000	0.0007
NUCLEAR EXPORT	117	0.51	2.08	0.0000	0.0008
TRNA TRANSPORT	29	0.66	2.08	0.0000	0.0008
MICROBODY LUMEN	41	0.61	2.08	0.0000	0.0008
ESCRT COMPLEX	23	0.69	2.08	0.0000	0.0008
REGULATION OF TRANSLATIONAL ELONGATION	20	0.70	2.08	0.0000	0.0009

DNA TEMPLATED TRANSCRIPTION TERMINATION	81	0.54	2.08	0.0000	0.0009
CIS GOLGI NETWORK	39	0.62	2.08	0.0000	0.0009
ELECTRON TRANSPORT CHAIN	82	0.53	2.07	0.0000	0.0011
ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS	69	0.54	2.06	0.0000	0.0011
MULTI ORGANISM LOCALIZATION	54	0.56	2.06	0.0000	0.0012
PROTEIN TRANSMEMBRANE TRANSPORT	44	0.60	2.06	0.0000	0.0012
REGULATION OF PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	91	0.51	2.06	0.0000	0.0012
MITOCHONDRIAL TRANSPORT	142	0.49	2.06	0.0000	0.0012
MULTI ORGANISM TRANSPORT	54	0.56	2.06	0.0000	0.0012
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX I BIOGENESIS	46	0.60	2.06	0.0000	0.0012
PORPHYRIN CONTAINING COMPOUND METABOLIC PROCESS	31	0.63	2.05	0.0000	0.0012
RRNA BINDING	50	0.58	2.06	0.0000	0.0012
TETRAPYRROLE BIOSYNTHETIC PROCESS	25	0.67	2.05	0.0017	0.0013
PROTEASOMAL PROTEIN CATABOLIC PROCESS	240	0.46	2.05	0.0000	0.0013
MRNA 3 END PROCESSING	56	0.55	2.05	0.0000	0.0013
REGULATION OF MITOPHAGY	36	0.62	2.04	0.0000	0.0015
GLYOXYLATE METABOLIC PROCESS	26	0.65	2.04	0.0000	0.0015
TRANSFERASE ACTIVITY TRANSFERRING ACYL GROUPS	201	0.46	2.04	0.0000	0.0016
EXORIBONUCLEASE ACTIVITY	31	0.65	2.03	0.0000	0.0016
MATURATION OF 5 8S RRNA FROM TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA	17	0.73	2.03	0.0000	0.0017
PURINE NTP DEPENDENT HELICASE ACTIVITY	84	0.52	2.03	0.0000	0.0017
ESTABLISHMENT OF PROTEIN LOCALIZATION TO ORGANELLE	297	0.44	2.02	0.0000	0.0019
OXIDATIVE PHOSPHORYLATION	71	0.53	2.02	0.0000	0.0019
VACUOLAR MEMBRANE	487	0.42	2.02	0.0000	0.0021
QUINONE METABOLIC PROCESS	19	0.71	2.02	0.0000	0.0022
LIGASE ACTIVITY FORMING CARBON OXYGEN BONDS	39	0.60	2.01	0.0000	0.0023
VACUOLAR TRANSPORT	205	0.46	2.01	0.0000	0.0023
RNA CATABOLIC PROCESS	195	0.45	2.01	0.0000	0.0023

ENDORIBONUCLEASE ACTIVITY PRODUCING 5 PHOSPHOMONOESTERS	22	0.67	2.01	0.0000	0.0024
CELLULAR IRON ION HOMEOSTASIS	38	0.60	2.01	0.0000	0.0024
MRNA CLEAVAGE FACTOR COMPLEX	16	0.72	2.00	0.0017	0.0024
TRANS GOLGI NETWORK MEMBRANE	58	0.54	2.01	0.0000	0.0024
PROTEIN LOCALIZATION TO ORGANELLE	473	0.42	2.01	0.0000	0.0024
TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	33	0.61	2.01	0.0000	0.0024
EXONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	39	0.59	2.01	0.0017	0.0024
PROTEIN CATABOLIC PROCESS	494	0.42	2.01	0.0000	0.0024
THIOESTER HYDROLASE ACTIVITY	31	0.62	2.00	0.0000	0.0026
LATE ENDOSOME MEMBRANE	80	0.51	2.00	0.0000	0.0026
OUTER MEMBRANE	169	0.46	2.00	0.0000	0.0027
SMALL MOLECULE CATABOLIC PROCESS	285	0.44	2.00	0.0000	0.0027
COATED MEMBRANE	78	0.52	1.99	0.0000	0.0027
PROTEASOME ACCESSORY COMPLEX	24	0.66	2.00	0.0017	0.0027
NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS DEADENYLATION DEPENDENT DECAY	53	0.57	1.99	0.0000	0.0029
BRANCHED CHAIN AMINO ACID METABOLIC PROCESS	23	0.67	1.99	0.0000	0.0030
LIGASE ACTIVITY	357	0.43	1.98	0.0000	0.0030
COP1 COATED VESICLE MEMBRANE	16	0.71	1.98	0.0000	0.0031
VESICLE COAT	42	0.59	1.98	0.0000	0.0031
REGULATION OF MITOCHONDRIAL FISSION	18	0.71	1.98	0.0017	0.0031
CARBOXYLIC ESTER HYDROLASE ACTIVITY	111	0.48	1.98	0.0000	0.0031
THIOESTER BIOSYNTHETIC PROCESS	48	0.56	1.98	0.0000	0.0032
NUCLEOBASE CONTAINING COMPOUND TRANSPORT	157	0.46	1.97	0.0000	0.0036
INTRINSIC COMPONENT OF ORGANELLE MEMBRANE	227	0.44	1.96	0.0000	0.0038
NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS NONSENSE MEDIATED DECAY	98	0.48	1.97	0.0000	0.0038
AMINO ACID BETAINE METABOLIC PROCESS	16	0.72	1.96	0.0018	0.0039
PROTEIN K11 LINKED UBIQUITINATION	23	0.65	1.96	0.0000	0.0039
NEGATIVE REGULATION OF HEART CONTRACTION	20	0.67	1.96	0.0018	0.0041

CELLULAR CARBOHYDRATE CATABOLIC PROCESS	26	0.63	1.96	0.0000	0.0043
GLYCOSYL COMPOUND METABOLIC PROCESS	306	0.42	1.96	0.0000	0.0044
ACYL COA BIOSYNTHETIC PROCESS	48	0.56	1.96	0.0000	0.0044
RNA MODIFICATION	18	0.70	1.96	0.0000	0.0044
CLEAVAGE INVOLVED IN RRNA PROCESSING	16	0.72	1.95	0.0017	0.0044
MULTI ORGANISM METABOLIC PROCESS	113	0.48	1.95	0.0000	0.0044
GLYCOSYL COMPOUND BIOSYNTHETIC PROCESS	98	0.49	1.95	0.0000	0.0045
GPI ANCHOR METABOLIC PROCESS	28	0.63	1.95	0.0016	0.0045
HELICASE ACTIVITY	135	0.46	1.95	0.0000	0.0046
RNA POLYMERASE COMPLEX	105	0.49	1.95	0.0000	0.0046
RNA PHOSPHODIESTER BOND HYDROLYSIS EXONUCLEOLYTIC	32	0.61	1.95	0.0000	0.0046
TRANS GOLGI NETWORK	156	0.46	1.95	0.0000	0.0046
GENERATION OF PRECURSOR METABOLITES AND ENERGY	255	0.43	1.95	0.0000	0.0046
POST GOLGI VESICLE MEDIATED TRANSPORT	71	0.51	1.95	0.0000	0.0047
RNA PHOSPHODIESTER BOND HYDROLYSIS ENDONUCLEOLYTIC	46	0.55	1.95	0.0000	0.0047
CELLULAR AMINO ACID METABOLIC PROCESS	298	0.42	1.94	0.0000	0.0048
MITOCHONDRIAL FUSION	17	0.68	1.94	0.0000	0.0049
POSTTRANSCRIPTIONAL REGULATION OF GENE EXPRESSION	404	0.41	1.94	0.0000	0.0049
RNA POLYMERASE II REPRESSING TRANSCRIPTION FACTOR BINDING	25	0.63	1.94	0.0000	0.0049
NUCLEAR PORE	66	0.51	1.94	0.0000	0.0052
FORMATION OF TRANSLATION PREINITIATION COMPLEX	17	0.70	1.94	0.0000	0.0052
UBIQUITIN LIKE PROTEIN TRANSFERASE ACTIVITY	367	0.41	1.93	0.0000	0.0053
NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS EXONUCLEOLYTIC	29	0.62	1.93	0.0000	0.0054
SMALL NUCLEOLAR RIBONUCLEOPROTEIN COMPLEX	17	0.70	1.93	0.0000	0.0054
RIBOSOMAL LARGE SUBUNIT ASSEMBLY	22	0.65	1.93	0.0000	0.0055
CELLULAR COMPONENT DISASSEMBLY	449	0.41	1.93	0.0000	0.0055
AUTOPHAGY	312	0.42	1.93	0.0000	0.0055

NUCLEIC ACID PHOSPHODIESTER BOND HYDROLYSIS	207	0.43	1.93	0.0000	0.0056
RESPIRATORY CHAIN	69	0.51	1.92	0.0000	0.0061
HEPARAN SULFATE PROTEOGLYCAN METABOLIC PROCESS	28	0.62	1.92	0.0000	0.0061
ENDOSOMAL PART	350	0.41	1.92	0.0000	0.0061
SULFUR COMPOUND METABOLIC PROCESS	315	0.41	1.92	0.0000	0.0062
FATTY ACID METABOLIC PROCESS	237	0.43	1.92	0.0000	0.0062
CAJAL BODY	44	0.55	1.92	0.0016	0.0062
PURINE NUCLEOSIDE BIOSYNTHETIC PROCESS	72	0.50	1.92	0.0000	0.0062
UBIQUITIN LIKE PROTEIN LIGASE BINDING	232	0.43	1.92	0.0000	0.0062
MEMBRANE DISASSEMBLY	40	0.56	1.92	0.0000	0.0062
PURINE RIBONUCLEOSIDE BIOSYNTHETIC PROCESS	72	0.50	1.92	0.0000	0.0062
INTRINSIC COMPONENT OF MITOCHONDRIAL INNER MEMBRANE	16	0.71	1.92	0.0035	0.0063
PHOSPHATIDIC ACID METABOLIC PROCESS	31	0.59	1.92	0.0000	0.0063
RIBONUCLEASE ACTIVITY	79	0.50	1.92	0.0000	0.0063
ORGANELLE SUBCOMPARTMENT	254	0.42	1.91	0.0000	0.0064
CUL4 RING E3 UBIQUITIN LIGASE COMPLEX	21	0.66	1.92	0.0000	0.0064
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 COMPLEX	15	0.71	1.91	0.0000	0.0064
PROTEIN K63 LINKED UBIQUITINATION	30	0.59	1.91	0.0017	0.0065
ASPARTATE FAMILY AMINO ACID CATABOLIC PROCESS	17	0.69	1.91	0.0053	0.0065
HEME METABOLIC PROCESS	25	0.61	1.91	0.0000	0.0067
REGULATION OF LIGASE ACTIVITY	113	0.47	1.91	0.0000	0.0067
LIPID CATABOLIC PROCESS	211	0.43	1.91	0.0000	0.0068
LIPOPROTEIN BIOSYNTHETIC PROCESS	76	0.49	1.90	0.0000	0.0071
SNRNA METABOLIC PROCESS	74	0.50	1.90	0.0000	0.0071
VACUOLE ORGANIZATION	132	0.46	1.90	0.0000	0.0071
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH CH GROUP OF DONORS	50	0.53	1.90	0.0000	0.0072
NUCLEOTIDE EXCISION REPAIR PREINCISION COMPLEX ASSEMBLY	24	0.62	1.90	0.0017	0.0072
NUCLEAR ENVELOPE DISASSEMBLY	40	0.56	1.90	0.0000	0.0073
SUGAR TRANSMEMBRANE TRANSPORTER ACTIVITY	26	0.61	1.90	0.0050	0.0073

CHEMOKINE ACTIVITY	30	-0.65	-2.20	0.0000	0.0073
MULTI ORGANISM MEMBRANE BUDDING	21	0.64	1.90	0.0000	0.0074
SNARE COMPLEX	48	0.55	1.90	0.0000	0.0074
COP1 COATED VESICLE	22	0.64	1.90	0.0017	0.0074
ENDOPLASMIC RETICULUM ORGANIZATION	32	0.58	1.90	0.0017	0.0075
GLYCOSYL COMPOUND CATABOLIC PROCESS	32	0.59	1.90	0.0000	0.0075
POSITIVE REGULATION OF MITOCHONDRION ORGANIZATION	143	0.45	1.90	0.0000	0.0075
LYMPHOCYTE CHEMOTAXIS	24	-0.67	-2.21	0.0000	0.0076
ASPARTATE FAMILY AMINO ACID BIOSYNTHETIC PROCESS	23	0.63	1.90	0.0000	0.0076
PHOSPHATASE COMPLEX	41	0.55	1.89	0.0000	0.0077
OLIGOSACCHARIDE LIPID INTERMEDIATE BIOSYNTHETIC PROCESS	18	0.67	1.89	0.0018	0.0078
METHYLATION	217	0.43	1.89	0.0000	0.0078
REGULATION OF LIPID CATABOLIC PROCESS	47	0.54	1.89	0.0000	0.0080
NCRNA CATABOLIC PROCESS	18	0.68	1.89	0.0000	0.0081
DOLICHOL LINKED OLIGOSACCHARIDE BIOSYNTHETIC PROCESS	18	0.67	1.89	0.0000	0.0081
REGULATION OF RESPONSE TO NUTRIENT LEVELS	156	0.44	1.89	0.0000	0.0082
RNA SECONDARY STRUCTURE UNWINDING	39	0.55	1.89	0.0000	0.0082
TRANSFERASE COMPLEX TRANSFERRING PHOSPHORUS CONTAINING GROUPS	209	0.43	1.89	0.0000	0.0082
PROTEIN SERINE THREONINE PHOSPHATASE ACTIVITY	57	0.53	1.89	0.0000	0.0083
FATTY ACYL COA METABOLIC PROCESS	45	0.54	1.88	0.0017	0.0083
IRON ION HOMEOSTASIS	60	0.52	1.88	0.0000	0.0089
COATED VESICLE	195	0.43	1.88	0.0000	0.0089
ENDONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	25	0.61	1.88	0.0017	0.0089
NUCLEAR ENVELOPE ORGANIZATION	69	0.50	1.88	0.0000	0.0089
MITOCHONDRIAL ELECTRON TRANSPORT NADH TO UBIQUINONE	37	0.55	1.88	0.0016	0.0089
PROTEIN N TERMINUS BINDING	90	0.48	1.88	0.0000	0.0089

OXIDOREDUCTION COENZYME METABOLIC PROCESS	94	0.47	1.88	0.0000	0.0089
REGULATION OF RESPONSE TO EXTRACELLULAR STIMULUS	156	0.44	1.88	0.0000	0.0089
PEROXISOMAL TRANSPORT	16	0.68	1.87	0.0000	0.0094
BETA TUBULIN BINDING	33	0.59	1.87	0.0000	0.0095
ORGANELLA SMALL RIBOSOMAL SUBUNIT	24	0.63	1.87	0.0017	0.0096
REGULATION OF MITOCHONDRIAL ORGANIZATION	186	0.43	1.87	0.0000	0.0097
NUCLEOTIDE EXCISION REPAIR DNA DAMAGE RECOGNITION	19	0.65	1.87	0.0000	0.0098
GOLGI ASSOCIATED VESICLE	71	0.49	1.87	0.0000	0.0099
VIRAL BUDDING	21	0.64	1.86	0.0000	0.0100
SIGNAL SEQUENCE BINDING	34	0.58	1.86	0.0000	0.0104
PROTEIN LOCALIZATION TO VACUOLE	37	0.55	1.86	0.0000	0.0105
COATED VESICLE MEMBRANE	109	0.46	1.86	0.0000	0.0106
MITOCHONDRIAL TRANSMEMBRANE TRANSPORT	47	0.53	1.86	0.0000	0.0106
MITOCHONDRIAL RNA METABOLIC PROCESS	21	0.63	1.86	0.0018	0.0106
PROTEIN IMPORT	137	0.44	1.86	0.0000	0.0106
OXIDOREDUCTASE ACTIVITY ACTING ON NAD P H QUINONE OR SIMILAR COMPOUND AS ACCEPTOR	42	0.54	1.86	0.0016	0.0108
REGULATION OF LIPID STORAGE	38	0.55	1.86	0.0016	0.0108
BROWN FAT CELL DIFFERENTIATION	28	0.60	1.85	0.0052	0.0109
COENZYME BINDING	165	0.43	1.85	0.0000	0.0111
MONOSACCHARIDE TRANSMEMBRANE TRANSPORTER ACTIVITY	16	0.68	1.85	0.0000	0.0111
NF KAPPAB BINDING	26	0.61	1.85	0.0033	0.0111
EXONUCLEASE ACTIVITY	66	0.50	1.85	0.0015	0.0111
OXIDOREDUCTASE ACTIVITY ACTING ON NAD P H	78	0.48	1.85	0.0000	0.0113
NCRNA TRANSCRIPTION	79	0.47	1.85	0.0000	0.0113
REGULATION OF TOR SIGNALING	61	0.50	1.85	0.0000	0.0114
RETROGRADE VESICLE MEDIATED TRANSPORT GOLGI TO ER	68	0.50	1.85	0.0000	0.0114
REGULATION OF PLASMA LIPOPROTEIN PARTICLE LEVELS	41	0.55	1.85	0.0017	0.0116
NUCLEOID	36	0.57	1.85	0.0017	0.0116
ORGANELLE DISASSEMBLY	153	0.43	1.84	0.0000	0.0116

CELLULAR CARBOHYDRATE METABOLIC PROCESS	117	0.44	1.85	0.0000	0.0116
KETONE BIOSYNTHETIC PROCESS	21	0.63	1.85	0.0034	0.0116
MONOSACCHARIDE BIOSYNTHETIC PROCESS	46	0.53	1.84	0.0017	0.0116
NUCLEOSIDE BISPHOSPHATE METABOLIC PROCESS	32	0.57	1.85	0.0032	0.0116
CARBOHYDRATE BIOSYNTHETIC PROCESS	101	0.46	1.84	0.0015	0.0118
MULTI ORGANISM ORGANELLE ORGANIZATION	21	0.64	1.84	0.0017	0.0118
UBIQUITIN LIKE PROTEIN CONJUGATING ENZYME BINDING	33	0.57	1.84	0.0016	0.0118
ACETYLTRANSFERASE ACTIVITY	82	0.47	1.84	0.0000	0.0119
MEMBRANE BIOGENESIS	28	0.58	1.84	0.0017	0.0119
RIBOSOME BINDING	42	0.54	1.84	0.0000	0.0119
HEME BIOSYNTHETIC PROCESS	19	0.63	1.84	0.0000	0.0119
ORGANOPHOSPHATE BIOSYNTHETIC PROCESS	398	0.39	1.84	0.0000	0.0121
METAL CLUSTER BINDING	57	0.51	1.84	0.0000	0.0122
ALDITOL PHOSPHATE METABOLIC PROCESS	33	0.56	1.84	0.0016	0.0122
NIK NF KAPPAB SIGNALING	74	0.49	1.84	0.0000	0.0122
REGULATION OF TRIGLYCERIDE METABOLIC PROCESS	31	0.57	1.83	0.0017	0.0124
RIBONUCLEOSIDE BISPHOSPHATE METABOLIC PROCESS	32	0.57	1.83	0.0017	0.0124
POSITIVE REGULATION OF DENDRITE MORPHOGENESIS	32	0.57	1.83	0.0017	0.0125
PROTEIN MODIFICATION BY SMALL PROTEIN REMOVAL	101	0.45	1.83	0.0000	0.0126
PURINE NUCLEOSIDE BISPHOSPHATE METABOLIC PROCESS	32	0.57	1.83	0.0000	0.0128
TRANSLATION PREINITIATION COMPLEX	15	0.69	1.83	0.0000	0.0128
NUCLEAR SPECK	163	0.42	1.83	0.0000	0.0128
CELLULAR PROTEIN COMPLEX ASSEMBLY	283	0.40	1.83	0.0000	0.0128
DNA DIRECTED RNA POLYMERASE II HOLOENZYME	80	0.47	1.83	0.0000	0.0128
RELAXATION OF MUSCLE	20	0.64	1.83	0.0000	0.0130
RIBONUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	40	0.53	1.83	0.0034	0.0131
POSITIVE REGULATION OF LIGASE ACTIVITY	93	0.45	1.83	0.0000	0.0133

NEGATIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	120	0.44	1.83	0.0000	0.0133
NCRNA 3 END PROCESSING	16	0.67	1.82	0.0035	0.0134
POSITIVE REGULATION OF LIPID STORAGE	18	0.65	1.82	0.0017	0.0134
NUCLEAR ENVELOPE REASSEMBLY	17	0.67	1.82	0.0035	0.0134
PROTEIN TARGETING	340	0.39	1.82	0.0000	0.0134
ISOMERASE ACTIVITY	132	0.44	1.82	0.0000	0.0134
GDP BINDING	48	0.52	1.82	0.0000	0.0134
RESPONSE TO X RAY	24	0.60	1.82	0.0035	0.0134
CELLULAR LIPID CATABOLIC PROCESS	132	0.44	1.82	0.0000	0.0138
PURINE RIBONUCLEOSIDE BISPHOSPHATE METABOLIC PROCESS	15	0.67	1.82	0.0034	0.0139
VIRION ASSEMBLY	30	0.58	1.82	0.0017	0.0139
TRANSFERASE ACTIVITY TRANSFERRING ALKYL OR ARYL OTHER THAN METHYL GROUPS	55	0.50	1.82	0.0015	0.0140
NUCLEAR TRANSCRIBED mRNA POLY A TAIL SHORTENING	23	0.61	1.82	0.0000	0.0140
NUCLEOBASE CONTAINING SMALL MOLECULE METABOLIC PROCESS	457	0.38	1.82	0.0000	0.0140
BLASTOCYST DEVELOPMENT	56	0.50	1.81	0.0000	0.0143
BASAL TRANSCRIPTION MACHINERY BINDING	21	0.63	1.82	0.0017	0.0143
PEPTIDYL LYSINE MODIFICATION	262	0.40	1.82	0.0000	0.0143
FC EPSILON RECEPTOR SIGNALING PATHWAY	116	0.44	1.81	0.0000	0.0144
LIGASE ACTIVITY FORMING CARBON NITROGEN BONDS	49	0.52	1.81	0.0000	0.0144
REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	246	0.40	1.81	0.0000	0.0145
OXIDOREDUCTASE ACTIVITY ACTING ON A SULFUR GROUP OF DONORS	46	0.52	1.81	0.0000	0.0145
POSITIVE REGULATION OF DNA TEMPLATED TRANSCRIPTION ELONGATION	19	0.62	1.81	0.0069	0.0146
NUCLEOTIDE EXCISION REPAIR DNA INCISION 3 TO LESION	17	0.64	1.81	0.0153	0.0151
MULTI ORGANISM MEMBRANE ORGANIZATION	27	0.58	1.81	0.0051	0.0151
PROTON TRANSPORTING TWO SECTOR ATPASE COMPLEX	39	0.54	1.81	0.0000	0.0152

RETROGRADE TRANSPORT ENDOSOME TO GOLGI	57	0.50	1.81	0.0016	0.0154
UBIQUITIN LIKE PROTEIN SPECIFIC PROTEASE ACTIVITY	89	0.46	1.80	0.0015	0.0158
TETRACYCLIC COMPOUND METABOLISM	48	0.51	1.80	0.0000	0.0159
SNAP RECEPTOR ACTIVITY	33	0.55	1.80	0.0016	0.0161
POLYSOME	37	0.54	1.80	0.0000	0.0166
COFACTOR BINDING	242	0.40	1.80	0.0000	0.0166
LYTIC VACUOLE MEMBRANE	223	0.40	1.80	0.0000	0.0166
NUCLEAR BODY	290	0.39	1.80	0.0000	0.0166
TRANSCRIPTION COUPLED NUCLEOTIDE EXCISION REPAIR	63	0.48	1.80	0.0000	0.0166
ACETYLTRANSFERASE COMPLEX	77	0.47	1.80	0.0000	0.0166
METHYLTRANSFERASE COMPLEX	74	0.47	1.80	0.0000	0.0167
NUCLEOTIDE EXCISION REPAIR PREINCISION COMPLEX STABILIZATION	17	0.64	1.80	0.0017	0.0169
ENDOMEMBRANE SYSTEM ORGANIZATION	412	0.38	1.79	0.0000	0.0169
HEPARAN SULFATE PROTEOGLYCAN BIOSYNTHETIC PROCESS	23	0.60	1.79	0.0086	0.0170
GOLGI TO PLASMA MEMBRANE TRANSPORT	35	0.55	1.79	0.0017	0.0170
PROTEIN ACETYLATION	101	0.44	1.79	0.0000	0.0174
RNA CAPPING	33	0.55	1.79	0.0049	0.0174
NEGATIVE REGULATION OF mRNA METABOLIC PROCESS	28	0.57	1.79	0.0053	0.0174
CHEMOKINE MEDIATED SIGNALING PATHWAY	54	-0.55	-2.13	0.0000	0.0174
TRANSITION METAL ION HOMEOSTASIS	92	0.46	1.79	0.0015	0.0174
FATTY ACYL COA BINDING	28	0.57	1.79	0.0050	0.0175
PEPTIDE N ACETYLTRANSFERASE ACTIVITY	47	0.51	1.79	0.0000	0.0175
VESICLE ORGANIZATION	251	0.40	1.79	0.0000	0.0176
AUTOPHAGOSOME MEMBRANE	21	0.61	1.79	0.0035	0.0179
NEGATIVE REGULATION OF TRANSCRIPTION FACTOR IMPORT INTO NUCLEUS	34	0.54	1.79	0.0000	0.0180
VITAMIN TRANSPORTER ACTIVITY	21	0.60	1.78	0.0052	0.0183
REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	317	0.38	1.78	0.0000	0.0185
N ACYLTRANSFERASE ACTIVITY	75	0.46	1.78	0.0000	0.0185
NEGATIVE REGULATION OF TOR SIGNALING	28	0.56	1.78	0.0052	0.0185

OXIDOREDUCTASE COMPLEX	84	0.46	1.78	0.0000	0.0185
CELLULAR AMINO ACID CATABOLIC PROCESS	101	0.44	1.78	0.0000	0.0185
MACROAUTOPHAGY	215	0.40	1.78	0.0000	0.0187
PHOSPHOLIPID METABOLIC PROCESS	328	0.38	1.78	0.0000	0.0188
NUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	48	0.50	1.78	0.0015	0.0188
SMALL RIBOSOMAL SUBUNIT	54	0.49	1.78	0.0016	0.0188
PROTEIN SUMOYLATION	103	0.44	1.78	0.0000	0.0189
OXIDOREDUCTASE ACTIVITY ACTING ON CH OH GROUP OF DONORS	111	0.43	1.78	0.0000	0.0189
POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	176	0.41	1.78	0.0000	0.0189
NEUTRAL LIPID METABOLIC PROCESS	77	0.46	1.78	0.0015	0.0190
PIGMENT METABOLIC PROCESS	48	0.49	1.78	0.0033	0.0192
FATTY ACID BETA OXIDATION USING ACYL COA DEHYDROGENASE	16	0.66	1.78	0.0102	0.0193
SULFUR COMPOUND BIOSYNTHETIC PROCESS	182	0.41	1.77	0.0000	0.0193
FATTY ACID TRANSPORT	52	0.50	1.77	0.0029	0.0193
DNA TEMPLATED TRANSCRIPTION INITIATION	178	0.41	1.77	0.0000	0.0194
MEDIATOR COMPLEX	32	0.55	1.77	0.0046	0.0195
ENDOSOME TO LYSOSOME TRANSPORT	33	0.54	1.77	0.0065	0.0196
NUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	191	0.40	1.77	0.0000	0.0196
REGULATION OF FATTY ACID OXIDATION	26	0.57	1.77	0.0050	0.0197
ANTIGEN PROCESSING AND PRESENTATION OF EXOGENOUS PEPTIDE ANTIGEN VIA MHC CLASS I	56	0.48	1.77	0.0000	0.0198
REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	163	0.41	1.77	0.0000	0.0199
PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	114	0.43	1.77	0.0000	0.0199
INTRINSIC COMPONENT OF GOLGI MEMBRANE	51	0.49	1.77	0.0017	0.0199
PSEUDOURIDINE SYNTHESIS	17	0.64	1.77	0.0069	0.0201
7 METHYLGUANOSINE RNA CAPPING	33	0.55	1.77	0.0000	0.0201
UBIQUITIN LIKE PROTEIN LIGASE ACTIVITY	176	0.41	1.77	0.0000	0.0201
FLAVIN ADENINE DINUCLEOTIDE BINDING	68	0.47	1.77	0.0016	0.0203

TRANSFORMING GROWTH FACTOR BETA BINDING	15	0.66	1.76	0.0086	0.0206
NEGATIVE REGULATION OF RNA SPLICING	18	0.63	1.76	0.0035	0.0210
LIGAND DEPENDENT NUCLEAR RECEPTOR TRANSCRIPTION COACTIVATOR ACTIVITY	44	0.51	1.76	0.0016	0.0210
GLYCEROLIPID METABOLIC PROCESS	326	0.38	1.76	0.0000	0.0210
PROTEIN MONOUBIQUITINATION	44	0.50	1.76	0.0016	0.0212
NUCLEOTIDE EXCISION REPAIR	93	0.44	1.76	0.0000	0.0221
REGULATION OF RNA STABILITY	127	0.42	1.76	0.0000	0.0221
N ACETYLTRANSFERASE ACTIVITY	66	0.47	1.76	0.0015	0.0221
MONOCARBOXYLIC ACID METABOLIC PROCESS	408	0.37	1.76	0.0000	0.0222
POSITIVE REGULATION OF LEUKOCYTE CHEMOTAXIS	70	-0.50	-2.09	0.0000	0.0225
LYSOSOMAL TRANSPORT	57	0.47	1.75	0.0017	0.0226
O ACYLTTRANSFERASE ACTIVITY	44	0.51	1.75	0.0033	0.0226
CYCLIN BINDING	18	0.62	1.75	0.0017	0.0227
PROTON TRANSPORTING ATP SYNTHASE COMPLEX	16	0.64	1.75	0.0071	0.0227
ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN VIA MHC CLASS I	79	0.46	1.75	0.0015	0.0227
GLYCEROLIPID CATABOLIC PROCESS	35	0.53	1.75	0.0017	0.0227
MYD88 DEPENDENT TOLL LIKE RECEPTOR SIGNALING PATHWAY	27	0.56	1.75	0.0050	0.0227
LONG CHAIN FATTY ACID TRANSPORT	38	0.52	1.75	0.0017	0.0229
NUCLEOBASE CONTAINING SMALL MOLECULE INTERCONVERSION	20	0.61	1.75	0.0017	0.0231
NUCLEAR TRANSPORT	295	0.38	1.75	0.0000	0.0234
METHIONINE METABOLIC PROCESS	18	0.61	1.75	0.0085	0.0234
MITOCHONDRION LOCALIZATION	28	0.56	1.75	0.0068	0.0234
RESPONSE TO ENDOPLASMIC RETICULUM STRESS	208	0.39	1.75	0.0000	0.0235
2 OXOGLUTARATE METABOLIC PROCESS	20	0.60	1.75	0.0102	0.0235
SPLICEOSOMAL SNRNP ASSEMBLY	30	0.55	1.74	0.0048	0.0237
ENDOPLASMIC RETICULUM GOLGI INTERMEDIATE COMPARTMENT	87	0.45	1.75	0.0000	0.0238
PROTEASE BINDING	86	0.45	1.74	0.0015	0.0238
CYTOCHROME COMPLEX ASSEMBLY	15	0.64	1.74	0.0037	0.0238
CELLULAR TRANSITION METAL ION HOMEOSTASIS	65	0.47	1.74	0.0015	0.0239

CELLULAR CARBOHYDRATE BIOSYNTHETIC PROCESS	38	0.52	1.74	0.0016	0.0240
HYDRO LYASE ACTIVITY	33	0.53	1.74	0.0049	0.0240
DNA PACKAGING COMPLEX	56	-0.52	-2.06	0.0000	0.0240
REGULATION OF ALPHA BETA T CELL ACTIVATION	56	-0.53	-2.10	0.0000	0.0243
POSITIVE REGULATION OF TRIGLYCERIDE METABOLIC PROCESS	20	0.61	1.74	0.0068	0.0245
CELLULAR RESPONSE TO AMINO ACID STARVATION	25	0.58	1.74	0.0036	0.0245
DNA GEOMETRIC CHANGE	67	0.46	1.74	0.0015	0.0246
REGULATION OF TRANSLATIONAL INITIATION	76	0.45	1.74	0.0000	0.0246
MANGANESE ION BINDING	47	0.50	1.74	0.0048	0.0247
DEPHOSPHORYLATION	249	0.38	1.74	0.0000	0.0247
PURINE RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS	50	0.49	1.74	0.0031	0.0250
NUCLEOTIDE EXCISION REPAIR DNA DUPLEX UNWINDING	17	0.63	1.74	0.0052	0.0251
LYSOPHOSPHOLIPID ACYLTRANSFERASE ACTIVITY	18	0.62	1.74	0.0158	0.0251
NADH DEHYDROGENASE COMPLEX	38	0.52	1.74	0.0049	0.0252
NUCLEUS ORGANIZATION	115	0.43	1.74	0.0000	0.0252
NADH DEHYDROGENASE ACTIVITY	33	0.53	1.73	0.0080	0.0253
PROTEIN ACYLATION	130	0.42	1.73	0.0000	0.0253
POSITIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER INVOLVED IN CELLULAR RESPONSE TO CHEMICAL STIMULUS	25	0.57	1.73	0.0052	0.0255
RIBONUCLEOSIDE CATABOLIC PROCESS	17	0.62	1.73	0.0054	0.0256
POSITIVE REGULATION OF RESPONSE TO NUTRIENT LEVELS	44	0.50	1.73	0.0032	0.0256
POLY PURINE TRACT BINDING	18	0.61	1.73	0.0052	0.0256
CHEMOKINE RECEPTOR BINDING	38	-0.56	-2.07	0.0000	0.0257
THIOL DEPENDENT UBIQUITIN SPECIFIC PROTEASE ACTIVITY	65	0.47	1.73	0.0015	0.0257
MRNA 3 UTR BINDING	45	0.50	1.73	0.0096	0.0260
POSITIVE REGULATION OF RESPONSE TO EXTRACELLULAR STIMULUS	44	0.50	1.73	0.0064	0.0261
REGULATION OF SPROUTING ANGIOGENESIS	26	-0.61	-2.07	0.0000	0.0261

HISTONE H3 ACETYLATION	37	0.52	1.73	0.0000	0.0261
ORGANIC CYCLIC COMPOUND CATABOLIC PROCESS	361	0.37	1.73	0.0000	0.0266
PHOSPHOLIPID CATABOLIC PROCESS	29	0.55	1.73	0.0113	0.0271
CIS TRANS ISOMERASE ACTIVITY	33	0.53	1.73	0.0032	0.0271
POSITIVE REGULATION OF VIRAL PROCESS	80	0.44	1.72	0.0015	0.0272
REGULATION OF THE FORCE OF HEART CONTRACTION	28	0.55	1.72	0.0070	0.0279
N TERMINAL PROTEIN AMINO ACID MODIFICATION	21	0.58	1.72	0.0117	0.0281
SCF DEPENDENT PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	20	0.60	1.72	0.0052	0.0284
QUINONE BINDING	16	0.63	1.72	0.0073	0.0287
GOLGI TO VACUOLE TRANSPORT	24	0.56	1.72	0.0053	0.0289
STEROL TRANSPORT	47	0.49	1.72	0.0015	0.0289
GOLGI STACK	104	0.42	1.72	0.0029	0.0292
REVERSE CHOLESTEROL TRANSPORT	16	0.61	1.72	0.0087	0.0292
REPRESSING TRANSCRIPTION FACTOR BINDING	50	0.48	1.72	0.0032	0.0294
REGULATION OF LYMPHOCYTE MIGRATION	32	-0.57	-2.02	0.0000	0.0294
TERMINATION OF RNA POLYMERASE II TRANSCRIPTION	46	0.49	1.71	0.0031	0.0295
4 IRON 4 SULFUR CLUSTER BINDING	38	0.51	1.71	0.0097	0.0295
PURINE NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS	50	0.49	1.71	0.0064	0.0295
PHOSPHOLIPID BIOSYNTHETIC PROCESS	215	0.39	1.71	0.0000	0.0295
POSITIVE REGULATION OF DENDRITE DEVELOPMENT	63	0.46	1.71	0.0015	0.0296
PROTEIN PEPTIDYL PROLYL ISOMERIZATION	32	0.53	1.71	0.0085	0.0298
NEGATIVE REGULATION OF NF KAPPAB IMPORT INTO NUCLEUS	16	0.61	1.71	0.0089	0.0299
POSITIVE REGULATION OF DNA TEMPLATED TRANSCRIPTION INITIATION	23	0.57	1.71	0.0051	0.0299
ACYL COA DEHYDROGENASE ACTIVITY	15	0.64	1.71	0.0091	0.0299
POSITIVE REGULATION OF CHEMOTAXIS	106	-0.46	-2.03	0.0000	0.0300
POSITIVE REGULATION OF LEUKOCYTE MIGRATION	96	-0.46	-2.03	0.0000	0.0303

POSITIVE REGULATION OF NEUTROPHIL MIGRATION	24	-0.62	-2.01	0.0000	0.0308
NEUTRAL LIPID BIOSYNTHETIC PROCESS	24	0.57	1.71	0.0117	0.0310
POSITIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	171	0.40	1.71	0.0000	0.0314
RNA POLYMERASE ACTIVITY	38	0.51	1.71	0.0078	0.0314
ATP BIOSYNTHETIC PROCESS	27	0.54	1.70	0.0052	0.0316
TBP CLASS PROTEIN BINDING	18	0.60	1.70	0.0141	0.0316
ACYLGLYCEROL BIOSYNTHETIC PROCESS	24	0.57	1.70	0.0118	0.0320
PROTEIN K48 LINKED UBIQUITINATION	40	0.50	1.70	0.0078	0.0321
REGULATION OF CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	33	-0.58	-2.03	0.0000	0.0321
EXON EXON JUNCTION COMPLEX	21	0.59	1.70	0.0071	0.0324
IRON ION TRANSPORT	48	0.49	1.70	0.0016	0.0324
PHOSPHATIDYLSERINE METABOLIC PROCESS	27	0.53	1.70	0.0068	0.0327
WATER SOLUBLE VITAMIN METABOLIC PROCESS	73	0.44	1.70	0.0015	0.0336
N METHYLTRANSFERASE ACTIVITY	68	0.45	1.70	0.0030	0.0336
LIPOPROTEIN METABOLIC PROCESS	106	0.42	1.69	0.0015	0.0340
GLYCEROPOHOSPHOLIPID METABOLIC PROCESS	272	0.37	1.69	0.0000	0.0341
ORGANELLE ENVELOPE LUMEN	71	0.45	1.70	0.0000	0.0341
REGULATION OF FATTY ACID BETA OXIDATION	15	0.62	1.69	0.0163	0.0342
REGULATION OF DNA TEMPLATED TRANSCRIPTION INITIATION	27	0.54	1.69	0.0066	0.0343
LIPID MODIFICATION	186	0.39	1.69	0.0000	0.0344
NUCLEASE ACTIVITY	163	0.40	1.69	0.0000	0.0344
MICROTUBULE ORGANIZING CENTER ORGANIZATION	76	0.44	1.69	0.0000	0.0347
RRNA TRANSCRIPTION	15	0.64	1.69	0.0124	0.0347
REGULATION OF SYNCYTIA FORMATION BY PLASMA MEMBRANE FUSION	22	-0.63	-1.97	0.0000	0.0347
SNRNA PROCESSING	19	0.59	1.69	0.0156	0.0348
FOLIC ACID CONTAINING COMPOUND METABOLIC PROCESS	24	0.55	1.69	0.0048	0.0348
LATE ENDOSOME	169	0.39	1.69	0.0000	0.0352
MACROMOLECULE METHYLATION	167	0.39	1.69	0.0000	0.0354

REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	245	0.38	1.69	0.0000	0.0356
NUCLEOSIDE MONOPHOSPHATE METABOLIC PROCESS	206	0.38	1.69	0.0000	0.0356
REGULATION OF GRANULOCYTE CHEMOTAXIS	34	-0.55	-1.96	0.0000	0.0356
NUCLEOSIDE PHOSPHATE BIOSYNTHETIC PROCESS	159	0.39	1.69	0.0000	0.0357
GOLGI ASSOCIATED VESICLE MEMBRANE	42	0.49	1.69	0.0132	0.0357
REGULATION OF TYPE 2 IMMUNE RESPONSE	24	-0.61	-1.99	0.0000	0.0357
ATPASE ACTIVITY COUPLED	282	0.37	1.69	0.0000	0.0360
UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS VIA THE MULTIVESICULAR BODY SORTING PATHWAY	16	0.62	1.69	0.0123	0.0360
NUCLEOTIDYLTRANSFERASE ACTIVITY	110	0.41	1.69	0.0015	0.0360
LONG CHAIN FATTY ACID METABOLIC PROCESS	64	0.46	1.68	0.0000	0.0361
MITOTIC NUCLEAR DIVISION	310	0.36	1.68	0.0000	0.0363
ER TO GOLGI TRANSPORT VESICLE MEMBRANE	33	0.50	1.68	0.0144	0.0363
REGULATION OF MYOBLAST FUSION	17	-0.67	-1.99	0.0000	0.0363
ORGANIC ANION TRANSPORT	332	0.36	1.68	0.0000	0.0364
VOLTAGE GATED CATION CHANNEL ACTIVITY	130	-0.41	-1.97	0.0000	0.0364
RNA POLYADENYLATION	28	0.55	1.68	0.0102	0.0368
PROTEASOME CORE COMPLEX	19	0.58	1.68	0.0067	0.0369
PEPTIDE RECEPTOR ACTIVITY	123	-0.42	-1.97	0.0000	0.0372
GLYCEROLIPID BIOSYNTHETIC PROCESS	190	0.38	1.68	0.0000	0.0377
ACID THIOL LIGASE ACTIVITY	16	0.62	1.68	0.0223	0.0380
RESPONSE TO STARVATION	136	0.40	1.68	0.0000	0.0380
FOLIC ACID METABOLIC PROCESS	15	0.63	1.68	0.0162	0.0380
METAPHASE PLATE CONGRESSION	33	0.52	1.68	0.0135	0.0380
ORGANIC ACID TRANSPORT	235	0.37	1.67	0.0000	0.0387
CELLULAR RESPONSE TO VASCULAR ENDOTHELIAL GROWTH FACTOR STIMULUS	29	-0.58	-1.97	0.0000	0.0391
POSITIVE REGULATION OF CATABOLIC PROCESS	351	0.36	1.67	0.0000	0.0393
ENDOSOME ORGANIZATION	52	0.47	1.67	0.0077	0.0398
SULFUR AMINO ACID BIOSYNTHETIC PROCESS	19	0.58	1.67	0.0136	0.0398

NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS	70	0.44	1.67	0.0015	0.0400
MRNA BINDING	135	0.40	1.67	0.0014	0.0402
REGULATION OF RYANODINE SENSITIVE CALCIUM RELEASE CHANNEL ACTIVITY	25	0.55	1.67	0.0174	0.0406
ALDITOL METABOLIC PROCESS	16	0.61	1.67	0.0088	0.0406
REGULATION OF CELL CYCLE PHASE TRANSITION	281	0.37	1.67	0.0000	0.0417
CELL CHEMOTAXIS	135	-0.42	-1.95	0.0000	0.0417
BLASTOCYST FORMATION	27	0.53	1.66	0.0101	0.0421
NUCLEAR LOCALIZATION SEQUENCE BINDING	19	0.59	1.66	0.0124	0.0422
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH OH GROUP OF DONORS NAD OR NADP AS ACCEPTOR	92	0.42	1.66	0.0030	0.0431
NITROGEN COMPOUND TRANSPORT	435	0.35	1.66	0.0000	0.0437
PHOSPHATASE ACTIVITY	241	0.37	1.66	0.0000	0.0440
GLOBAL GENOME NUCLEOTIDE EXCISION REPAIR	26	0.54	1.66	0.0179	0.0441
2 IRON 2 SULFUR CLUSTER BINDING	18	0.59	1.66	0.0153	0.0444
NEGATIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	37	0.49	1.66	0.0082	0.0444
HYDROGEN EXPORTING ATPASE ACTIVITY	24	0.55	1.66	0.0212	0.0447
VITAMIN D RECEPTOR BINDING	17	0.59	1.65	0.0189	0.0452
CYSTEINE TYPE PEPTIDASE ACTIVITY	144	0.39	1.65	0.0014	0.0453
ACYLGLYCEROL O ACYLTRANSFERASE ACTIVITY	26	0.54	1.65	0.0067	0.0459
POSITIVE REGULATION OF LIPID CATABOLIC PROCESS	25	0.53	1.65	0.0177	0.0459
ALPHA AMINO ACID METABOLIC PROCESS	206	0.37	1.65	0.0013	0.0460
TRANSCRIPTION ELONGATION FACTOR COMPLEX	40	0.49	1.65	0.0109	0.0461
TRICARBOXYLIC ACID METABOLIC PROCESS	34	0.51	1.65	0.0087	0.0461
NUCLEOTIDE SUGAR METABOLIC PROCESS	31	0.51	1.65	0.0099	0.0462
PTERIDINE CONTAINING COMPOUND METABOLIC PROCESS	31	0.52	1.65	0.0105	0.0462
ERAD PATHWAY	67	0.44	1.65	0.0031	0.0466
LIGASE ACTIVITY FORMING CARBON SULFUR BONDS	33	0.51	1.65	0.0101	0.0471
RESPONSE TO UV	100	0.41	1.65	0.0014	0.0472

RESPONSE TO MONOAMINE	32	0.51	1.65	0.0136	0.0472
REGULATION OF PROTEIN TARGETING TO MITOCHONDRION	86	0.42	1.65	0.0015	0.0472
MITOCHONDRIAL MEMBRANE ORGANIZATION	73	0.43	1.65	0.0076	0.0473
NAD BINDING	52	0.47	1.64	0.0015	0.0479
ESTABLISHMENT OF PROTEIN LOCALIZATION TO MEMBRANE	227	0.37	1.64	0.0000	0.0484
GOLGI TO PLASMA MEMBRANE PROTEIN TRANSPORT	24	0.54	1.64	0.0126	0.0485
MEMBRANE FUSION	139	0.39	1.64	0.0014	0.0495
ESTABLISHMENT OF PROTEIN LOCALIZATION TO VACUOLE	24	0.54	1.64	0.0203	0.0498
REGULATION OF SPINDLE ORGANIZATION	17	0.59	1.64	0.0199	0.0499
MEMBRANE LIPID METABOLIC PROCESS	154	0.39	1.64	0.0000	0.0505
POSITIVE REGULATION OF PROTEIN CATABOLIC PROCESS	232	0.36	1.64	0.0000	0.0506
TRNA SPECIFIC RIBONUCLEASE ACTIVITY	15	0.61	1.64	0.0190	0.0509
ACTIVATION OF MAPKK ACTIVITY	45	0.47	1.64	0.0063	0.0512
COFACTOR TRANSPORT	22	0.56	1.63	0.0269	0.0512
TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	141	0.39	1.63	0.0028	0.0513
CYTOSOLIC PART	175	0.38	1.63	0.0000	0.0515
REGULATION OF LYMPHOCYTE CHEMOTAXIS	17	-0.66	-1.92	0.0000	0.0521
INNATE IMMUNE RESPONSE ACTIVATING CELL SURFACE RECEPTOR SIGNALING PATHWAY	91	0.42	1.63	0.0117	0.0527
REGULATION OF PROTEIN STABILITY	196	0.37	1.63	0.0000	0.0530
REGULATION OF NFAT PROTEIN IMPORT INTO NUCLEUS	15	0.60	1.63	0.0295	0.0530
REGULATION OF PROTEIN HOMODIMERIZATION ACTIVITY	20	0.57	1.63	0.0199	0.0531
ALPHA AMINO ACID CATABOLIC PROCESS	85	0.42	1.63	0.0092	0.0533
U4 U6 X U5 TRI SNRNP COMPLEX	18	0.58	1.63	0.0162	0.0533
ORGANELLE ASSEMBLY	407	0.35	1.63	0.0000	0.0534
POSITIVE REGULATION OF VIRAL TRANSCRIPTION	35	0.50	1.63	0.0119	0.0534
PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE ACTIVITY	24	0.54	1.63	0.0171	0.0534
STEROL TRANSPORTER ACTIVITY	16	0.59	1.63	0.0252	0.0535

MLL1 2 COMPLEX	21	0.55	1.63	0.0208	0.0539
PROTON TRANSPORTING V TYPE ATPASE COMPLEX	21	0.56	1.63	0.0202	0.0540
POSITIVE REGULATION OF LYMPHOCYTE MIGRATION	22	-0.60	-1.91	0.0022	0.0541
NUCLEOTIDE SUGAR BIOSYNTHETIC PROCESS	18	0.58	1.63	0.0243	0.0543
MONOSACCHARIDE METABOLIC PROCESS	157	0.39	1.62	0.0000	0.0545
MACROMOLECULE TRANSMEMBRANE TRANSPORTER ACTIVITY	21	0.56	1.62	0.0102	0.0553
NEGATIVE REGULATION OF TRANSFERASE ACTIVITY	309	0.36	1.62	0.0000	0.0559
CELLULAR RESPONSE TO STARVATION	101	0.40	1.62	0.0030	0.0562
FERRIC IRON TRANSPORT	33	0.49	1.62	0.0189	0.0562
REGULATION OF LEUKOCYTE CHEMOTAXIS	82	-0.45	-1.91	0.0000	0.0562
PIGMENT BIOSYNTHETIC PROCESS	41	0.48	1.62	0.0095	0.0563
REGULATION OF MITOTIC CELL CYCLE	408	0.34	1.62	0.0000	0.0564
RNA POLYMERASE BINDING	28	0.51	1.62	0.0152	0.0566
REGULATION OF ESTABLISHMENT OF PLANAR POLARITY	106	0.40	1.62	0.0043	0.0567
LIPID DIGESTION	20	0.57	1.62	0.0190	0.0567
CARBOHYDRATE TRANSMEMBRANE TRANSPORT	18	0.57	1.62	0.0169	0.0575
PEPTIDYL THREONINE MODIFICATION	43	0.47	1.62	0.0159	0.0576
DNA REPAIR	379	0.35	1.62	0.0000	0.0576
PROTON TRANSPORTING TWO SECTOR ATPASE COMPLEX PROTON TRANSPORTING DOMAIN	15	0.61	1.62	0.0322	0.0576
ATPASE ACTIVITY	368	0.34	1.61	0.0000	0.0577
PRE AUTOPHAGOSOMAL STRUCTURE	21	0.55	1.62	0.0269	0.0577
EMBRYONIC FORELIMB MORPHOGENESIS	29	-0.57	-1.91	0.0000	0.0577
VACUOLE FUSION	17	0.58	1.61	0.0201	0.0577
COFACTOR TRANSPORTER ACTIVITY	18	0.57	1.61	0.0204	0.0577
REGULATION OF RELEASE OF SEQUESTERED CALCIUM ION INTO CYTOSOL BY SARCOPLASMIC RETICULUM	23	0.54	1.61	0.0256	0.0579
NEGATIVE REGULATION OF AUTOPHAGY	45	0.46	1.61	0.0170	0.0579
CARBOHYDRATE CATABOLIC PROCESS	94	0.41	1.61	0.0058	0.0580

PHOSPHORIC ESTER HYDROLASE ACTIVITY	330	0.35	1.61	0.0000	0.0582
NUCLEOCYTOPLASMIC TRANSPORTER ACTIVITY	22	0.56	1.61	0.0256	0.0583
PROTEIN LIPID COMPLEX SUBUNIT ORGANIZATION	31	0.51	1.61	0.0165	0.0583
REGULATION OF CELL CYCLE PROCESS	480	0.34	1.61	0.0000	0.0583
PYRIMIDINE RIBONUCLEOSIDE METABOLIC PROCESS	25	0.53	1.61	0.0247	0.0592
TRANSLATION INITIATION FACTOR BINDING	24	0.54	1.61	0.0178	0.0595
SMALL MOLECULE BIOSYNTHETIC PROCESS	389	0.34	1.61	0.0000	0.0600
LEUKOCYTE APOPTOTIC PROCESS	18	0.58	1.61	0.0211	0.0614
MISFOLDED OR INCOMPLETELY SYNTHESIZED PROTEIN CATABOLIC PROCESS	15	0.60	1.60	0.0259	0.0618
PROTEIN REFOLDING	16	-0.65	-1.89	0.0000	0.0618
RETROGRADE TRANSPORT VESICLE RECYCLING WITHIN GOLGI	15	0.60	1.60	0.0294	0.0620
PROTEIN AUTOUBIQUITINATION	40	0.47	1.60	0.0033	0.0621
POSITIVE REGULATION OF GENE EXPRESSION EPIGENETIC	56	0.44	1.60	0.0048	0.0625
PYRIMIDINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	34	0.49	1.60	0.0223	0.0628
VIRAL LIFE CYCLE	242	0.36	1.60	0.0000	0.0630
TRIVALENT INORGANIC CATION TRANSPORT	33	0.49	1.60	0.0172	0.0632
INTERFERON GAMMA MEDIATED SIGNALING PATHWAY	43	-0.49	-1.89	0.0000	0.0635
ORGANONITROGEN COMPOUND CATABOLIC PROCESS	298	0.35	1.60	0.0000	0.0639
PHOSPHATASE REGULATOR ACTIVITY	73	0.43	1.60	0.0078	0.0639
PROTEIN KINASE COMPLEX	80	0.41	1.60	0.0090	0.0645
CUL3 RING UBIQUITIN LIGASE COMPLEX	57	0.43	1.60	0.0099	0.0645
PROTEIN DEPHOSPHORYLATION	175	0.37	1.60	0.0014	0.0650
TRANSFERASE ACTIVITY TRANSFERRING HEXOSYL GROUPS	153	0.37	1.60	0.0014	0.0651
NUCLEAR REPLICATION FORK	34	0.48	1.59	0.0216	0.0656
REGULATION OF MACROPHAGE DERIVED FOAM CELL DIFFERENTIATION	25	0.52	1.59	0.0348	0.0656
ORGANIC ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	155	0.37	1.59	0.0014	0.0662

ORGANIC ACID TRANSMEMBRANE TRANSPORT	95	0.40	1.59	0.0015	0.0663
RNA POLYMERASE II CARBOXY TERMINAL DOMAIN KINASE ACTIVITY	15	0.60	1.59	0.0249	0.0664
TRANSCRIPTION COACTIVATOR ACTIVITY	266	0.35	1.59	0.0000	0.0665
REGULATION OF DNA TEMPLATED TRANSCRIPTION ELONGATION	36	0.47	1.59	0.0149	0.0666
ENERGY COUPLED PROTON TRANSPORT DOWN ELECTROCHEMICAL GRADIENT	17	0.57	1.59	0.0215	0.0671
REGULATION OF SENSORY PERCEPTION OF PAIN	34	0.49	1.59	0.0173	0.0673
REGULATION OF PROTEIN PHOSPHATASE TYPE 2A ACTIVITY	22	0.54	1.59	0.0254	0.0675
CLATHRIN COATED VESICLE	133	0.38	1.59	0.0014	0.0679
PROTEIN LIPID COMPLEX REMODELING	21	0.54	1.59	0.0231	0.0679
REGULATION OF SENSORY PERCEPTION	34	0.49	1.59	0.0148	0.0679
VASODILATION	24	0.52	1.59	0.0215	0.0680
POSITIVE REGULATION OF MULTI ORGANISM PROCESS	138	0.38	1.59	0.0000	0.0688
REGULATION OF STEROL TRANSPORT	35	0.47	1.58	0.0165	0.0698
PLASMA LIPOPROTEIN PARTICLE CLEARANCE	21	0.54	1.58	0.0426	0.0699
NEGATIVE REGULATION OF CELLULAR CATABOLIC PROCESS	137	0.37	1.58	0.0055	0.0700
CELLULAR MODIFIED AMINO ACID METABOLIC PROCESS	189	0.36	1.58	0.0013	0.0701
PLASMA LIPOPROTEIN PARTICLE REMODELING	21	0.54	1.58	0.0365	0.0705
PURINE CONTAINING COMPOUND METABOLIC PROCESS	347	0.34	1.58	0.0000	0.0707
ATP SYNTHESIS COUPLED PROTON TRANSPORT	17	0.57	1.58	0.0270	0.0707
ORGANELLE FISSION	414	0.34	1.58	0.0000	0.0708
MODULATION BY HOST OF VIRAL PROCESS	15	0.57	1.58	0.0457	0.0708
RNA STABILIZATION	30	0.49	1.58	0.0322	0.0708
MACROMOLECULAR COMPLEX REMODELING	21	0.54	1.58	0.0243	0.0709
LIPID BIOSYNTHETIC PROCESS	466	0.33	1.58	0.0000	0.0717
LYMPHOCYTE APOPTOTIC PROCESS	15	0.60	1.58	0.0297	0.0717
G PROTEIN COUPLED PURINERGIC RECEPTOR SIGNALING PATHWAY	18	0.56	1.58	0.0314	0.0718

VITAMIN TRANSPORT	29	0.49	1.58	0.0229	0.0718
NEGATIVE REGULATION OF BLOOD PRESSURE	42	0.46	1.58	0.0159	0.0718
NEGATIVE REGULATION OF BLOOD CIRCULATION	33	0.49	1.58	0.0251	0.0718
NEGATIVE REGULATION OF MITOCHONDRION ORGANIZATION	34	0.49	1.58	0.0085	0.0718
CARBOHYDRATE TRANSPORTER ACTIVITY	36	0.48	1.58	0.0178	0.0718
UBIQUITIN LIKE PROTEIN CONJUGATING ENZYME ACTIVITY	25	0.52	1.58	0.0321	0.0719
POSITIVE REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	94	0.39	1.58	0.0107	0.0724
DICARBOXYLIC ACID METABOLIC PROCESS	92	0.39	1.58	0.0060	0.0725
EARLY ENDOSOME	255	0.35	1.57	0.0000	0.0733
NUCLEOTIDE BINDING DOMAIN LEUCINE RICH REPEAT CONTAINING RECEPTOR SIGNALING PATHWAY	25	0.52	1.57	0.0202	0.0734
NEGATIVE REGULATION OF PEPTIDYL SERINE PHOSPHORYLATION	22	0.53	1.57	0.0251	0.0735
MODIFIED AMINO ACID TRANSPORT	23	0.52	1.57	0.0271	0.0736
HISTONE mRNA METABOLIC PROCESS	26	0.52	1.57	0.0261	0.0738
ORGANELLE FUSION	112	0.39	1.57	0.0029	0.0739
ATPASE BINDING	66	0.42	1.57	0.0121	0.0742
PHAGOSOME ACIDIFICATION	24	0.52	1.57	0.0220	0.0745
RNA POLYMERASE CORE ENZYME BINDING	18	0.56	1.57	0.0327	0.0745
MAINTENANCE OF LOCATION	122	0.38	1.57	0.0014	0.0750
REGULATION OF NEUTROPHIL CHEMOTAXIS	24	-0.58	-1.87	0.0022	0.0754
THREONINE TYPE PEPTIDASE ACTIVITY	20	0.53	1.57	0.0377	0.0756
MITOCHONDRIAL GENOME MAINTENANCE	18	0.55	1.57	0.0365	0.0766
REGULATION OF CELLULAR AMINO ACID METABOLIC PROCESS	60	0.42	1.57	0.0180	0.0767
DEFENSE RESPONSE TO VIRUS	120	-0.41	-1.86	0.0000	0.0770
PIGMENT GRANULE LOCALIZATION	22	0.52	1.56	0.0347	0.0776
ORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	15	0.58	1.56	0.0363	0.0776
ENERGY RESERVE METABOLIC PROCESS	60	0.42	1.56	0.0127	0.0776
RESPONSE TO INCREASED OXYGEN LEVELS	22	0.53	1.56	0.0369	0.0776

THYMUS DEVELOPMENT	43	0.45	1.56	0.0142	0.0777
CCR CHEMOKINE RECEPTOR BINDING	22	-0.58	-1.86	0.0000	0.0778
REGULATION OF TELOMERE MAINTENANCE	57	0.42	1.56	0.0202	0.0778
T CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	48	-0.48	-1.86	0.0054	0.0779
REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	39	0.46	1.56	0.0241	0.0780
TRANSCRIPTION FACTOR TFIID COMPLEX	18	0.55	1.56	0.0315	0.0781
HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS IN LINEAR AMIDES	74	0.41	1.56	0.0102	0.0781
1 PHOSPHATIDYLINOSITOL BINDING	17	0.56	1.56	0.0370	0.0781
REGULATION OF PROTEIN CATABOLIC PROCESS	349	0.33	1.56	0.0000	0.0788
PROTEIN PHOSPHATASE 2A BINDING	26	0.51	1.56	0.0315	0.0789
ELECTRON CARRIER ACTIVITY	98	0.40	1.56	0.0085	0.0789
AMMONIUM ION METABOLIC PROCESS	151	0.37	1.56	0.0027	0.0792
PROTEIN LOCALIZATION TO CELL SURFACE	21	0.53	1.56	0.0382	0.0792
ANION TRANSPORT	441	0.33	1.56	0.0000	0.0792
THYROID HORMONE RECEPTOR BINDING	26	0.50	1.56	0.0235	0.0793
REGULATION OF CHROMOSOME SEGREGATION	74	0.40	1.56	0.0091	0.0793
EARLY ENDOSOME MEMBRANE	89	0.40	1.56	0.0118	0.0794
SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX	51	0.43	1.56	0.0228	0.0794
POSITIVE REGULATION OF PROTEOLYSIS	323	0.34	1.56	0.0000	0.0794
INTERACTION WITH SYMBIONT	43	0.45	1.56	0.0144	0.0803
LIPASE ACTIVITY	107	0.39	1.56	0.0044	0.0804
RESPONSE TO HYPEROXIA	22	0.53	1.56	0.0374	0.0804
PYRIMIDINE RIBONUCLEOTIDE METABOLIC PROCESS	22	0.53	1.56	0.0253	0.0805
REGULATION OF CHOLESTEROL TRANSPORT	35	0.47	1.55	0.0242	0.0806
VOLTAGE GATED POTASSIUM CHANNEL ACTIVITY	88	-0.42	-1.84	0.0000	0.0808
REGULATION OF CELLULAR KETONE METABOLIC PROCESS	149	0.36	1.55	0.0041	0.0809
MEMBRANE PROTEIN PROTEOLYSIS	29	0.49	1.55	0.0233	0.0810
PROTEASOME COMPLEX	69	0.41	1.55	0.0138	0.0810
TELOMERIC DNA BINDING	25	0.51	1.55	0.0309	0.0810

ADAPTIVE IMMUNE RESPONSE	185	-0.37	-1.85	0.0000	0.0810
FC RECEPTOR SIGNALING PATHWAY	169	0.36	1.55	0.0027	0.0811
REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	133	0.37	1.55	0.0056	0.0816
APOPTOTIC MITOCHONDRIAL CHANGES	45	0.45	1.55	0.0174	0.0818
REGULATION OF NEUTROPHIL MIGRATION	29	-0.55	-1.85	0.0000	0.0825
NEGATIVE REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	16	0.57	1.55	0.0357	0.0831
COLLAGEN TRIMER	75	-0.43	-1.83	0.0000	0.0833
CELLULAR RESPONSE TO INTERFERON GAMMA	81	-0.43	-1.83	0.0000	0.0834
LIPID STORAGE	25	0.51	1.55	0.0399	0.0836
POSITIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	102	0.38	1.55	0.0099	0.0838
RESPONSE TO INTERFERON GAMMA	101	-0.41	-1.83	0.0000	0.0847
MAST CELL ACTIVATION	19	-0.61	-1.84	0.0023	0.0848
PROTEIN DESTABILIZATION	30	0.49	1.55	0.0267	0.0849
GLUCAN METABOLIC PROCESS	46	0.44	1.55	0.0155	0.0849
CHROMATIN MODIFICATION	454	0.32	1.55	0.0000	0.0849
SPLICEOSOMAL TRI SNRNP COMPLEX	23	0.52	1.55	0.0275	0.0850
INTRAMOLECULAR TRANSFERASE ACTIVITY	22	0.53	1.55	0.0537	0.0850
POSITIVE REGULATION OF DENDRITIC SPINE DEVELOPMENT	34	0.48	1.54	0.0252	0.0852
PROTEIN LOCALIZATION TO ENDOPLASMIC RETICULUM	103	0.39	1.54	0.0117	0.0853
REGULATION OF ENDOTHELIAL CELL CHEMOTAXIS	16	-0.64	-1.83	0.0023	0.0855
NEGATIVE REGULATION OF CARBOHYDRATE METABOLIC PROCESS	39	0.45	1.54	0.0157	0.0863
NEGATIVE REGULATION OF TRANSLATIONAL INITIATION	20	0.53	1.54	0.0409	0.0867
PROTON TRANSPORTING TWO SECTOR ATPASE COMPLEX CATALYTIC DOMAIN	16	0.56	1.54	0.0388	0.0867
NUCLEAR ENVELOPE	356	0.33	1.54	0.0000	0.0867
NUCLEOSOME BINDING	39	0.45	1.54	0.0291	0.0868
CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	71	0.41	1.54	0.0111	0.0868
ORGANIC ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	127	0.37	1.54	0.0043	0.0868

PHOSPHATIDYLINOSITOL 3 PHOSPHATE BINDING	29	0.49	1.54	0.0334	0.0869
LIVER REGENERATION	17	0.55	1.54	0.0444	0.0875
PROTEIN PHOSPHATASE TYPE 2A REGULATOR ACTIVITY	19	0.55	1.54	0.0501	0.0875
SCF UBIQUITIN LIGASE COMPLEX	31	0.48	1.54	0.0464	0.0876
REGULATION OF EXOSOMAL SECRETION	15	0.57	1.54	0.0426	0.0877
POSITIVE REGULATION OF G1 S TRANSITION OF MITOTIC CELL CYCLE	22	0.52	1.54	0.0497	0.0881
REGULATION OF PROTEIN LOCALIZATION TO CELL SURFACE	24	0.51	1.54	0.0268	0.0882
FORELIMB MORPHOGENESIS	35	-0.52	-1.82	0.0000	0.0883
POSITIVE REGULATION OF ALPHA BETA T CELL ACTIVATION	42	-0.49	-1.82	0.0025	0.0883
RNA POLYMERASE II CORE BINDING	15	0.58	1.54	0.0266	0.0885
GLUTAMINE METABOLIC PROCESS	23	0.52	1.54	0.0364	0.0887
ATP DEPENDENT DNA HELICASE ACTIVITY	29	0.48	1.54	0.0372	0.0890
DNA HELICASE ACTIVITY	45	0.44	1.54	0.0263	0.0892
COVALENT CHROMATIN MODIFICATION	294	0.33	1.53	0.0012	0.0895
PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROCESS	110	0.37	1.53	0.0058	0.0899
CELLULAR RESPONSE TO TOPOLOGICALLY INCORRECT PROTEIN	108	0.38	1.53	0.0132	0.0900
PHOSPHATIDYLGLYCEROL METABOLIC PROCESS	29	0.48	1.53	0.0200	0.0900
LIPID LOCALIZATION	232	0.34	1.53	0.0000	0.0904
DICARBOXYLIC ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	31	0.47	1.53	0.0372	0.0908
NEGATIVE REGULATION OF SMOOTH MUSCLE CONTRACTION	15	0.57	1.53	0.0435	0.0911
CELLULAR GLUCAN METABOLIC PROCESS	46	0.44	1.53	0.0145	0.0911
PYRIMIDINE NUCLEOTIDE BIOSYNTHETIC PROCESS	26	0.49	1.53	0.0347	0.0915
T CELL RECEPTOR SIGNALING PATHWAY	124	0.37	1.53	0.0072	0.0915
POSITIVE REGULATION OF CELL GROWTH	134	0.37	1.53	0.0043	0.0916
PRECATALYTIC SPLICEOSOME	19	0.54	1.53	0.0489	0.0920
UBIQUITIN LIKE PROTEIN BINDING	106	0.38	1.53	0.0088	0.0924
ORGANELLE TRANSPORT ALONG MICROTUBULE	49	0.43	1.53	0.0194	0.0924
DRUG BINDING	97	0.38	1.53	0.0130	0.0929

NUCLEAR UBIQUITIN LIGASE COMPLEX	38	0.45	1.53	0.0256	0.0934
REGULATION OF DNA METABOLIC PROCESS	292	0.33	1.53	0.0000	0.0936
GLUCOSE METABOLIC PROCESS	101	0.38	1.53	0.0121	0.0937
CALCIUM DEPENDENT CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	18	0.54	1.52	0.0381	0.0939
PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	164	0.35	1.52	0.0123	0.0944
PH REDUCTION	33	0.47	1.52	0.0361	0.0953
TRANS GOLGI NETWORK TRANSPORT VESICLE	25	0.49	1.52	0.0527	0.0964
NEUROTRANSMITTER UPTAKE	15	0.56	1.52	0.0525	0.0971
PHOSPHOTRANSFERASE ACTIVITY FOR OTHER SUBSTITUTED PHOSPHATE GROUPS	17	0.54	1.52	0.0421	0.0987
NEGATIVE REGULATION OF LEUKOCYTE APOPTOTIC PROCESS	35	-0.51	-1.80	0.0000	0.0990
DISULFIDE OXIDOREDUCTASE ACTIVITY	29	0.48	1.51	0.0368	0.1007
ACYLGLYCEROL CATABOLIC PROCESS	25	0.49	1.51	0.0390	0.1009
TRANSCRIPTIONAL REPRESSOR COMPLEX	67	0.40	1.51	0.0195	0.1010
POSITIVE REGULATION OF CARDIAC MUSCLE CELL PROLIFERATION	17	0.55	1.51	0.0511	0.1017
REGULATION OF AUTOPHAGY	219	0.34	1.51	0.0013	0.1019
POSITIVE REGULATION OF CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	24	-0.55	-1.80	0.0047	0.1024
RETINOIC ACID METABOLIC PROCESS	16	-0.62	-1.79	0.0046	0.1025
PROTEIN TARGETING TO MEMBRANE	133	0.36	1.51	0.0100	0.1029
REGULATION OF DNA REPLICATION	143	0.36	1.51	0.0055	0.1034
G2 DNA DAMAGE CHECKPOINT	30	0.46	1.51	0.0390	0.1039
CARBON OXYGEN LYASE ACTIVITY	52	0.42	1.51	0.0243	0.1042
REGULATION OF CHEMOTAXIS	162	-0.38	-1.79	0.0000	0.1046
REGULATION OF POSITIVE CHEMOTAXIS	21	-0.57	-1.79	0.0023	0.1051
FERROUS IRON BINDING	19	0.53	1.51	0.0436	0.1053
INTESTINAL ABSORPTION	25	0.50	1.51	0.0485	0.1057
R SMAD BINDING	20	-0.57	-1.79	0.0144	0.1060
U2 SNRNP	16	0.54	1.51	0.0545	0.1064
EXECUTION PHASE OF APOPTOSIS	50	0.42	1.50	0.0244	0.1067
NEUTRAL LIPID CATABOLIC PROCESS	25	0.49	1.50	0.0566	0.1067
LOCALIZATION WITHIN MEMBRANE	111	0.37	1.50	0.0074	0.1077
3 5 CYCLIC AMP PHOSPHODIESTERASE ACTIVITY	15	0.56	1.50	0.0480	0.1082

HYDROLASE ACTIVITY HYDROLYZING O GLYCOSYL COMPOUNDS	75	0.39	1.50	0.0137	0.1084
PURINERGIC RECEPTOR ACTIVITY	23	0.51	1.50	0.0498	0.1084
GLUCAN BIOSYNTHETIC PROCESS	16	0.54	1.50	0.0503	0.1084
REGULATION OF CARDIAC MUSCLE CONTRACTION	64	0.41	1.50	0.0214	0.1085
REGULATION OF SISTER CHROMATID SEGREGATION	57	0.41	1.50	0.0283	0.1096
REGULATION OF CELL MIGRATION INVOLVED IN SPROUTING ANGIOGENESIS	19	-0.58	-1.78	0.0093	0.1099
PROTEIN K63 LINKED DEUBIQUITINATION	21	0.51	1.50	0.0371	0.1111
OXIDOREDUCTASE ACTIVITY OXIDIZING METAL IONS	17	0.55	1.50	0.0348	0.1114
REGULATION OF T HELPER CELL DIFFERENTIATION	22	-0.56	-1.77	0.0068	0.1115
HEXOSE METABOLIC PROCESS	134	0.36	1.50	0.0135	0.1116
NUCLEAR MEMBRANE	239	0.33	1.50	0.0013	0.1117
NUCLEAR TRANSCRIPTIONAL REPRESSOR COMPLEX	19	0.51	1.50	0.0494	0.1118
ENDOPLASMIC RETICULUM GOLGI INTERMEDIATE COMPARTMENT MEMBRANE	52	0.42	1.50	0.0264	0.1118
ER ASSOCIATED UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	57	0.41	1.50	0.0266	0.1118
MODULATION BY SYMBIONT OF HOST CELLULAR PROCESS	24	0.50	1.50	0.0412	0.1119
LEUKOCYTE CHEMOTAXIS	94	-0.40	-1.77	0.0000	0.1120
PROTEIN METHYLATION	99	0.37	1.49	0.0231	0.1121
POLYSACCHARIDE METABOLIC PROCESS	65	0.40	1.49	0.0188	0.1122
TOLL LIKE RECEPTOR SIGNALING PATHWAY	77	0.39	1.49	0.0138	0.1122
ENDORIBONUCLEASE ACTIVITY	39	0.44	1.49	0.0257	0.1131
ATP HYDROLYSIS COUPLED TRANSMEMBRANE TRANSPORT	34	0.46	1.49	0.0419	0.1131
NEGATIVE REGULATION OF CATABOLIC PROCESS	182	0.34	1.49	0.0026	0.1133
POLYSACCHARIDE BIOSYNTHETIC PROCESS	30	0.47	1.49	0.0458	0.1134
REGULATION OF mRNA SPLICING VIA SPliceosome	46	0.42	1.49	0.0349	0.1135
PROTEIN PHOSPHATASE TYPE 2A COMPLEX	17	0.54	1.49	0.0559	0.1141

RESPONSE TO LIPOPROTEIN PARTICLE	19	0.52	1.49	0.0624	0.1141
ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN	140	0.35	1.49	0.0128	0.1147
ORGANOPHOSPHATE CATABOLIC PROCESS	102	0.37	1.49	0.0101	0.1150
PHOSPHOLIPASE ACTIVITY	88	0.37	1.49	0.0176	0.1150
NON CANONICAL WNT SIGNALING PATHWAY	136	0.36	1.49	0.0129	0.1152
CATION SUGAR SYMPORTER ACTIVITY	15	0.55	1.49	0.0554	0.1153
GLYCOGEN BIOSYNTHETIC PROCESS	16	0.54	1.49	0.0731	0.1154
XENOPHAGY	81	0.38	1.49	0.0233	0.1155
POSITIVE REGULATION OF AUTOPHAGY	65	0.40	1.49	0.0369	0.1161
DNA INTEGRITY CHECKPOINT	122	0.36	1.48	0.0101	0.1181
PROTEIN ALKYLATION	99	0.37	1.48	0.0117	0.1183
3'5' EXONUCLEASE ACTIVITY	44	0.43	1.48	0.0329	0.1190
CONDENSED CHROMOSOME	164	0.34	1.48	0.0056	0.1191
INO80 TYPE COMPLEX	18	0.52	1.48	0.0451	0.1192
PHOSPHOLIPID DEPHOSPHORYLATION	25	0.49	1.48	0.0604	0.1193
LIPID TRANSPORTER ACTIVITY	96	0.37	1.48	0.0201	0.1195
CELLULAR ALDEHYDE METABOLIC PROCESS	72	0.39	1.48	0.0211	0.1196
NEGATIVE REGULATION OF MITOTIC NUCLEAR DIVISION	28	0.47	1.48	0.0510	0.1197
DICARBOXYLIC ACID TRANSPORT	68	0.39	1.48	0.0262	0.1211
CYTOPLASMIC PATTERNrecognition RECEPTOR SIGNALING PATHWAY	30	0.46	1.48	0.0376	0.1212
ACETYL COA METABOLIC PROCESS	25	0.49	1.48	0.0466	0.1213
REGULATION OF VIRAL RELEASE FROM HOST CELL	27	0.48	1.48	0.0509	0.1214
THYROID HORMONE METABOLIC PROCESS	16	0.54	1.48	0.0699	0.1220
TRANSCRIPTIONALLY ACTIVE CHROMATIN	18	0.52	1.48	0.0552	0.1227
POSITIVE REGULATION OF ACTIN CYTOSKELETON REORGANIZATION	15	0.53	1.48	0.0569	0.1228
ESTROGEN METABOLIC PROCESS	15	0.54	1.48	0.0635	0.1228
PROTEIN LOCALIZATION TO CYTOSKELETON	25	0.48	1.48	0.0450	0.1229
PHAGOSOME MATURATION	35	0.45	1.48	0.0417	0.1229
RESPONSE TO ISCHEMIA	24	0.49	1.48	0.0414	0.1233
ESTROGEN RECEPTOR BINDING	35	0.44	1.48	0.0448	0.1233
ORGANELLE LOCALIZATION	359	0.31	1.47	0.0000	0.1257
MANNOSYLATION	25	0.48	1.47	0.0509	0.1280

FILOPODIUM ASSEMBLY	16	-0.60	-1.75	0.0069	0.1280
POSITIVE REGULATION OF HEART GROWTH	24	0.48	1.47	0.0568	0.1281
FAT CELL DIFFERENTIATION	98	0.37	1.47	0.0165	0.1282
CELLULAR KETONE METABOLIC PROCESS	55	0.40	1.47	0.0385	0.1282
MONOCARBOXYLIC ACID TRANSPORT	110	0.36	1.47	0.0144	0.1282
ANAPHASE PROMOTING COMPLEX	18	0.53	1.47	0.0496	0.1282
REACTIVE NITROGEN SPECIES METABOLIC PROCESS	16	0.53	1.47	0.0713	0.1284
HYDROGEN TRANSPORT	115	0.35	1.47	0.0142	0.1286
S ACYLTRANSFERASE ACTIVITY	27	0.47	1.47	0.0491	0.1288
CELL DIVISION	399	0.31	1.47	0.0000	0.1288
GLYCOLIPID BINDING	18	0.51	1.47	0.0589	0.1289
SINGLE ORGANISM MEMBRANE FUSION	113	0.36	1.47	0.0086	0.1290
GLYCOLIPID BIOSYNTHETIC PROCESS	52	0.41	1.47	0.0403	0.1292
REGULATION OF ALTERNATIVE mRNA SPLICING VIA SPLICEOSOME	28	0.46	1.47	0.0529	0.1302
INTRINSIC APOPTOTIC SIGNALING PATHWAY	122	0.35	1.47	0.0126	0.1302
LIPOSACCHARIDE METABOLIC PROCESS	95	0.37	1.47	0.0198	0.1303
NEUROPEPTIDE HORMONE ACTIVITY	27	-0.53	-1.75	0.0074	0.1310
VESICLE LOCALIZATION	203	0.33	1.46	0.0040	0.1314
REGULATION OF SULFUR METABOLIC PROCESS	17	0.53	1.46	0.0747	0.1316
REGULATION OF TRANSCRIPTION ELONGATION FROM RNA POLYMERASE II PROMOTER	22	0.49	1.46	0.0489	0.1319
POSITIVE REGULATION OF GROWTH	213	0.33	1.46	0.0013	0.1323
REGULATION OF T CELL MIGRATION	20	-0.56	-1.74	0.0089	0.1330
CYTOKINE ACTIVITY	165	-0.36	-1.74	0.0000	0.1336
REGULATION OF CHROMATIN BINDING	15	0.54	1.46	0.0651	0.1336
DELAYED RECTIFIER POTASSIUM CHANNEL ACTIVITY	36	-0.50	-1.74	0.0070	0.1340
NEGATIVE REGULATION OF RESPONSE TO REACTIVE OXYGEN SPECIES	17	-0.59	-1.74	0.0069	0.1341
GOLGI TO ENDOSOME TRANSPORT	17	0.52	1.46	0.0646	0.1346
REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	23	0.49	1.46	0.0526	0.1347
REGULATION OF CELL PROLIFERATION INVOLVED IN HEART MORPHOGENESIS	15	0.54	1.46	0.0655	0.1349
TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	36	0.44	1.46	0.0379	0.1352

TRANSPORT VESICLE	283	0.32	1.46	0.0012	0.1378
NEGATIVE REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	62	0.39	1.45	0.0294	0.1378
POSITIVE REGULATION OF PEPTIDYL THREONINE PHOSPHORYLATION	23	0.49	1.45	0.0561	0.1379
CELLULAR RESPONSE TO REACTIVE NITROGEN SPECIES	18	0.51	1.45	0.0757	0.1379
AMMONIUM TRANSMEMBRANE TRANSPORTER ACTIVITY	26	0.47	1.45	0.0559	0.1379
AMINOPEPTIDASE ACTIVITY	37	0.44	1.45	0.0460	0.1379
ADRENERGIC RECEPTOR SIGNALING PATHWAY	18	0.51	1.45	0.0757	0.1381
NEGATIVE REGULATION OF LIPID STORAGE	17	0.52	1.45	0.0829	0.1382
REGULATION OF LIPOPROTEIN LIPASE ACTIVITY	15	0.54	1.45	0.0761	0.1383
REGULATION OF FATTY ACID METABOLIC PROCESS	72	0.38	1.45	0.0280	0.1384
REGULATION OF DENDRITE EXTENSION	18	0.51	1.45	0.0636	0.1387
PYRIMIDINE NUCLEOSIDE BIOSYNTHETIC PROCESS	25	0.47	1.45	0.0567	0.1394
MAGNESIUM ION BINDING	172	0.34	1.45	0.0134	0.1406
GABA RECEPTOR BINDING	15	0.54	1.45	0.0726	0.1413
NEGATIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	57	0.39	1.45	0.0469	0.1416
CYTOPLASMIC SEQUESTERING OF PROTEIN	35	0.43	1.45	0.0510	0.1417
REGULATION OF PROTEIN TARGETING	267	0.32	1.45	0.0038	0.1418
CHOLESTEROL EFFLUX	26	0.47	1.45	0.0528	0.1418
RESPONSE TO OXIDATIVE STRESS	306	0.31	1.45	0.0025	0.1419
OLIGOSACCHARIDE METABOLIC PROCESS	57	0.39	1.45	0.0484	0.1420
HISTONE METHYLTRANSFERASE COMPLEX	60	0.39	1.45	0.0475	0.1421
REGULATION OF PROTEIN COMPLEX ASSEMBLY	322	0.31	1.45	0.0037	0.1423
PURINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	120	0.35	1.45	0.0201	0.1423
SPHINGOLIPID METABOLIC PROCESS	117	0.35	1.45	0.0215	0.1435
NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	330	0.31	1.45	0.0012	0.1436
PYRIMIDINE NUCLEOSIDE METABOLIC PROCESS	39	0.43	1.44	0.0475	0.1447
POLY PYRIMIDINE TRACT BINDING	17	0.52	1.44	0.0668	0.1447

ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY	148	0.34	1.44	0.0120	0.1451
CELL CYCLE CHECKPOINT	163	0.33	1.44	0.0195	0.1451
PROTEIN KINASE C BINDING	47	-0.45	-1.72	0.0000	0.1451
LYASE ACTIVITY	151	0.34	1.44	0.0148	0.1454
STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	89	0.37	1.44	0.0164	0.1454
DNA DOUBLE STRAND BREAK PROCESSING	17	0.53	1.44	0.0727	0.1456
NEGATIVE REGULATION OF CELL CYCLE PROCESS	181	0.33	1.44	0.0121	0.1456
GOLGI CISTERNA	75	0.38	1.44	0.0501	0.1459
UDP GLYCOSYLTRANSFERASE ACTIVITY	105	0.36	1.44	0.0271	0.1460
NUCLEAR TRANSCRIPTION FACTOR COMPLEX	112	0.35	1.44	0.0236	0.1461
INTRINSIC APOPTOTIC SIGNALING PATHWAY BY P53 CLASS MEDIATOR	42	0.42	1.44	0.0463	0.1462
MYELIN SHEATH	148	0.34	1.44	0.0127	0.1462
NEGATIVE REGULATION OF VASCULATURE DEVELOPMENT	75	-0.41	-1.72	0.0060	0.1465
CELLULAR MONOVALENT INORGANIC CATION HOMEOSTASIS	82	0.37	1.44	0.0198	0.1465
REGULATION OF COENZYME METABOLIC PROCESS	45	0.41	1.44	0.0533	0.1466
POSITIVE REGULATION OF ACUTE INFLAMMATORY RESPONSE	27	-0.52	-1.72	0.0098	0.1475
RESPONSE TO ARSENIC CONTAINING SUBSTANCE	29	0.46	1.44	0.0583	0.1476
NEGATIVE REGULATION OF LYMPHOCYTE APOPTOTIC PROCESS	24	-0.52	-1.72	0.0101	0.1484
POSITIVE REGULATION OF COAGULATION	24	0.46	1.44	0.0561	0.1490
LYTIC VACUOLE	436	0.30	1.44	0.0000	0.1490
VESICLE MEMBRANE	450	0.30	1.44	0.0000	0.1493
PROTEIN METHYLTRANSFERASE ACTIVITY	68	0.38	1.44	0.0463	0.1495
ER TO GOLGI TRANSPORT VESICLE	46	0.41	1.44	0.0413	0.1495
PYRIMIDINE NUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	15	0.53	1.44	0.0734	0.1496
HISTONE H4 ACETYLATION	40	0.42	1.44	0.0417	0.1498
NEUROPEPTIDE RECEPTOR ACTIVITY	42	-0.46	-1.72	0.0052	0.1499
SERINE FAMILY AMINO ACID METABOLIC PROCESS	37	0.43	1.43	0.0495	0.1514

TRANSFERASE ACTIVITY TRANSFERRING GLYCOSYL GROUPS	216	0.32	1.43	0.0080	0.1526
PCG PROTEIN COMPLEX	39	0.42	1.43	0.0621	0.1528
CELLULAR RESPONSE TO UV	54	0.40	1.43	0.0427	0.1533
REGULATION OF GLUCONEOGENESIS	34	0.44	1.43	0.0507	0.1536
POSITIVE REGULATION OF DENDRITE EXTENSION	18	0.51	1.43	0.0819	0.1538
PHOSPHORIC DIESTER HYDROLASE ACTIVITY	86	0.36	1.43	0.0176	0.1551
PROTEIN LOCALIZATION TO GOLGI APPARATUS	23	0.48	1.43	0.0675	0.1562
CYTOPLASMIC SEQUESTERING OF TRANSCRIPTION FACTOR	15	0.54	1.43	0.0833	0.1568
REGULATION OF VACUOLE ORGANIZATION	37	0.42	1.43	0.0597	0.1572
TRANSCRIPTION FACTOR BINDING	457	0.30	1.43	0.0011	0.1573
NEGATIVE REGULATION OF LIPID TRANSPORT	25	0.46	1.43	0.0699	0.1575
NEGATIVE REGULATION OF RESPONSE TO NUTRIENT LEVELS	30	0.44	1.43	0.0658	0.1575
PROTEIN DISULFIDE OXIDOREDUCTASE ACTIVITY	22	0.49	1.43	0.0720	0.1576
MODIFICATION BY SYMBIONT OF HOST MORPHOLOGY OR PHYSIOLOGY	38	0.42	1.43	0.0529	0.1576
POSITIVE REGULATION OF BLOOD PRESSURE	34	0.44	1.43	0.0761	0.1577
APOPTOTIC SIGNALING PATHWAY	242	0.32	1.43	0.0104	0.1577
REGULATION OF CELLULAR PROTEIN LOCALIZATION	479	0.30	1.42	0.0000	0.1581
DRUG TRANSMEMBRANE TRANSPORT	17	0.52	1.42	0.0688	0.1586
IMPORT INTO CELL	34	0.43	1.42	0.0600	0.1589
PHOSPHATIDYLINOSITOL METABOLIC PROCESS	176	0.33	1.42	0.0154	0.1591
POLYSACCHARIDE CATABOLIC PROCESS	20	0.49	1.42	0.0860	0.1595
CYTOSOLIC RIBOSOME	85	0.36	1.42	0.0432	0.1598
CELLULAR PIGMENTATION	41	0.42	1.42	0.0613	0.1599
DOUBLE STRAND BREAK REPAIR	124	0.34	1.42	0.0247	0.1599
CELL CYCLE PHASE TRANSITION	213	0.32	1.42	0.0078	0.1600
POSITIVE REGULATION OF WOUND HEALING	42	0.42	1.42	0.0604	0.1608
AGGRESOME	29	0.44	1.42	0.0670	0.1621
NEGATIVE REGULATION OF RESPONSE TO CYTOKINE STIMULUS	36	0.43	1.42	0.0548	0.1622

MAINTENANCE OF PROTEIN LOCALIZATION IN ORGANELLE	28	0.45	1.42	0.0592	0.1627
ORGANIC HYDROXY COMPOUND TRANSPORT	139	0.34	1.42	0.0156	0.1628
PROTEIN EXPORT FROM NUCLEUS	29	0.45	1.42	0.0546	0.1634
DNA REPLICATION	166	0.33	1.42	0.0080	0.1639
MEMBRANE LIPID BIOSYNTHETIC PROCESS	96	0.35	1.42	0.0330	0.1639
PALMITOYLTRANSFERASE ACTIVITY	31	0.43	1.42	0.0723	0.1641
POLYUBIQUITIN BINDING	36	0.42	1.42	0.0710	0.1647
REGULATION OF BLOOD VESSEL ENDOTHELIAL CELL MIGRATION	49	-0.44	-1.70	0.0132	0.1655
MAINTENANCE OF LOCATION IN CELL	84	0.36	1.41	0.0352	0.1662
JNK CASCADE	72	0.37	1.41	0.0490	0.1669
PROTEIN HYDROXYLATION	18	-0.56	-1.70	0.0128	0.1675
REGULATION OF ISOTYPE SWITCHING	20	-0.54	-1.70	0.0100	0.1689
NUCLEAR CHROMOSOME TELOMERIC REGION	95	0.35	1.41	0.0389	0.1702
DNA DEPENDENT DNA REPLICATION	77	0.36	1.41	0.0438	0.1703
REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	110	0.35	1.41	0.0345	0.1703
REGULATION OF INTERLEUKIN 10 PRODUCTION	37	-0.46	-1.69	0.0076	0.1704
U12 TYPE SPliceosomal COMPLEX	23	0.47	1.41	0.0730	0.1704
MULTICELLULAR ORGANISM GROWTH	67	0.38	1.41	0.0339	0.1705
NEGATIVE REGULATION OF CANONICAL WNT SIGNALING PATHWAY	152	0.34	1.41	0.0204	0.1709
REGULATION OF COFACTOR METABOLIC PROCESS	45	0.41	1.41	0.0753	0.1710
POSITIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	25	0.46	1.41	0.0767	0.1711
REGULATION OF LIPID METABOLIC PROCESS	245	0.31	1.41	0.0087	0.1711
NEGATIVE REGULATION OF LIPID CATABOLIC PROCESS	18	0.50	1.41	0.0863	0.1713
REGULATION OF MEMBRANE PROTEIN ECTODOMAIN PROTEOLYSIS	20	-0.54	-1.69	0.0070	0.1715
POSITIVE REGULATION OF INTERLEUKIN 1 BETA PRODUCTION	21	-0.53	-1.69	0.0263	0.1718
CENTROSOME	408	0.30	1.41	0.0000	0.1729
NEGATIVE REGULATION OF KIDNEY DEVELOPMENT	17	-0.57	-1.69	0.0113	0.1730

EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT	67	-0.41	-1.68	0.0057	0.1737
NEGATIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	119	0.34	1.41	0.0262	0.1737
NON RECOMBINATIONAL REPAIR	53	0.40	1.40	0.0437	0.1742
DEMETHYLASE ACTIVITY	31	0.43	1.40	0.0815	0.1744
REGULATION OF LEUKOCYTE APOPTOTIC PROCESS	66	-0.41	-1.68	0.0057	0.1756
CHROMOSOMAL REGION	264	0.31	1.40	0.0102	0.1759
MYELOID LEUKOCYTE MIGRATION	79	-0.39	-1.68	0.0000	0.1759
DETECTION OF MECHANICAL STIMULUS INVOLVED IN SENSORY PERCEPTION	22	-0.53	-1.68	0.0113	0.1763
POSITIVE REGULATION OF SYNAPSE ASSEMBLY	55	0.39	1.40	0.0554	0.1765
REGULATION OF TRANSLATION IN RESPONSE TO STRESS	19	0.49	1.40	0.1076	0.1775
RESPONSE TO HYDROGEN PEROXIDE	92	0.36	1.40	0.0421	0.1777
POSITIVE REGULATION OF I KAPPAB KINASE NF KAPPAB SIGNALING	157	0.32	1.40	0.0254	0.1782
ESTABLISHMENT OF PROTEIN LOCALIZATION TO ENDOPLASMIC RETICULUM	85	0.36	1.40	0.0460	0.1784
SERINE TYPE EXOPEPTIDASE ACTIVITY	17	0.50	1.40	0.1164	0.1793
SULFUR AMINO ACID METABOLIC PROCESS	39	0.42	1.40	0.0715	0.1796
NUCLEOSOMAL DNA BINDING	27	0.44	1.40	0.0829	0.1797
PROTEIN STABILIZATION	120	0.34	1.40	0.0258	0.1799
PROTEIN HOMOTETRAMERIZATION	55	0.38	1.40	0.0696	0.1799
REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	332	0.30	1.40	0.0085	0.1800
POSITIVE REGULATION OF CARDIAC MUSCLE TISSUE DEVELOPMENT	26	0.45	1.40	0.0876	0.1800
ANTIGEN PROCESSING AND PRESENTATION	161	0.33	1.40	0.0189	0.1803
REGULATION OF CARBOHYDRATE METABOLIC PROCESS	149	0.33	1.40	0.0262	0.1804
DOUBLE STRANDED RNA BINDING	54	0.38	1.40	0.0670	0.1812
RIBONUCLEOPROTEIN GRANULE	132	0.33	1.40	0.0323	0.1812
U2 TYPE SPliceosomal COMPLEX	25	0.46	1.39	0.0807	0.1819
REGULATION OF VIRAL TRANSCRIPTION	56	0.39	1.39	0.0512	0.1819
MUSCLE CELL CELLULAR HOMEOSTASIS	18	0.49	1.39	0.0927	0.1827
PROTEIN LOCALIZATION TO CHROMOSOME	41	0.41	1.39	0.0564	0.1828

FATTY ACID BINDING	27	0.44	1.39	0.0840	0.1828
HISTONE UBIQUITINATION	28	0.45	1.39	0.0666	0.1829
CHROMOSOME TELOMERIC REGION	123	0.34	1.39	0.0281	0.1838
VOLTAGE GATED ION CHANNEL ACTIVITY	177	-0.35	-1.67	0.0000	0.1840
NUCLEAR NUCLEOSOME	15	-0.59	-1.67	0.0214	0.1840
REGULATION OF SYNAPTIC VESICLE TRANSPORT	29	0.43	1.39	0.0848	0.1845
NEGATIVE REGULATION OF RESPONSE TO EXTRACELLULAR STIMULUS	30	0.44	1.39	0.0786	0.1847
KINETOCHORE	97	0.35	1.39	0.0419	0.1855
PHOSPHATIDYLINOSITOL 3 KINASE COMPLEX	17	0.51	1.39	0.0979	0.1863
POSITIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	54	0.38	1.39	0.0661	0.1863
PYRIMIDINE NUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	17	0.51	1.39	0.0810	0.1865
REGULATION OF MULTI ORGANISM PROCESS	391	0.29	1.39	0.0047	0.1867
S-ADENOSYLMETHIONINE METABOLIC PROCESS	18	0.50	1.39	0.0810	0.1867
MANNOSYLTRANSFERASE ACTIVITY	18	0.49	1.39	0.1082	0.1871
GENE SILENCING BY RNA	108	0.34	1.39	0.0398	0.1873
ORGANIC CATION TRANSPORT	19	0.48	1.39	0.0909	0.1873
CORTICAL CYTOSKELETON	65	0.37	1.39	0.0631	0.1886
CELLULAR MODIFIED AMINO ACID BIOSYNTHETIC PROCESS	46	0.40	1.39	0.0522	0.1890
TRANSLATION REGULATOR ACTIVITY	30	0.43	1.39	0.0890	0.1891
DRUG TRANSPORT	22	0.47	1.38	0.0889	0.1898
DRUG TRANSPORTER ACTIVITY	18	0.49	1.38	0.1009	0.1898
LEUKOCYTE MIGRATION	223	-0.33	-1.65	0.0000	0.1905
REGULATION OF ALPHA BETA T CELL DIFFERENTIATION	40	-0.46	-1.66	0.0079	0.1906
INTERMEDIATE FILAMENT	124	-0.35	-1.66	0.0000	0.1911
NEGATIVE REGULATION OF T CELL DIFFERENTIATION	27	-0.50	-1.66	0.0075	0.1912
REGULATION OF MONOCYTE CHEMOTAXIS	18	-0.55	-1.66	0.0092	0.1918
CHROMOSOME SEGREGATION	225	0.31	1.38	0.0130	0.1929
CARTILAGE CONDENSATION	20	-0.53	-1.66	0.0162	0.1933
REGULATION OF LIPID TRANSPORT	87	0.35	1.38	0.0496	0.1936
PYRIMIDINE CONTAINING COMPOUND METABOLIC PROCESS	61	0.37	1.38	0.0635	0.1936

GLUTAMINE FAMILY AMINO ACID METABOLIC PROCESS	60	0.37	1.38	0.0581	0.1938
GTPASE ACTIVITY	206	0.32	1.38	0.0146	0.1942
PRE mRNA BINDING	21	0.47	1.38	0.0930	0.1944
POSITIVE REGULATION OF SODIUM ION TRANSPORT	30	0.44	1.38	0.0873	0.1944
MITOCHONDRIAL MORPHOGENESIS	17	0.50	1.38	0.1014	0.1944
AMMONIUM TRANSMEMBRANE TRANSPORT	22	0.47	1.38	0.1045	0.1946
FATTY ACID BIOSYNTHETIC PROCESS	92	0.35	1.38	0.0477	0.1947
HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS	123	0.33	1.38	0.0371	0.1947
TRANSITION METAL ION TRANSPORT	96	0.35	1.38	0.0524	0.1947
REGULATION OF DNA REPAIR	67	0.37	1.38	0.0552	0.1949
CYTOPLASMIC MICROTUBULE	43	0.40	1.38	0.0832	0.1955
NEGATIVE REGULATION OF LIPASE ACTIVITY	15	0.51	1.38	0.1103	0.1955
CYTOSKELETON DEPENDENT CYTOKINESIS	32	0.42	1.38	0.0835	0.1958
PHOSPHOLIPASE BINDING	18	0.48	1.38	0.0964	0.1960
NAD METABOLIC PROCESS	51	0.38	1.38	0.0598	0.1962
PROTEIN LOCALIZATION TO LYSOSOME	16	0.50	1.38	0.1020	0.1963
RIBONUCLEOTIDE CATABOLIC PROCESS	26	0.44	1.38	0.1048	0.1963
CELLULAR RESPONSE TO ESTROGEN STIMULUS	37	0.41	1.38	0.0846	0.1965
PROTEIN K48 LINKED DEUBIQUITINATION	17	0.51	1.38	0.0973	0.1969
CHROMOSOME LOCALIZATION	49	0.39	1.37	0.0604	0.1978
DNA DEPENDENT ATPASE ACTIVITY	70	0.37	1.37	0.0465	0.2009
INTESTINAL EPITHELIAL CELL DIFFERENTIATION	15	0.50	1.37	0.1200	0.2018
PURINERGIC RECEPTOR SIGNALING PATHWAY	26	0.45	1.37	0.0953	0.2019
NUCLEAR IMPORT	112	0.34	1.37	0.0313	0.2020
NUCLEAR EUCHROMATIN	20	0.47	1.37	0.0855	0.2025
CHROMATIN SILENCING	60	-0.41	-1.65	0.0000	0.2028
REGULATION OF ALPHA BETA T CELL PROLIFERATION	17	-0.55	-1.64	0.0256	0.2029
INSULIN RECEPTOR SIGNALING PATHWAY	72	0.36	1.37	0.0595	0.2032
MODIFICATION OF MORPHOLOGY OR PHYSIOLOGY OF OTHER ORGANISM	71	0.37	1.37	0.0646	0.2035
COENZYME A METABOLIC PROCESS	17	0.49	1.37	0.1138	0.2039

G PROTEIN COUPLED CHEMOATTRACTANT RECEPTOR ACTIVITY	23	-0.51	-1.64	0.0143	0.2041
MITOTIC CYTOKINESIS	25	0.45	1.37	0.0959	0.2044
GUANYL NUCLEOTIDE BINDING	332	0.30	1.37	0.0074	0.2044
REGULATION OF CELLULAR AMINE METABOLIC PROCESS	79	0.35	1.37	0.0574	0.2056
HYDROGEN ION TRANSMEMBRANE TRANSPORT	86	0.35	1.37	0.0652	0.2056
MONOCYTE CHEMOTAXIS	27	-0.48	-1.62	0.0177	0.2056
MEMBRANE PROTEIN ECTODOMAIN PROTEOLYSIS	17	0.49	1.37	0.1020	0.2058
CYTOPLASMIC mRNA PROCESSING BODY	63	0.37	1.37	0.0470	0.2060
INTRAMOLECULAR OXIDOREDUCTASE ACTIVITY	48	0.39	1.37	0.0770	0.2064
ADAPTIVE IMMUNE RESPONSE BASED ON SOMATIC RECOMBINATION OF IMMUNE RECEPTORS BUILT FROM IMMUNOGLOBULIN SUPERFAMILY DOMAINS	97	-0.36	-1.62	0.0000	0.2067
REGULATION OF LEUKOCYTE MIGRATION	132	-0.35	-1.63	0.0000	0.2068
CARDIAC RIGHT VENTRICLE MORPHOGENESIS	15	-0.58	-1.62	0.0313	0.2073
WNT ACTIVATED RECEPTOR ACTIVITY	21	0.46	1.36	0.0926	0.2074
NEGATIVE REGULATION OF LYMPHOCYTE DIFFERENTIATION	34	-0.45	-1.63	0.0193	0.2075
AMIDE TRANSMEMBRANE TRANSPORTER ACTIVITY	17	-0.56	-1.63	0.0147	0.2081
RESPONSE TO PROTOZOAN	18	-0.54	-1.62	0.0267	0.2088
PYrimidine nucleoside catabolic process	15	0.50	1.36	0.1243	0.2090
PROXIMAL DISTAL PATTERN FORMATION	31	-0.48	-1.63	0.0025	0.2096
CELL AGGREGATION	20	-0.53	-1.63	0.0238	0.2097
TRANSFERASE ACTIVITY TRANSFERRING SULFUR CONTAINING GROUPS	56	0.37	1.36	0.0761	0.2098
NEGATIVE REGULATION OF TELOMERE MAINTENANCE	23	0.45	1.36	0.0947	0.2100
AMINO ACID TRANSPORT	114	0.33	1.36	0.0394	0.2100
NUCLEOBASE CONTAINING COMPOUND KINASE ACTIVITY	42	0.39	1.36	0.0862	0.2101

REGULATION OF SYMBIOSIS ENCOMPASSING MUTUALISM THROUGH PARASITISM	171	0.32	1.36	0.0284	0.2102
REGULATION OF NUCLEASE ACTIVITY	22	-0.52	-1.64	0.0158	0.2107
POSITIVE REGULATION OF TRANSLATIONAL INITIATION	20	0.47	1.36	0.1043	0.2108
SPERM CAPACITATION	16	0.49	1.36	0.1248	0.2108
NUCLEOSIDE DIPHOSPHATE METABOLIC PROCESS	73	0.35	1.36	0.0712	0.2109
THYMIC T CELL SELECTION	19	-0.53	-1.63	0.0389	0.2110
KIDNEY MESENCHYME DEVELOPMENT	18	-0.54	-1.63	0.0194	0.2116
INACTIVATION OF MAPK ACTIVITY	26	0.44	1.36	0.1123	0.2119
TRANSLATION REPRESSOR ACTIVITY	17	0.49	1.36	0.1052	0.2119
REGULATION OF B CELL APOPTOTIC PROCESS	17	-0.56	-1.63	0.0137	0.2121
AMINE METABOLIC PROCESS	120	0.33	1.36	0.0424	0.2122
DNA DIRECTED RNA POLYMERASE III COMPLEX	18	0.48	1.36	0.1197	0.2128
SWI SNF SUPERFAMILY TYPE COMPLEX	64	0.36	1.36	0.0615	0.2138
REGULATION OF TUMOR NECROSIS FACTOR BIOSYNTHETIC PROCESS	16	-0.55	-1.61	0.0494	0.2141
NEGATIVE REGULATION OF CYCLIC NUCLEOTIDE METABOLIC PROCESS	40	-0.44	-1.62	0.0078	0.2142
REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	129	0.33	1.36	0.0414	0.2143
SPINDLE POLE	107	0.33	1.36	0.0389	0.2150
POSITIVE REGULATION OF CELLULAR COMPONENT BIOGENESIS	359	0.29	1.36	0.0083	0.2150
ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	258	0.30	1.36	0.0266	0.2152
REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	149	0.32	1.36	0.0341	0.2153
SINGLE STRANDED RNA BINDING	59	0.37	1.36	0.0826	0.2154
PROTEIN OLIGOMERIZATION	379	0.29	1.36	0.0095	0.2155
POSITIVE REGULATION OF TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	17	0.49	1.36	0.1135	0.2155
MAP KINASE KINASE KINASE ACTIVITY	17	0.48	1.35	0.1222	0.2157
REGULATION OF mRNA METABOLIC PROCESS	100	0.34	1.35	0.0494	0.2158
HISTONE BINDING	132	0.32	1.35	0.0401	0.2158
TERMINAL BOUTON	62	0.37	1.35	0.0740	0.2158

CELLULAR PROTEIN COMPLEX LOCALIZATION	18	0.49	1.35	0.1224	0.2169
POSITIVE REGULATION OF MITOTIC CELL CYCLE	110	0.34	1.35	0.0466	0.2171
QUATERNARY AMMONIUM GROUP TRANSPORT	16	0.49	1.35	0.1322	0.2175
ORGANIC HYDROXY COMPOUND CATABOLIC PROCESS	59	0.37	1.35	0.0783	0.2180
NEGATIVE REGULATION OF MUSCLE CONTRACTION	22	0.46	1.35	0.1139	0.2181
IN UTERO EMBRYONIC DEVELOPMENT	280	0.30	1.35	0.0120	0.2186
SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENE SEGMENTS	17	0.48	1.35	0.1261	0.2197
CELL CYCLE G1 S PHASE TRANSITION	93	0.34	1.35	0.0606	0.2198
ORGANIC HYDROXY COMPOUND METABOLIC PROCESS	419	0.29	1.35	0.0083	0.2200
CELL GROWTH	120	0.33	1.35	0.0416	0.2201
LYSOPHOSPHOLIPASE ACTIVITY	17	0.48	1.35	0.1290	0.2207
MITOPHAGY IN RESPONSE TO MITOCHONDRIAL DEPOLARIZATION	109	0.33	1.35	0.0440	0.2211
MEMBRANE DOCKING	59	0.37	1.35	0.0768	0.2223
ANTIOXIDANT ACTIVITY	59	0.37	1.35	0.0744	0.2224
AUTOPHAGOSOME	64	0.36	1.35	0.0788	0.2226
REGULATION OF GLUCOSE METABOLIC PROCESS	96	0.34	1.35	0.0590	0.2227
REGULATION OF RETINOIC ACID RECEPTOR SIGNALING PATHWAY	15	-0.56	-1.59	0.0300	0.2232
REGULATION OF MEMBRANE PERMEABILITY	55	0.37	1.35	0.0814	0.2232
LONG TERM SYNAPTIC POTENTIATION	37	-0.45	-1.60	0.0080	0.2234
POSITIVE REGULATION OF NEURAL PRECURSOR CELL PROLIFERATION	39	-0.43	-1.60	0.0294	0.2236
VITAMIN METABOLIC PROCESS	100	0.33	1.35	0.0495	0.2239
NEGATIVE REGULATION OF CYTOKINE PRODUCTION INVOLVED IN IMMUNE RESPONSE	17	-0.53	-1.60	0.0267	0.2245
ANION TRANSMEMBRANE TRANSPORT	225	0.30	1.35	0.0159	0.2245
T CELL SELECTION	32	-0.45	-1.61	0.0132	0.2251
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE BY HORMONE	32	-0.45	-1.59	0.0176	0.2251
REGULATION OF IMMUNOGLOBULIN PRODUCTION	39	-0.43	-1.60	0.0148	0.2252
LEFT RIGHT PATTERN FORMATION	19	-0.52	-1.60	0.0276	0.2253

TAXIS	394	-0.30	-1.60	0.0000	0.2254
NEUROPEPTIDE SIGNALING PATHWAY	90	-0.37	-1.59	0.0000	0.2263
PROTEIN TETRAMERIZATION	106	0.33	1.34	0.0552	0.2268
POTASSIUM CHANNEL ACTIVITY	115	-0.35	-1.60	0.0000	0.2272
RESPONSE TO VIRUS	196	-0.32	-1.59	0.0000	0.2273
RESPONSE TO XENOBIOTIC STIMULUS	67	0.35	1.34	0.0691	0.2276
RESPONSE TO MITOCHONDRIAL DEPOLARISATION	109	0.33	1.34	0.0534	0.2276
POSITIVE REGULATION OF POTASSIUM ION TRANSPORT	34	0.41	1.34	0.0880	0.2277
REGULATION OF CYTOPLASMIC TRANSPORT	430	0.28	1.34	0.0106	0.2277
POSITIVE REGULATION OF PROTEIN COMPLEX ASSEMBLY	172	0.31	1.34	0.0360	0.2277
HYDROGEN ION TRANSMEMBRANE TRANSPORTER ACTIVITY	83	0.35	1.34	0.0620	0.2277
ORGAN REGENERATION	78	0.35	1.34	0.0729	0.2278
RNA POLYMERASE III ACTIVITY	18	0.48	1.34	0.1190	0.2283
COLLAGEN FIBRIL ORGANIZATION	35	-0.44	-1.60	0.0243	0.2287
REGULATION OF NUCLEAR DIVISION	141	0.32	1.34	0.0389	0.2287
NEURON MATURATION	27	-0.49	-1.59	0.0273	0.2291
GRANULOCYTE MIGRATION	60	-0.40	-1.58	0.0027	0.2308
REGULATION OF FATTY ACID BIOSYNTHETIC PROCESS	33	-0.45	-1.58	0.0127	0.2310
NUCLEAR PERIPHERY	103	0.33	1.34	0.0627	0.2316
INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE BY P53 CLASS MEDIATOR	24	0.44	1.34	0.1086	0.2317
B CELL HOMEOSTASIS	19	0.46	1.34	0.1227	0.2319
PROTEIN LOCALIZATION TO CILIUM	22	0.46	1.34	0.1138	0.2320
DEVELOPMENTAL PIGMENTATION	36	0.41	1.34	0.0949	0.2329
PROTEIN C TERMINUS BINDING	169	0.31	1.34	0.0409	0.2339
POSITIVE REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	55	-0.39	-1.58	0.0110	0.2343
REGULATION OF MYELINATION	29	0.42	1.34	0.1150	0.2345
POSITIVE REGULATION OF GLYCOGEN METABOLIC PROCESS	15	-0.54	-1.57	0.0446	0.2347
G PROTEIN COUPLED RECEPTOR ACTIVITY	374	-0.29	-1.57	0.0000	0.2357
REGULATION OF HYDROGEN PEROXIDE INDUCED CELL DEATH	16	-0.54	-1.58	0.0305	0.2359
NEUROPEPTIDE BINDING	20	-0.51	-1.57	0.0501	0.2360

IMMUNE EFFECTOR PROCESS	356	-0.30	-1.57	0.0000	0.2363
PARTURITION	19	-0.52	-1.57	0.0315	0.2367
G1 S TRANSITION OF MITOTIC CELL CYCLE	93	0.34	1.33	0.0751	0.2379
ALPHA TUBULIN BINDING	22	0.46	1.33	0.1321	0.2381
RESPONSE TO TOXIC SUBSTANCE	214	0.30	1.33	0.0296	0.2382
CELL REDOX HOMEOSTASIS	60	0.36	1.33	0.0731	0.2383
REGULATION OF B CELL MEDIATED IMMUNITY	33	-0.45	-1.57	0.0129	0.2384
NEURON FATE SPECIFICATION	30	-0.47	-1.58	0.0102	0.2387
SULFOTRANSFERASE ACTIVITY	44	0.39	1.33	0.0918	0.2391
REGULATION OF TRANSCRIPTION REGULATORY REGION DNA BINDING	33	0.40	1.33	0.1084	0.2392
CORTICAL ACTIN CYTOSKELETON	46	0.38	1.33	0.0926	0.2393
STEROID BINDING	83	0.34	1.33	0.0714	0.2395
CELLULAR AMINO ACID BIOSYNTHETIC PROCESS	84	0.34	1.33	0.0701	0.2405
REGULATION OF B CELL PROLIFERATION	52	-0.39	-1.57	0.0164	0.2405
NLS BEARING PROTEIN IMPORT INTO NUCLEUS	21	0.45	1.33	0.1376	0.2411
CARBOHYDRATE DERIVATIVE CATABOLIC PROCESS	151	0.31	1.33	0.0474	0.2416
PHOSPHOPROTEIN BINDING	57	0.36	1.33	0.0836	0.2417
REGULATION OF INFLAMMATORY RESPONSE TO ANTIGENIC STIMULUS	17	-0.53	-1.57	0.0410	0.2417
SPLICEOSOMAL COMPLEX ASSEMBLY	35	0.41	1.33	0.1152	0.2420
NEGATIVE REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	23	-0.48	-1.56	0.0287	0.2423
ETHANOLAMINE CONTAINING COMPOUND METABOLIC PROCESS	78	0.34	1.33	0.0779	0.2424
NEGATIVE REGULATION OF CYTOPLASMIC TRANSPORT	103	0.33	1.33	0.0480	0.2424
REGULATION OF STRIATED MUSCLE CONTRACTION	76	0.35	1.33	0.0800	0.2431
PHOSPHATIDYLINOSITOL BINDING	186	0.30	1.33	0.0404	0.2432
REGULATION OF CARDIAC MUSCLE CELL CONTRACTION	27	0.43	1.33	0.1100	0.2433
NUCLEAR CHROMOSOME	413	0.28	1.33	0.0142	0.2440
BETA CATENIN BINDING	80	0.34	1.33	0.0654	0.2441
COMPLEX OF COLLAGEN TRIMERS	22	-0.49	-1.56	0.0323	0.2441
MAST CELL GRANULE	19	-0.50	-1.56	0.0316	0.2444
RECEPTOR AGONIST ACTIVITY	16	-0.54	-1.56	0.0547	0.2446

ALCOHOL CATABOLIC PROCESS	52	0.37	1.33	0.0866	0.2448
VESICLE DOCKING	49	0.37	1.33	0.0758	0.2449
ACTIVE TRANSMEMBRANE TRANSPORTER ACTIVITY	318	0.29	1.32	0.0255	0.2455
PROTEIN HOMOOLIGOMERIZATION	235	0.30	1.32	0.0341	0.2455
REGULATION OF PROTEIN COMPLEX DISASSEMBLY	179	0.31	1.32	0.0326	0.2456
REGULATION OF INTERLEUKIN 2 BIOSYNTHETIC PROCESS	16	-0.54	-1.56	0.0342	0.2456
CELL CYCLE G2 M PHASE TRANSITION	115	0.32	1.32	0.0629	0.2456
SISTER CHROMATID SEGREGATION	150	0.31	1.32	0.0455	0.2457
WNT SIGNALING PATHWAY	329	0.29	1.32	0.0134	0.2457
REGULATION OF RESPONSE TO FOOD	16	0.49	1.32	0.1456	0.2457
REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	33	0.41	1.32	0.1113	0.2460
REGULATION OF BINDING	250	0.29	1.32	0.0287	0.2465
POSITIVE REGULATION OF INSULIN SECRETION INVOLVED IN CELLULAR RESPONSE TO GLUCOSE STIMULUS	23	0.45	1.32	0.1327	0.2466
MODULATION BY VIRUS OF HOST MORPHOLOGY OR PHYSIOLOGY	30	0.42	1.32	0.1269	0.2474
ACETYLGLUCOSAMINYLTRANSFERASE ACTIVITY	43	0.39	1.32	0.1100	0.2487
RESPONSE TO REACTIVE OXYGEN SPECIES	164	0.30	1.32	0.0505	0.2488
DNA DAMAGE RESPONSE DETECTION OF DNA DAMAGE	33	0.41	1.32	0.1045	0.2488
PYRUVATE METABOLIC PROCESS	57	0.36	1.32	0.1019	0.2488
POSITIVE REGULATION OF NEURON PROJECTION DEVELOPMENT	218	0.30	1.32	0.0326	0.2489
INTRINSIC COMPONENT OF EXTERNAL SIDE OF PLASMA MEMBRANE	17	0.47	1.32	0.1380	0.2490
REGULATION OF LYMPHOCYTE APOPTOTIC PROCESS	47	-0.40	-1.55	0.0186	0.2491
CYCLIN DEPENDENT PROTEIN SERINE THREONINE KINASE REGULATOR ACTIVITY	24	0.43	1.32	0.1237	0.2491
RESPONSE TO IONIZING RADIATION	122	0.32	1.32	0.0636	0.2492
MUSCLE CELL FATE COMMITMENT	15	-0.54	-1.55	0.0554	0.2503
MACROMITOPHAGY	109	0.33	1.32	0.0596	0.2505

NEGATIVE REGULATION OF CELL DIVISION	53	0.37	1.32	0.1003	0.2513
REGULATION OF PROTEIN POLYMERIZATION	147	0.31	1.32	0.0635	0.2515
NEGATIVE REGULATION OF PROTEIN KINASE B SIGNALING	34	0.41	1.32	0.1281	0.2515
DORSAL VENTRAL NEURAL TUBE PATTERNING	15	-0.55	-1.55	0.0404	0.2520
RAB GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	27	0.42	1.32	0.1261	0.2525
POSITIVE REGULATION OF CANONICAL WNT SIGNALING PATHWAY	110	0.32	1.32	0.0725	0.2530
DNA RECOMBINATION	163	0.31	1.32	0.0521	0.2530
POTASSIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	138	-0.33	-1.55	0.0000	0.2536
CYTOSOLIC LARGE RIBOSOMAL SUBUNIT	47	0.37	1.32	0.1173	0.2540
REGULATION OF MITOCHONDRIAL MEMBRANE POTENTIAL	48	0.37	1.31	0.0789	0.2547
SPINDLE ASSEMBLY	59	0.36	1.31	0.0988	0.2547
PIGMENT GRANULE ORGANIZATION	20	0.46	1.31	0.1431	0.2555
MYOSIN V BINDING	16	0.47	1.31	0.1519	0.2556
CELLULAR RESPONSE TO HYDROGEN PEROXIDE	54	0.37	1.31	0.1058	0.2564
ALPHA AMINO ACID BIOSYNTHETIC PROCESS	69	0.35	1.31	0.0769	0.2567
I KAPPAB KINASE NF KAPPAB SIGNALING	61	0.35	1.31	0.1060	0.2573
NEGATIVE REGULATION OF CALCIUM MEDIATED SIGNALING	16	0.48	1.31	0.1491	0.2577
AP TYPE MEMBRANE COAT ADAPTOR COMPLEX	35	0.40	1.31	0.1140	0.2580
SEX DETERMINATION	22	-0.48	-1.54	0.0378	0.2583
NEGATIVE REGULATION OF ALPHA BETA T CELL ACTIVATION	18	-0.53	-1.54	0.0249	0.2599
REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	125	0.31	1.31	0.0678	0.2599
EXTERNAL SIDE OF PLASMA MEMBRANE	183	-0.32	-1.54	0.0040	0.2600
IRE1 MEDIATED UNFOLDED PROTEIN RESPONSE	51	0.37	1.31	0.1130	0.2601
POSITIVE REGULATION OF APOPTOTIC SIGNALING PATHWAY	149	0.31	1.31	0.0440	0.2601
NEPHRON TUBULE FORMATION	18	-0.52	-1.54	0.0373	0.2602

WNT SIGNALING PATHWAY CALCIUM MODULATING PATHWAY	39	0.38	1.31	0.1099	0.2604
HISTONE MONOUBIQUITINATION	18	0.46	1.31	0.1450	0.2607
REGIONALIZATION	291	-0.30	-1.54	0.0000	0.2610
CARBOHYDRATE TRANSPORT	79	0.34	1.31	0.0921	0.2613
UDP GALACTOSYLTRANSFERASE ACTIVITY	25	0.42	1.31	0.1327	0.2621
NEGATIVE REGULATION OF I KAPPAB KINASE NF KAPPAB SIGNALING	46	0.37	1.31	0.1068	0.2622
PURINE CONTAINING COMPOUND CATABOLIC PROCESS	46	0.37	1.31	0.1188	0.2624
CONDENSED CHROMOSOME CENTROMERIC REGION	79	0.34	1.31	0.0849	0.2631
POLYPEPTIDE N ACETYLGALACTOSAMINYLTRANSFERASE ACTIVITY	17	0.47	1.31	0.1408	0.2632
NEGATIVE REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	29	0.41	1.31	0.1330	0.2642
LIPID HOMEOSTASIS	97	0.32	1.30	0.0716	0.2643
REGULATION OF MICROTUBULE BASED PROCESS	202	0.29	1.31	0.0519	0.2643
POSITIVE REGULATION OF FAT CELL DIFFERENTIATION	44	0.37	1.30	0.1066	0.2643
REGULATION OF DOUBLE STRAND BREAK REPAIR	35	0.39	1.30	0.1195	0.2645
REGULATION OF CELL GROWTH	354	0.28	1.30	0.0169	0.2646
TOXIN TRANSPORT	36	0.39	1.30	0.1028	0.2646
WNT PROTEIN BINDING	28	0.41	1.30	0.1325	0.2658
CELLULAR METABOLIC COMPOUND SALVAGE	33	0.40	1.30	0.1109	0.2658
MONOVALENT INORGANIC CATION HOMEOSTASIS	106	0.32	1.30	0.0658	0.2659
CYTOCHROME COMPLEX	17	0.46	1.30	0.1690	0.2660
TRANSLATION REGULATOR ACTIVITY NUCLEIC ACID BINDING	16	0.47	1.30	0.1301	0.2660
PIGMENTATION	77	0.34	1.30	0.0956	0.2661
PHOSPHATIDYLCHOLINE METABOLIC PROCESS	59	0.36	1.30	0.1113	0.2661
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT1 PROTEIN	16	-0.52	-1.53	0.0400	0.2664
POSITIVE REGULATION OF FATTY ACID BIOSYNTHETIC PROCESS	17	-0.51	-1.53	0.0404	0.2666

VOLTAGE GATED CALCIUM CHANNEL ACTIVITY	40	-0.42	-1.53	0.0054	0.2670
POSITIVE REGULATION OF mRNA PROCESSING	29	0.41	1.30	0.1426	0.2674
POSITIVE REGULATION OF RECEPTOR ACTIVITY	43	0.38	1.30	0.1111	0.2678
POSITIVE REGULATION OF PEPTIDASE ACTIVITY	134	0.31	1.30	0.0512	0.2679
CLATHRIN VESICLE COAT	22	0.44	1.30	0.1328	0.2679
RNA POLYMERASE II TRANSCRIPTION FACTOR COMPLEX	88	0.33	1.30	0.0856	0.2679
RESPONSE TO INTERLEUKIN 4	27	-0.46	-1.53	0.0282	0.2679
RNA POLYMERASE II ACTIVATING TRANSCRIPTION FACTOR BINDING	34	-0.43	-1.53	0.0332	0.2682
NEGATIVE REGULATION OF DNA REPLICATION	45	0.37	1.30	0.1151	0.2684
REGULATION OF DENDRITE MORPHOGENESIS	73	0.34	1.30	0.0921	0.2685
POSITIVE REGULATION OF B CELL PROLIFERATION	36	-0.43	-1.53	0.0129	0.2686
COMPLEMENT ACTIVATION	34	-0.43	-1.53	0.0254	0.2693
POSITIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	312	0.28	1.30	0.0348	0.2700
REGULATION OF OXIDATIVE STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	26	-0.45	-1.53	0.0381	0.2701
POSITIVE REGULATION OF BLOOD VESSEL ENDOTHELIAL CELL MIGRATION	24	-0.46	-1.52	0.0460	0.2705
DETOXIFICATION	65	0.35	1.30	0.0989	0.2709
CYTOKINE MEDIATED SIGNALING PATHWAY	368	-0.29	-1.53	0.0000	0.2711
ESC E Z COMPLEX	15	0.48	1.30	0.1574	0.2711
ACTIVATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	82	0.33	1.30	0.1060	0.2712
POSITIVE REGULATION OF INTERLEUKIN 1 PRODUCTION	26	-0.45	-1.52	0.0288	0.2720
NUCLEOSIDE PHOSPHATE CATABOLIC PROCESS	61	0.35	1.30	0.1027	0.2722
PROLINE RICH REGION BINDING	19	0.45	1.30	0.1476	0.2725
COATED PIT	61	0.35	1.30	0.1030	0.2725
PYrimidine Nucleobase Metabolic Process	17	0.47	1.30	0.1446	0.2725
RESPONSE TO MUSCLE ACTIVITY	17	0.45	1.30	0.1725	0.2726
ADIPOSE TISSUE DEVELOPMENT	31	0.41	1.30	0.1514	0.2727

REGULATION OF ORGANELLE ASSEMBLY	135	0.31	1.30	0.0720	0.2727
POSITIVE REGULATION OF RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	24	0.43	1.29	0.1531	0.2736
OXIDOREDUCTASE ACTIVITY ACTING ON SINGLE DONORS WITH INCORPORATION OF MOLECULAR OXYGEN	25	-0.46	-1.52	0.0291	0.2741
REGULATION OF CARDIAC MUSCLE TISSUE DEVELOPMENT	42	0.38	1.29	0.1188	0.2746
GLYCINE METABOLIC PROCESS	15	0.48	1.29	0.1675	0.2747
REGULATION OF CYTOKINESIS	56	0.36	1.29	0.1138	0.2749
REFLEX	20	0.44	1.29	0.1488	0.2761
NEGATIVE REGULATION OF BINDING	111	0.32	1.29	0.0754	0.2763
CELLULAR SODIUM ION HOMEOSTASIS	18	0.46	1.29	0.1672	0.2764
POSITIVE REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	226	0.29	1.29	0.0396	0.2764
PROTEIN LOCALIZATION TO NUCLEUS	140	0.31	1.29	0.0688	0.2773
EXCITATORY POSTSYNAPTIC POTENTIAL	27	0.41	1.29	0.1453	0.2775
INTRACELLULAR RECEPTOR SIGNALING PATHWAY	151	0.30	1.29	0.0624	0.2776
PHOSPHATE TRANSMEMBRANE TRANSPORTER ACTIVITY	27	0.42	1.29	0.1395	0.2779
ACTIVATION OF INNATE IMMUNE RESPONSE	178	0.30	1.29	0.0581	0.2781
SYNTAXIN 1 BINDING	16	0.47	1.29	0.1631	0.2784
REGULATION OF CELLULAR RESPIRATION	20	0.44	1.29	0.1528	0.2786
ESTABLISHMENT OF LOCALIZATION BY MOVEMENT ALONG MICROTUBULE	80	0.33	1.29	0.0953	0.2787
REGULATION OF TRANSCRIPTION FACTOR IMPORT INTO NUCLEUS	83	0.33	1.29	0.1043	0.2794
REGULATION OF NUCLEOSIDE METABOLIC PROCESS	44	0.37	1.29	0.1290	0.2795
AXO DENDRITIC TRANSPORT	33	0.40	1.29	0.1518	0.2796
NEGATIVE REGULATION OF CELL CYCLE	366	0.28	1.29	0.0256	0.2797
REPLISOME	26	0.41	1.29	0.1419	0.2799
SPINDLE MICROTUBULE	50	0.36	1.29	0.1086	0.2801
POSITIVE REGULATION OF NUCLEASE ACTIVITY	15	-0.53	-1.51	0.0468	0.2832
LYMPHOCYTE MEDIATED IMMUNITY	82	-0.35	-1.51	0.0093	0.2832
NEGATIVE REGULATION OF JNK CASCADE	30	0.40	1.29	0.1451	0.2835
SAGA TYPE COMPLEX	27	0.41	1.29	0.1388	0.2835

REGULATION OF ATP METABOLIC PROCESS	44	0.37	1.28	0.1284	0.2852
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE	74	0.34	1.28	0.1031	0.2862
NEGATIVE REGULATION OF CALCIUM ION TRANSPORT INTO CYTOSOL	17	0.46	1.28	0.1661	0.2862
NEGATIVE REGULATION OF CHROMOSOME ORGANIZATION	85	0.33	1.28	0.1096	0.2864
REGULATION OF SYNAPTIC TRANSMISSION GABAERGIC	27	0.41	1.28	0.1546	0.2864
RECYCLING ENDOSOME MEMBRANE	38	0.38	1.28	0.1242	0.2865
CYCLIC NUCLEOTIDE CATABOLIC PROCESS	17	0.46	1.28	0.1589	0.2866
PLASMA MEMBRANE RAFT	79	0.33	1.28	0.0942	0.2867
ALCOHOL METABOLIC PROCESS	310	0.28	1.28	0.0380	0.2869
RETINOID X RECEPTOR BINDING	17	0.45	1.28	0.1849	0.2869
NEGATIVE REGULATION OF SEQUENCE SPECIFIC DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	117	0.31	1.28	0.0858	0.2870
PURINE NUCLEOSIDE BISPHOSPHATE BIOSYNTHETIC PROCESS	16	0.46	1.28	0.1804	0.2870
NUCLEAR MATRIX	81	0.33	1.28	0.0978	0.2871
REGULATION OF PROTEIN IMPORT	160	0.29	1.28	0.0740	0.2882
REGULATION OF MAMMARY GLAND EPITHELIAL CELL PROLIFERATION	15	0.48	1.28	0.1746	0.2884
NEGATIVE REGULATION OF INTRACELLULAR SIGNAL TRANSDUCTION	395	0.27	1.28	0.0214	0.2893
POSITIVE REGULATION OF FATTY ACID METABOLIC PROCESS	33	0.39	1.28	0.1323	0.2897
SPINDLE	236	0.29	1.28	0.0556	0.2907
EMBRYONIC HEMOPOIESIS	16	0.46	1.28	0.1676	0.2922
ATPASE ACTIVITY COUPLED TO MOVEMENT OF SUBSTANCES	113	0.31	1.28	0.1094	0.2923
NEGATIVE REGULATION OF STRIATED MUSCLE CELL APOPTOTIC PROCESS	16	-0.52	-1.51	0.0377	0.2924
REGULATION OF CELLULAR PH	63	0.34	1.28	0.1095	0.2927
INNATE IMMUNE RESPONSE	411	-0.28	-1.51	0.0000	0.2932
POSITIVE REGULATION OF TELOMERE MAINTENANCE	40	0.37	1.28	0.1458	0.2933
POSITIVE REGULATION OF INTERLEUKIN 10 PRODUCTION	27	-0.45	-1.51	0.0308	0.2935

OXIDOREDUCTASE ACTIVITY ACTING ON A HEME GROUP OF DONORS	20	0.44	1.28	0.1609	0.2935
INTRACILIARY TRANSPORT PARTICLE B	17	0.45	1.28	0.1581	0.2942
RESPONSE TO ACIDIC PH	19	-0.49	-1.50	0.0501	0.2943
RETINA VASCULATURE DEVELOPMENT IN CAMERA TYPE EYE	15	0.48	1.28	0.1556	0.2944
HYDROLASE ACTIVITY ACTING ON GLYCOSYL BONDS	96	0.32	1.28	0.0882	0.2947
PHOSPHATIDYLINOSITOL PHOSPHATE KINASE ACTIVITY	15	0.47	1.27	0.1850	0.2949
INTERCALATED DISC	46	0.37	1.27	0.1374	0.2950
RESPONSE TO FATTY ACID	74	0.33	1.27	0.1035	0.2951
IMMUNE RESPONSE REGULATING CELL SURFACE RECEPTOR SIGNALING PATHWAY	241	0.28	1.27	0.0623	0.2956
PROTEIN LIPID COMPLEX ASSEMBLY	19	0.45	1.27	0.1564	0.2965
REGULATION OF CARDIAC MUSCLE CELL DIFFERENTIATION	17	0.45	1.27	0.1863	0.2970
AU RICH ELEMENT BINDING	23	0.42	1.27	0.1684	0.2976
NEGATIVE REGULATION OF ORGANELLE ASSEMBLY	20	0.44	1.27	0.1682	0.2999
MONOAMINE TRANSPORT	20	0.44	1.27	0.1710	0.3005
REGULATION OF CANONICAL WNT SIGNALING PATHWAY	220	0.29	1.27	0.0488	0.3019
EPIDERMAL GROWTH FACTOR RECEPTOR BINDING	27	0.41	1.27	0.1621	0.3020
ENDOPLASMIC RETICULUM CALCIUM ION HOMEOSTASIS	19	0.44	1.27	0.1847	0.3020
NEGATIVE REGULATION OF OXIDATIVE STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	18	-0.51	-1.50	0.0502	0.3020
REGULATION OF RHODOPSIN MEDIATED SIGNALING PATHWAY	25	0.42	1.27	0.1628	0.3021
REGULATION OF CLATHRIN MEDIATED ENDOCYTOSIS	15	0.47	1.27	0.1818	0.3021
NEGATIVE REGULATION OF GENE EXPRESSION EPIGENETIC	75	-0.36	-1.50	0.0176	0.3021
ORGANIC ACID BIOSYNTHETIC PROCESS	232	0.28	1.27	0.0539	0.3023
MRNA CLEAVAGE	20	0.44	1.27	0.1716	0.3023
MITOTIC SISTER CHROMATID SEGREGATION	74	0.33	1.27	0.1343	0.3023
HISTONE METHYLATION	75	0.33	1.27	0.1216	0.3024

CELLULAR RESPONSE TO REACTIVE OXYGEN SPECIES	93	0.32	1.27	0.0830	0.3024
RIBONUCLEOSIDE BISPHOSPHATE BIOSYNTHETIC PROCESS	16	0.46	1.27	0.1678	0.3026
NEGATIVE REGULATION OF NUCLEAR DIVISION	40	0.37	1.27	0.1510	0.3028
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH NH GROUP OF DONORS	24	0.42	1.27	0.1531	0.3030
NEGATIVE REGULATION OF WNT SIGNALING PATHWAY	184	0.29	1.27	0.0692	0.3030
NEGATIVE REGULATION OF INTERLEUKIN 1 PRODUCTION	15	-0.51	-1.50	0.0585	0.3033
EMBRYONIC AXIS SPECIFICATION	32	-0.42	-1.49	0.0521	0.3033
HORMONE RECEPTOR BINDING	139	0.30	1.27	0.1086	0.3034
NEGATIVE REGULATION OF DNA METABOLIC PROCESS	90	0.32	1.27	0.1015	0.3035
NEGATIVE REGULATION OF B CELL ACTIVATION	26	-0.46	-1.50	0.0372	0.3036
MICROTUBULE NUCLEATION	18	0.45	1.27	0.1783	0.3037
RETROMER COMPLEX	19	0.44	1.27	0.1889	0.3047
CORNIFIED ENVELOPE	32	-0.43	-1.49	0.0372	0.3050
RESPONSE TO NITRIC OXIDE	19	0.44	1.26	0.1658	0.3052
POSITIVE REGULATION OF CELL PROJECTION ORGANIZATION	279	0.28	1.26	0.0640	0.3054
CHROMOSOME CENTROMERIC REGION	143	0.30	1.26	0.0845	0.3055
CIRCADIAN RHYTHM	123	0.31	1.26	0.0846	0.3056
PROTEIN FOLDING	187	0.29	1.26	0.0684	0.3056
REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	126	0.31	1.26	0.0842	0.3057
POSITIVE REGULATION OF TOR SIGNALING	25	0.41	1.26	0.1740	0.3058
STEROID HORMONE MEDIATED SIGNALING PATHWAY	113	0.31	1.26	0.0891	0.3060
HUMORAL IMMUNE RESPONSE MEDIATED BY CIRCULATING IMMUNOGLOBULIN	27	-0.43	-1.49	0.0496	0.3061
CELL DIFFERENTIATION IN SPINAL CORD	50	-0.38	-1.49	0.0170	0.3068
PEPTIDYL ARGININE MODIFICATION	16	0.45	1.26	0.1853	0.3068
CELL VOLUME HOMEOSTASIS	26	0.41	1.26	0.1567	0.3069
NUCLEAR INNER MEMBRANE	46	0.36	1.26	0.1341	0.3070
CHOLESTEROL HOMEOSTASIS	52	0.35	1.26	0.1392	0.3071
CELLULAR RESPONSE TO GLUCOSE STARVATION	26	0.41	1.26	0.1678	0.3072

REGULATION OF TRIGLYCERIDE BIOSYNTHETIC PROCESS	16	0.47	1.26	0.1727	0.3082
NEGATIVE REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	26	0.41	1.26	0.1867	0.3084
PHOSPHATIDYLINOSITOL 3 5 BISPHOSPHATE BINDING	18	0.45	1.26	0.1898	0.3085
POSITIVE REGULATION OF OSTEOCLAST DIFFERENTIATION	21	-0.47	-1.49	0.0422	0.3085
CARBOXYLIC ACID BIOSYNTHETIC PROCESS	232	0.28	1.26	0.0608	0.3087
PHOSPHOLIPID TRANSPORT	56	0.35	1.26	0.1256	0.3087
NEGATIVE REGULATION OF MACROAUTOPHAGY	18	0.45	1.26	0.2034	0.3088
INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	62	0.33	1.26	0.1262	0.3096
CELLULAR RESPONSE TO EXTRACELLULAR STIMULUS	169	0.29	1.26	0.0854	0.3097
CELLULAR RESPONSE TO OXIDATIVE STRESS	161	0.29	1.26	0.0862	0.3107
CHROMATIN REMODELING	118	0.30	1.26	0.0972	0.3113
ONE CARBON METABOLIC PROCESS	20	0.45	1.26	0.1893	0.3113
TELOMERE MAINTENANCE VIA TELOMERASE	15	0.47	1.26	0.1915	0.3115
LONG TERM MEMORY	27	0.41	1.26	0.1906	0.3116
ATRIOVENTRICULAR VALVE MORPHOGENESIS	16	-0.50	-1.48	0.0782	0.3135
ENDORIBONUCLEASE COMPLEX	20	0.43	1.26	0.1661	0.3144
REGULATION OF OLIGODENDROCYTE DIFFERENTIATION	27	0.40	1.26	0.1757	0.3145
REGULATION OF T CELL DIFFERENTIATION	90	-0.34	-1.48	0.0122	0.3145
PRONUCLEUS	15	0.46	1.26	0.2092	0.3146
INCLUSION BODY	63	0.33	1.26	0.1473	0.3146
REGULATION OF CARDIAC MUSCLE CONTRACTION BY CALCIUM ION SIGNALING	21	0.43	1.26	0.1855	0.3147
INTRACELLULAR LIPID TRANSPORT	19	0.44	1.26	0.1874	0.3148
SEGMENT SPECIFICATION	16	-0.52	-1.48	0.0611	0.3151
NUCLEOSIDE BISPHOSPHATE BIOSYNTHETIC PROCESS	16	0.46	1.25	0.1703	0.3154
NEGATIVE REGULATION OF KINASE ACTIVITY	230	0.28	1.25	0.0562	0.3158
REGULATION OF JNK CASCADE	146	0.30	1.25	0.0815	0.3161

REGULATION OF LEUKOCYTE PROLIFERATION	166	-0.30	-1.48	0.0035	0.3164
EUCHROMATIN	27	0.41	1.25	0.1711	0.3170
REGULATION OF CIRCADIAN RHYTHM	91	0.31	1.25	0.1108	0.3170
POSITIVE REGULATION OF INNATE IMMUNE RESPONSE	216	0.28	1.25	0.0663	0.3173
AGING	229	0.28	1.25	0.0701	0.3180
SMOOTH MUSCLE CONTRACTION	42	0.37	1.25	0.1469	0.3182
PROTEIN EXIT FROM ENDOPLASMIC RETICULUM	18	0.45	1.25	0.2076	0.3187
REACTIVE OXYGEN SPECIES METABOLIC PROCESS	84	0.32	1.25	0.1092	0.3194
CELLULAR RESPONSE TO INORGANIC SUBSTANCE	126	0.30	1.25	0.1215	0.3195
REGULATION OF CELLULAR RESPONSE TO HEAT	65	0.33	1.25	0.1309	0.3196
HEPATICOBILIARY SYSTEM DEVELOPMENT	117	0.30	1.25	0.1060	0.3197
ACUTE INFLAMMATORY RESPONSE	62	0.34	1.25	0.1626	0.3198
NEGATIVE REGULATION OF CYTOSKELETON ORGANIZATION	184	0.29	1.25	0.0844	0.3207
RESPONSE TO EPIDERMAL GROWTH FACTOR	28	0.40	1.25	0.1707	0.3208
PYRIDOXAL PHOSPHATE BINDING	48	0.36	1.25	0.1654	0.3211
REGULATION OF INSULIN SECRETION INVOLVED IN CELLULAR RESPONSE TO GLUCOSE STIMULUS	44	0.36	1.25	0.1661	0.3212
MITOTIC CELL CYCLE CHECKPOINT	117	0.31	1.25	0.1216	0.3218
PHOSPHATIDYLINOSITOL DEPHOSPHORYLATION	19	0.44	1.25	0.1993	0.3220
CELLULAR RESPONSE TO STEROID HORMONE STIMULUS	194	0.29	1.25	0.0760	0.3232
CELL CYCLE ARREST	132	0.30	1.25	0.1036	0.3239
AXON CYTOPLASM	30	0.39	1.25	0.1597	0.3247
LYMPHOCYTE ACTIVATION INVOLVED IN IMMUNE RESPONSE	80	-0.34	-1.48	0.0182	0.3252
NEGATIVE REGULATION OF INNATE IMMUNE RESPONSE	28	0.39	1.25	0.1728	0.3257
CELL DIFFERENTIATION INVOLVED IN KIDNEY DEVELOPMENT	35	-0.40	-1.47	0.0322	0.3257
POSITIVE REGULATION OF LEUKOCYTE PROLIFERATION	110	-0.33	-1.48	0.0000	0.3259
PYRIMIDINE NUCLEOTIDE METABOLIC PROCESS	38	0.37	1.25	0.1542	0.3262

INTERSTRAND CROSS LINK REPAIR	27	0.40	1.25	0.1786	0.3262
REGULATION OF I KAPPAB KINASE NF KAPPAB SIGNALING	205	0.28	1.24	0.0771	0.3268
THYROID GLAND DEVELOPMENT	23	-0.46	-1.47	0.0350	0.3270
EXOPEPTIDASE ACTIVITY	94	0.31	1.24	0.1354	0.3273
OXIDOREDUCTASE ACTIVITY ACTING ON THE ALDEHYDE OR OXO GROUP OF DONORS	40	0.37	1.24	0.1651	0.3276
NADP BINDING	38	0.38	1.24	0.1692	0.3283
REGULATION OF VASCULATURE DEVELOPMENT	216	-0.30	-1.47	0.0000	0.3286
FIBRONECTIN BINDING	22	-0.46	-1.47	0.0597	0.3286
REGULATION OF MESONEPHROS DEVELOPMENT	26	-0.43	-1.47	0.0437	0.3295
ORGANELLE MEMBRANE FUSION	84	0.32	1.24	0.1555	0.3297
SOMATIC DIVERSIFICATION OF IMMUNOGLOBULINS	22	0.41	1.24	0.1726	0.3298
GLYCOSYLATION	223	0.28	1.24	0.0714	0.3299
14 3 3 PROTEIN BINDING	17	-0.49	-1.47	0.0862	0.3301
STEROL HOMEOSTASIS	52	0.35	1.24	0.1483	0.3302
AMIDE BINDING	216	0.28	1.24	0.0901	0.3305
HISTONE DEMETHYLASE ACTIVITY	24	0.41	1.24	0.1872	0.3305
TETRAHYDROFOLATE METABOLIC PROCESS	16	0.45	1.24	0.1864	0.3306
ORGANOPHOSPHATE ESTER TRANSPORT	85	0.32	1.24	0.1166	0.3315
CELL DIVISION SITE	50	0.35	1.24	0.1591	0.3319
MONOVALENT INORGANIC ANION HOMEOSTASIS	16	0.45	1.24	0.1996	0.3320
REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	195	0.28	1.24	0.0978	0.3320
REGULATION OF mRNA 3 END PROCESSING	27	0.40	1.24	0.1772	0.3321
REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	83	0.32	1.24	0.1403	0.3322
CYTOKINESIS	69	0.33	1.24	0.1451	0.3324
POLYOL METABOLIC PROCESS	86	0.32	1.24	0.1256	0.3327
HORMONE MEDIATED SIGNALING PATHWAY	143	0.29	1.24	0.1257	0.3329
RUFFLE ORGANIZATION	19	0.44	1.24	0.1946	0.3332
POSITIVE REGULATION OF mRNA 3 END PROCESSING	16	0.45	1.24	0.1969	0.3332

REGULATION OF NEURAL PRECURSOR CELL PROLIFERATION	69	-0.35	-1.46	0.0171	0.3333
G PROTEIN COUPLED AMINE RECEPTOR ACTIVITY	39	-0.39	-1.46	0.0350	0.3340
MONOOXYGENASE ACTIVITY	57	-0.36	-1.46	0.0222	0.3350
CHROMATIN BINDING	390	0.26	1.24	0.0486	0.3357
SYNAPTIC TRANSMISSION GLUTAMATERGIC	21	0.42	1.24	0.1642	0.3367
RETINOIC ACID RECEPTOR BINDING	27	0.39	1.24	0.1801	0.3373
REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	193	0.29	1.24	0.1011	0.3376
RESPONSE TO OXYGEN RADICAL	17	0.44	1.23	0.2142	0.3388
SKELETAL MUSCLE CELL DIFFERENTIATION	51	-0.38	-1.46	0.0339	0.3388
FAT SOLUBLE VITAMIN METABOLIC PROCESS	27	-0.43	-1.46	0.0564	0.3388
REGULATION OF B CELL ACTIVATION	91	-0.33	-1.46	0.0183	0.3390
REGULATION OF DIGESTIVE SYSTEM PROCESS	35	0.37	1.23	0.1821	0.3390
PEPTIDE CROSS LINKING	43	-0.39	-1.46	0.0347	0.3405
GALACTOSYLTRANSFERASE ACTIVITY	28	0.39	1.23	0.1973	0.3406
RENAL WATER HOMEOSTASIS	26	0.40	1.23	0.1993	0.3415
RESPONSE TO EXTRACELLULAR STIMULUS	405	0.26	1.23	0.0537	0.3415
CONDENSED NUCLEAR CHROMOSOME CENTROMERIC REGION	15	-0.51	-1.46	0.0813	0.3423
PROTEIN MATURATION	228	0.28	1.23	0.0926	0.3430
REGULATION OF ANION TRANSPORT	126	0.30	1.23	0.1097	0.3435
REGULATION OF VIRAL ENTRY INTO HOST CELL	25	0.41	1.23	0.1929	0.3435
REGENERATION	147	0.29	1.23	0.1213	0.3436
POSITIVE REGULATION OF WNT SIGNALING PATHWAY	143	0.29	1.23	0.1015	0.3436
PATTERNrecognition RECEPTOR SIGNALING PATHWAY	98	0.31	1.23	0.1301	0.3437
NEGATIVE REGULATION OF CHROMOSOME SEGREGATION	25	0.41	1.23	0.1939	0.3437
NEGATIVE REGULATION OF PLATELET ACTIVATION	17	0.43	1.23	0.2142	0.3438
PROTEIN LOCALIZATION TO MEMBRANE	328	0.26	1.23	0.0636	0.3439
ENDONUCLEASE ACTIVITY	95	0.31	1.23	0.1230	0.3439
CYTOPLASMIC MICROTUBULE ORGANIZATION	38	0.36	1.23	0.1499	0.3440

NEGATIVE REGULATION OF PHOSPHORYLATION	386	0.26	1.23	0.0619	0.3441
REGULATION OF NEURON APOPTOTIC PROCESS	166	0.29	1.23	0.0910	0.3444
POST TRANSLATIONAL PROTEIN MODIFICATION	24	0.40	1.23	0.2145	0.3444
ENDOTHELIAL CELL DIFFERENTIATION	67	0.33	1.23	0.1461	0.3446
PROTEIN COMPLEX INVOLVED IN CELL ADHESION	30	-0.43	-1.45	0.0442	0.3455
TUBULIN BINDING	227	0.28	1.23	0.0875	0.3455
GAMMA TUBULIN BINDING	20	0.43	1.23	0.2143	0.3459
EMBRYONIC PLACENTA MORPHOGENESIS	22	-0.45	-1.45	0.0699	0.3460
RAN GTPASE BINDING	30	0.38	1.23	0.1905	0.3468
CELLULAR RESPONSE TO LIPID	412	0.26	1.23	0.0499	0.3469
HISTONE METHYLTRANSFERASE ACTIVITY	52	0.35	1.23	0.1708	0.3478
STEROID HYDROXYLASE ACTIVITY	18	-0.48	-1.45	0.0583	0.3484
CEREBELLAR CORTEX FORMATION	22	-0.45	-1.45	0.0707	0.3491
DEATH RECEPTOR ACTIVITY	20	-0.46	-1.44	0.0614	0.3491
B CELL MEDIATED IMMUNITY	51	-0.37	-1.45	0.0292	0.3496
REGULATION OF MYOTUBE DIFFERENTIATION	51	-0.38	-1.45	0.0382	0.3496
MITOTIC DNA INTEGRITY CHECKPOINT	84	0.31	1.23	0.1503	0.3498
POLYOL TRANSPORT	16	-0.49	-1.45	0.0678	0.3500
HORMONE ACTIVITY	96	-0.33	-1.45	0.0176	0.3507
T CELL DIFFERENTIATION INVOLVED IN IMMUNE RESPONSE	29	-0.44	-1.45	0.0510	0.3512
LOW DENSITY LIPOPROTEIN PARTICLE RECEPTOR BINDING	17	0.44	1.22	0.2338	0.3515
RECOMBINATIONAL REPAIR	57	0.33	1.22	0.1780	0.3516
EPITHELIAL CELL FATE COMMITMENT	15	0.44	1.22	0.2220	0.3521
BLOC COMPLEX	16	0.44	1.22	0.1971	0.3522
NUCLEAR CHROMOSOME SEGREGATION	189	0.28	1.22	0.0872	0.3524
ERYTHROCYTE DEVELOPMENT	17	-0.48	-1.44	0.0657	0.3538
LIPOPROTEIN PARTICLE RECEPTOR BINDING	22	0.41	1.22	0.2142	0.3553
CARBOHYDRATE DERIVATIVE TRANSPORT	47	0.35	1.22	0.1705	0.3555
PROTEINACEOUS EXTRACELLULAR MATRIX	322	-0.27	-1.44	0.0000	0.3556
EXTRACELLULAR MATRIX	386	-0.27	-1.44	0.0000	0.3578

NEGATIVE REGULATION OF HOMOTYPIC CELL CELL ADHESION	84	-0.33	-1.44	0.0237	0.3585
POSITIVE REGULATION OF DEVELOPMENTAL GROWTH	140	0.29	1.22	0.1337	0.3589
ISOPRENOID BIOSYNTHETIC PROCESS	25	0.40	1.22	0.2074	0.3589
REGULATION OF PROTEIN BINDING	149	0.29	1.22	0.1240	0.3591
SEMAPHORIN RECEPTOR BINDING	22	-0.46	-1.44	0.0612	0.3594
POSITIVE REGULATION OF DEPHOSPHORYLATION	44	0.35	1.22	0.1726	0.3600
REGULATION OF INTERLEUKIN 1 BETA PRODUCTION	37	-0.39	-1.44	0.0366	0.3606
REGULATION OF TYPE I INTERFERON MEDIATED SIGNALING PATHWAY	30	-0.41	-1.43	0.0536	0.3607
REGULATION OF CELL CYCLE CHECKPOINT	24	0.41	1.22	0.1829	0.3612
PROTEIN MANNOSYLATION	17	0.44	1.22	0.2139	0.3613
RESPONSE TO IRON ION	30	0.38	1.22	0.2079	0.3613
REGULATION OF AUTOPHAGOSOME ASSEMBLY	31	0.38	1.22	0.2085	0.3614
ATPASE COMPLEX	24	0.40	1.22	0.2003	0.3616
REGULATION OF NEURON DEATH	217	0.27	1.22	0.1088	0.3623
NEGATIVE REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	16	0.45	1.22	0.2236	0.3624
CYTOPLASMIC STRESS GRANULE	30	0.38	1.22	0.2091	0.3625
PROTEIN PHOSPHORYLATED AMINO ACID BINDING	23	0.41	1.22	0.2177	0.3627
NEGATIVE REGULATION OF FIBROBLAST PROLIFERATION	23	0.41	1.22	0.2281	0.3640
CELL AGING	55	0.34	1.21	0.1712	0.3647
CELLULAR COMPONENT DISASSEMBLY INVOLVED IN EXECUTION PHASE OF APOPTOSIS	39	0.36	1.21	0.1768	0.3648
PHOSPHOLIPASE A2 ACTIVITY	29	0.39	1.21	0.2000	0.3650
NEGATIVE REGULATION OF LYMPHOCYTE MEDIATED IMMUNITY	24	-0.44	-1.43	0.0588	0.3657
CARBOXY TERMINAL DOMAIN PROTEIN KINASE COMPLEX	20	0.42	1.21	0.2213	0.3665
REGULATION OF DENDRITE DEVELOPMENT	115	0.30	1.21	0.1360	0.3666
REGULATION OF SMOOTH MUSCLE CELL MIGRATION	46	0.34	1.21	0.1766	0.3667

PROTEIN SERINE THREONINE KINASE ACTIVITY	401	0.26	1.21	0.0648	0.3667
PHOSPHATIDYLETHANOLAMINE ACYL CHAIN REMODELING	22	0.40	1.21	0.2194	0.3681
INTRAMOLECULAR OXIDOREDUCTASE ACTIVITY TRANSPOSING S S BONDS	21	0.41	1.21	0.2101	0.3686
SCAFFOLD PROTEIN BINDING	43	0.35	1.21	0.1773	0.3699
SNARE BINDING	111	0.30	1.21	0.1360	0.3699
CLATHRIN COAT	43	0.35	1.21	0.1948	0.3700
NEGATIVE REGULATION OF T CELL RECEPTOR SIGNALING PATHWAY	15	0.46	1.21	0.2201	0.3700
POSITIVE REGULATION OF NEURON DEATH	57	0.33	1.21	0.1888	0.3702
PROTEIN TYROSINE KINASE BINDING	51	0.34	1.21	0.2048	0.3706
LEUKOCYTE MEDIATED IMMUNITY	118	-0.31	-1.43	0.0000	0.3709
CELLULAR RESPONSE TO INSULIN STIMULUS	135	0.29	1.21	0.1546	0.3710
ATRIOVENTRICULAR VALVE DEVELOPMENT	19	-0.47	-1.43	0.0771	0.3711
NEGATIVE REGULATION OF BMP SIGNALING PATHWAY	37	0.36	1.21	0.1957	0.3712
REGULATION OF DEFENSE RESPONSE TO VIRUS BY HOST	103	0.30	1.21	0.1437	0.3712
CILIUM MOVEMENT	24	0.40	1.21	0.2153	0.3713
REGULATION OF DNA BIOSYNTHETIC PROCESS	82	0.31	1.21	0.1634	0.3713
AMINO ACID TRANSMEMBRANE TRANSPORT	60	0.33	1.21	0.1861	0.3714
MHC PROTEIN BINDING	19	-0.47	-1.43	0.0679	0.3716
CYCLIC NUCLEOTIDE BIOSYNTHETIC PROCESS	32	-0.40	-1.43	0.0560	0.3716
KINASE INHIBITOR ACTIVITY	86	0.31	1.21	0.1597	0.3729
OXIDOREDUCTASE ACTIVITY ACTING ON THE ALDEHYDE OR OXO GROUP OF DONORS NAD OR NADP AS ACCEPTOR	31	0.37	1.21	0.2240	0.3730
REGULATION OF CELL DIVISION	238	0.27	1.21	0.0859	0.3731
REGULATION OF CARDIAC MUSCLE CELL PROLIFERATION	25	0.39	1.21	0.2185	0.3732
REGULATION OF WNT SIGNALING PATHWAY	288	0.27	1.21	0.0851	0.3737
POSITIVE REGULATION OF EXOCYTOSIS	75	0.32	1.21	0.1807	0.3740
INTRINSIC COMPONENT OF ENDOPLASMIC RETICULUM MEMBRANE	106	0.29	1.21	0.1506	0.3740

CELL PROJECTION CYTOPLASM	47	0.34	1.21	0.1897	0.3742
TRIGLYCERIDE CATABOLIC PROCESS	20	0.42	1.21	0.2104	0.3744
IONOTROPIC GLUTAMATE RECEPTOR BINDING	22	0.41	1.21	0.2211	0.3753
GLYCOPROTEIN METABOLIC PROCESS	306	0.26	1.20	0.0825	0.3754
REGULATION OF SYNAPSE ASSEMBLY	73	0.32	1.21	0.1816	0.3754
H4 HISTONE ACETYLTRANSFERASE COMPLEX	16	0.44	1.20	0.2540	0.3768
MITOCHONDRIAL ELECTRON TRANSPORT CYTOCHROME C TO OXYGEN	15	0.45	1.20	0.2447	0.3769
RECYCLING ENDOSOME	115	0.30	1.20	0.1542	0.3774
BASOLATERAL PLASMA MEMBRANE	191	0.27	1.20	0.1208	0.3779
NEGATIVE REGULATION OF NEURON APOPTOTIC PROCESS	117	0.29	1.20	0.1464	0.3780
LIGAND DEPENDENT NUCLEAR RECEPTOR BINDING	21	0.41	1.20	0.2407	0.3797
MYD88 INDEPENDENT TOLL LIKE RECEPTOR SIGNALING PATHWAY	28	0.39	1.20	0.2166	0.3800
NEGATIVE REGULATION OF SMOOTH MUSCLE CELL MIGRATION	15	0.44	1.20	0.2420	0.3800
ANDROGEN RECEPTOR SIGNALING PATHWAY	38	0.36	1.20	0.2022	0.3800
DAMAGED DNA BINDING	48	0.34	1.20	0.1894	0.3801
SNRNA BINDING	33	0.37	1.20	0.2147	0.3801
ANTEROGRADE AXONAL TRANSPORT	23	0.40	1.20	0.2373	0.3801
CELLULAR RESPONSE TO EXTERNAL STIMULUS	238	0.27	1.20	0.1127	0.3803
REGULATION OF CHROMOSOME ORGANIZATION	239	0.27	1.20	0.1158	0.3805
INNER EAR MORPHOGENESIS	87	-0.33	-1.42	0.0226	0.3805
ENDOTHELIAL CELL DEVELOPMENT	41	0.35	1.20	0.2146	0.3808
REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	83	-0.33	-1.42	0.0300	0.3814
POSITIVE REGULATION OF INTRACELLULAR TRANSPORT	325	0.26	1.20	0.0851	0.3818
APICAL PLASMA MEMBRANE	264	0.26	1.20	0.0948	0.3818
RECEPTOR SIGNALING PROTEIN SERINE THREONINE KINASE ACTIVITY	82	0.31	1.20	0.1813	0.3818
LIPID TRANSLOCATION	21	0.41	1.20	0.2424	0.3819
CORECEPTOR ACTIVITY	35	0.35	1.20	0.1924	0.3820
CHROMOSOME SEPARATION	18	0.42	1.20	0.2590	0.3827

NECROTIC CELL DEATH	27	0.39	1.20	0.2437	0.3827
REGULATION OF DNA DEPENDENT DNA REPLICATION	36	0.36	1.20	0.2029	0.3831
POSITIVE REGULATION OF BINDING	118	0.29	1.20	0.1591	0.3832
REGULATION OF STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	179	0.28	1.20	0.1265	0.3833
CELLULAR RESPONSE TO IONIZING RADIATION	43	0.34	1.20	0.1910	0.3833
CHAPERONE BINDING	69	0.32	1.20	0.2047	0.3835
REGULATION OF ADAPTIVE IMMUNE RESPONSE	105	-0.31	-1.42	0.0103	0.3839
POTASSIUM ION TRANSPORT	148	-0.30	-1.42	0.0139	0.3845
NEGATIVE REGULATION OF RESPONSE TO OXIDATIVE STRESS	31	-0.41	-1.41	0.0590	0.3849
SPERM MOTILITY	37	-0.39	-1.41	0.0541	0.3856
NEURON FATE COMMITMENT	64	-0.35	-1.42	0.0358	0.3857
EAR MORPHOGENESIS	107	-0.31	-1.41	0.0131	0.3863
MICROTUBULE CYTOSKELETON ORGANIZATION	276	0.26	1.20	0.1029	0.3867
MACROMOLECULE DEACYLATION	61	0.33	1.20	0.1966	0.3867
MYOFILAMENT	22	-0.45	-1.41	0.0782	0.3872
POSITIVE REGULATION OF LIPID METABOLIC PROCESS	119	0.29	1.19	0.1460	0.3874
REGULATION OF TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	20	0.41	1.19	0.2285	0.3874
POSITIVE REGULATION OF STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	122	0.29	1.20	0.1394	0.3875
RESPONSE TO EPINEPHRINE	15	0.44	1.19	0.2429	0.3875
HISTONE DEACETYLASE BINDING	92	0.30	1.19	0.1699	0.3875
PHOSPHOLIPASE C ACTIVITY	29	0.38	1.19	0.2230	0.3876
DYNEIN BINDING	23	0.41	1.19	0.2385	0.3877
REGULATION OF HEART MORPHOGENESIS	29	0.38	1.19	0.2245	0.3877
HSP70 PROTEIN BINDING	25	-0.42	-1.41	0.0879	0.3885
REGULATION OF CAMP MEDIATED SIGNALING	23	-0.44	-1.41	0.0866	0.3889
REGULATION OF DENDRITIC SPINE MORPHOGENESIS	30	0.37	1.19	0.2145	0.3892
PROTEIN HETEROOLIGOMERIZATION	86	0.31	1.19	0.1619	0.3893
RESPONSE TO INORGANIC SUBSTANCE	422	0.25	1.19	0.0817	0.3894
CELLULAR RESPONSE TO INTERLEUKIN 4	23	-0.43	-1.41	0.0627	0.3898

POSITIVE REGULATION OF MESONEPHROS DEVELOPMENT	22	-0.44	-1.41	0.0852	0.3900
REGULATION OF PH	77	0.31	1.19	0.1980	0.3909
CELLULAR RESPONSE TO ANTIBIOTIC	16	-0.49	-1.41	0.0736	0.3915
T TUBULE	41	0.35	1.19	0.2056	0.3916
REGULATION OF DEFENSE RESPONSE TO VIRUS	154	0.28	1.19	0.1362	0.3918
MONOSACCHARIDE TRANSPORT	44	0.35	1.19	0.2237	0.3934
DEMETHYLATION	40	0.35	1.19	0.2042	0.3935
RESPONSE TO INTERLEUKIN 1	98	0.30	1.19	0.1617	0.3940
PHOSPHATIDYLCHOLINE BIOSYNTHETIC PROCESS	24	0.39	1.19	0.2381	0.3983
AMINO SUGAR METABOLIC PROCESS	34	0.37	1.19	0.2101	0.3985
RETINOL METABOLIC PROCESS	26	0.38	1.19	0.2399	0.4001
CELL DIFFERENTIATION IN HINDBRAIN	21	-0.44	-1.39	0.0775	0.4004
RECEPTOR SIGNALING COMPLEX SCAFFOLD ACTIVITY	20	-0.45	-1.39	0.0950	0.4005
CERAMIDE METABOLIC PROCESS	59	0.33	1.19	0.2112	0.4013
INWARD RECTIFIER POTASSIUM CHANNEL ACTIVITY	21	-0.45	-1.39	0.0853	0.4014
REGULATION OF METANEPHROS DEVELOPMENT	23	-0.43	-1.39	0.0900	0.4015
OOCYTE DIFFERENTIATION	32	-0.41	-1.40	0.0771	0.4017
CYTOKINE RECEPTOR BINDING	220	-0.28	-1.40	0.0000	0.4017
REGULATION OF SMOOTHENED SIGNALING PATHWAY	58	-0.34	-1.39	0.0480	0.4020
RESPONSE TO TOPOLOGICALLY INCORRECT PROTEIN	143	-0.29	-1.40	0.0189	0.4021
ENDOTHELIUM DEVELOPMENT	85	0.30	1.18	0.1758	0.4023
ACTIN MYOSIN FILAMENT SLIDING	35	-0.38	-1.39	0.0579	0.4024
REGULATION OF MACROPHAGE DIFFERENTIATION	20	0.41	1.18	0.2437	0.4025
AMINO ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	71	0.31	1.18	0.1909	0.4025
REGULATION OF RECEPTOR INTERNALIZATION	33	-0.39	-1.40	0.0628	0.4025
NEGATIVE REGULATION OF CELL AGING	15	-0.50	-1.40	0.0973	0.4025
POSITIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY	49	0.34	1.18	0.2083	0.4026
POSITIVE REGULATION OF KIDNEY DEVELOPMENT	40	-0.38	-1.40	0.0679	0.4026
TRANSCRIPTION COREPRESSOR ACTIVITY	179	0.27	1.18	0.1444	0.4032

CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	115	-0.31	-1.40	0.0202	0.4032
NEGATIVE REGULATION OF LEUKOCYTE MEDIATED IMMUNITY	33	-0.39	-1.40	0.0857	0.4036
CELLULAR RESPONSE TO ORGANIC CYCLIC COMPOUND	419	0.25	1.18	0.1051	0.4038
REGULATION OF CELLULAR CARBOHYDRATE CATABOLIC PROCESS	37	0.35	1.18	0.2326	0.4040
NUCLEOTIDE EXCISION REPAIR DNA INCISION	31	0.36	1.18	0.2541	0.4041
POSITIVE REGULATION OF CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	150	0.28	1.18	0.1521	0.4041
ANTERIOR POSTERIOR PATTERN SPECIFICATION	185	-0.28	-1.39	0.0000	0.4042
AMMONIUM TRANSPORT	52	0.33	1.18	0.2173	0.4042
POSITIVE REGULATION OF CYTOPLASMIC TRANSPORT	254	0.26	1.18	0.1319	0.4049
REGULATION OF GENE EXPRESSION EPIGENETIC	180	0.27	1.18	0.1532	0.4052
ISOPRENOID BINDING	27	-0.42	-1.39	0.0844	0.4053
LYMPHOCYTE HOMEOSTASIS	44	0.34	1.18	0.2318	0.4055
REGULATION OF HORMONE BIOSYNTHETIC PROCESS	17	0.42	1.18	0.2533	0.4056
RESPONSE TO TEMPERATURE STIMULUS	130	0.29	1.18	0.1507	0.4056
NEGATIVE REGULATION OF INTRACELLULAR TRANSPORT	123	0.29	1.18	0.1784	0.4057
NEGATIVE REGULATION OF ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY	19	0.41	1.18	0.2534	0.4069
REGULATION OF SEQUENCE SPECIFIC DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	320	0.26	1.18	0.1137	0.4081
POSITIVE REGULATION OF MYOTUBE DIFFERENTIATION	25	-0.43	-1.39	0.0976	0.4082
REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	18	0.42	1.18	0.2577	0.4083
NEGATIVE REGULATION OF PROTEIN CATABOLIC PROCESS	100	0.29	1.18	0.1744	0.4084
SKELETAL MUSCLE CONTRACTION	30	-0.40	-1.39	0.0762	0.4086
REGULATION OF PLASMA MEMBRANE ORGANIZATION	64	0.32	1.18	0.2140	0.4086
AXON ENSHEATHMENT	81	0.30	1.18	0.2054	0.4092

POSITIVE REGULATION OF EMBRYONIC DEVELOPMENT	32	0.36	1.18	0.2306	0.4094
POSITIVE REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	15	0.44	1.18	0.2384	0.4095
REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	138	0.28	1.18	0.1667	0.4097
REGULATION OF ACTIN CYTOSKELETON REORGANIZATION	30	0.37	1.18	0.2467	0.4098
REGULATION OF CARBOHYDRATE BIOSYNTHETIC PROCESS	81	0.30	1.18	0.1817	0.4099
BASAL LAMINA	18	0.41	1.18	0.2469	0.4101
CELL FATE SPECIFICATION	69	-0.33	-1.39	0.0537	0.4102
TRANSPORT VESICLE MEMBRANE	122	0.29	1.18	0.1637	0.4103
MICROTUBULE BASED PROCESS	409	0.25	1.18	0.1047	0.4104
REGULATION OF ALPHA AMINO 3 HYDROXY 5 METHYL 4 ISOXAZOLE PROPIONATE SELECTIVE GLUTAMATE RECEPTOR ACTIVITY	19	-0.45	-1.38	0.1000	0.4110
PHOSPHOLIPID TRANSPORTER ACTIVITY	45	0.34	1.18	0.2259	0.4113
REGULATION OF DEPHOSPHORYLATION	134	0.28	1.18	0.1593	0.4122
POSITIVE REGULATION OF MUSCLE TISSUE DEVELOPMENT	52	0.33	1.18	0.2197	0.4131
ANION HOMEOSTASIS	36	0.35	1.18	0.2347	0.4137
REGULATION OF OXIDATIVE STRESS INDUCED CELL DEATH	40	-0.37	-1.38	0.0873	0.4142
PERICENTRIOLAR MATERIAL	17	0.41	1.17	0.2440	0.4142
NEGATIVE REGULATION OF PROTEIN COMPLEX DISASSEMBLY	137	0.28	1.17	0.1696	0.4156
NEGATIVE REGULATION OF CELLULAR RESPONSE TO OXIDATIVE STRESS	31	-0.41	-1.38	0.0820	0.4158
PHOSPHATIDYLINOSITOL PHOSPHATE BINDING	111	0.29	1.17	0.1789	0.4161
ODONTOGENESIS	101	0.29	1.17	0.1797	0.4162
NEGATIVE REGULATION OF LYASE ACTIVITY	26	-0.42	-1.38	0.0887	0.4163
POSITIVE REGULATION OF DNA REPLICATION	78	0.31	1.17	0.1864	0.4169
HORMONE METABOLIC PROCESS	138	0.28	1.17	0.1868	0.4171
REGULATION OF CARBOHYDRATE CATABOLIC PROCESS	37	0.35	1.17	0.2335	0.4172
RESPONSE TO LIGHT STIMULUS	243	0.26	1.17	0.1354	0.4173

REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	27	0.37	1.17	0.2365	0.4174
REGULATION OF KIDNEY DEVELOPMENT	54	-0.35	-1.38	0.0628	0.4175
SITE OF DOUBLE STRAND BREAK	29	0.38	1.17	0.2405	0.4194
CALCIUM DEPENDENT PROTEIN BINDING	53	0.32	1.17	0.2374	0.4197
TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	22	0.40	1.17	0.2542	0.4198
CELLULAR RESPONSE TO KETONE	66	0.31	1.17	0.1912	0.4202
REGULATION OF T Helper 1 TYPE IMMUNE RESPONSE	19	-0.45	-1.38	0.0947	0.4208
REGULATION OF APPETITE	21	0.40	1.17	0.2658	0.4214
PROTEIN LOCALIZATION TO CENTROSOME	15	0.43	1.17	0.2597	0.4215
DORSAL VENTRAL PATTERN FORMATION	84	-0.32	-1.38	0.0457	0.4222
REGULATION OF SYNAPTIC TRANSMISSION GLUTAMATERGIC	47	0.33	1.17	0.2166	0.4229
REGULATION OF CYTOSKELETON ORGANIZATION	433	0.25	1.17	0.1018	0.4229
RNA POLYMERASE II TRANSCRIPTION FACTOR BINDING	96	0.29	1.17	0.1841	0.4230
POSITIVE REGULATION OF CELL CYCLE PHASE TRANSITION	57	0.32	1.17	0.2117	0.4230
POSITIVE REGULATION OF DNA REPAIR	31	0.36	1.17	0.2410	0.4230
REGULATION OF T CELL PROLIFERATION	114	-0.30	-1.37	0.0313	0.4246
RESPONSE TO MANGANESE ION	16	0.43	1.17	0.2683	0.4249
GLUCOSAMINE CONTAINING COMPOUND METABOLIC PROCESS	20	0.40	1.17	0.2626	0.4250
POSITIVE REGULATION OF ENDOTHELIAL CELL PROLIFERATION	63	0.31	1.17	0.2231	0.4251
MAMMARY GLAND LOBULE DEVELOPMENT	16	0.42	1.17	0.2857	0.4251
REGULATION OF MEMBRANE LIPID DISTRIBUTION	35	0.35	1.17	0.2186	0.4266
PROTEIN POLYMERIZATION	57	0.32	1.17	0.2083	0.4267
LEUKOCYTE PROLIFERATION	72	-0.33	-1.37	0.0471	0.4278
REGULATION OF RESPONSE TO REACTIVE OXYGEN SPECIES	30	-0.40	-1.37	0.1007	0.4283
NATURAL KILLER CELL ACTIVATION	37	-0.38	-1.37	0.0539	0.4286

INDOLALKYLAMINE METABOLIC PROCESS	15	-0.48	-1.37	0.1192	0.4286
REGULATION OF PEPTIDYL THREONINE PHOSPHORYLATION	34	0.36	1.16	0.2585	0.4289
HINDLIMB MORPHOGENESIS	36	-0.39	-1.37	0.0758	0.4299
LYMPHOCYTE ACTIVATION	292	-0.27	-1.36	0.0000	0.4300
MALE MEIOSIS	32	-0.39	-1.37	0.0821	0.4301
NEGATIVE REGULATION OF CHEMOKINE PRODUCTION	16	0.42	1.16	0.2817	0.4302
REGULATION OF NECROTIC CELL DEATH	23	0.39	1.16	0.2721	0.4304
POSITIVE REGULATION OF CELL CYCLE	284	0.25	1.16	0.1358	0.4307
ALCOHOL TRANSMEMBRANE TRANSPORTER ACTIVITY	22	-0.42	-1.37	0.0973	0.4307
ENSHEATHMENT OF NEURONS	81	0.30	1.16	0.2158	0.4308
CALCIUM ION TRANSMEMBRANE TRANSPORT	143	-0.29	-1.37	0.0328	0.4313
RESPONSE TO INSULIN	193	0.26	1.16	0.1696	0.4322
REGULATION OF RECEPTOR ACTIVITY	112	0.29	1.16	0.2041	0.4324
REGULATION OF HEAT GENERATION	15	-0.47	-1.36	0.1163	0.4325
RESPONSE TO METAL ION	297	0.25	1.16	0.1255	0.4330
CHROMATIN DNA BINDING	72	0.31	1.16	0.2282	0.4339
REGULATION OF GENERATION OF PRECURSOR METABOLITES AND ENERGY	79	0.30	1.16	0.2031	0.4342
GLUTAMATE RECEPTOR BINDING	34	0.35	1.16	0.2525	0.4343
LEUKOCYTE CELL CELL ADHESION	222	-0.27	-1.35	0.0083	0.4351
CELLULAR RESPONSE TO PROSTAGLANDIN E STIMULUS	18	0.41	1.16	0.2882	0.4354
CELLULAR RESPONSE TO LEPTIN STIMULUS	15	0.43	1.16	0.2807	0.4354
AROMATIC AMINO ACID FAMILY CATABOLIC PROCESS	17	-0.46	-1.35	0.1230	0.4358
SUBPALLIUM DEVELOPMENT	19	0.40	1.16	0.2815	0.4360
POSITIVE REGULATION OF B CELL ACTIVATION	61	-0.33	-1.35	0.0593	0.4363
GLOMERULAR EPITHELIUM DEVELOPMENT	18	-0.45	-1.36	0.0984	0.4363
GROWTH FACTOR ACTIVITY	142	-0.29	-1.36	0.0293	0.4364
DOPAMINE RECEPTOR SIGNALING PATHWAY	26	-0.40	-1.36	0.0882	0.4370
B CELL PROLIFERATION	28	-0.39	-1.35	0.0850	0.4371
PML BODY	81	0.30	1.16	0.2131	0.4377
atrial septum development	17	-0.46	-1.36	0.1164	0.4378

MUSCLE FILAMENT SLIDING	35	-0.38	-1.36	0.0693	0.4385
CYTOSOLIC TRANSPORT	187	0.27	1.16	0.1751	0.4386
INFLAMMATORY RESPONSE	381	-0.26	-1.36	0.0000	0.4386
LYMPHOCYTE DIFFERENTIATION	187	-0.27	-1.36	0.0300	0.4390
FUCOSYLATION	20	-0.43	-1.35	0.1042	0.4391
POSITIVE REGULATION OF NF KAPPAB TRANSCRIPTION FACTOR ACTIVITY	117	0.28	1.16	0.2102	0.4395
SYMPORter ACTIVITY	134	0.27	1.16	0.1997	0.4396
CYCLIC NUCLEOTIDE PHOSPHODIESTERASE ACTIVITY	25	0.38	1.16	0.2571	0.4396
UNSATURATED FATTY ACID METABOLIC PROCESS	73	0.30	1.16	0.2130	0.4398
CEREBRAL CORTEX NEURON DIFFERENTIATION	19	-0.44	-1.36	0.0993	0.4400
ANION CATION SYMPORter ACTIVITY	50	0.32	1.16	0.2321	0.4401
EAR DEVELOPMENT	185	-0.28	-1.36	0.0225	0.4402
REGULATION OF HETEROtYPIC CELL CELL ADHESION	18	-0.45	-1.35	0.1190	0.4406
PRESPLICEOSOME	19	0.39	1.16	0.2819	0.4412
STEROID HORMONE RECEPTOR BINDING	75	0.30	1.16	0.2214	0.4413
INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO ENDOPLASMIC RETICULUM STRESS	29	0.35	1.16	0.2509	0.4413
REGULATION OF OSTEOBLAST PROLIFERATION	21	-0.43	-1.36	0.0773	0.4417
CALCIUM INDEPENDENT CELL CELL ADHESION VIA PLASMA MEMBRANE CELL ADHESION MOLECULES	19	-0.43	-1.35	0.1136	0.4422
NUCLEOTIDE TRANSPORT	23	0.39	1.16	0.2623	0.4422
T CELL DIFFERENTIATION	117	-0.29	-1.35	0.0373	0.4425
ACTININ BINDING	27	0.36	1.15	0.2697	0.4433
REGULATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	184	0.27	1.15	0.1809	0.4434
POSITIVE T CELL SELECTION	19	-0.45	-1.35	0.1214	0.4435
LYSOSOME LOCALIZATION	20	-0.43	-1.34	0.1117	0.4436
POSITIVE REGULATION OF ALPHA BETA T CELL DIFFERENTIATION	32	-0.38	-1.35	0.0866	0.4438
CELL FATE COMMITMENT	219	-0.26	-1.35	0.0042	0.4438
CATION CHANNEL ACTIVITY	277	-0.26	-1.34	0.0090	0.4442
L ASCORBIC ACID BINDING	19	-0.44	-1.35	0.1256	0.4442
REGULATION OF RNA SPLICING	79	0.30	1.15	0.2215	0.4444

EPITHELIAL CELL DIFFERENTIATION INVOLVED IN KIDNEY DEVELOPMENT	23	-0.42	-1.34	0.0993	0.4446
SOLUTE PROTON ANTIPORTER ACTIVITY	16	-0.46	-1.34	0.1132	0.4448
CELL JUNCTION ASSEMBLY	115	0.28	1.15	0.2025	0.4462
MAMMARY GLAND ALVEOLUS DEVELOPMENT	16	0.42	1.15	0.2910	0.4468
HSP90 PROTEIN BINDING	24	-0.42	-1.34	0.1090	0.4470
REGULATION OF INTERLEUKIN 1 PRODUCTION	46	-0.36	-1.34	0.0652	0.4476
NEGATIVE REGULATION OF MITOTIC CELL CYCLE	167	0.26	1.15	0.1729	0.4478
REGULATION OF PHOSPHATASE ACTIVITY	105	0.28	1.15	0.2125	0.4478
REGULATION OF ORGAN MORPHOGENESIS	232	0.26	1.15	0.1544	0.4485
PROTEIN DEALKYLATION	27	0.37	1.15	0.2513	0.4486
POSITIVE REGULATION OF ORGANELLE ASSEMBLY	45	0.33	1.15	0.2595	0.4486
REGULATION OF LYMPHOCYTE DIFFERENTIATION	113	-0.29	-1.34	0.0411	0.4490
INDOLE CONTAINING COMPOUND METABOLIC PROCESS	24	-0.41	-1.34	0.1104	0.4491
POSITIVE REGULATION OF CARDIAC MUSCLE HYPERTROPHY	21	0.39	1.15	0.2639	0.4507
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH CH GROUP OF DONORS NAD OR NADP AS ACCEPTOR	21	0.40	1.15	0.2919	0.4510
CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	28	0.37	1.15	0.2702	0.4512
REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	67	0.31	1.15	0.2511	0.4512
SINGLE STRANDED DNA BINDING	74	0.30	1.15	0.2197	0.4514
PDZ DOMAIN BINDING	85	0.29	1.15	0.2345	0.4515
APOPTOTIC PROCESS INVOLVED IN DEVELOPMENT	18	0.40	1.15	0.2712	0.4520
SIGNAL TRANSDUCTION BY PROTEIN PHOSPHORYLATION	365	0.25	1.15	0.1532	0.4525
MICROTUBULE POLYMERIZATION	24	0.38	1.15	0.3058	0.4527
POSITIVE REGULATION OF mRNA METABOLIC PROCESS	42	0.33	1.15	0.2472	0.4543
RENAL SYSTEM PROCESS	86	0.29	1.15	0.2365	0.4549
NEGATIVE REGULATION OF STRESS ACTIVATED MAPK CASCADE	36	0.34	1.15	0.2534	0.4552

POSITIVE REGULATION OF RECEPTOR INTERNALIZATION	21	-0.42	-1.33	0.1394	0.4556
GATED CHANNEL ACTIVITY	299	-0.26	-1.33	0.0000	0.4560
REGULATION OF LYMPHOCYTE MEDIATED IMMUNITY	95	-0.30	-1.33	0.0406	0.4563
CHLORIDE CHANNEL COMPLEX	46	-0.35	-1.33	0.0802	0.4568
REGULATION OF HISTONE DEACETYLATION	19	-0.43	-1.33	0.1361	0.4570
POSITIVE REGULATION OF T CELL PROLIFERATION	74	-0.32	-1.33	0.0678	0.4574
BHLH TRANSCRIPTION FACTOR BINDING	26	-0.40	-1.33	0.0919	0.4576
AXONAL GROWTH CONE	19	-0.44	-1.33	0.1290	0.4579
LEUKOCYTE ACTIVATION	354	-0.25	-1.33	0.0057	0.4582
HUMORAL IMMUNE RESPONSE	105	-0.29	-1.33	0.0316	0.4583
FIBROBLAST GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	75	0.30	1.14	0.2342	0.4587
REGULATION OF COAGULATION	84	0.29	1.14	0.2355	0.4588
ACTIVATING TRANSCRIPTION FACTOR BINDING	54	-0.33	-1.33	0.0771	0.4593
REGULATION OF RESPONSE TO BIOTIC STIMULUS	193	0.26	1.14	0.1994	0.4594
RESPONSE TO MORPHINE	26	-0.40	-1.33	0.1182	0.4602
REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	17	0.41	1.14	0.2759	0.4602
PHOSPHATIDYLINOSITOL BISPHOSPHATE BINDING	68	0.30	1.14	0.2654	0.4602
REGULATION OF ACTIN FILAMENT BASED MOVEMENT	32	0.36	1.14	0.2689	0.4603
CELL CELL CONTACT ZONE	59	0.31	1.14	0.2324	0.4604
POSITIVE REGULATION OF MUSCLE HYPERSTROPHY	21	0.39	1.14	0.2734	0.4605
L AMINO ACID TRANSPORT	52	0.32	1.14	0.2558	0.4606
PHAGOCYTIC VESICLE	70	0.30	1.14	0.2336	0.4606
SULFUR COMPOUND CATABOLIC PROCESS	38	0.34	1.14	0.2914	0.4607
PITUITARY GLAND DEVELOPMENT	42	-0.36	-1.32	0.0904	0.4607
DNA REPAIR COMPLEX	33	0.36	1.14	0.2796	0.4607
POSITIVE REGULATION OF DNA METABOLIC PROCESS	160	0.27	1.14	0.1953	0.4608
MICROTUBULE BINDING	166	0.27	1.14	0.1951	0.4608
POSITIVE REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	31	0.35	1.14	0.2500	0.4608

REGULATION OF APOPTOTIC SIGNALING PATHWAY	324	0.25	1.14	0.1757	0.4609
REGULATION OF SMOOTH MUSCLE CONTRACTION	60	0.31	1.14	0.2562	0.4611
PEPTIDYL PROLINE MODIFICATION	46	0.32	1.14	0.2625	0.4612
TOLL LIKE RECEPTOR 4 SIGNALING PATHWAY	16	0.42	1.14	0.3045	0.4613
CLATHRIN COAT OF COATED PIT	16	0.42	1.14	0.3035	0.4613
ADP BINDING	30	-0.39	-1.32	0.0991	0.4614
MONOCARBOXYLIC ACID BIOSYNTHETIC PROCESS	143	0.27	1.14	0.2122	0.4629
PHOTORECEPTOR CONNECTING CILIUM	27	0.36	1.14	0.2832	0.4629
EXTRACELLULAR STRUCTURE ORGANIZATION	277	-0.26	-1.32	0.0138	0.4629
CALCIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	121	-0.28	-1.32	0.0280	0.4631
POSITIVE REGULATION OF HEART RATE	22	0.38	1.14	0.2531	0.4631
GENE SILENCING	164	0.27	1.14	0.1907	0.4632
POSITIVE REGULATION OF PROTEIN POLYMERIZATION	78	0.30	1.14	0.2474	0.4633
NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	124	0.28	1.14	0.2486	0.4635
REGULATION OF NEUROLOGICAL SYSTEM PROCESS	64	0.31	1.14	0.2414	0.4636
NEGATIVE REGULATION OF PROTEIN POLYMERIZATION	43	0.33	1.14	0.2739	0.4636
STEROID HORMONE RECEPTOR ACTIVITY	55	0.32	1.14	0.2813	0.4637
SISTER CHROMATID COHESION	101	0.29	1.14	0.2475	0.4638
CILIARY MEMBRANE	69	-0.31	-1.32	0.0588	0.4642
REGULATION OF CATECHOLAMINE SECRETION	43	-0.35	-1.32	0.0951	0.4643
CLATHRIN COATED ENDOCYTIC VESICLE	46	0.33	1.14	0.2824	0.4652
PHOSPHATE ION TRANSPORT	17	-0.45	-1.32	0.1373	0.4652
NEGATIVE REGULATION OF ERK1 AND ERK2 CASCADE	47	-0.35	-1.32	0.0847	0.4653
T HELPER 1 TYPE IMMUNE RESPONSE	16	-0.45	-1.32	0.1484	0.4654
RNA POLYMERASE II CORE PROMOTER SEQUENCE SPECIFIC DNA BINDING	47	-0.34	-1.32	0.0758	0.4658
APICAL PART OF CELL	325	0.24	1.14	0.1594	0.4658
VOLTAGE GATED SODIUM CHANNEL ACTIVITY	19	-0.42	-1.32	0.1394	0.4659
MEMBRANE RAFT ORGANIZATION	16	0.41	1.14	0.3080	0.4661

NEGATIVE REGULATION OF MYOTUBE DIFFERENTIATION	18	-0.44	-1.32	0.1406	0.4667
LEADING EDGE MEMBRANE	120	-0.29	-1.32	0.0284	0.4668
REGULATION OF WOUND HEALING	115	0.28	1.14	0.2100	0.4670
INTRASPECIES INTERACTION BETWEEN ORGANISMS	41	-0.35	-1.32	0.1002	0.4670
REGULATION OF MAP KINASE ACTIVITY	292	0.25	1.14	0.1840	0.4672
POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	41	-0.35	-1.32	0.0928	0.4672
CGMP METABOLIC PROCESS	23	-0.41	-1.32	0.1259	0.4676
REGULATION OF SMAD PROTEIN IMPORT INTO NUCLEUS	15	0.42	1.14	0.3137	0.4677
DNA STRAND ELONGATION	26	0.37	1.14	0.2746	0.4685
SECONDARY ACTIVE TRANSMEMBRANE TRANSPORTER ACTIVITY	204	0.26	1.14	0.1836	0.4686
MICROTUBULE BASED MOVEMENT	159	0.26	1.14	0.2072	0.4689
REGULATION OF PROTEIN KINASE B SIGNALING	108	0.28	1.13	0.2290	0.4690
REGULATION OF PATHWAY RESTRICTED SMAD PROTEIN PHOSPHORYLATION	58	0.31	1.13	0.2637	0.4691
ZINC ION HOMEOSTASIS	20	0.40	1.13	0.2929	0.4708
REGULATION OF PROTEIN SERINE THREONINE KINASE ACTIVITY	424	0.24	1.13	0.1566	0.4720
CELLULAR RESPONSE TO LIGHT STIMULUS	77	0.30	1.13	0.2427	0.4724
TRANSMEMBRANE RECEPTOR PROTEIN SERINE THREONINE KINASE ACTIVITY	16	0.41	1.13	0.3081	0.4729
SODIUM CHANNEL COMPLEX	16	-0.45	-1.31	0.1290	0.4731
CARDIAC EPITHELIAL TO MESENCHYMAL TRANSITION	24	0.37	1.13	0.2964	0.4734
COLUMNAR CUBOIDAL EPITHELIAL CELL DEVELOPMENT	44	0.33	1.13	0.2624	0.4744
ALPHA BETA T CELL DIFFERENTIATION	42	-0.35	-1.31	0.0923	0.4750
NEGATIVE REGULATION OF CARTILAGE DEVELOPMENT	25	-0.41	-1.31	0.1357	0.4755
NEGATIVE REGULATION OF STRESS ACTIVATED PROTEIN KINASE SIGNALING CASCADE	36	0.34	1.13	0.2741	0.4755
RESPONSE TO ISOQUINOLINE ALKALOID	26	-0.40	-1.31	0.1456	0.4758
COLLAGEN BINDING	56	-0.33	-1.31	0.0909	0.4764
ENDOCRINE PROCESS	41	-0.35	-1.31	0.0970	0.4765

NEGATIVE REGULATION OF CHONDROCYTE DIFFERENTIATION	19	-0.43	-1.31	0.1363	0.4768
NEGATIVE REGULATION OF PROTEIN BINDING	68	0.30	1.13	0.2655	0.4771
RESPONSE TO TRANSITION METAL NANOPARTICLE	125	0.27	1.13	0.2245	0.4773
NEGATIVE REGULATION OF CELL ACTIVATION	134	-0.28	-1.31	0.0364	0.4774
PRESYNAPTIC MEMBRANE	54	0.32	1.13	0.2590	0.4776
HISTONE DEUBIQUITINATION	18	0.40	1.13	0.3210	0.4776
ENDOCARDIAL CUSHION MORPHOGENESIS	22	0.38	1.13	0.3127	0.4777
CHROMATIN DISASSEMBLY	15	-0.45	-1.31	0.1514	0.4777
REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	87	-0.30	-1.31	0.0592	0.4777
REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY BY P53 CLASS MEDIATOR	20	0.39	1.13	0.3102	0.4779
POSITIVE REGULATION OF FIBROBLAST PROLIFERATION	51	0.31	1.13	0.2593	0.4781
CLATHRIN COATED VESICLE MEMBRANE	63	0.30	1.13	0.2692	0.4784
CENTROSOME CYCLE	41	0.33	1.13	0.2843	0.4785
REGULATION OF FIBROBLAST PROLIFERATION	75	0.29	1.13	0.2779	0.4789
CENTRAL NERVOUS SYSTEM NEURON DIFFERENTIATION	156	-0.27	-1.30	0.0511	0.4790
CYCLIC NUCLEOTIDE METABOLIC PROCESS	55	-0.33	-1.30	0.0899	0.4791
INTERMEDIATE FILAMENT CYTOSKELETON	163	-0.27	-1.30	0.0383	0.4799
ACTIVATION OF PROTEIN KINASE B ACTIVITY	18	-0.43	-1.30	0.1326	0.4800
POSITIVE REGULATION OF B CELL MEDIATED IMMUNITY	23	-0.40	-1.30	0.1442	0.4801
SIGNAL TRANSDUCTION INVOLVED IN REGULATION OF GENE EXPRESSION	18	-0.44	-1.30	0.1176	0.4803
PROTEIN DNA COMPLEX DISASSEMBLY	15	-0.45	-1.30	0.1477	0.4804
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE BY RENIN ANGIOTENSIN	20	-0.43	-1.30	0.1075	0.4809
RESPONSE TO COCAINE	44	-0.35	-1.30	0.0782	0.4814
NUCLEOTIDE RECEPTOR ACTIVITY	19	0.40	1.13	0.2917	0.4820
HEPARAN SULFATE SULFOTRANSFERASE ACTIVITY	15	0.42	1.13	0.3019	0.4821

RESPONSE TO RADIATION	357	0.24	1.13	0.1823	0.4822
SENSORY PERCEPTION OF MECHANICAL STIMULUS	130	-0.28	-1.30	0.0517	0.4837
REGULATION OF CENTROSOME DUPLICATION	29	0.35	1.12	0.2942	0.4855
EMBRYONIC DIGIT MORPHOGENESIS	56	0.31	1.12	0.2726	0.4861
NEUROMUSCULAR JUNCTION DEVELOPMENT	34	0.34	1.12	0.2878	0.4861
REGULATION OF HOMOTYPIC CELL CELL ADHESION	246	-0.25	-1.30	0.0095	0.4862
DIGESTIVE SYSTEM DEVELOPMENT	130	-0.28	-1.29	0.0512	0.4868
UNSATURATED FATTY ACID BIOSYNTHETIC PROCESS	44	0.33	1.12	0.2824	0.4869
POSITIVE REGULATION OF IMMUNOGLOBULIN MEDIATED IMMUNE RESPONSE	23	-0.40	-1.30	0.1600	0.4871
LEUKOCYTE HOMEOSTASIS	53	0.32	1.12	0.2939	0.4871
INTERACTION WITH HOST	117	0.27	1.12	0.2402	0.4872
SOCIAL BEHAVIOR	41	-0.35	-1.29	0.1460	0.4872
B CELL ACTIVATION	112	-0.28	-1.29	0.0465	0.4876
POSITIVE REGULATION OF ADHERENS JUNCTION ORGANIZATION	20	-0.41	-1.29	0.1332	0.4876
REGULATION OF MONONUCLEAR CELL MIGRATION	15	-0.45	-1.29	0.1648	0.4890
POSITIVE REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	16	-0.44	-1.29	0.1528	0.4890
NUCLEOSOME DISASSEMBLY	15	-0.45	-1.29	0.1535	0.4891
REGULATION OF LAMELLIPODUM ORGANIZATION	32	0.35	1.12	0.3089	0.4894
NEGATIVE REGULATION OF PHOSPHATE METABOLIC PROCESS	490	0.24	1.12	0.1604	0.4896
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE MEDIATED BY A CHEMICAL SIGNAL	42	0.33	1.12	0.2798	0.4897
POSITIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	441	0.24	1.12	0.1849	0.4900
REGULATION OF RESPONSE TO CYTOKINE STIMULUS	117	0.27	1.12	0.2514	0.4900
FATTY ACID DERIVATIVE BIOSYNTHETIC PROCESS	36	-0.36	-1.29	0.1096	0.4901
KERATINIZATION	38	-0.36	-1.29	0.1081	0.4910

RETINAL GANGLION CELL AXON GUIDANCE	18	0.39	1.12	0.3131	0.4910
SENSORY PERCEPTION OF TASTE	32	-0.37	-1.29	0.1371	0.4913
NEGATIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	77	-0.30	-1.29	0.0548	0.4914
NEGATIVE REGULATION OF PHOSPHORUS METABOLIC PROCESS	490	0.24	1.12	0.1771	0.4916
POLYSACCHARIDE BINDING	19	0.38	1.12	0.3134	0.4917
PRIMARY AMINO COMPOUND METABOLIC PROCESS	15	-0.44	-1.29	0.1701	0.4919
CELLULAR RESPONSE TO HEAT	28	0.36	1.12	0.3046	0.4920
PROTEIN KINASE C ACTIVITY	15	-0.45	-1.29	0.1442	0.4922
POSITIVE REGULATION OF MYOBLAST DIFFERENTIATION	21	0.39	1.12	0.3028	0.4923
MONOCARBOXYLIC ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	40	0.33	1.12	0.2815	0.4925
TERPENOID METABOLIC PROCESS	87	-0.29	-1.29	0.0638	0.4925
POSITIVE REGULATION OF SEQUESTERING OF CALCIUM ION	15	0.41	1.12	0.3277	0.4927
CELLULAR RESPONSE TO DEXAMETHASONE STIMULUS	24	0.37	1.12	0.3014	0.4932
CALCIUM CHANNEL COMPLEX	54	0.32	1.12	0.3011	0.4936
CELL CORTEX PART	100	0.28	1.12	0.2478	0.4943
TRANSFORMING GROWTH FACTOR BETA RECEPTOR BINDING	48	0.32	1.12	0.3057	0.4944
PROTEIN DEGLYCOSYLATION	19	0.39	1.12	0.3215	0.4944
RESPONSE TO CALCIUM ION	106	0.28	1.12	0.2588	0.4947
REGULATION OF PROTEIN HOMOOLIGOMERIZATION	16	0.41	1.12	0.3256	0.4948
HOMEOSTASIS OF NUMBER OF CELLS	150	0.26	1.12	0.2460	0.4950
RECEPTOR INTERNALIZATION	46	0.32	1.12	0.2670	0.4955
POSITIVE REGULATION OF RESPONSE TO EXTERNAL STIMULUS	259	-0.25	-1.28	0.0099	0.4961
CANONICAL WNT SIGNALING PATHWAY	92	0.28	1.12	0.2582	0.4965
GOLGI CISTERNA MEMBRANE	59	0.30	1.12	0.2879	0.4966
REGULATION OF GLUCOSE TRANSPORT	83	0.28	1.12	0.2758	0.4967
NEGATIVE REGULATION OF PROTEIN SERINE THREONINE KINASE ACTIVITY	118	0.27	1.12	0.2621	0.4974
NADH METABOLIC PROCESS	34	0.34	1.12	0.3073	0.4985
ACTIVE ION TRANSMEMBRANE TRANSPORTER ACTIVITY	160	0.26	1.12	0.2350	0.4987

REGULATION OF VASODILATION	46	0.32	1.11	0.2894	0.4989
RETINOIC ACID RECEPTOR SIGNALING PATHWAY	17	0.40	1.11	0.3043	0.4990
TRANSCRIPTIONAL ACTIVATOR ACTIVITY RNA POLYMERASE II CORE PROMOTER PROXIMAL REGION SEQUENCE SPECIFIC BINDING	205	-0.26	-1.28	0.0171	0.5001
RUFFLE MEMBRANE	72	-0.30	-1.28	0.0873	0.5009
PHAGOCYTIC CUP	16	-0.44	-1.28	0.1701	0.5013
CHEMOKINE BINDING	19	-0.43	-1.28	0.1597	0.5014
NEGATIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY BY P53 CLASS MEDIATOR	17	0.40	1.11	0.2958	0.5015
REGULATION OF CHOLESTEROL METABOLIC PROCESS	21	0.38	1.11	0.3237	0.5023
NEGATIVE REGULATION OF RESPONSE TO EXTERNAL STIMULUS	246	0.25	1.11	0.2358	0.5024
INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	57	0.30	1.11	0.2846	0.5025
REGULATION OF HEART GROWTH	35	0.34	1.11	0.3108	0.5027
MESONEPHROS DEVELOPMENT	84	0.29	1.11	0.2964	0.5030
NUCLEOBASE METABOLIC PROCESS	34	0.34	1.11	0.3157	0.5031
NUCLEOTIDE PHOSPHORYLATION	53	0.31	1.11	0.2973	0.5032
NEGATIVE REGULATION OF NEURON DEATH	149	0.26	1.11	0.2497	0.5039
CYTOSKELETON DEPENDENT INTRACELLULAR TRANSPORT	95	0.28	1.11	0.2533	0.5045
DEOXYRIBONUCLEOTIDE METABOLIC PROCESS	29	0.35	1.11	0.3089	0.5046
POSITIVE REGULATION OF GLIAL CELL DIFFERENTIATION	29	0.36	1.11	0.2991	0.5047
CELLULAR RESPONSE TO BIOTIC STIMULUS	145	0.26	1.11	0.2479	0.5047
POSITIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	30	0.35	1.11	0.3179	0.5049
TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY	78	0.29	1.11	0.2817	0.5049
ICOSANOID BIOSYNTHETIC PROCESS	36	-0.36	-1.28	0.1211	0.5050
PARASYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	15	0.41	1.11	0.3488	0.5053
PROTEIN DEMETHYLATION	27	0.37	1.11	0.3026	0.5054

NEGATIVE REGULATION OF COAGULATION	47	0.32	1.11	0.2980	0.5055
RNA DEPENDENT DNA BIOSYNTHETIC PROCESS	19	0.39	1.11	0.3214	0.5056
G PROTEIN COUPLED RECEPTOR BINDING	219	-0.25	-1.28	0.0340	0.5056
NUCLEOTIDE TRANSMEMBRANE TRANSPORTER ACTIVITY	17	0.40	1.11	0.3345	0.5065
FOREBRAIN REGIONALIZATION	25	-0.39	-1.28	0.1531	0.5071
REGULATION OF PROTEIN SUMOYLATION	18	0.38	1.11	0.3315	0.5074
CELL MORPHOGENESIS INVOLVED IN NEURON DIFFERENTIATION	330	-0.24	-1.27	0.0107	0.5076
EMBRYONIC HINDLIMB MORPHOGENESIS	29	-0.38	-1.28	0.1393	0.5081
AMPA GLUTAMATE RECEPTOR COMPLEX	26	0.36	1.11	0.3077	0.5085
REGULATION OF LEUKOCYTE MEDIATED IMMUNITY	130	-0.27	-1.27	0.0433	0.5087
POSITIVE REGULATION OF VASCULATURE DEVELOPMENT	121	-0.28	-1.27	0.0625	0.5090
RESPONSE TO ACTIVITY	63	0.30	1.11	0.2935	0.5097
CHEMOATTRACTANT ACTIVITY	22	-0.40	-1.27	0.1462	0.5101
TRANSCRIPTIONAL ACTIVATOR ACTIVITY RNA POLYMERASE II TRANSCRIPTION REGULATORY REGION SEQUENCE SPECIFIC BINDING	288	-0.24	-1.27	0.0164	0.5102
GLUCOCORTICOID METABOLIC PROCESS	15	-0.44	-1.27	0.1792	0.5108
NEUROMUSCULAR PROCESS	90	-0.29	-1.27	0.0927	0.5109
RESPONSE TO NERVE GROWTH FACTOR	36	0.34	1.11	0.3197	0.5117
CENTROSOME DUPLICATION	28	0.35	1.11	0.3122	0.5117
EYE PHOTORECEPTOR CELL DEVELOPMENT	27	0.36	1.11	0.3271	0.5119
AMINE BIOSYNTHETIC PROCESS	18	0.39	1.11	0.3270	0.5121
POSITIVE REGULATION OF TYPE I INTERFERON PRODUCTION	66	0.30	1.10	0.2839	0.5139
REGULATION OF ERBB SIGNALING PATHWAY	75	0.29	1.10	0.2756	0.5140
REGULATION OF INNATE IMMUNE RESPONSE	304	0.24	1.10	0.2455	0.5145
SPERM PRINCIPAL PIECE	15	0.41	1.10	0.3203	0.5146
ECTODERMAL PLACODE MORPHOGENESIS	15	0.41	1.10	0.3223	0.5147
HYDROGEN PEROXIDE CATABOLIC PROCESS	15	0.41	1.10	0.3467	0.5147

CGMP BINDING	16	-0.44	-1.27	0.1942	0.5149
POSITIVE REGULATION OF PROTEIN BINDING	68	0.29	1.10	0.3151	0.5170
NEGATIVE REGULATION OF CELL CELL ADHESION	115	-0.28	-1.26	0.0775	0.5172
SOMITE DEVELOPMENT	73	-0.30	-1.26	0.1066	0.5173
VENTRICULAR SYSTEM DEVELOPMENT	24	0.36	1.10	0.3344	0.5175
APICAL JUNCTION ASSEMBLY	36	0.33	1.10	0.2927	0.5176
RECEPTOR SIGNALING PROTEIN ACTIVITY	157	0.26	1.10	0.2713	0.5176
BRUSH BORDER MEMBRANE	49	0.32	1.10	0.3060	0.5178
NEGATIVE REGULATION OF ADAPTIVE IMMUNE RESPONSE	28	-0.38	-1.26	0.1847	0.5184
POSITIVE REGULATION OF PROTEIN DEACETYLATION	16	-0.44	-1.26	0.1663	0.5197
STEROID DEHYDROGENASE ACTIVITY	22	0.37	1.10	0.3357	0.5198
POSITIVE REGULATION OF NEURON DIFFERENTIATION	289	0.24	1.10	0.2346	0.5198
ORGANIC HYDROXY COMPOUND BIOSYNTHETIC PROCESS	155	0.26	1.10	0.2575	0.5200
RESPONSE TO NUTRIENT	179	0.25	1.10	0.2676	0.5201
RECEPTOR CLUSTERING	40	-0.35	-1.27	0.1303	0.5204
SIDE OF MEMBRANE	333	-0.24	-1.27	0.0169	0.5209
N GLYCAN PROCESSING	18	0.39	1.10	0.3531	0.5212
RESPONSE TO CAFFEINE	18	0.39	1.10	0.3407	0.5215
SINGLE ORGANISM CELL ADHESION	401	-0.24	-1.27	0.0114	0.5217
NEGATIVE REGULATION OF ACTIN FILAMENT POLYMERIZATION	32	0.35	1.10	0.3333	0.5225
ECTODERMAL PLACODE FORMATION	15	0.41	1.10	0.3397	0.5230
NEGATIVE REGULATION OF MUSCLE CELL APOPTOTIC PROCESS	29	-0.37	-1.26	0.1711	0.5243
NEGATIVE REGULATION OF PROTEIN COMPLEX ASSEMBLY	86	0.29	1.10	0.2779	0.5244
POSITIVE REGULATION OF EPITHELIAL CELL PROLIFERATION	139	0.26	1.10	0.2666	0.5247
PROTEOGLYCAN BINDING	24	-0.39	-1.26	0.1675	0.5255
RESPONSE TO AMMONIUM ION	48	0.31	1.10	0.3164	0.5259
REGULATION OF ORGANIC ACID TRANSPORT	46	0.32	1.10	0.3349	0.5260
DNA CONFORMATION CHANGE	187	0.25	1.10	0.2666	0.5261
CELLULAR RESPONSE TO CALCIUM ION	41	0.32	1.10	0.3242	0.5262
L AMINO ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	48	0.31	1.10	0.3242	0.5264

DENDRITE MORPHOGENESIS	38	-0.34	-1.26	0.1464	0.5265
ESTABLISHMENT OF PROTEIN LOCALIZATION TO PLASMA MEMBRANE	85	0.28	1.10	0.2958	0.5270
DE NOVO PROTEIN FOLDING	17	-0.43	-1.26	0.1915	0.5271
CELL PROLIFERATION IN FOREBRAIN	27	-0.38	-1.26	0.1757	0.5271
RECEPTOR ACTIVATOR ACTIVITY	32	0.34	1.10	0.3262	0.5272
SODIUM INDEPENDENT ORGANIC ANION TRANSPORT	15	-0.45	-1.26	0.1801	0.5275
HEAT SHOCK PROTEIN BINDING	77	0.29	1.10	0.3306	0.5277
ANTIPORTER ACTIVITY	63	0.29	1.10	0.2908	0.5278
MONOSACCHARIDE BINDING	59	-0.31	-1.26	0.1380	0.5279
B CELL DIFFERENTIATION	75	-0.30	-1.26	0.1045	0.5282
NEGATIVE REGULATION OF SECRETION	176	-0.26	-1.26	0.0444	0.5288
POSITIVE REGULATION OF LAMELLIPOD IUM ORGANIZATION	22	0.36	1.09	0.3405	0.5300
POSITIVE REGULATION OF ATPASE ACTIVITY	36	0.33	1.09	0.3273	0.5307
REGULATION OF DNA BINDING	81	0.28	1.09	0.2987	0.5312
OSTEOBLAST DIFFERENTIATION	119	0.27	1.09	0.2966	0.5315
ACTIVATION OF PHOSPHOLIPASE C ACTIVITY	26	-0.38	-1.25	0.1805	0.5317
DNA DEPENDENT DNA REPLICATION MAINTENANCE OF FIDELITY	19	0.38	1.09	0.3530	0.5317
ADHERENS JUNCTION ASSEMBLY	30	0.34	1.09	0.3288	0.5317
REGULATION OF DEFENSE RESPONSE TO VIRUS BY VIRUS	26	0.36	1.09	0.3087	0.5321
TRANSMISSION OF NERVE IMPULSE	51	-0.32	-1.25	0.1025	0.5324
INOSITOL PHOSPHATE PHOSPHATASE ACTIVITY	19	0.38	1.09	0.3519	0.5326
PHOSPHATIDYLCHOLINE ACYL CHAIN REMODELING	25	0.36	1.09	0.3322	0.5326
REGULATION OF N METHYL D ASPARTATE SELECTIVE GLUTAMATE RECEPTOR ACTIVITY	15	-0.44	-1.25	0.1820	0.5327
REGULATION OF INTERFERON GAMMA PRODUCTION	81	-0.29	-1.25	0.0943	0.5328
NEURON PROJECTION MORPHOGENESIS	353	-0.23	-1.25	0.0233	0.5328
MEMBRANE DEPOLARIZATION DURING ACTION POTENTIAL	37	-0.34	-1.25	0.1390	0.5330
LEUKOCYTE MEDIATED CYTOTOXICITY	21	-0.41	-1.25	0.1725	0.5331
CYTOKINE PRODUCTION INVOLVED IN IMMUNE RESPONSE	16	-0.42	-1.25	0.1882	0.5332

POSITIVE REGULATION OF CHROMATIN MODIFICATION	75	-0.30	-1.25	0.0855	0.5332
ALCOHOL BINDING	95	-0.28	-1.25	0.0798	0.5334
REGULATION OF MUSCLE HYPERTROPHY	34	0.33	1.09	0.3398	0.5336
MICROTUBULE BUNDLE FORMATION	43	-0.34	-1.25	0.1308	0.5339
DIENCEPHALON DEVELOPMENT	77	-0.29	-1.25	0.0972	0.5340
ECTODERMAL PLACODE DEVELOPMENT	15	0.41	1.09	0.3554	0.5343
RESPONSE TO DIETARY EXCESS	21	0.37	1.09	0.3570	0.5347
PROTEOGLYCAN METABOLIC PROCESS	78	0.28	1.09	0.2945	0.5348
PEPTIDYL CYSTEINE MODIFICATION	19	0.38	1.09	0.3516	0.5348
POSITIVE REGULATION OF HEART CONTRACTION	34	0.33	1.09	0.3090	0.5349
NECROPTOTIC PROCESS	20	0.38	1.09	0.3243	0.5350
RESPONSE TO LEPTIN	18	0.39	1.09	0.3467	0.5354
NEGATIVE REGULATION OF BLOOD VESSEL ENDOTHELIAL CELL MIGRATION	22	-0.39	-1.25	0.1636	0.5360
SENSORY PERCEPTION OF CHEMICAL STIMULUS	57	-0.30	-1.25	0.1170	0.5365
CELLULAR COMPONENT ASSEMBLY INVOLVED IN MORPHOGENESIS	197	0.25	1.09	0.2768	0.5366
NEGATIVE REGULATION OF ERBB SIGNALING PATHWAY	39	0.32	1.09	0.3317	0.5368
REGULATION OF NEUROTRANSMITTER RECEPTOR ACTIVITY	30	-0.36	-1.25	0.1717	0.5371
REGULATION OF ACTIN FILAMENT LENGTH	130	0.26	1.09	0.2837	0.5373
REGULATION OF ANTIGEN PROCESSING AND PRESENTATION	16	-0.43	-1.24	0.1856	0.5384
PERIPHERAL NERVOUS SYSTEM DEVELOPMENT	64	-0.31	-1.24	0.1173	0.5388
PROTEIN ACTIVATION CASCADE	55	-0.31	-1.24	0.1202	0.5391
COPPER ION BINDING	43	0.31	1.09	0.3039	0.5393
POTASSIUM CHANNEL COMPLEX	90	-0.29	-1.24	0.1075	0.5395
TRANSCRIPTION FACTOR ACTIVITY RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC BINDING	82	-0.29	-1.24	0.1194	0.5396
TRABECULA FORMATION	23	0.36	1.09	0.3257	0.5396
POSITIVE REGULATION OF PHOSPHOLIPASE ACTIVITY	50	-0.31	-1.24	0.1193	0.5400
POSITIVE REGULATION OF LYMPHOCYTE DIFFERENTIATION	66	-0.30	-1.24	0.1379	0.5415
COPULATION	15	-0.43	-1.24	0.1835	0.5416

SOMITOGENESIS	59	-0.31	-1.24	0.1429	0.5419
NEURON PROJECTION GUIDANCE	183	-0.25	-1.24	0.0412	0.5419
CARBOHYDRATE DERIVATIVE TRANSPORTER ACTIVITY	32	0.34	1.09	0.3333	0.5421
STRUCTURAL CONSTITUENT OF CYTOSKELETON	78	-0.29	-1.24	0.1147	0.5422
CAMP BIOSYNTHETIC PROCESS	16	-0.43	-1.24	0.2222	0.5423
LEUKOTRIENE BIOSYNTHETIC PROCESS	15	-0.44	-1.24	0.2046	0.5425
POSITIVE REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	28	0.35	1.09	0.3456	0.5427
INTEGRIN MEDIATED SIGNALING PATHWAY	78	-0.29	-1.24	0.1371	0.5432
RHYTHMIC PROCESS	267	0.24	1.09	0.2619	0.5432
REGULATION OF ANION TRANSMEMBRANE TRANSPORT	27	0.34	1.09	0.3408	0.5433
PROTEIN N LINKED GLYCOSYLATION	67	0.29	1.09	0.3199	0.5433
GLANDULAR EPITHELIAL CELL DEVELOPMENT	18	0.39	1.09	0.3770	0.5434
ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN VIA MHC CLASS II	71	0.29	1.08	0.3198	0.5435
RESPONSE TO CADMIUM ION	31	0.34	1.08	0.3624	0.5437
DETECTION OF TEMPERATURE STIMULUS	15	0.40	1.08	0.3512	0.5438
REGULATION OF CELL CELL ADHESION	313	-0.24	-1.24	0.0405	0.5440
NEGATIVE REGULATION OF ENDOTHELIAL CELL MIGRATION	36	-0.35	-1.24	0.1658	0.5441
CARDIOCYTE DIFFERENTIATION	94	0.27	1.08	0.3100	0.5441
REGULATION OF RESPONSE TO OXIDATIVE STRESS	57	-0.31	-1.24	0.1429	0.5442
NEURAL TUBE PATTERNING	32	-0.35	-1.23	0.1646	0.5447
REGULATION OF KERATINOCYTE PROLIFERATION	22	-0.39	-1.23	0.1908	0.5448
NUCLEAR HETEROCHROMATIN	29	-0.36	-1.23	0.1471	0.5449
EXPLORATION BEHAVIOR	22	-0.39	-1.23	0.1800	0.5452
CELL FATE DETERMINATION	41	-0.33	-1.24	0.1279	0.5452
POSITIVE REGULATION OF CALCIUM ION IMPORT	50	-0.32	-1.23	0.1440	0.5454
NEGATIVE REGULATION OF HORMONE SECRETION	72	-0.30	-1.23	0.1078	0.5454

NEGATIVE REGULATION OF G PROTEIN COUPLED RECEPTOR PROTEIN SIGNALING PATHWAY	37	-0.33	-1.23	0.1503	0.5458
REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	126	-0.26	-1.23	0.0572	0.5459
SPINAL CORD DEVELOPMENT	97	-0.28	-1.23	0.1075	0.5460
TRANSCRIPTION FACTOR ACTIVITY DIRECT LIGAND REGULATED SEQUENCE SPECIFIC DNA BINDING	44	0.31	1.08	0.3443	0.5461
METHYLATED HISTONE BINDING	43	0.31	1.08	0.3375	0.5461
POSITIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY	45	0.32	1.08	0.3442	0.5461
PHOSPHATIDYLINOSITOL ACYL CHAIN REMODELING	16	0.40	1.08	0.3479	0.5461
REGULATION OF TRANSMEMBRANE TRANSPORT	389	-0.23	-1.23	0.0062	0.5462
POSITIVE REGULATION OF LOCOMOTION	371	-0.23	-1.23	0.0352	0.5463
RESPONSE TO GAMMA RADIATION	44	0.32	1.08	0.3311	0.5464
DIGESTIVE TRACT MORPHOGENESIS	44	-0.32	-1.23	0.1578	0.5464
RESPONSE TO INTERFERON ALPHA	19	-0.41	-1.23	0.1881	0.5465
FOREBRAIN DEVELOPMENT	337	-0.23	-1.23	0.0266	0.5468
MEMBRANE MICRODOMAIN	266	0.24	1.08	0.2605	0.5469
CLATHRIN COATED ENDOCYTIC VESICLE MEMBRANE	33	0.33	1.08	0.3555	0.5470
REGULATION OF NEUROBLAST PROLIFERATION	26	-0.36	-1.23	0.1803	0.5473
DEOXYRIBONUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	15	0.40	1.08	0.3421	0.5473
POSITIVE REGULATION OF CELL ACTIVATION	234	-0.24	-1.23	0.0412	0.5474
PHOSPHOLIPID BINDING	326	0.23	1.08	0.2693	0.5474
RESPONSE TO TRANSFORMING GROWTH FACTOR BETA	135	0.26	1.08	0.3090	0.5475
DYNEIN COMPLEX	24	0.36	1.08	0.3569	0.5475
NEGATIVE REGULATION OF HEMOPOIESIS	109	-0.27	-1.23	0.0932	0.5476
VENTRICULAR SEPTUM DEVELOPMENT	51	0.30	1.08	0.3328	0.5477
STEROL BINDING	41	-0.33	-1.23	0.1649	0.5484
POSITIVE REGULATION OF DNA BINDING	39	0.32	1.08	0.3444	0.5493
CYTOSOLIC SMALL RIBOSOMAL SUBUNIT	31	0.34	1.08	0.3540	0.5501

REGULATION OF CELLULAR EXTRAVASATION	21	-0.38	-1.22	0.1971	0.5501
RECEPTOR METABOLIC PROCESS	73	0.28	1.08	0.3025	0.5515
CHD TYPE COMPLEX	16	0.39	1.08	0.3704	0.5517
NEGATIVE REGULATION OF SMOOTHENED SIGNALING PATHWAY	23	-0.38	-1.22	0.1840	0.5517
ACIDIC AMINO ACID TRANSPORT	21	0.37	1.08	0.3484	0.5518
CEREBELLAR CORTEX MORPHOGENESIS	29	-0.36	-1.22	0.1694	0.5525
PROTEIN DNA COMPLEX SUBUNIT ORGANIZATION	155	0.25	1.08	0.2935	0.5527
COLUMNAR CUBOIDAL EPITHELIAL CELL DIFFERENTIATION	103	0.27	1.08	0.2994	0.5529
POSITIVE REGULATION OF CYTOKINE PRODUCTION INVOLVED IN IMMUNE RESPONSE	29	0.34	1.08	0.3475	0.5530
REGULATION OF CENTROSOME CYCLE	34	0.33	1.08	0.3591	0.5531
EMBRYONIC PATTERN SPECIFICATION	56	-0.31	-1.22	0.1264	0.5531
DNA CATABOLIC PROCESS	24	0.36	1.08	0.3596	0.5541
POSITIVE REGULATION OF TRANSMEMBRANE RECEPTOR PROTEIN SERINE THREONINE KINASE SIGNALING PATHWAY	93	0.27	1.08	0.3170	0.5548
STEROID METABOLIC PROCESS	185	0.25	1.08	0.2922	0.5565
PHOTORECEPTOR OUTER SEGMENT	61	-0.30	-1.22	0.1441	0.5576
TRABECULA MORPHOGENESIS	38	0.33	1.08	0.3492	0.5588
POSITIVE REGULATION OF LYMPHOCYTE MEDIATED IMMUNITY	59	-0.30	-1.22	0.1390	0.5594
HISTONE ACETYLTRANSFERASE BINDING	26	-0.37	-1.22	0.2086	0.5595
POSITIVE REGULATION OF CELL JUNCTION ASSEMBLY	23	-0.38	-1.22	0.2128	0.5599
POSITIVE REGULATION OF CELL CELL ADHESION	192	-0.25	-1.22	0.0769	0.5599
CENTROMERE COMPLEX ASSEMBLY	30	-0.36	-1.21	0.1769	0.5599
REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	27	-0.36	-1.21	0.1859	0.5600
EPIDERMIS MORPHOGENESIS	26	-0.37	-1.21	0.2063	0.5603
SYNAPTIC SIGNALING	392	-0.23	-1.21	0.0440	0.5605
POSITIVE REGULATION OF LEUKOCYTE DIFFERENTIATION	112	-0.27	-1.21	0.0836	0.5606
REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	50	0.30	1.07	0.3499	0.5607

REGULATION OF CELLULAR SENESCENCE	24	-0.37	-1.22	0.1843	0.5609
ANION ANION ANTIPORTER ACTIVITY	20	0.36	1.07	0.3687	0.5609
ZYMOGEN ACTIVATION	97	0.27	1.07	0.3304	0.5612
REGULATION OF RESPIRATORY GASEOUS EXCHANGE	22	-0.38	-1.21	0.2009	0.5613
PROTEIN TRANSPORT ALONG MICROTUBULE	23	-0.37	-1.22	0.2117	0.5614
PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	27	-0.36	-1.21	0.1827	0.5615
POSITIVE REGULATION OF INFLAMMATORY RESPONSE	98	-0.27	-1.22	0.1185	0.5617
REGULATION OF CYTOKINE PRODUCTION INVOLVED IN IMMUNE RESPONSE	49	-0.30	-1.21	0.1769	0.5621
CELLULAR HORMONE METABOLIC PROCESS	81	0.28	1.07	0.3042	0.5621
POSITIVE REGULATION OF LIPID BIOSYNTHETIC PROCESS	62	-0.30	-1.21	0.1875	0.5622
ANDROGEN METABOLIC PROCESS	24	-0.37	-1.21	0.1873	0.5622
KINESIN COMPLEX	47	-0.32	-1.20	0.1654	0.5622
DNA METHYLATION INVOLVED IN GAMETE GENERATION	18	-0.40	-1.21	0.1995	0.5623
PEPTIDE HORMONE RECEPTOR BINDING	17	-0.41	-1.22	0.1905	0.5623
REGULATION OF ACTIN FILAMENT BASED PROCESS	279	0.24	1.07	0.2929	0.5624
POSITIVE REGULATION OF T HELPER CELL DIFFERENTIATION	16	-0.42	-1.20	0.2250	0.5625
REGULATION OF HEMOPOIESIS	267	-0.23	-1.21	0.0563	0.5626
NUCLEOBASE BIOSYNTHETIC PROCESS	15	0.40	1.07	0.3735	0.5628
KERATINOCYTE DIFFERENTIATION	82	-0.28	-1.21	0.1366	0.5629
PHOTOTRANSDUCTION	40	-0.33	-1.22	0.1557	0.5629
REGULATION OF RECEPTOR BINDING	15	0.40	1.07	0.3590	0.5631
OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN	105	-0.27	-1.21	0.1137	0.5631
NEGATIVE REGULATION OF LEUKOCYTE DIFFERENTIATION	72	-0.29	-1.21	0.1269	0.5632
POSITIVE REGULATION OF GLUCOSE TRANSPORT	35	-0.33	-1.21	0.1700	0.5633
GERM CELL NUCLEUS	20	-0.39	-1.21	0.2105	0.5636
POSITIVE REGULATION OF CELL ADHESION	312	-0.23	-1.21	0.0459	0.5641

AROMATIC AMINO ACID FAMILY METABOLIC PROCESS	25	-0.36	-1.21	0.1760	0.5642
RESPONSE TO SALT STRESS	18	-0.40	-1.21	0.2028	0.5643
K63 LINKED POLYUBIQUITIN BINDING	15	0.40	1.07	0.3724	0.5644
CELL CELL JUNCTION ASSEMBLY	66	0.29	1.07	0.3245	0.5646
METALLOPEPTIDASE ACTIVITY	166	0.25	1.07	0.3356	0.5649
REGULATION OF MUSCLE CONTRACTION	142	0.26	1.07	0.3186	0.5651
NEGATIVE REGULATION OF SIGNAL TRANSDUCTION IN ABSENCE OF LIGAND	29	-0.35	-1.21	0.1881	0.5652
NEGATIVE REGULATION OF NUCLEOTIDE METABOLIC PROCESS	59	-0.30	-1.20	0.1799	0.5654
MRNA SPlice SITE SELECTION	16	0.39	1.07	0.3759	0.5660
REGULATION OF NIK NF KAPPAB SIGNALING	34	0.33	1.07	0.3585	0.5662
EMBRYO IMPLANTATION	36	-0.33	-1.20	0.1933	0.5664
ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE OR POLYSACCHARIDE ANTIGEN VIA MHC CLASS II	71	0.29	1.07	0.3370	0.5669
CELLULAR RESPONSE TO RADIATION	115	0.26	1.07	0.3247	0.5669
CYTOPLASMIC REGION	252	0.24	1.07	0.3053	0.5670
NEGATIVE REGULATION OF MAPK CASCADE	135	0.26	1.07	0.3353	0.5670
REGULATION OF HORMONE LEVELS	423	0.23	1.07	0.2909	0.5670
ALPHA BETA T CELL ACTIVATION	48	-0.31	-1.20	0.1723	0.5671
POSITIVE REGULATION OF TYROSINE PHOSPHORYLATION OF STAT5 PROTEIN	15	0.40	1.07	0.3714	0.5671
REGULATION OF CHONDROCYTE DIFFERENTIATION	44	-0.32	-1.20	0.1578	0.5674
ENDOTHELIAL CELL MIGRATION	52	-0.31	-1.20	0.1886	0.5674
RESPONSE TO PLATELET DERIVED GROWTH FACTOR	15	-0.43	-1.20	0.2169	0.5677
RESPONSE TO WATER	15	-0.42	-1.20	0.2437	0.5678
NEGATIVE REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	23	-0.37	-1.20	0.2118	0.5683
SENSORY PERCEPTION	427	-0.22	-1.20	0.0136	0.5684
REGULATION OF NITRIC OXIDE BIOSYNTHETIC PROCESS	47	-0.31	-1.20	0.1851	0.5686
CHAPERONE MEDIATED PROTEIN FOLDING	40	-0.32	-1.20	0.1787	0.5687
SMAD PROTEIN SIGNAL TRANSDUCTION	55	-0.30	-1.20	0.1550	0.5688

NONMOTILE PRIMARY CILIUM	114	-0.26	-1.20	0.0952	0.5696
POSITIVE REGULATION OF CALCIUM ION TRANSPORT	99	-0.27	-1.19	0.1415	0.5698
NEGATIVE REGULATION OF NEURON DIFFERENTIATION	178	-0.24	-1.19	0.0952	0.5699
PATTERN SPECIFICATION PROCESS	384	-0.22	-1.19	0.0252	0.5705
LEUKOCYTE DIFFERENTIATION	262	-0.23	-1.19	0.0351	0.5705
RESPONSE TO IMMOBILIZATION STRESS	20	-0.38	-1.19	0.2244	0.5705
MALE MEIOSIS I	15	-0.41	-1.19	0.2387	0.5706
METANEPHROS DEVELOPMENT	78	-0.28	-1.20	0.1441	0.5707
NEGATIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY IN ABSENCE OF LIGAND	29	-0.35	-1.20	0.1995	0.5707
POSITIVE REGULATION OF TUMOR NECROSIS FACTOR SUPERFAMILY CYTOKINE PRODUCTION	54	-0.31	-1.20	0.1760	0.5708
DENDRITIC SPINE ORGANIZATION	17	-0.40	-1.19	0.2477	0.5709
SOLUTE CATION SYMPORTER ACTIVITY	93	-0.27	-1.19	0.1346	0.5710
SYNAPSE ASSEMBLY	65	-0.29	-1.19	0.1667	0.5710
REGULATION OF MORPHOGENESIS OF A BRANCHING STRUCTURE	53	-0.30	-1.19	0.1816	0.5712
POSITIVE REGULATION OF AMINE TRANSPORT	32	-0.35	-1.19	0.2228	0.5713
NUCLEAR CHROMATIN	229	0.24	1.07	0.3085	0.5714
INTRACILIARY TRANSPORT	23	-0.37	-1.19	0.2273	0.5716
NEGATIVE REGULATION OF PROTEIN PROCESSING	28	-0.35	-1.19	0.2117	0.5717
REGULATION OF GLYCOPROTEIN METABOLIC PROCESS	33	0.33	1.07	0.3601	0.5724
REGULATION OF ENDOTHELIAL CELL MIGRATION	110	-0.26	-1.19	0.1137	0.5737
CHROMATIN	352	0.23	1.07	0.2848	0.5739
REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	44	0.31	1.07	0.3526	0.5740
NEGATIVE REGULATION OF LEUKOCYTE MIGRATION	28	0.34	1.07	0.3694	0.5745
ESTABLISHMENT OF EPITHELIAL CELL POLARITY	21	0.36	1.07	0.3699	0.5750
NEGATIVE REGULATION OF LIPID METABOLIC PROCESS	61	0.29	1.07	0.3510	0.5751
FEMALE SEX DIFFERENTIATION	106	-0.26	-1.19	0.1443	0.5752

REGULATION OF TUMOR NECROSIS FACTOR SUPERFAMILY CYTOKINE PRODUCTION	94	-0.27	-1.19	0.1344	0.5754
MULTI MULTICELLULAR ORGANISM PROCESS	185	-0.24	-1.19	0.0837	0.5756
REGULATION OF INTERLEUKIN 5 PRODUCTION	17	0.39	1.06	0.3636	0.5771
PURINERGIC NUCLEOTIDE RECEPTOR SIGNALING PATHWAY	20	0.37	1.06	0.3933	0.5772
TOR SIGNALING	15	0.40	1.06	0.3933	0.5773
CENTRIOLAR SATELLITE	20	0.37	1.06	0.3768	0.5780
MICROTUBULE ASSOCIATED COMPLEX	108	0.27	1.06	0.3438	0.5781
POSITIVE REGULATION OF MAPK CASCADE	415	0.22	1.06	0.2937	0.5782
POSITIVE REGULATION OF RESPONSE TO CYTOKINE STIMULUS	29	0.34	1.06	0.3704	0.5783
MUSCLE HYPERTROPHY	28	0.34	1.06	0.3780	0.5783
NEGATIVE REGULATION OF EPITHELIAL CELL APOPTOTIC PROCESS	34	0.33	1.06	0.3901	0.5800
RESPONSE TO COLD	40	0.31	1.06	0.3618	0.5800
CLATHRIN ADAPTOR COMPLEX	25	0.35	1.06	0.3882	0.5802
ORGAN INDUCTION	16	0.39	1.06	0.3948	0.5802
POSITIVE REGULATION OF DEFENSE RESPONSE	316	0.23	1.06	0.3207	0.5803
SH2 DOMAIN BINDING	26	-0.35	-1.18	0.2253	0.5804
REGULATION OF PHOSPHOLIPASE ACTIVITY	61	-0.29	-1.18	0.1888	0.5804
TRANSLATION ELONGATION FACTOR ACTIVITY	18	0.38	1.06	0.3986	0.5805
LRR DOMAIN BINDING	15	0.39	1.06	0.3759	0.5806
DENDRITIC CELL DIFFERENTIATION	29	-0.34	-1.18	0.2161	0.5810
CELLULAR RESPONSE TO HORMONE STIMULUS	489	0.22	1.06	0.3014	0.5818
NEGATIVE REGULATION OF APOPTOTIC SIGNALING PATHWAY	181	0.25	1.06	0.3250	0.5819
NEGATIVE REGULATION OF WOUND HEALING	56	0.29	1.06	0.3514	0.5820
EXTRACELLULAR MATRIX BINDING	48	-0.30	-1.18	0.1917	0.5829
MAINTENANCE OF CELL NUMBER	126	0.26	1.06	0.3526	0.5829
CELL ACTIVATION	494	-0.22	-1.18	0.0365	0.5832
REGULATION OF LEUKOCYTE DIFFERENTIATION	202	-0.24	-1.18	0.0870	0.5836
MALE GERM CELL NUCLEUS	16	-0.41	-1.18	0.2483	0.5837
REGULATION OF AXON GUIDANCE	39	-0.32	-1.18	0.2030	0.5839

NEGATIVE REGULATION OF RESPONSE TO BIOTIC STIMULUS	26	0.34	1.06	0.3873	0.5846
NEUROPILIN BINDING	15	-0.41	-1.18	0.2261	0.5848
ARTERY MORPHOGENESIS	49	0.30	1.06	0.3575	0.5848
REGULATION OF ATPASE ACTIVITY	52	0.30	1.06	0.3899	0.5849
SKELETAL MUSCLE ORGAN DEVELOPMENT	124	-0.25	-1.18	0.1329	0.5853
TRIGLYCERIDE LIPASE ACTIVITY	17	0.38	1.06	0.3949	0.5853
CELL CORTEX REGION	15	-0.41	-1.18	0.2318	0.5864
REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO PLASMA MEMBRANE	43	0.31	1.06	0.3581	0.5873
ZINC II ION TRANSPORT	25	0.34	1.06	0.3761	0.5874
RHO PROTEIN SIGNAL TRANSDUCTION	43	-0.31	-1.17	0.1814	0.5884
COCHLEA DEVELOPMENT	38	-0.32	-1.18	0.1933	0.5886
POSITIVE REGULATION OF TYROSINE PHOSPHORYLATION OF STAT3 PROTEIN	34	-0.34	-1.18	0.2163	0.5886
AMINE CATABOLIC PROCESS	19	-0.38	-1.18	0.2257	0.5887
TISSUE MIGRATION	75	-0.27	-1.18	0.1631	0.5887
RESPONSE TO ALKALOID	128	-0.25	-1.18	0.1337	0.5894
LYMPHOCYTE COSTIMULATION	55	-0.30	-1.18	0.1763	0.5903
CATION TRANSPORTING ATPASE ACTIVITY	56	0.29	1.06	0.3555	0.5905
MAMMARY GLAND MORPHOGENESIS	39	-0.32	-1.17	0.2085	0.5905
NEGATIVE REGULATION OF ANION TRANSPORT	31	0.34	1.06	0.3789	0.5907
ALCOHOL BIOSYNTHETIC PROCESS	98	0.27	1.05	0.3602	0.5908
POSITIVE REGULATION OF ORGAN GROWTH	35	0.32	1.06	0.4047	0.5909
TRANSFORMING GROWTH FACTOR BETA RECEPTOR SIGNALING PATHWAY	92	0.26	1.05	0.3613	0.5911
OMEGA PEPTIDASE ACTIVITY	15	0.39	1.05	0.3856	0.5912
PHENOL CONTAINING COMPOUND METABOLIC PROCESS	70	0.28	1.05	0.3509	0.5912
ORGAN MATURATION	16	-0.41	-1.17	0.2368	0.5914
JAK STAT CASCADE	43	-0.31	-1.17	0.1924	0.5914
PEPTIDE TRANSPORT	67	-0.28	-1.17	0.1750	0.5922
ANDROGEN RECEPTOR BINDING	37	0.32	1.05	0.3577	0.5924
NOSE DEVELOPMENT	15	-0.41	-1.17	0.2512	0.5929
ION ANTIPORTER ACTIVITY	43	0.30	1.05	0.3690	0.5930
MYOSIN FILAMENT	20	-0.38	-1.17	0.2447	0.5932
BODY FLUID SECRETION	67	-0.28	-1.17	0.1630	0.5935

CENTRAL NERVOUS SYSTEM PROJECTION NEURON AXONOGENESIS	21	-0.38	-1.17	0.2488	0.5936
POSITIVE REGULATION OF SEQUENCE SPECIFIC DNA BINDING TRANSCRIPTION FACTOR ACTIVITY	206	0.24	1.05	0.3712	0.5940
REGULATION OF ASTROCYTE DIFFERENTIATION	26	-0.35	-1.17	0.2402	0.5941
B CELL RECEPTOR SIGNALING PATHWAY	31	-0.34	-1.17	0.2081	0.5941
DRUG METABOLIC PROCESS	19	0.37	1.05	0.3975	0.5943
SMOOTH MUSCLE TISSUE DEVELOPMENT	15	0.39	1.05	0.3950	0.5947
NEGATIVE REGULATION OF CELL PROJECTION ORGANIZATION	133	-0.25	-1.17	0.1628	0.5948
REGULATION OF AMINE TRANSPORT	70	-0.28	-1.17	0.1821	0.5951
POSITIVE REGULATION OF BIOMINERAL TISSUE DEVELOPMENT	36	-0.33	-1.17	0.2187	0.5951
NEGATIVE REGULATION OF PROTEIN MATURATION	28	-0.35	-1.17	0.2494	0.5954
METAL ION TRANSMEMBRANE TRANSPORTER ACTIVITY	393	-0.22	-1.17	0.0387	0.5956
POSITIVE REGULATION OF PROTEIN EXPORT FROM NUCLEUS	17	-0.39	-1.17	0.2511	0.5958
MYOSIN COMPLEX	60	-0.29	-1.17	0.1902	0.5958
REGULATION OF DENDRITIC SPINE DEVELOPMENT	54	0.29	1.05	0.3910	0.5962
CELL CELL ADHESION VIA PLASMA MEMBRANE ADHESION MOLECULES	157	-0.24	-1.17	0.1215	0.5963
BLOOD VESSEL REMODELING	30	0.33	1.05	0.3970	0.5964
POSITIVE REGULATION OF CARBOHYDRATE METABOLIC PROCESS	68	0.28	1.05	0.3756	0.5964
STAT CASCADE	43	-0.31	-1.17	0.2264	0.5965
ORGANIC ACID SODIUM SYMPORTER ACTIVITY	27	0.34	1.05	0.3752	0.5967
TRANSCRIPTIONAL REPRESSOR ACTIVITY RNA POLYMERASE II ACTIVATING TRANSCRIPTION FACTOR BINDING	52	-0.29	-1.16	0.2102	0.5972
POSITIVE REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR PRODUCTION	24	0.35	1.05	0.4043	0.5972
LYSINE N METHYLTRANSFERASE ACTIVITY	46	0.30	1.05	0.3968	0.5972
SKIN DEVELOPMENT	185	-0.23	-1.16	0.1176	0.5990

REGULATION OF ENERGY HOMEOSTASIS	17	0.37	1.05	0.3869	0.5991
POSITIVE REGULATION OF NEUROTRANSMITTER TRANSPORT	16	0.38	1.05	0.4178	0.6015
ORGAN GROWTH	63	-0.28	-1.16	0.1718	0.6026
REGULATION OF ENDOCRINE PROCESS	43	-0.31	-1.16	0.2272	0.6027
POSITIVE REGULATION OF RELEASE OF SEQUESTERED CALCIUM ION INTO CYTOSOL	35	-0.31	-1.16	0.2317	0.6028
NEGATIVE REGULATION OF CELL ADHESION	192	-0.24	-1.16	0.0898	0.6033
LOCOMOTORY BEHAVIOR	165	-0.24	-1.16	0.1255	0.6034
RNA POLYMERASE II TRANSCRIPTION COACTIVATOR ACTIVITY	35	-0.33	-1.16	0.2293	0.6041
REGULATION OF SYNAPSE ORGANIZATION	105	0.26	1.05	0.3752	0.6045
CALCIUM ION REGULATED EXOCYTOSIS OF NEUROTRANSMITTER	31	-0.34	-1.16	0.2123	0.6052
NEGATIVE REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORT	21	-0.37	-1.16	0.2579	0.6053
REGULATION OF SKELETAL MUSCLE TISSUE DEVELOPMENT	47	-0.31	-1.16	0.2109	0.6054
CEREBELLAR PURKINJE CELL LAYER DEVELOPMENT	22	-0.37	-1.16	0.2411	0.6055
MYELOID CELL DEVELOPMENT	35	-0.32	-1.16	0.2143	0.6057
VENTRAL SPINAL CORD DEVELOPMENT	43	-0.31	-1.16	0.2464	0.6062
POSITIVE REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	54	-0.30	-1.16	0.2280	0.6067
POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	73	-0.28	-1.15	0.2046	0.6082
FOREBRAIN CELL MIGRATION	58	-0.29	-1.15	0.2099	0.6087
HYALURONAN METABOLIC PROCESS	25	-0.35	-1.15	0.2517	0.6095
REGULATION OF NEURON MIGRATION	28	0.33	1.04	0.3798	0.6100
DIOXYGENASE ACTIVITY	79	0.27	1.04	0.3828	0.6100
RIBONUCLEOSIDE DIPHOSPHATE METABOLIC PROCESS	57	0.29	1.04	0.3956	0.6103
HEART DEVELOPMENT	435	0.22	1.04	0.3381	0.6105
SODIUM ION HOMEOSTASIS	25	0.35	1.04	0.3989	0.6111
POSITIVE REGULATION OF MICROTUBULE POLYMERIZATION	18	0.37	1.04	0.3907	0.6116
MYELINATION IN PERIPHERAL NERVOUS SYSTEM	21	0.35	1.04	0.4030	0.6116

RESPONSE TO CORTICOSTERONE	25	-0.35	-1.15	0.2536	0.6123
NEGATIVE REGULATION OF MAP KINASE ACTIVITY	69	0.28	1.04	0.3802	0.6129
POSITIVE REGULATION OF IMMUNOGLOBULIN PRODUCTION	25	-0.35	-1.15	0.2518	0.6132
METANEPHRIC NEPHRON MORPHOGENESIS	21	-0.35	-1.15	0.2586	0.6138
DNA PACKAGING	123	-0.25	-1.15	0.1783	0.6147
CHROMATIN ASSEMBLY OR DISASSEMBLY	109	-0.25	-1.15	0.1869	0.6156
PHOSPHATE ION TRANSMEMBRANE TRANSPORTER ACTIVITY	16	-0.40	-1.15	0.3064	0.6156
NEGATIVE REGULATION OF RESPONSE TO ENDOPLASMIC RETICULUM STRESS	33	0.32	1.04	0.3972	0.6160
CYSTEINE TYPE ENDOPEPTIDASE INHIBITOR ACTIVITY INVOLVED IN APOPTOTIC PROCESS	19	-0.37	-1.15	0.2740	0.6161
SEGMENTATION	85	-0.27	-1.15	0.2026	0.6162
OVARIAN FOLLICLE DEVELOPMENT	54	-0.29	-1.15	0.2119	0.6165
ENDOCYTIC VESICLE MEMBRANE	121	0.25	1.04	0.3858	0.6165
POSITIVE REGULATION OF INTERFERON GAMMA PRODUCTION	57	-0.29	-1.15	0.2294	0.6165
PROTEIN LIPID COMPLEX	32	0.32	1.04	0.3898	0.6165
SPINDLE CHECKPOINT	24	0.35	1.04	0.4178	0.6165
MESENCHYMAL TO EPITHELIAL TRANSITION	15	-0.40	-1.15	0.2931	0.6167
REGULATION OF HORMONE METABOLIC PROCESS	23	0.34	1.04	0.3997	0.6168
REGULATION OF STAT CASCADE	126	-0.25	-1.15	0.1433	0.6171
REGULATION OF CALCIUM MEDIATED SIGNALING	68	0.28	1.04	0.4053	0.6174
REGULATION OF JAK STAT CASCADE	126	-0.25	-1.15	0.1464	0.6175
MITOTIC G2 M TRANSITION CHECKPOINT	16	0.38	1.04	0.4097	0.6176
REGULATION OF VASCULAR PERMEABILITY	26	-0.35	-1.15	0.2730	0.6176
IMMUNOGLOBULIN PRODUCTION	33	0.32	1.04	0.4157	0.6177
MOTOR ACTIVITY	100	-0.25	-1.15	0.1941	0.6180
GLYCOSAMINOGLYCAN BINDING	179	-0.24	-1.15	0.1288	0.6181
REGULATION OF ACTIVIN RECEPTOR SIGNALING PATHWAY	20	0.37	1.04	0.4125	0.6214
CYTOKINE RECEPTOR ACTIVITY	83	-0.27	-1.14	0.2059	0.6242
ASSOCIATIVE LEARNING	68	-0.27	-1.14	0.2203	0.6247

REGULATION OF CYTOSOLIC CALCIUM ION CONCENTRATION	186	-0.23	-1.14	0.1434	0.6249
REGULATION OF TRANSFORMING GROWTH FACTOR BETA PRODUCTION	23	0.35	1.04	0.3989	0.6250
TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHWAY	459	0.22	1.04	0.3811	0.6252
POSITIVE REGULATION OF G PROTEIN COUPLED RECEPTOR PROTEIN SIGNALING PATHWAY	23	-0.35	-1.14	0.2699	0.6255
HEART VALVE DEVELOPMENT	33	-0.32	-1.14	0.2537	0.6255
REGULATION OF INSULIN LIKE GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	20	-0.36	-1.14	0.2768	0.6257
REGULATION OF ENDOTHELIAL CELL DIFFERENTIATION	27	0.33	1.04	0.4125	0.6257
DETECTION OF LIGHT STIMULUS	54	-0.29	-1.14	0.2245	0.6259
ORGANIC HYDROXY COMPOUND TRANSMEMBRANE TRANSPORTER ACTIVITY	53	0.29	1.04	0.3957	0.6261
ADULT BEHAVIOR	122	-0.24	-1.14	0.1846	0.6262
CELLULAR BIOGENIC AMINE CATABOLIC PROCESS	19	-0.38	-1.14	0.2854	0.6267
NEGATIVE REGULATION OF IMMUNE RESPONSE	94	-0.25	-1.13	0.1854	0.6268
NEGATIVE REGULATION OF DENDRITE DEVELOPMENT	24	-0.35	-1.14	0.2824	0.6269
POSITIVE REGULATION OF SMOOTHENED SIGNALING PATHWAY	23	-0.35	-1.14	0.2957	0.6270
CARDIAC ATRIUM DEVELOPMENT	28	-0.34	-1.13	0.2736	0.6273
NUCLEUS LOCALIZATION	20	-0.36	-1.13	0.2998	0.6274
EMBRYONIC ORGAN MORPHOGENESIS	261	-0.22	-1.13	0.1033	0.6275
KERATIN FILAMENT	50	-0.29	-1.14	0.2367	0.6275
EXTRACELLULAR MATRIX DISASSEMBLY	67	-0.28	-1.13	0.2325	0.6275
RETINOL DEHYDROGENASE ACTIVITY	15	-0.39	-1.14	0.2933	0.6275
RUFFLE	143	-0.24	-1.13	0.1855	0.6276
PHAGOCYTOSIS ENGULFMENT	16	-0.38	-1.14	0.2757	0.6277
DEFENSE RESPONSE TO OTHER ORGANISM	335	-0.22	-1.13	0.1067	0.6277
ACTIN MONOMER BINDING	23	-0.35	-1.13	0.2938	0.6277
NEGATIVE REGULATION OF IMMUNE EFFECTOR PROCESS	79	-0.27	-1.13	0.2175	0.6278
MAMMARY GLAND DEVELOPMENT	113	-0.25	-1.14	0.1698	0.6278
OVULATION CYCLE	104	-0.25	-1.14	0.1863	0.6280

VIRUS RECEPTOR ACTIVITY	61	-0.28	-1.13	0.2158	0.6281
IRON ION BINDING	104	-0.25	-1.13	0.1787	0.6283
ENDOCRINE SYSTEM DEVELOPMENT	118	-0.24	-1.13	0.1749	0.6284
POSITIVE REGULATION OF JAK STAT CASCADE	64	-0.27	-1.13	0.2203	0.6285
POSITIVE REGULATION OF NEUROBLAST PROLIFERATION	19	-0.38	-1.14	0.3022	0.6285
MYELOID LEUKOCYTE ACTIVATION	87	-0.26	-1.14	0.1914	0.6287
METANEPHROS MORPHOGENESIS	28	-0.33	-1.13	0.2902	0.6291
POSITIVE REGULATION OF CHOLESTEROL TRANSPORT	16	0.38	1.03	0.4234	0.6293
LEUKOCYTE DEGRANULATION	27	-0.34	-1.14	0.2754	0.6294
GROWTH	371	0.22	1.03	0.3691	0.6296
REGULATION OF CELL ACTIVATION	387	-0.21	-1.14	0.0988	0.6297
NEGATIVE REGULATION OF FATTY ACID METABOLIC PROCESS	17	-0.38	-1.13	0.2804	0.6304
HETEROPHILIC CELL CELL ADHESION VIA PLASMA MEMBRANE CELL ADHESION MOLECULES	41	-0.31	-1.13	0.2574	0.6310
NEGATIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	25	0.34	1.03	0.4194	0.6353
GLUTAMINE FAMILY AMINO ACID CATABOLIC PROCESS	23	0.34	1.03	0.4335	0.6354
POSITIVE REGULATION OF CELL CYCLE PROCESS	211	0.23	1.03	0.3799	0.6356
ATPASE REGULATOR ACTIVITY	27	-0.32	-1.13	0.2824	0.6357
REGULATION OF HOMEOSTATIC PROCESS	397	0.22	1.03	0.3770	0.6359
CARDIAC SEPTUM DEVELOPMENT	82	0.26	1.03	0.4003	0.6363
PEPTIDYL SERINE MODIFICATION	137	0.25	1.03	0.4027	0.6364
NEGATIVE REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	83	0.27	1.03	0.3962	0.6365
CELL SURFACE RECEPTOR SIGNALING PATHWAY INVOLVED IN CELL CELL SIGNALING	68	0.28	1.03	0.4168	0.6366
POSITIVE REGULATION OF STEROL TRANSPORT	16	0.38	1.03	0.4319	0.6367
REGULATION OF mRNA CATABOLIC PROCESS	26	0.33	1.03	0.4213	0.6369
MITOTIC SPINDLE ORGANIZATION	56	0.28	1.03	0.4081	0.6371
CELLULAR RESPONSE TO PROSTAGLANDIN STIMULUS	22	0.34	1.03	0.4081	0.6372
REGULATION OF ICOSANOID SECRETION	17	0.37	1.03	0.4155	0.6385

PHOSPHATIDYLGLYCEROL ACYL CHAIN REMODELING	16	0.38	1.03	0.4412	0.6388
MOTOR NEURON AXON GUIDANCE	26	-0.34	-1.12	0.2802	0.6394
MICROTUBULE ORGANIZING CENTER PART	116	0.25	1.03	0.3907	0.6419
SPLEEN DEVELOPMENT	34	0.32	1.03	0.4185	0.6426
LUNG ALVEOLUS DEVELOPMENT	40	0.30	1.03	0.4119	0.6431
CHROMOSOME ORGANIZATION INVOLVED IN MEIOTIC CELL CYCLE	41	-0.30	-1.12	0.2918	0.6434
PEPTIDYL LYSINE METHYLATION	62	0.28	1.03	0.4111	0.6437
SECRETORY GRANULE ORGANIZATION	25	0.34	1.03	0.4159	0.6449
POSITIVE REGULATION OF MYELOID LEUKOCYTE DIFFERENTIATION	45	-0.29	-1.12	0.2601	0.6462
REGULATION OF PROTEIN KINASE A SIGNALING	17	-0.37	-1.12	0.3191	0.6471
CELLULAR RESPONSE TO ALKALOID	31	-0.31	-1.12	0.2776	0.6474
REGULATION OF LIPID BIOSYNTHETIC PROCESS	117	-0.25	-1.12	0.2158	0.6478
EPITHELIAL CELL DIFFERENTIATION	441	0.21	1.02	0.4057	0.6481
REGULATION OF CELL ADHESION MEDIATED BY INTEGRIN	35	-0.31	-1.12	0.2960	0.6481
POSITIVE REGULATION OF PATHWAY RESTRICTED SMAD PROTEIN PHOSPHORYLATION	47	0.29	1.02	0.4121	0.6484
ISOPRENOID METABOLIC PROCESS	106	-0.25	-1.12	0.2055	0.6485
NEUTRAL AMINO ACID TRANSMEMBRANE TRANSPORTER ACTIVITY	28	0.33	1.02	0.4164	0.6486
CELLULAR DEFENSE RESPONSE	43	-0.30	-1.12	0.2857	0.6486
CARTILAGE DEVELOPMENT INVOLVED IN ENDOCHONDRAL BONE MORPHOGENESIS	18	-0.37	-1.12	0.2766	0.6487
REGULATION OF FIBROBLAST MIGRATION	24	0.34	1.02	0.4281	0.6488
LUNG CELL DIFFERENTIATION	24	0.33	1.02	0.4350	0.6488
CENTRAL NERVOUS SYSTEM NEURON AXONOGENESIS	25	-0.33	-1.12	0.2760	0.6488
CELLULAR GLUCOSE HOMEOSTASIS	71	-0.27	-1.12	0.2278	0.6489
NEGATIVE REGULATION OF RECEPTOR MEDIATED ENDOCYTOSIS	16	0.38	1.02	0.4288	0.6490
POSITIVE REGULATION OF EPITHELIAL CELL DIFFERENTIATION	50	-0.28	-1.12	0.2500	0.6490
ENDOPLASMIC RETICULUM SUBCOMPARTMENT	15	0.38	1.02	0.4262	0.6491

EXTRINSIC APOPTOTIC SIGNALING PATHWAY IN ABSENCE OF LIGAND	26	-0.34	-1.12	0.2895	0.6491
TRANSCRIPTION COFACTOR BINDING	21	0.35	1.02	0.4375	0.6493
SYNAPTIC VESICLE CYCLE	83	-0.26	-1.12	0.2423	0.6493
RESPONSE TO ATP	28	-0.34	-1.12	0.2879	0.6497
SIGNAL TRANSDUCTION IN ABSENCE OF LIGAND	26	-0.34	-1.12	0.3096	0.6498
ADAPTATION OF SIGNALING PATHWAY	20	-0.37	-1.12	0.3318	0.6499
HEART PROCESS	82	0.26	1.02	0.4311	0.6506
NEGATIVE REGULATION OF T CELL PROLIFERATION	40	-0.30	-1.12	0.2656	0.6507
REGULATION OF CGMP METABOLIC PROCESS	27	-0.34	-1.12	0.2815	0.6508
NONMOTILE PRIMARY CILIUM ASSEMBLY	19	0.36	1.02	0.4433	0.6511
ENDOPEPTIDASE ACTIVITY	344	0.22	1.02	0.4082	0.6513
PERIPHERAL NERVOUS SYSTEM AXON ENSHEATHMENT	21	0.35	1.02	0.4561	0.6520
PROTEIN PHOSPHATASE BINDING	107	0.25	1.02	0.4061	0.6533
GLUTAMATE METABOLIC PROCESS	26	0.33	1.02	0.4364	0.6534
POSITIVE REGULATION OF ATP METABOLIC PROCESS	21	0.35	1.02	0.4325	0.6535
SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	103	0.25	1.02	0.4149	0.6535
ENDOCARDIAL CUSHION FORMATION	15	0.38	1.02	0.4086	0.6536
AMMONIUM ION BINDING	63	0.28	1.02	0.4071	0.6537
DEACETYLASE ACTIVITY	51	0.28	1.02	0.4179	0.6537
CEREBRAL CORTEX DEVELOPMENT	99	0.25	1.02	0.4032	0.6537
STRUCTURE SPECIFIC DNA BINDING	102	0.25	1.02	0.4242	0.6538
BASAL PLASMA MEMBRANE	31	0.32	1.02	0.4512	0.6539
REGULATION OF PEPTIDASE ACTIVITY	322	0.22	1.02	0.4095	0.6539
TISSUE REMODELING	83	0.26	1.02	0.4364	0.6541
MONOCARBOXYLIC ACID BINDING	47	0.29	1.02	0.4080	0.6542
TUMOR NECROSIS FACTOR MEDiated SIGNALING PATHWAY	105	0.25	1.02	0.4184	0.6547
POSITIVE REGULATION OF CELL DEVELOPMENT	438	0.21	1.02	0.4325	0.6548
MODULATION OF GROWTH OF SYMBIONT INVOLVED IN INTERACTION WITH HOST	16	0.37	1.02	0.4363	0.6550
EPIDERMAL CELL DIFFERENTIATION	120	-0.24	-1.11	0.2331	0.6554
POSITIVE REGULATION OF SMOOTH MUSCLE CELL MIGRATION	28	0.33	1.02	0.4527	0.6555

POSITIVE REGULATION OF PROTEIN TARGETING TO MEMBRANE	18	0.36	1.02	0.4530	0.6556
REGULATION OF EPITHELIAL CELL APOPTOTIC PROCESS	55	0.28	1.02	0.4237	0.6557
POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	40	0.30	1.02	0.4213	0.6578
CENTRIOLE	81	0.26	1.02	0.4275	0.6580
RAC PROTEIN SIGNAL TRANSDUCTION	16	0.38	1.02	0.4441	0.6583
POSITIVE REGULATION OF IMMUNE EFFECTOR PROCESS	131	-0.24	-1.11	0.2145	0.6595
POSITIVE REGULATION OF CYTOSKELETON ORGANIZATION	158	0.24	1.01	0.4333	0.6610
REGULATION OF CELLULAR COMPONENT SIZE	298	0.22	1.01	0.4220	0.6611
POSITIVE REGULATION OF KINASE ACTIVITY	423	0.21	1.01	0.4456	0.6614
REGULATION OF T CELL MEDIATED CYTOTOXICITY	18	0.36	1.01	0.4207	0.6614
SYNAPTIC TRANSMISSION DOPAMINERGIC	16	0.36	1.01	0.4444	0.6615
REGULATION OF PLATELET ACTIVATION	29	0.32	1.01	0.4315	0.6616
REGULATION OF FAT CELL DIFFERENTIATION	95	0.25	1.01	0.4290	0.6617
TRANSCRIPTIONAL REPRESSOR ACTIVITY RNA POLYMERASE II CORE PROMOTER PROXIMAL REGION SEQUENCE SPECIFIC BINDING	90	0.26	1.01	0.4399	0.6617
MONOSACCHARIDE CATABOLIC PROCESS	50	0.29	1.01	0.4295	0.6617
POSITIVE REGULATION OF NITRIC OXIDE SYNTHASE ACTIVITY	18	0.36	1.01	0.4426	0.6618
PHAGOCYTIC VESICLE MEMBRANE	45	0.29	1.01	0.4362	0.6618
NEGATIVE REGULATION OF MYOBLAST DIFFERENTIATION	23	0.33	1.01	0.4283	0.6621
G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY COUPLED TO CYCLIC NUCLEOTIDE SECOND MESSENGER	156	-0.23	-1.11	0.2128	0.6632
BINDING OF SPERM TO ZONA PELLUCIDA	29	0.32	1.01	0.4216	0.6636
ORGANOPHOSPHATE ESTER TRANSMEMBRANE TRANSPORTER ACTIVITY	21	0.34	1.01	0.4462	0.6642
CADHERIN BINDING	28	0.32	1.01	0.4574	0.6654

POSITIVE REGULATION OF CHROMOSOME SEGREGATION	21	0.35	1.01	0.4480	0.6654
TRANSCRIPTION FACTOR ACTIVITY RNA POLYMERASE II CORE PROMOTER PROXIMAL REGION SEQUENCE SPECIFIC BINDING	293	-0.21	-1.11	0.1667	0.6655
KINASE REGULATOR ACTIVITY	174	0.23	1.01	0.4198	0.6657
GROWTH FACTOR BINDING	116	0.25	1.01	0.4298	0.6659
DENDRITIC CELL MIGRATION	17	-0.38	-1.11	0.3318	0.6662
LAMININ BINDING	27	-0.33	-1.11	0.3161	0.6667
DNA ALKYLATION	44	-0.29	-1.11	0.2961	0.6669
DNA METHYLATION	44	-0.29	-1.11	0.2816	0.6670
REGULATION OF AXONOGENESIS	159	-0.23	-1.11	0.2081	0.6672
REGULATION OF NUCLEOTIDE CATABOLIC PROCESS	33	0.31	1.01	0.4520	0.6672
REGULATION OF CYCLIC NUCLEOTIDE METABOLIC PROCESS	143	-0.23	-1.11	0.2000	0.6678
REGULATION OF STEROID METABOLIC PROCESS	64	0.27	1.01	0.4621	0.6680
REGULATION OF CYTOKINE PRODUCTION INVOLVED IN INFLAMMATORY RESPONSE	17	-0.38	-1.10	0.3296	0.6691
POSITIVE REGULATION OF STEM CELL PROLIFERATION	53	-0.27	-1.10	0.2965	0.6693
NEGATIVE REGULATION OF LEUKOCYTE PROLIFERATION	56	-0.28	-1.10	0.2787	0.6696
ARF GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	23	0.33	1.01	0.4470	0.6699
SPERM EGGrecognition	39	0.30	1.01	0.4511	0.6701
PROTEIN LOCALIZATION TO CELL PERIPHERY	136	0.24	1.01	0.4476	0.6706
CARBOHYDRATE HOMEOSTASIS	154	-0.23	-1.10	0.2211	0.6707
PERICARDIUM DEVELOPMENT	17	-0.38	-1.10	0.3079	0.6708
NEGATIVE REGULATION OF IMMUNE SYSTEM PROCESS	310	-0.21	-1.10	0.1724	0.6709
LIMBIC SYSTEM DEVELOPMENT	97	-0.25	-1.10	0.2605	0.6713
COCHLEA MORPHOGENESIS	20	-0.36	-1.10	0.3558	0.6715
SYNAPSE ORGANIZATION	136	-0.23	-1.10	0.2140	0.6716
PODOSOME	23	-0.35	-1.10	0.2974	0.6716
TRANSCRIPTION FACTOR ACTIVITY RNA POLYMERASE II TRANSCRIPTION FACTOR BINDING	122	0.24	1.01	0.4517	0.6729

REGULATION OF GLUTAMATE SECRETION	15	0.36	1.01	0.4365	0.6730
HISTONE H3 DEACETYLATION	20	0.35	1.01	0.4316	0.6732
REGULATION OF INSULIN RECEPTOR SIGNALING PATHWAY	40	-0.30	-1.10	0.2846	0.6737
HISTONE EXCHANGE	32	-0.31	-1.10	0.3144	0.6738
REGULATION OF PEPTIDE SECRETION	189	-0.22	-1.10	0.2190	0.6738
RHO GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	62	-0.27	-1.10	0.2590	0.6745
ENTRY INTO CELL OF OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	76	-0.25	-1.10	0.2676	0.6753
REPLICATION FORK	53	0.28	1.01	0.4609	0.6754
REGULATION OF MUSCLE CELL APOPTOTIC PROCESS	40	-0.30	-1.10	0.2952	0.6755
AXIS SPECIFICATION	86	-0.26	-1.10	0.2209	0.6759
MEMBRANE DEPOLARIZATION	57	-0.27	-1.10	0.3055	0.6760
REGULATION OF STRIATED MUSCLE CELL APOPTOTIC PROCESS	20	-0.35	-1.10	0.3287	0.6761
SARCOMERE ORGANIZATION	25	-0.33	-1.09	0.3540	0.6761
ENTRY INTO OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	76	-0.25	-1.10	0.2922	0.6762
PYRIDINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	19	-0.35	-1.10	0.3473	0.6763
LAMELLAR BODY	17	-0.37	-1.10	0.3254	0.6766
TRANSCRIPTION FACTOR COMPLEX	265	0.22	1.00	0.4261	0.6768
BRUSH BORDER	93	0.25	1.00	0.4359	0.6768
REGULATION OF ACUTE INFLAMMATORY RESPONSE	65	-0.27	-1.10	0.2373	0.6772
POSITIVE REGULATION OF ADAPTIVE IMMUNE RESPONSE	64	-0.27	-1.10	0.2800	0.6779
NEGATIVE REGULATION OF DEFENSE RESPONSE TO VIRUS	16	0.37	1.00	0.4413	0.6780
NEGATIVE REGULATION OF NOTCH SIGNALING PATHWAY	24	-0.34	-1.09	0.3070	0.6781
SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS VIA GERMLINE RECOMBINATION WITHIN A SINGLE LOCUS	27	0.32	1.00	0.4476	0.6783
NEGATIVE REGULATION OF HOMEOSTATIC PROCESS	107	0.25	1.00	0.4466	0.6784
POSITIVE REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION	147	0.24	1.00	0.4498	0.6785

REGULATION OF PHOSPHOLIPASE C ACTIVITY	37	-0.30	-1.10	0.3112	0.6787
PROTEIN HETROTETRAMERIZATION	20	0.35	1.00	0.4598	0.6788
REGULATION OF HISTONE H3 K9 METHYLATION	15	-0.38	-1.09	0.3386	0.6795
MOVEMENT IN ENVIRONMENT OF OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	76	-0.25	-1.09	0.2672	0.6798
EPITHELIAL STRUCTURE MAINTENANCE	19	-0.36	-1.09	0.3174	0.6801
RESPONSE TO EXOGENOUS DSRNA	34	0.30	1.00	0.4570	0.6806
REGULATION OF DOPAMINE SECRETION	22	-0.35	-1.09	0.3244	0.6806
REGULATION OF VESICLE MEDIATED TRANSPORT	414	0.21	1.00	0.4681	0.6808
MITOGEN ACTIVATED PROTEIN KINASE BINDING	24	0.33	1.00	0.4740	0.6808
REGULATION OF MICROTUBULE POLYMERIZATION	31	0.31	1.00	0.4499	0.6809
DNA SECONDARY STRUCTURE BINDING	20	-0.35	-1.09	0.3611	0.6812
NEGATIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	21	0.35	1.00	0.4489	0.6813
RESPONSE TO ACID CHEMICAL	281	0.22	1.00	0.4631	0.6814
REGULATION OF STEM CELL PROLIFERATION	78	-0.25	-1.09	0.2832	0.6819
ENTRY INTO HOST	76	-0.25	-1.09	0.2653	0.6821
REGULATION OF T CELL RECEPTOR SIGNALING PATHWAY	26	0.33	1.00	0.4509	0.6822
REGULATION OF SYNAPTIC VESICLE EXOCYTOSIS	19	0.34	1.00	0.4522	0.6822
NEURON MIGRATION	102	-0.24	-1.09	0.2799	0.6824
BICARBONATE TRANSMEMBRANE TRANSPORTER ACTIVITY	17	0.36	1.00	0.4536	0.6824
GLUCOSE HOMEOSTASIS	154	-0.23	-1.09	0.2148	0.6828
DENDRITE MEMBRANE	19	-0.35	-1.09	0.3539	0.6829
VESICLE CYTOSKELETAL TRAFFICKING	35	0.30	1.00	0.4868	0.6829
NEGATIVE REGULATION OF ORGANIC ACID TRANSPORT	17	0.37	1.00	0.4541	0.6829
MUSCLE ORGAN MORPHOGENESIS	67	-0.27	-1.09	0.3219	0.6832
NEGATIVE REGULATION OF EPITHELIAL CELL MIGRATION	50	-0.28	-1.09	0.3039	0.6832
E BOX BINDING	30	-0.32	-1.09	0.3118	0.6838
FEMALE GAMETE GENERATION	80	-0.26	-1.09	0.3015	0.6845
RESPONSE TO TUMOR NECROSIS FACTOR	197	0.23	1.00	0.4763	0.6847

STEROL BIOSYNTHETIC PROCESS	37	0.30	1.00	0.4631	0.6847
INSULIN RECEPTOR BINDING	29	0.32	1.00	0.4692	0.6848
SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	308	0.22	1.00	0.4490	0.6849
MESONEPHRIC TUBULE MORPHOGENESIS	49	0.28	1.00	0.4590	0.6853
OSTEOCLAST DIFFERENTIATION	28	0.32	1.00	0.4655	0.6877
PHOSPHATIDYLCHOLINE BINDING	18	0.35	1.00	0.4500	0.6878
ROUGH ENDOPLASMIC RETICULUM MEMBRANE	20	0.34	1.00	0.4551	0.6880
POSITIVE REGULATION OF NUCLEOSIDE METABOLIC PROCESS	21	0.35	1.00	0.4660	0.6881
SOMATIC CELL DNA RECOMBINATION	27	0.32	1.00	0.4699	0.6882
MITOGEN ACTIVATED PROTEIN KINASE KINASE BINDING	15	0.36	1.00	0.4576	0.6883
PIGMENT CELL DIFFERENTIATION	26	0.32	1.00	0.4564	0.6884
NEGATIVE REGULATION OF DEVELOPMENTAL GROWTH	78	-0.25	-1.09	0.2790	0.6899
NEGATIVE REGULATION OF STEROID METABOLIC PROCESS	20	-0.34	-1.09	0.3237	0.6901
SODIUM CHANNEL ACTIVITY	35	-0.30	-1.08	0.3264	0.6911
CELLULAR RESPONSE TO FATTY ACID	46	0.29	1.00	0.4737	0.6912
ANTIGEN BINDING	38	-0.29	-1.08	0.3166	0.6919
REGULATION OF TRANSMEMBRANE RECEPTOR PROTEIN SERINE THREONINE KINASE SIGNALING PATHWAY	182	0.23	0.99	0.4641	0.6921
POTASSIUM ION HOMEOSTASIS	17	0.36	0.99	0.4461	0.6922
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH NH GROUP OF DONORS NAD OR NADP AS ACCEPTOR	15	0.37	0.99	0.4841	0.6924
POSITIVE REGULATION OF STAT CASCADE	64	-0.27	-1.08	0.3031	0.6930
DOPAMINE METABOLIC PROCESS	22	0.34	0.99	0.4476	0.6931
RESPONSE TO ORGANOPHOSPHORUS	126	-0.23	-1.08	0.2862	0.6932
ESTABLISHMENT OF ENDOTHELIAL BARRIER	28	0.32	0.99	0.4783	0.6933
ENDOCARDIAL CUSHION DEVELOPMENT	31	0.31	0.99	0.4697	0.6933
PROTEIN SELF ASSOCIATION	36	0.30	0.99	0.4679	0.6933
CAMERA TYPE EYE MORPHOGENESIS	98	0.25	0.99	0.4820	0.6934
REGULATION OF PROTEIN INSERTION INTO MITOCHONDRIAL MEMBRANE	23	0.32	0.99	0.4741	0.6935

INVOLVED IN APOPTOTIC SIGNALING PATHWAY					
EXTRINSIC COMPONENT OF ORGANELLE MEMBRANE	20	0.34	0.99	0.4764	0.6936
CELLULAR RESPONSE TO INTERLEUKIN 1	71	0.26	0.99	0.4639	0.6936
POSITIVE REGULATION OF PHOSPHATASE ACTIVITY	27	0.32	0.99	0.4917	0.6936
POSITIVE REGULATION OF HEMOPOIESIS	140	-0.23	-1.08	0.2625	0.6939
CELLULAR RESPONSE TO ESTRADIOL STIMULUS	28	0.31	0.99	0.4795	0.6948
MYOBLAST DIFFERENTIATION	35	-0.30	-1.08	0.3122	0.6951
EPIDERMIS DEVELOPMENT	218	-0.22	-1.08	0.2375	0.6954
CEREBRAL CORTEX RADially ORIENTED CELL MIGRATION	26	-0.32	-1.08	0.3546	0.6954
POSITIVE REGULATION OF CELL MATRIX ADHESION	38	-0.29	-1.08	0.3152	0.6956
I BAND	110	-0.24	-1.08	0.2730	0.6958
VIRAL ENTRY INTO HOST CELL	76	-0.25	-1.08	0.3068	0.6962
T CELL MEDIATED IMMUNITY	20	-0.34	-1.08	0.3425	0.6965
MOVEMENT IN HOST ENVIRONMENT	76	-0.25	-1.08	0.3251	0.6965
CYTOLYSIS	15	-0.38	-1.08	0.3592	0.6965
REGULATION OF HORMONE SECRETION	239	-0.21	-1.08	0.2364	0.6966
PRIMARY ALCOHOL METABOLIC PROCESS	40	-0.29	-1.08	0.3621	0.6967
POSITIVE REGULATION OF PEPTIDYL SERINE PHOSPHORYLATION	77	-0.26	-1.07	0.3138	0.6968
MUSCLE ORGAN DEVELOPMENT	255	-0.21	-1.08	0.2545	0.6969
EMBRYONIC ORGAN DEVELOPMENT	378	-0.20	-1.08	0.1716	0.6969
REGULATION OF CELL AGING	30	-0.31	-1.07	0.3563	0.6970
MYELOID CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	37	-0.30	-1.08	0.3222	0.6971
TRANSCRIPTIONAL ACTIVATOR ACTIVITY RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC BINDING	23	-0.34	-1.08	0.3510	0.6973
CALCIUM DEPENDENT PHOSPHOLIPID BINDING	48	-0.28	-1.08	0.3217	0.6973
ENTRY INTO HOST CELL	76	-0.25	-1.08	0.3077	0.6974
REGULATION OF TELOMERASE ACTIVITY	36	0.30	0.99	0.4508	0.6974
CEREBRAL CORTEX RADIAL GLIA GUIDED MIGRATION	17	-0.36	-1.08	0.3357	0.6975

CARTILAGE DEVELOPMENT	139	-0.22	-1.07	0.2420	0.6976
NEGATIVE REGULATION OF CYTOKINE PRODUCTION	181	-0.22	-1.07	0.2621	0.6977
AMEBOIDAL TYPE CELL MIGRATION	143	-0.23	-1.07	0.2809	0.6977
CALCIUM ION IMPORT	53	-0.27	-1.07	0.3194	0.6978
POSITIVE REGULATION OF SKELETAL MUSCLE TISSUE DEVELOPMENT	25	-0.33	-1.07	0.3540	0.6980
CELLULAR RESPONSE TO CARBOHYDRATE STIMULUS	69	-0.26	-1.08	0.2845	0.6981
REGULATION OF INTERLEUKIN 6 BIOSYNTHETIC PROCESS	15	-0.38	-1.07	0.3684	0.6983
SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS	33	0.30	0.99	0.4668	0.6983
ENDOCYTIC RECYCLING	23	0.33	0.99	0.4735	0.6984
NEPHRIC DUCT DEVELOPMENT	15	-0.38	-1.07	0.3601	0.6985
NEUTRAL AMINO ACID TRANSPORT	30	0.31	0.99	0.4680	0.6991
EMBRYONIC MORPHOGENESIS	496	-0.20	-1.07	0.2044	0.6992
NITRIC OXIDE SYNTHASE BINDING	18	0.34	0.99	0.4804	0.6996
NEGATIVE REGULATION OF HYDROLASE ACTIVITY	327	0.21	0.99	0.5048	0.7003
REGULATION OF TUMOR NECROSIS FACTOR MEDIATED SIGNALING PATHWAY	40	0.29	0.99	0.4881	0.7004
RENAL SYSTEM PROCESS INVOLVED IN REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE	18	0.36	0.99	0.4727	0.7010
MACROPHAGE DIFFERENTIATION	17	-0.35	-1.07	0.3457	0.7014
POSITIVE REGULATION OF PROTEIN LOCALIZATION TO CELL PERIPHERY	33	0.30	0.99	0.4678	0.7021
CORE PROMOTER BINDING	133	0.23	0.99	0.4854	0.7023
BLOOD COAGULATION INTRINSIC PATHWAY	16	0.36	0.99	0.4648	0.7033
PEPTIDASE ACTIVATOR ACTIVITY	34	0.30	0.99	0.4677	0.7052
SPERMATID DIFFERENTIATION	105	0.24	0.99	0.4846	0.7053
POSITIVE REGULATION OF VIRAL GENOME REPPLICATION	27	0.32	0.99	0.4736	0.7054
REGULATION OF NEURON PROJECTION DEVELOPMENT	384	0.21	0.99	0.5023	0.7056
MULTICELLULAR ORGANISMAL MACROMOLECULE METABOLIC PROCESS	71	-0.25	-1.07	0.3183	0.7058
RELEASE OF CYTOCHROME C FROM MITOCHONDRIA	17	0.35	0.99	0.4608	0.7059

G PROTEIN BETA GAMMA SUBUNIT COMPLEX BINDING	21	0.34	0.98	0.4860	0.7060
REGULATION OF MYOBLAST DIFFERENTIATION	45	0.29	0.99	0.4927	0.7060
PROTEIN INSERTION INTO MEMBRANE	17	0.36	0.98	0.4786	0.7070
EPITHELIAL CELL APOPTOTIC PROCESS	24	0.32	0.98	0.4553	0.7071
RESPONSE TO LEAD ION	20	0.34	0.98	0.4876	0.7072
CARBON CARBON LYASE ACTIVITY	49	0.28	0.98	0.4944	0.7073
REGULATION OF CARDIAC MUSCLE CONTRACTION BY REGULATION OF THE RELEASE OF SEQUESTERED CALCIUM ION	17	0.36	0.98	0.4836	0.7073
AXONEME ASSEMBLY	26	-0.32	-1.07	0.3367	0.7075
POSITIVE REGULATION OF PROTEIN LOCALIZATION TO PLASMA MEMBRANE	33	0.30	0.98	0.4850	0.7081
CELLULAR RESPONSE TO TOXIC SUBSTANCE	24	-0.33	-1.07	0.3515	0.7086
REPRODUCTIVE BEHAVIOR	26	-0.32	-1.07	0.3454	0.7087
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY BINDING	42	-0.28	-1.07	0.3496	0.7089
PROTEIN KINASE A BINDING	36	0.30	0.98	0.4968	0.7095
REGULATION OF IMMUNOGLOBULIN SECRETION	15	0.36	0.98	0.4621	0.7098
POSITIVE REGULATION OF MYELOID LEUKOCYTE MEDIATED IMMUNITY	15	0.37	0.98	0.4922	0.7100
ATP GENERATION FROM ADP	36	0.29	0.98	0.4891	0.7103
COMPLEMENT BINDING	15	0.38	0.98	0.4753	0.7113
RESPONSE TO FLUID SHEAR STRESS	32	0.30	0.98	0.4958	0.7118
PROTEIN KINASE C ACTIVATING G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY	31	0.30	0.98	0.4912	0.7120
CATION CHANNEL COMPLEX	157	-0.22	-1.06	0.2852	0.7141
SEMAPHORIN PLEXIN SIGNALING PATHWAY	35	-0.30	-1.06	0.3604	0.7146
POSITIVE REGULATION OF VASOCONSTRICITION	34	-0.30	-1.06	0.3598	0.7150
POSITIVE REGULATION OF NERVOUS SYSTEM DEVELOPMENT	407	0.21	0.98	0.5483	0.7154
POSITIVE REGULATION OF SYNAPTIC TRANSMISSION	104	0.24	0.98	0.4772	0.7155
POSITIVE REGULATION OF STEROID METABOLIC PROCESS	21	0.33	0.98	0.4992	0.7155
ODONTOGENESIS OF DENTIN CONTAINING TOOTH	73	0.26	0.98	0.4931	0.7162

SARCOLEMMA	113	0.24	0.98	0.4978	0.7163
ACTIN NUCLEATION	19	0.35	0.98	0.4913	0.7169
NEGATIVE REGULATION OF CATECHOLAMINE SECRETION	16	-0.37	-1.06	0.3846	0.7170
VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	73	-0.25	-1.06	0.3219	0.7179
REGULATION OF CHROMATIN ORGANIZATION	133	-0.23	-1.06	0.3060	0.7180
RESPONSE TO PH	36	-0.30	-1.06	0.3564	0.7184
OOGENESIS	53	-0.27	-1.06	0.3360	0.7188
NEGATIVE REGULATION OF CELL SUBSTRATE ADHESION	46	0.28	0.98	0.5093	0.7189
POSITIVE REGULATION OF DNA RECOMBINATION	16	-0.37	-1.06	0.3643	0.7190
POSITIVE REGULATION OF PROTEIN INSERTION INTO MITOCHONDRIAL MEMBRANE INVOLVED IN APOPTOTIC SIGNALING PATHWAY	23	0.32	0.98	0.4733	0.7191
DNA METHYLATION OR DEMETHYLATION	52	-0.27	-1.06	0.3636	0.7194
DECIDUALIZATION	18	-0.36	-1.06	0.3759	0.7194
REGULATION OF WATER LOSS VIA SKIN	15	-0.37	-1.06	0.3806	0.7196
NEGATIVE REGULATION OF CELL DEVELOPMENT	276	-0.20	-1.06	0.2896	0.7197
NEGATIVE REGULATION OF OSSIFICATION	64	0.27	0.98	0.4946	0.7204
FIBROBLAST GROWTH FACTOR BINDING	23	0.33	0.98	0.4967	0.7215
REGULATION OF SUBSTRATE ADHESION DEPENDENT CELL SPREADING	37	0.29	0.98	0.4691	0.7218
NEGATIVE REGULATION OF DEFENSE RESPONSE	122	0.24	0.98	0.4972	0.7220
CARDIAC MUSCLE CELL DIFFERENTIATION	72	0.25	0.98	0.5008	0.7220
PROTEIN SERINE THREONINE KINASE INHIBITOR ACTIVITY	29	0.30	0.97	0.4846	0.7221
ACID AMINO ACID LIGASE ACTIVITY	19	0.34	0.97	0.4921	0.7234
MUSCLE TISSUE DEVELOPMENT	254	-0.21	-1.06	0.2805	0.7236
DNA REPLICATION INDEPENDENT NUCLEOSOME ASSEMBLY	35	0.29	0.97	0.4763	0.7237
BETA CATENIN DESTRUCTION COMPLEX DISASSEMBLY	21	0.33	0.97	0.5069	0.7239
PROTEIN PALMITOYLATION	22	0.33	0.97	0.4809	0.7239

NEGATIVE REGULATION OF ENDOTHELIAL CELL APOPTOTIC PROCESS	26	0.32	0.97	0.4947	0.7241
REGULATION OF EXCRETION	25	-0.31	-1.06	0.3599	0.7243
REGULATION OF HUMORAL IMMUNE RESPONSE	42	-0.28	-1.06	0.3720	0.7254
REGULATION OF CILIUM ASSEMBLY	47	0.27	0.97	0.5066	0.7260
HIPPO SIGNALING	24	0.32	0.97	0.4833	0.7267
TRANSMITTER GATED CHANNEL ACTIVITY	25	-0.32	-1.06	0.3668	0.7282
CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	465	-0.19	-1.06	0.2532	0.7284
SIGNAL PEPTIDE PROCESSING	20	0.34	0.97	0.5062	0.7285
REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	91	0.25	0.97	0.5184	0.7285
ADP METABOLIC PROCESS	42	0.28	0.97	0.5153	0.7293
BILE ACID METABOLIC PROCESS	27	0.31	0.97	0.5025	0.7293
CELL SUBSTRATE JUNCTION ASSEMBLY	38	0.29	0.97	0.5126	0.7293
STEROID BIOSYNTHETIC PROCESS	96	0.24	0.97	0.5122	0.7294
GASTRULATION WITH MOUTH FORMING SECOND	27	0.31	0.97	0.5083	0.7303
BILE ACID BIOSYNTHETIC PROCESS	18	0.35	0.97	0.5009	0.7304
RESPONSE TO DRUG	390	0.21	0.97	0.5421	0.7305
CELL JUNCTION ORGANIZATION	167	0.22	0.97	0.5124	0.7305
REGULATION OF ACTIN FILAMENT BUNDLE ASSEMBLY	71	0.26	0.97	0.4945	0.7306
REGULATION OF MUSCLE SYSTEM PROCESS	186	0.22	0.97	0.5463	0.7315
REGULATION OF PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	53	0.27	0.97	0.5064	0.7316
REGULATION OF MUSCLE TISSUE DEVELOPMENT	93	0.24	0.97	0.5313	0.7317
RESPONSE TO INTERLEUKIN 6	23	0.32	0.97	0.5009	0.7319
NEGATIVE REGULATION OF POTASSIUM ION TRANSPORT	32	-0.30	-1.05	0.3790	0.7322
RENAL TUBULE DEVELOPMENT	73	-0.25	-1.05	0.3650	0.7325
PHOTORECEPTOR DISC MEMBRANE	15	-0.38	-1.05	0.3916	0.7326
TELENCEPHALON GLIAL CELL MIGRATION	17	-0.36	-1.05	0.3583	0.7328
REGULATION OF VASOCONSTRICITION	62	-0.26	-1.05	0.3704	0.7331
REGULATION OF CARTILAGE DEVELOPMENT	59	-0.27	-1.05	0.3716	0.7332
COBALAMIN METABOLIC PROCESS	17	0.35	0.97	0.5091	0.7334

AXON EXTENSION	35	-0.29	-1.05	0.3639	0.7338
REGULATION OF EPIDERMAL GROWTH FACTOR ACTIVATED RECEPTOR ACTIVITY	21	0.33	0.97	0.4966	0.7339
HISTONE H3 K4 METHYLATION	28	0.30	0.97	0.4914	0.7340
NEGATIVE REGULATION OF AMINE TRANSPORT	25	-0.32	-1.05	0.3611	0.7343
REGULATION OF BMP SIGNALING PATHWAY	67	0.26	0.97	0.5185	0.7343
FEEDING BEHAVIOR	85	-0.24	-1.05	0.3354	0.7344
NEGATIVE REGULATION OF PEPTIDE SECRETION	47	-0.27	-1.05	0.3653	0.7344
SITE OF POLARIZED GROWTH	138	-0.22	-1.05	0.3227	0.7345
CELLULAR COMPONENT MAINTENANCE	16	-0.37	-1.05	0.4119	0.7346
REGULATION OF STRIATED MUSCLE CELL DIFFERENTIATION	79	-0.25	-1.05	0.3544	0.7348
PHOTORECEPTOR INNER SEGMENT	33	-0.30	-1.05	0.3623	0.7352
EMBRYONIC DIGESTIVE TRACT DEVELOPMENT	30	-0.31	-1.05	0.3890	0.7352
PHOSPHATIDYLINOSITOL 4 5 BISPHOSPHATE BINDING	48	0.28	0.97	0.5135	0.7360
SINGLE ORGANISM BEHAVIOR	343	-0.20	-1.05	0.2727	0.7364
CILIUM MORPHOGENESIS	157	0.22	0.97	0.5463	0.7366
G1 DNA DAMAGE CHECKPOINT	61	0.26	0.97	0.4938	0.7367
CELLULAR RESPONSE TO BMP STIMULUS	87	0.24	0.96	0.5110	0.7383
METALLOEXOPEPTIDASE ACTIVITY	46	0.27	0.96	0.5255	0.7385
ACTIVATION OF IMMUNE RESPONSE	332	0.21	0.96	0.5603	0.7385
DNA REPLICATION INDEPENDENT NUCLEOSOME ORGANIZATION	35	0.29	0.96	0.5261	0.7385
POSITIVE REGULATION OF ACTIN FILAMENT POLYMERIZATION	58	0.27	0.96	0.5228	0.7386
BLOOD COAGULATION FIBRIN CLOT FORMATION	23	0.32	0.96	0.5053	0.7388
RESPONSE TO INTERFERON BETA	20	-0.33	-1.05	0.3886	0.7388
RESPONSE TO PROSTAGLANDIN E	23	0.33	0.96	0.4958	0.7389
RESPIRATORY GASEOUS EXCHANGE	45	0.28	0.96	0.5233	0.7389
POSITIVE REGULATION OF RNA SPLICING	22	0.32	0.96	0.5075	0.7394
NEPHRON EPITHELIUM DEVELOPMENT	87	-0.24	-1.05	0.3449	0.7402
POSITIVE REGULATION OF ERK1 AND ERK2 CASCADE	148	0.22	0.96	0.5335	0.7405
PRESYNAPSE	265	0.21	0.96	0.5637	0.7405

REGULATION OF DEVELOPMENTAL GROWTH	263	0.21	0.96	0.5687	0.7412
DEFENSE RESPONSE TO BACTERIUM	134	-0.23	-1.05	0.3382	0.7414
GLYCERALDEHYDE 3 PHOSPHATE METABOLIC PROCESS	16	0.35	0.96	0.5094	0.7415
GLAND DEVELOPMENT	371	0.20	0.96	0.5780	0.7420
NEURON SPINE	110	0.24	0.96	0.5258	0.7421
TELOMERE ORGANIZATION	75	0.25	0.96	0.5339	0.7421
REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY	141	0.23	0.96	0.5629	0.7422
TELOMERASE HOLOENZYME COMPLEX	19	0.34	0.96	0.5018	0.7423
REGULATION OF NF KAPPAB IMPORT INTO NUCLEUS	41	0.28	0.96	0.5141	0.7428
ACTIVATION OF PROTEIN KINASE ACTIVITY	242	0.21	0.96	0.5661	0.7429
HIPPOCAMPUS DEVELOPMENT	70	-0.25	-1.04	0.3952	0.7433
SECRETORY GRANULE MEMBRANE	74	0.25	0.96	0.5457	0.7435
NEURON PROJECTION EXTENSION	49	-0.27	-1.04	0.4158	0.7436
PROTEIN KINASE B SIGNALING	34	-0.29	-1.04	0.3614	0.7438
POSITIVE REGULATION OF TRANSMEMBRANE TRANSPORT	121	-0.22	-1.04	0.3370	0.7441
REGULATION OF EPITHELIAL CELL DIFFERENTIATION	111	-0.23	-1.04	0.3442	0.7441
EXTRINSIC COMPONENT OF CYTOPLASMIC SIDE OF PLASMA MEMBRANE	89	-0.24	-1.04	0.3363	0.7442
POSITIVE REGULATION OF STRIATED MUSCLE CELL DIFFERENTIATION	47	-0.27	-1.04	0.3911	0.7446
POSITIVE REGULATION OF CALCIUM ION DEPENDENT EXOCYTOSIS	24	0.31	0.96	0.5061	0.7449
POSITIVE REGULATION OF CIRCADIAN RHYTHM	20	-0.34	-1.04	0.3785	0.7450
RESPONSE TO STEROID HORMONE	450	0.20	0.96	0.5751	0.7459
SYNAPTIC VESICLE ENDOCYTOSIS	17	0.35	0.96	0.5120	0.7461
RAC GTPASE BINDING	34	-0.29	-1.04	0.4090	0.7462
CHONDROCYTE DEVELOPMENT	20	0.33	0.96	0.5347	0.7467
PROTEIN BINDING INVOLVED IN CELL ADHESION	17	-0.36	-1.04	0.3995	0.7468
MULTI ORGANISM BEHAVIOR	68	-0.25	-1.04	0.3675	0.7476
ENDOPLASMIC RETICULUM TO CYTOSOL TRANSPORT	19	0.34	0.96	0.5105	0.7478
LAMELLIPODIA	159	-0.22	-1.04	0.3346	0.7479
TETRACYCLIC POLYPIRROLEDOPHERIN BINDING	85	-0.24	-1.04	0.3571	0.7480

SECOND MESSENGER MEDIATED SIGNALING	144	0.23	0.96	0.5684	0.7480
GROWTH FACTOR RECEPTOR BINDING	113	0.23	0.96	0.5477	0.7481
BINDING BRIDGING	157	0.22	0.96	0.5658	0.7481
HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS IN CYCLIC AMIDINES	26	0.31	0.96	0.5169	0.7483
NEGATIVE REGULATION OF EPITHELIAL CELL DIFFERENTIATION	34	0.30	0.96	0.5632	0.7483
REGULATION OF RESPONSE TO INTERFERON GAMMA	21	0.33	0.96	0.5299	0.7484
L ALPHA AMINO ACID TRANSMEMBRANE TRANSPORT	30	0.30	0.96	0.5395	0.7485
HAIR CELL DIFFERENTIATION	32	0.29	0.96	0.5287	0.7486
REGULATION OF PRI MIRNA TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	16	0.35	0.96	0.5063	0.7487
CLUSTER OF ACTIN BASED CELL PROJECTIONS	122	0.23	0.96	0.5396	0.7492
EXCITATORY SYNAPSE	179	-0.21	-1.04	0.3553	0.7496
UNFOLDED PROTEIN BINDING	73	-0.25	-1.04	0.3839	0.7497
REGULATION OF T CELL APOPTOTIC PROCESS	27	-0.31	-1.04	0.4020	0.7499
REGULATION OF MEGAKARYOCYTE DIFFERENTIATION	16	-0.36	-1.04	0.3941	0.7509
INOSITOL PHOSPHATE METABOLIC PROCESS	52	0.27	0.95	0.5462	0.7511
ENDOSOME LUMEN	20	-0.33	-1.04	0.3850	0.7517
NEURON PROJECTION TERMINUS	124	0.23	0.95	0.5623	0.7518
REGULATION OF PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	19	-0.34	-1.04	0.3865	0.7518
POSITIVE REGULATION OF GLIOGENESIS	43	0.27	0.95	0.5219	0.7520
FILOPODIUM MEMBRANE	18	-0.35	-1.04	0.4227	0.7524
NEUTROPHIL MEDIATED IMMUNITY	17	0.35	0.95	0.5036	0.7531
REGULATION OF BONE REMODELING	39	0.29	0.95	0.5250	0.7536
LIPID PHOSPHORYLATION	93	0.24	0.95	0.5676	0.7538
NEGATIVE REGULATION OF NERVOUS SYSTEM DEVELOPMENT	243	-0.20	-1.04	0.3584	0.7541
ALKALI METAL ION BINDING	20	0.33	0.95	0.5347	0.7550
REGULATION OF SISTER CHROMATID COHESION	17	0.34	0.95	0.5203	0.7551
SIGNAL RELEASE	158	-0.22	-1.03	0.3370	0.7566

NEGATIVE REGULATION OF AXONOGENESIS	63	-0.26	-1.03	0.3946	0.7567
ENDOCRINE PANCREAS DEVELOPMENT	38	0.28	0.95	0.5378	0.7568
NEGATIVE REGULATION OF INTERLEUKIN 6 PRODUCTION	31	-0.30	-1.03	0.3883	0.7570
RESPONSE TO BMP	87	0.24	0.95	0.5680	0.7577
ENZYME INHIBITOR ACTIVITY	307	0.21	0.95	0.5960	0.7578
REGULATION OF CELL KILLING	53	0.26	0.95	0.5433	0.7578
CYTOKINE PRODUCTION	105	-0.23	-1.03	0.3555	0.7579
ESTABLISHMENT OR MAINTENANCE OF EPITHELIAL CELL APICAL BASAL POLARITY	24	0.31	0.95	0.5309	0.7580
REGULATION OF ORGAN GROWTH	63	0.26	0.95	0.5572	0.7581
REGULATION OF P38MAPK CASCADE	25	0.31	0.95	0.5415	0.7581
PYRIMIDINE CONTAINING COMPOUND CATABOLIC PROCESS	24	0.31	0.95	0.5273	0.7584
NICOTINAMIDE NUCLEOTIDE BIOSYNTHETIC PROCESS	15	0.35	0.95	0.5195	0.7585
LENS FIBER CELL DIFFERENTIATION	24	0.32	0.95	0.5193	0.7587
NEGATIVE REGULATION OF STAT CASCADE	43	0.27	0.95	0.5320	0.7587
POSITIVE REGULATION OF PHOSPHATIDYLINOSITOL 3 KINASE SIGNALING	58	0.26	0.95	0.5485	0.7598
NEURONAL POSTSYNAPTIC DENSITY	47	0.27	0.95	0.5532	0.7600
DNA STRAND ELONGATION INVOLVED IN DNA REPLICATION	21	0.32	0.95	0.5406	0.7602
NEGATIVE REGULATION OF ALCOHOL BIOSYNTHETIC PROCESS	17	-0.34	-1.03	0.4015	0.7602
REGULATION OF MYELOID CELL DIFFERENTIATION	157	-0.21	-1.03	0.3626	0.7604
METANEPHRIC NEPHRON DEVELOPMENT	31	-0.30	-1.03	0.3922	0.7607
POSITIVE REGULATION OF SUBSTRATE ADHESION DEPENDENT CELL SPREADING	26	0.31	0.95	0.5317	0.7610
POSITIVE REGULATION OF CELL KILLING	32	0.29	0.95	0.5349	0.7611
PLATELET DEGRANULATION	98	0.24	0.95	0.5637	0.7611
BETA CATENIN TCF COMPLEX ASSEMBLY	35	-0.29	-1.03	0.4373	0.7612
RESPONSE TO MUSCLE STRETCH	19	-0.34	-1.03	0.4092	0.7612
APPENDAGE DEVELOPMENT	155	-0.21	-1.03	0.3827	0.7613
NEGATIVE REGULATION OF TRANSPORT	406	0.20	0.95	0.6339	0.7614
VESICLE LUMEN	89	-0.24	-1.03	0.3773	0.7615

FIBRINOLYSIS	20	0.33	0.95	0.5513	0.7616
REGULATION OF PHAGOCYTOSIS	59	-0.25	-1.03	0.4227	0.7617
NEGATIVE REGULATION OF PROTEIN SECRETION	93	-0.23	-1.03	0.3842	0.7618
STRAND DISPLACEMENT	22	-0.33	-1.03	0.3911	0.7620
NEGATIVE REGULATION OF STRIATED MUSCLE CELL DIFFERENTIATION	25	-0.31	-1.03	0.3986	0.7620
NEGATIVE REGULATION OF CYTOKINE SECRETION	35	-0.29	-1.03	0.3960	0.7622
EPITHELIAL CELL PROLIFERATION	82	-0.24	-1.03	0.3509	0.7622
REGULATION OF CGMP BIOSYNTHETIC PROCESS	20	-0.34	-1.03	0.4319	0.7628
NARROW PORE CHANNEL ACTIVITY	15	-0.36	-1.03	0.3867	0.7629
TEMPERATURE HOMEOSTASIS	23	0.32	0.95	0.5469	0.7630
GAP JUNCTION CHANNEL ACTIVITY	15	-0.36	-1.03	0.4123	0.7633
REGULATION OF CELL MATURATION	17	0.34	0.94	0.5437	0.7634
TRANSITION METAL ION TRANSMEMBRANE TRANSPORTER ACTIVITY	37	-0.28	-1.03	0.3760	0.7636
SODIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	128	-0.22	-1.03	0.3651	0.7637
GTPASE BINDING	273	0.21	0.94	0.6231	0.7637
DENDRITE DEVELOPMENT	74	-0.24	-1.03	0.4090	0.7638
NEGATIVE REGULATION OF NEURAL PRECURSOR CELL PROLIFERATION	20	-0.33	-1.03	0.4083	0.7639
REGULATION OF BLOOD PRESSURE	153	0.22	0.95	0.5919	0.7639
TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE ACTIVITY	62	0.26	0.95	0.5541	0.7639
METHYL CPG BINDING	16	-0.35	-1.03	0.4223	0.7641
NEGATIVE REGULATION OF HEMATOPOIETIC PROGENITOR CELL DIFFERENTIATION	16	-0.36	-1.02	0.4297	0.7642
NEGATIVE REGULATION OF TISSUE REMODELING	17	-0.35	-1.02	0.4123	0.7645
SOLUTE PROTON SYMPORTER ACTIVITY	25	-0.31	-1.02	0.3929	0.7647
NEGATIVE REGULATION OF JAK STAT CASCADE	43	0.27	0.94	0.5377	0.7652
REGULATION OF HEART CONTRACTION	209	0.21	0.94	0.5839	0.7653
NEGATIVE REGULATION OF RESPONSE TO WOUNDING	142	0.22	0.94	0.5945	0.7654
REGULATION OF CELL CYCLE ARREST	91	0.24	0.94	0.5575	0.7655
ACTIVATION OF JUN KINASE ACTIVITY	30	0.30	0.94	0.5382	0.7657
POSITIVE REGULATION OF BLOOD CIRCULATION	89	-0.23	-1.02	0.3943	0.7665

STEROL METABOLIC PROCESS	107	0.23	0.94	0.6085	0.7666
CAMP METABOLIC PROCESS	33	0.29	0.94	0.5353	0.7666
POTASSIUM CHANNEL REGULATOR ACTIVITY	43	0.27	0.94	0.5366	0.7675
RESPONSE TO OXYGEN LEVELS	284	0.21	0.94	0.6248	0.7676
OLIGODENDROCYTE DEVELOPMENT	30	0.30	0.94	0.5546	0.7683
REGULATION OF ODONTOGENESIS	23	-0.31	-1.02	0.4161	0.7686
MICROTUBULE PLUS END	16	0.34	0.94	0.5394	0.7686
AXON	390	0.20	0.94	0.6316	0.7687
RECEPTOR REGULATOR ACTIVITY	44	0.27	0.94	0.5585	0.7688
NEUROMUSCULAR JUNCTION	49	0.26	0.94	0.5461	0.7688
CELL DIFFERENTIATION INVOLVED IN EMBRYONIC PLACENTA DEVELOPMENT	25	0.31	0.94	0.5751	0.7689
REGULATION OF ENDOCYTOSIS	179	0.21	0.94	0.6003	0.7689
CELL MATURATION	110	0.23	0.94	0.5851	0.7690
REGULATION OF RESPIRATORY SYSTEM PROCESS	16	0.35	0.94	0.5290	0.7691
POSITIVE REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	31	0.29	0.94	0.5381	0.7691
EXOCYTOSIS	278	0.21	0.94	0.6247	0.7692
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT5 PROTEIN	19	0.34	0.94	0.5372	0.7693
REGULATION OF ACTIN NUCLEATION	25	0.31	0.94	0.5461	0.7693
CALCIUM MEDIATED SIGNALING	76	0.25	0.94	0.5857	0.7697
REGULATION OF ANATOMICAL STRUCTURE SIZE	427	0.20	0.94	0.6435	0.7698
MICROTUBULE	318	0.20	0.94	0.6201	0.7699
PROTEIN HETERO DIMERIZATION ACTIVITY	376	0.20	0.94	0.6525	0.7701
POSITIVE REGULATION OF GLUCOSE METABOLIC PROCESS	34	-0.29	-1.02	0.4077	0.7701
PROTEIN DNA COMPLEX	114	-0.22	-1.02	0.3731	0.7704
INNERVATION	19	0.33	0.94	0.5262	0.7706
SENSORY ORGAN MORPHOGENESIS	228	-0.20	-1.02	0.3722	0.7715
LIMB DEVELOPMENT	155	-0.21	-1.02	0.3784	0.7719
BEHAVIOR	463	-0.18	-1.02	0.3627	0.7720
POSITIVE REGULATION OF REPRODUCTIVE PROCESS	50	0.26	0.94	0.5604	0.7722
CELL LEADING EDGE	322	-0.19	-1.02	0.3706	0.7722
EXTRINSIC APOPTOTIC SIGNALING PATHWAY	82	0.24	0.94	0.5710	0.7722

POSTTRANSCRIPTIONAL GENE SILENCING	40	0.28	0.94	0.5554	0.7723
REGULATION OF OSTEOCLAST DIFFERENTIATION	55	-0.26	-1.02	0.4006	0.7725
REGULATION OF ESTABLISHMENT OR MAINTENANCE OF CELL POLARITY	20	0.32	0.94	0.5380	0.7726
NEGATIVE REGULATION OF AXON EXTENSION	36	-0.28	-1.02	0.4235	0.7729
REGULATION OF CARDIAC CONDUCTION	64	0.25	0.94	0.5712	0.7730
RESPONSE TO AMINE	43	0.27	0.94	0.5475	0.7730
NEGATIVE REGULATION OF CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	109	-0.22	-1.02	0.3947	0.7730
PRESYNAPTIC PROCESS INVOLVED IN SYNAPTIC TRANSMISSION	105	-0.23	-1.02	0.4151	0.7731
CAMP BINDING	22	0.32	0.94	0.5526	0.7732
BASAL PART OF CELL	48	0.27	0.94	0.5759	0.7737
CELLULAR SENESCENCE	27	0.30	0.94	0.5628	0.7739
PHOSPHATIDYLETHANOLAMINE METABOLIC PROCESS	16	0.35	0.94	0.5745	0.7739
REGULATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY INVOLVED IN APOPTOTIC SIGNALING PATHWAY	18	-0.34	-1.02	0.4371	0.7740
EYE MORPHOGENESIS	128	0.22	0.93	0.5940	0.7751
PHOSPHATASE INHIBITOR ACTIVITY	27	0.30	0.93	0.5484	0.7752
POSITIVE REGULATION OF BMP SIGNALING PATHWAY	28	0.30	0.93	0.5638	0.7753
INTERMEDIATE FILAMENT BASED PROCESS	40	0.27	0.93	0.5539	0.7753
ZINC ION TRANSMEMBRANE TRANSPORTER ACTIVITY	22	0.32	0.93	0.5445	0.7755
HISTONE LYSINE N METHYLTRANSFERASE ACTIVITY	41	0.28	0.93	0.5594	0.7755
NEGATIVE REGULATION OF PROTEIN TYROSINE KINASE ACTIVITY	19	0.32	0.93	0.5255	0.7756
PHOSPHOTRANSFERASE ACTIVITY PHOSPHATE GROUP AS ACCEPTOR	34	0.28	0.93	0.5792	0.7768
PLATELET ALPHA GRANULE	71	0.25	0.93	0.5930	0.7769
REGULATION OF GLIAL CELL PROLIFERATION	19	0.33	0.93	0.5722	0.7769
SODIUM ION TRANSPORT	135	0.22	0.93	0.5942	0.7770
CARBOXY LYASE ACTIVITY	35	-0.28	-1.01	0.4163	0.7773

ANCHORED COMPONENT OF MEMBRANE	123	-0.22	-1.02	0.4150	0.7775
DEVELOPMENTAL GROWTH INVOLVED IN MORPHOGENESIS	98	-0.23	-1.01	0.4199	0.7777
SCAVENGER RECEPTOR ACTIVITY	39	-0.27	-1.02	0.4339	0.7778
TRANSMEMBRANE RECEPTOR PROTEIN SERINE THREONINE KINASE SIGNALING PATHWAY	177	0.22	0.93	0.6274	0.7779
NEGATIVE REGULATION OF BEHAVIOR	15	0.34	0.93	0.5400	0.7780
REGULATION OF CAMP METABOLIC PROCESS	119	-0.22	-1.02	0.4022	0.7781
ANCHORED COMPONENT OF PLASMA MEMBRANE	30	0.29	0.93	0.5445	0.7781
PRIMARY CILIUM	173	-0.21	-1.02	0.3976	0.7784
BETA AMYLOID BINDING	32	0.29	0.93	0.5733	0.7784
REGULATION OF EPITHELIAL CELL PROLIFERATION	258	0.21	0.93	0.6380	0.7796
NADP METABOLIC PROCESS	24	0.31	0.93	0.5607	0.7798
CELL CORTEX	208	0.21	0.93	0.6171	0.7801
NUCLEOBASE CONTAINING COMPOUND TRANSMEMBRANE TRANSPORTER ACTIVITY	29	0.30	0.93	0.5635	0.7802
LIPOPOLYSACCHARIDE BINDING	15	0.35	0.93	0.5547	0.7803
REGULATION OF MUSCLE ORGAN DEVELOPMENT	93	0.24	0.93	0.5973	0.7805
REGULATION OF ORGAN FORMATION	32	0.28	0.93	0.5535	0.7807
REGULATION OF SODIUM ION TRANSPORT	67	0.24	0.93	0.5716	0.7808
POSITIVE REGULATION OF INTERLEUKIN 2 PRODUCTION	29	0.29	0.93	0.5668	0.7810
ATPASE COUPLED ION TRANSMEMBRANE TRANSPORTER ACTIVITY	67	0.25	0.93	0.5926	0.7826
SYNAPTIC MEMBRANE	244	-0.20	-1.01	0.4089	0.7827
OLFFACTORY LOBE DEVELOPMENT	34	-0.28	-1.01	0.4319	0.7829
POSITIVE REGULATION OF PHAGOCYTOSIS	41	-0.27	-1.01	0.4457	0.7830
CALCIUM ION TRANSPORT	204	-0.20	-1.01	0.4432	0.7831
SKELETAL SYSTEM DEVELOPMENT	423	-0.19	-1.01	0.4198	0.7832
ICOSANOID TRANSPORT	20	-0.32	-1.01	0.4408	0.7834
PLATELET MORPHOGENESIS	17	-0.34	-1.01	0.4104	0.7834
GUANOSINE CONTAINING COMPOUND METABOLIC PROCESS	38	0.27	0.93	0.6000	0.7838

REGULATION OF DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	27	-0.30	-1.01	0.4152	0.7838
HETEROCHROMATIN	62	-0.25	-1.01	0.4318	0.7839
ARTERY DEVELOPMENT	72	0.25	0.93	0.6076	0.7839
NEGATIVE REGULATION OF MUSCLE TISSUE DEVELOPMENT	31	-0.29	-1.01	0.4430	0.7842
ER NUCLEUS SIGNALING PATHWAY	29	0.30	0.93	0.5693	0.7845
RESPONSE TO HEAT	76	0.24	0.93	0.5886	0.7847
POSTSYNAPTIC MEMBRANE	191	-0.20	-1.01	0.4357	0.7851
REGULATION OF TRANSCRIPTION INVOLVED IN CELL FATE COMMITMENT	19	0.32	0.93	0.5379	0.7852
CEREBRAL CORTEX CELL MIGRATION	40	-0.28	-1.01	0.4380	0.7853
NOTCH RECEPTOR PROCESSING	15	-0.35	-1.01	0.4480	0.7853
PEPTIDYL TYROSINE DEPHOSPHORYLATION	94	0.23	0.93	0.6050	0.7853
RESPONSE TO VITAMIN D	32	-0.29	-1.01	0.4444	0.7855
NEGATIVE REGULATION OF DNA BINDING	38	0.28	0.93	0.5928	0.7856
HETEROTYPIC CELL CELL ADHESION	24	-0.30	-1.01	0.4574	0.7862
CELL PROJECTION MEMBRANE	264	-0.20	-1.00	0.4688	0.7880
NEGATIVE REGULATION OF TRANSMEMBRANE RECEPTOR PROTEIN SERINE THREONINE KINASE SIGNALING PATHWAY	86	0.24	0.92	0.6102	0.7881
REGULATION OF INTERLEUKIN 12 PRODUCTION	45	-0.27	-1.01	0.4165	0.7882
PROTEIN TARGETING TO PLASMA MEMBRANE	22	-0.32	-1.00	0.4665	0.7883
CAMERA TYPE EYE PHOTORECEPTOR CELL DIFFERENTIATION	15	-0.35	-1.01	0.4296	0.7888
MYELOID DENDRITIC CELL ACTIVATION	22	-0.32	-1.00	0.4681	0.7888
PHARYNGEAL SYSTEM DEVELOPMENT	17	-0.34	-1.01	0.4377	0.7889
CHONDROCYTE DIFFERENTIATION	58	-0.25	-1.00	0.4273	0.7891
NEGATIVE REGULATION OF OSTEOBLAST DIFFERENTIATION	38	-0.28	-1.00	0.4507	0.7892
CONTRACTILE FIBER	191	-0.20	-1.00	0.4083	0.7892
EXTRACELLULAR MATRIX COMPONENT	114	-0.22	-1.00	0.4247	0.7893
MAST CELL MEDIATED IMMUNITY	17	-0.34	-1.00	0.4576	0.7894
REGULATION OF GLYCOGEN METABOLIC PROCESS	31	-0.29	-1.00	0.4586	0.7895
GLAND MORPHOGENESIS	94	-0.23	-1.01	0.4218	0.7895
ENDODEOXYRIBONUCLEASE ACTIVITY	35	-0.28	-1.00	0.4678	0.7896

PLASMA MEMBRANE RECEPTOR COMPLEX	158	-0.21	-1.00	0.4317	0.7896
NUCLEOSIDE TRIPHOSPHATASE REGULATOR ACTIVITY	291	-0.19	-1.00	0.4732	0.7896
ANTERIOR POSTERIOR AXIS SPECIFICATION	46	-0.27	-1.00	0.4462	0.7898
CYSTEINE TYPE ENDOPEPTIDASE REGULATOR ACTIVITY INVOLVED IN APOPTOTIC PROCESS	34	-0.28	-1.00	0.4192	0.7899
INORGANIC ANION TRANSPORT	116	-0.22	-1.01	0.4028	0.7899
POSITIVE REGULATION OF NF KAPPAB IMPORT INTO NUCLEUS	23	-0.32	-1.00	0.4314	0.7900
LOW DENSITY LIPOPROTEIN PARTICLE BINDING	15	-0.35	-1.00	0.4554	0.7900
POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	117	0.22	0.92	0.6223	0.7902
PASSIVE TRANSMEMBRANE TRANSPORTER ACTIVITY	420	-0.19	-1.00	0.4552	0.7902
POSITIVE REGULATION OF INTERLEUKIN 6 PRODUCTION	61	0.25	0.92	0.5907	0.7903
HIGH DENSITY LIPOPROTEIN PARTICLE	21	0.31	0.92	0.5390	0.7903
PYRIDINE NUCLEOTIDE BIOSYNTHETIC PROCESS	15	0.35	0.92	0.5605	0.7904
INFLAMMATORY RESPONSE TO ANTIGENIC STIMULUS	23	-0.31	-1.00	0.4567	0.7907
RESPONSE TO STEROL	21	-0.31	-1.00	0.4344	0.7926
NEGATIVE REGULATION OF NF KAPPAB TRANSCRIPTION FACTOR ACTIVITY	53	0.25	0.92	0.6035	0.7942
EPITHELIAL TO MESENCHYMAL TRANSITION	54	0.26	0.92	0.5894	0.7943
INOSITOL PHOSPHATE MEDIATED SIGNALING	17	0.34	0.92	0.5729	0.7943
LACTATION	40	-0.26	-1.00	0.4655	0.7943
SPINAL CORD MOTOR NEURON DIFFERENTIATION	31	-0.28	-1.00	0.4450	0.7943
POSITIVE REGULATION OF LEUKOCYTE MEDIATED IMMUNITY	72	-0.24	-1.00	0.4790	0.7944
RESPONSE TO ANGIOTENSIN	15	-0.35	-1.00	0.4512	0.7945
NEUROTRANSMITTER RECEPTOR ACTIVITY	61	-0.25	-1.00	0.4583	0.7946
REGULATION OF SKELETAL MUSCLE CELL DIFFERENTIATION	15	-0.35	-1.00	0.4736	0.7947

TRANSCRIPTIONAL REPRESSOR ACTIVITY RNA POLYMERASE II TRANSCRIPTION REGULATORY REGION SEQUENCE SPECIFIC BINDING	145	-0.21	-1.00	0.4415	0.7947
PEPTIDE CATABOLIC PROCESS	21	0.31	0.92	0.5561	0.7948
CELL SURFACE RECEPTOR SIGNALING PATHWAY INVOLVED IN HEART DEVELOPMENT	16	-0.34	-1.00	0.4447	0.7948
EXTRINSIC COMPONENT OF PLASMA MEMBRANE	125	-0.22	-1.00	0.4526	0.7949
REGULATION OF PROTEIN ACTIVATION CASCADE	29	-0.29	-1.00	0.4442	0.7949
REGULATION OF CYTOKINE SECRETION	112	-0.22	-0.99	0.4605	0.7951
EXTRINSIC APOPTOTIC SIGNALING PATHWAY VIA DEATH DOMAIN RECEPTORS	29	-0.29	-1.00	0.4730	0.7952
HEPARIN BINDING	138	-0.21	-1.00	0.4667	0.7958
SYNAPTONEMAL COMPLEX ORGANIZATION	16	-0.35	-0.99	0.4528	0.7959
NEGATIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	81	0.24	0.92	0.6136	0.7970
NEURONAL ACTION POTENTIAL	26	-0.30	-0.99	0.4716	0.7971
SUPEROXIDE METABOLIC PROCESS	31	0.29	0.92	0.6180	0.7971
POSITIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	53	0.26	0.92	0.5714	0.7973
MULTICELLULAR ORGANISMAL SIGNALING	116	-0.22	-0.99	0.4919	0.7978
REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	242	-0.20	-0.99	0.4820	0.7980
CALCIUM CHANNEL REGULATOR ACTIVITY	36	0.28	0.92	0.6065	0.7983
MULTI ORGANISM REPRODUCTIVE BEHAVIOR	20	-0.31	-0.99	0.4939	0.7991
REGULATION OF T CELL MEDIATED IMMUNITY	44	0.27	0.92	0.5839	0.8006
NEUROMUSCULAR PROCESS CONTROLLING BALANCE	47	-0.26	-0.99	0.4613	0.8008
FATTY ACID DERIVATIVE TRANSPORT	20	-0.32	-0.99	0.4714	0.8009
MUSCULOSKELETAL MOVEMENT	40	-0.27	-0.99	0.4571	0.8010
REGULATION OF CYTOKINE PRODUCTION	480	-0.18	-0.99	0.5000	0.8011
INTERMEDIATE FILAMENT ORGANIZATION	20	-0.31	-0.99	0.4758	0.8013
SMAD BINDING	65	-0.24	-0.99	0.4724	0.8015
T CELL PROLIFERATION	31	0.28	0.92	0.5921	0.8016

POSITIVE REGULATION OF PROTEIN TYROSINE KINASE ACTIVITY	34	-0.28	-0.99	0.4925	0.8017
DEVELOPMENT OF PRIMARY SEXUAL CHARACTERISTICS	184	-0.20	-0.99	0.5057	0.8020
ACTIN MEDIATED CELL CONTRACTION	69	-0.24	-0.99	0.4535	0.8023
NOTOCHORD DEVELOPMENT	18	-0.32	-0.99	0.4654	0.8024
RESPONSE TO PURINE CONTAINING COMPOUND	148	-0.20	-0.99	0.5037	0.8024
MULTICELLULAR ORGANISMAL MOVEMENT	40	-0.27	-0.99	0.4566	0.8026
EXOCYTIC VESICLE	130	0.22	0.92	0.6278	0.8029
REGULATION OF RECEPTOR MEDIATED ENDOCYTOSIS	70	0.24	0.92	0.6184	0.8031
REGULATION OF MITOCHONDRIAL MEMBRANE PERMEABILITY INVOLVED IN APOPTOTIC PROCESS	16	0.34	0.92	0.5749	0.8032
REGULATION OF AMINO ACID TRANSPORT	25	0.30	0.92	0.5892	0.8035
CILIUM ORGANIZATION	144	0.22	0.92	0.6474	0.8035
CHROMATIN SILENCING AT RDNA	18	0.33	0.92	0.5739	0.8038
CORE PROMOTER PROXIMAL REGION DNA BINDING	289	-0.19	-0.98	0.5079	0.8043
POSITIVE REGULATION OF CELL DIVISION	117	-0.21	-0.99	0.5017	0.8043
POSITIVE REGULATION OF CYCLIC NUCLEOTIDE METABOLIC PROCESS	100	-0.22	-0.99	0.4774	0.8044
VENTRICULAR CARDIAC MUSCLE CELL ACTION POTENTIAL	15	-0.35	-0.99	0.4735	0.8044
LEARNING	122	-0.22	-0.99	0.4928	0.8052
OVULATION CYCLE PROCESS	80	-0.23	-0.99	0.4711	0.8055
SPHINGOLIPID BIOSYNTHETIC PROCESS	65	0.24	0.91	0.6092	0.8057
CLATHRIN MEDIATED ENDOCYTOSIS	35	0.28	0.91	0.5648	0.8058
RNA POLYMERASE II TRANSCRIPTION COFACTOR ACTIVITY	83	0.23	0.91	0.6114	0.8060
CYSTEINE TYPE ENDOPEPTIDASE INHIBITOR ACTIVITY	40	-0.27	-0.99	0.4721	0.8060
POSITIVE REGULATION OF T CELL MEDIATED IMMUNITY	27	0.29	0.91	0.5793	0.8061
CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	30	0.28	0.91	0.6034	0.8064
COGNITION	226	0.21	0.91	0.6900	0.8065
RENAL SYSTEM VASCULATURE DEVELOPMENT	19	0.32	0.91	0.5743	0.8067

NEGATIVE REGULATION OF GROWTH	209	0.21	0.91	0.6827	0.8067
VERY LOW DENSITY LIPOPROTEIN PARTICLE	16	0.33	0.91	0.5827	0.8067
METALLOCARBOXYPEPTIDASE ACTIVITY	25	-0.29	-0.99	0.4758	0.8067
REGULATION OF PROTEIN DEACETYLATION	28	0.29	0.91	0.6144	0.8067
NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	45	0.26	0.91	0.5918	0.8067
REGULATION OF SYNAPSE STRUCTURE OR ACTIVITY	219	0.20	0.91	0.6706	0.8068
DEVELOPMENTAL GROWTH	302	0.20	0.91	0.7099	0.8070
OXIDOREDUCTASE ACTIVITY ACTING ON THE CH NH2 GROUP OF DONORS	16	0.33	0.91	0.5888	0.8070
EPITHELIAL CELL DEVELOPMENT	172	0.21	0.91	0.6635	0.8070
DEOXYRIBONUCLEASE ACTIVITY	49	-0.25	-0.98	0.4826	0.8070
PROTEIN TYROSINE PHOSPHATASE ACTIVITY	97	0.23	0.91	0.6257	0.8072
NEUROTRANSMITTER METABOLIC PROCESS	22	0.31	0.91	0.5946	0.8073
RESPONSE TO AMINO ACID	99	0.23	0.91	0.6366	0.8073
SOLUTE SODIUM SYMPORTER ACTIVITY	46	0.26	0.91	0.5895	0.8080
ENTEROENDOCRINE CELL DIFFERENTIATION	19	-0.32	-0.98	0.4582	0.8084
POSITIVE REGULATION OF CYTOKINE PRODUCTION	316	-0.19	-0.98	0.5077	0.8084
REGULATION OF BIOMINERAL TISSUE DEVELOPMENT	68	-0.24	-0.98	0.4715	0.8087
NEGATIVE REGULATION OF CELL GROWTH	156	0.21	0.91	0.6539	0.8104
BRAIN MORPHOGENESIS	32	0.28	0.91	0.6151	0.8111
DEAMINASE ACTIVITY	25	0.29	0.91	0.6021	0.8113
CELLULAR RESPONSE TO LITHIUM ION	17	0.33	0.91	0.5722	0.8113
COP9 SIGNALOSOME	28	0.29	0.91	0.5973	0.8114
PHOSPHOLIPID TRANSLOCATING ATPASE ACTIVITY	16	0.33	0.91	0.5949	0.8116
POSTREPLICATION REPAIR	43	0.26	0.91	0.5987	0.8116
SODIUM CHANNEL REGULATOR ACTIVITY	30	0.29	0.91	0.5932	0.8117
MAIN AXON	50	0.26	0.91	0.6018	0.8120
NEGATIVE REGULATION OF VIRAL TRANSCRIPTION	21	0.31	0.91	0.5784	0.8122
QUATERNARY AMMONIUM GROUP BINDING	44	-0.26	-0.98	0.4761	0.8123

MICROVILLUS ORGANIZATION	18	-0.33	-0.98	0.4863	0.8123
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT PROTEIN	63	0.24	0.91	0.6235	0.8128
INNER EAR RECEPTOR STEREOCILIA ORGANIZATION	20	-0.31	-0.98	0.4528	0.8129
MACROLIDE BINDING	16	0.34	0.91	0.5851	0.8131
NEGATIVE REGULATION OF PROTEOLYSIS	267	0.20	0.91	0.7036	0.8133
POSITIVE REGULATION OF EPITHELIAL CELL MIGRATION	96	0.23	0.91	0.6383	0.8133
POSITIVE REGULATION OF RESPONSE TO WOUNDING	140	-0.21	-0.98	0.5110	0.8133
NEURAL TUBE FORMATION	87	0.23	0.91	0.6350	0.8134
RESPONSE TO GONADOTROPIN	25	0.29	0.91	0.5829	0.8135
REGULATION OF FEEDING BEHAVIOR	19	0.31	0.91	0.6096	0.8135
REGULATION OF POSTSYNAPTIC MEMBRANE POTENTIAL	54	0.25	0.91	0.6315	0.8136
POSITIVE REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	22	0.31	0.91	0.6034	0.8137
PLATELET AGGREGATION	36	-0.27	-0.98	0.4974	0.8137
FK506 BINDING	16	0.34	0.91	0.5697	0.8138
HEART TRABECULA MORPHOGENESIS	25	0.29	0.91	0.5889	0.8138
REGULATION OF MUSCLE CELL DIFFERENTIATION	142	0.21	0.91	0.6806	0.8138
DEVELOPMENTAL PROGRAMMED CELL DEATH	20	-0.32	-0.98	0.4629	0.8138
REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION	194	0.20	0.91	0.6881	0.8138
REGULATION OF EPITHELIAL TO MESENCHYMAL TRANSITION	61	0.25	0.90	0.6157	0.8148
CELLULAR RESPONSE TO PH	15	-0.34	-0.98	0.4881	0.8149
CYCLIC NUCLEOTIDE MEDIATED SIGNALING	45	0.26	0.90	0.6124	0.8158
POSITIVE REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	111	0.22	0.90	0.6662	0.8167
HINDBRAIN MORPHOGENESIS	38	-0.27	-0.98	0.4706	0.8170
POSITIVE REGULATION OF LIPID TRANSPORT	48	0.26	0.90	0.6077	0.8171
SKELETAL SYSTEM MORPHOGENESIS	186	-0.20	-0.98	0.5160	0.8173

OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN NAD P H AS ONE DONOR AND INCORPORATION OF ONE ATOM OF OXYGEN	24	-0.30	-0.98	0.4774	0.8179
SMOOTH MUSCLE CELL DIFFERENTIATION	29	0.28	0.90	0.6174	0.8181
GLANDULAR EPITHELIAL CELL DIFFERENTIATION	38	0.27	0.90	0.6149	0.8183
REGULATION OF IMMUNE EFFECTOR PROCESS	349	0.19	0.90	0.7347	0.8185
VENTRICULAR CARDIAC MUSCLE TISSUE DEVELOPMENT	43	-0.26	-0.98	0.5065	0.8186
REGULATION OF ERK1 AND ERK2 CASCADE	208	-0.20	-0.98	0.5190	0.8186
REGULATION OF VACUOLAR TRANSPORT	27	0.29	0.90	0.6082	0.8188
REGULATION OF MAST CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	26	-0.30	-0.97	0.5025	0.8193
SENSORY ORGAN DEVELOPMENT	463	-0.18	-0.97	0.5822	0.8195
ORGANIC ACID BINDING	175	0.21	0.90	0.7130	0.8198
CONNECTIVE TISSUE DEVELOPMENT	185	-0.20	-0.98	0.5413	0.8199
OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN 2 OXOGLUTARATE AS ONE DONOR AND INCORPORATION OF ONE ATOM EACH OF OXYGEN INTO BOTH DONORS	39	-0.27	-0.97	0.4756	0.8200
ENDOCHONDRAL OSSIFICATION	24	0.29	0.90	0.6047	0.8201
NEGATIVE REGULATION OF CELLULAR RESPONSE TO TRANSFORMING GROWTH FACTOR BETA STIMULUS	54	0.25	0.90	0.6128	0.8201
TRANSCRIPTIONAL REPRESSOR ACTIVITY RNA POLYMERASE II TRANSCRIPTION FACTOR BINDING	80	-0.23	-0.97	0.5117	0.8203
REGULATION OF CALCIUM ION IMPORT	93	-0.22	-0.97	0.5250	0.8206
POSITIVE REGULATION OF CATION TRANSMEMBRANE TRANSPORT	89	-0.23	-0.97	0.5235	0.8206
PALATE DEVELOPMENT	78	-0.23	-0.98	0.5126	0.8206
NEGATIVE REGULATION OF CELL MATRIX ADHESION	26	-0.29	-0.97	0.5035	0.8209

C21 STEROID HORMONE METABOLIC PROCESS	20	-0.32	-0.97	0.5228	0.8215
FOREBRAIN GENERATION OF NEURONS	64	-0.23	-0.97	0.5084	0.8216
RESPONSE TO MINERALOCORTICOID	34	-0.27	-0.97	0.5124	0.8216
RESPONSE TO DSRNA	59	0.25	0.90	0.6160	0.8217
SPROUTING ANGIOGENESIS	44	-0.26	-0.97	0.5079	0.8220
WIDE PORE CHANNEL ACTIVITY	22	0.30	0.90	0.5923	0.8221
ENTRAINMENT OF CIRCADIAN CLOCK BY PHOTOPERIOD	17	0.33	0.90	0.6048	0.8221
HOMOTYPIC CELL CELL ADHESION	48	-0.25	-0.97	0.5273	0.8224
DIVALENT INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	157	-0.20	-0.97	0.5424	0.8228
REGULATION OF CELL MATRIX ADHESION	82	-0.23	-0.97	0.5100	0.8230
NEURON PROJECTION DEVELOPMENT	484	-0.18	-0.97	0.5691	0.8231
RESPONSE TO KETONE	166	0.21	0.90	0.6957	0.8236
BONE RESORPTION	19	0.32	0.90	0.5956	0.8237
REGULATION OF RESPONSE TO WOUNDING	364	0.19	0.90	0.7608	0.8237
NEGATIVE REGULATION OF MUSCLE CELL DIFFERENTIATION	53	0.25	0.90	0.6187	0.8238
TISSUE REGENERATION	47	0.25	0.90	0.6174	0.8239
REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR PRODUCTION	29	0.29	0.90	0.6145	0.8239
WW DOMAIN BINDING	25	0.29	0.90	0.6130	0.8241
REGULATION OF NATURAL KILLER CELL ACTIVATION	22	-0.31	-0.97	0.5059	0.8242
CONDENSED NUCLEAR CHROMOSOME	75	0.23	0.90	0.6519	0.8243
NEGATIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	181	0.21	0.90	0.6927	0.8243
NEGATIVE REGULATION OF RECEPTOR ACTIVITY	27	0.29	0.90	0.6000	0.8243
SIGNAL TRANSDUCTION IN RESPONSE TO DNA DAMAGE	82	0.23	0.90	0.6628	0.8243
LAMELLIPOD IUM ORGANIZATION	35	0.27	0.90	0.5944	0.8243
EYE DEVELOPMENT	304	0.19	0.90	0.7454	0.8244
MYELOID LEUKOCYTE DIFFERENTIATION	88	0.23	0.90	0.6491	0.8244
GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	262	0.20	0.90	0.7367	0.8246
GENETIC IMPRINTING	18	0.32	0.90	0.5870	0.8247

PHOSPHATIDYLINOSITOL 4 PHOSPHATE BINDING	19	0.31	0.90	0.6122	0.8248
BONE MORPHOGENESIS	74	-0.23	-0.97	0.4884	0.8248
REGULATION OF CATION CHANNEL ACTIVITY	84	0.23	0.90	0.6667	0.8248
REGULATION OF T CELL CYTOKINE PRODUCTION	18	0.32	0.89	0.5974	0.8248
RESPONSE TO ANTIBIOTIC	42	0.27	0.89	0.6390	0.8249
POSITIVE REGULATION OF PROTEIN OLIGOMERIZATION	18	-0.32	-0.97	0.4717	0.8250
REGULATION OF CELLULAR RESPONSE TO INSULIN STIMULUS	53	-0.25	-0.97	0.5245	0.8251
KIDNEY VASCULATURE DEVELOPMENT	19	0.32	0.90	0.6161	0.8251
REGULATION OF CATENIN IMPORT INTO NUCLEUS	26	0.29	0.90	0.5986	0.8253
POSITIVE REGULATION OF CALCIUM ION TRANSPORT INTO CYTOSOL	48	-0.25	-0.97	0.5346	0.8256
MUSCLE STRUCTURE DEVELOPMENT	400	-0.18	-0.97	0.5714	0.8258
MIRNA BINDING	16	-0.33	-0.97	0.5023	0.8259
PROTEOGLYCAN BIOSYNTHETIC PROCESS	56	0.24	0.89	0.6425	0.8259
MATING BEHAVIOR	20	-0.31	-0.96	0.5245	0.8261
ACTIN FILAMENT BASED PROCESS	404	-0.18	-0.97	0.6331	0.8263
REGULATION OF ACTIVATED T CELL PROLIFERATION	32	-0.27	-0.96	0.5066	0.8267
BILE ACID AND BILE SALT TRANSPORT	23	-0.30	-0.96	0.4903	0.8267
REGULATION OF INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	29	-0.28	-0.96	0.5327	0.8269
VENTRICULAR SEPTUM MORPHOGENESIS	28	0.28	0.89	0.6246	0.8270
LABYRINTHINE LAYER BLOOD VESSEL DEVELOPMENT	18	0.31	0.89	0.6317	0.8270
RESPONSE TO OSMOTIC STRESS	57	-0.24	-0.97	0.5123	0.8271
ANATOMICAL STRUCTURE MATURATION	35	-0.27	-0.97	0.4962	0.8272
MITOTIC SPINDLE ASSEMBLY	33	0.27	0.89	0.6053	0.8273
REGULATION OF MAST CELL DEGRANULATION	26	-0.30	-0.97	0.4905	0.8273
CORE PROMOTER SEQUENCE SPECIFIC DNA BINDING	87	0.23	0.89	0.6476	0.8274
STARTLE RESPONSE	24	-0.29	-0.97	0.4965	0.8274
CILIARY BASAL BODY	66	0.24	0.89	0.6530	0.8274

CARDIAC VENTRICLE MORPHOGENESIS	57	-0.24	-0.97	0.5387	0.8276
RESPONSE TO PROGESTERONE	44	-0.25	-0.96	0.4744	0.8277
NEGATIVE REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRINSIC APOPTOTIC SIGNALING PATHWAY	17	0.33	0.89	0.6293	0.8278
REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	58	-0.24	-0.96	0.5324	0.8280
CORONARY VASCULATURE DEVELOPMENT	35	0.27	0.89	0.6466	0.8281
REGULATION OF MULTICELLULAR ORGANISM GROWTH	60	0.24	0.89	0.6443	0.8281
NEURAL CREST CELL MIGRATION	49	0.25	0.89	0.6486	0.8282
HEART GROWTH	24	0.29	0.89	0.6117	0.8282
SODIUM ION TRANSMEMBRANE TRANSPORT	87	0.23	0.89	0.6844	0.8282
CELLULAR RESPONSE TO ABIOTIC STIMULUS	228	0.20	0.89	0.7388	0.8283
REGULATION OF DNA TEMPLATED TRANSCRIPTION IN RESPONSE TO STRESS	60	0.24	0.89	0.6524	0.8284
POSITIVE REGULATION OF CELLULAR RESPONSE TO TRANSFORMING GROWTH FACTOR BETA STIMULUS	24	0.30	0.89	0.5906	0.8285
POSITIVE REGULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR SIGNALING PATHWAY	24	0.30	0.89	0.6088	0.8286
RETINA MORPHOGENESIS IN CAMERA TYPE EYE	42	-0.26	-0.96	0.5302	0.8286
POSITIVE REGULATION OF NATURAL KILLER CELL ACTIVATION	16	-0.33	-0.96	0.5304	0.8287
TRIGLYCERIDE RICH LIPOPROTEIN PARTICLE	16	0.33	0.89	0.6124	0.8287
GASTRULATION	140	0.21	0.89	0.7106	0.8288
POSITIVE REGULATION OF BEHAVIOR	24	-0.29	-0.96	0.5138	0.8288
NEGATIVE REGULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR SIGNALING PATHWAY	54	0.25	0.89	0.6334	0.8289
PHOSPHATIDYLINOSITOL 3 4 BISPHOSPHATE BINDING	18	-0.33	-0.96	0.5211	0.8292
ION GATED CHANNEL ACTIVITY	40	-0.25	-0.96	0.5230	0.8294
POSITIVE REGULATION OF CHONDROCYTE DIFFERENTIATION	19	-0.31	-0.96	0.5332	0.8296

NEUROMUSCULAR SYNAPTIC TRANSMISSION	26	0.29	0.89	0.6070	0.8298
POSITIVE REGULATION OF ACTIN FILAMENT BUNDLE ASSEMBLY	46	0.26	0.89	0.6302	0.8299
DOPAMINERGIC NEURON DIFFERENTIATION	27	-0.29	-0.96	0.5155	0.8300
REGULATION OF GENE EXPRESSION BY GENETIC IMPRINTING	15	0.33	0.89	0.6061	0.8315
POSITIVE REGULATION OF HOMEOSTATIC PROCESS	191	0.20	0.89	0.7041	0.8318
REGULATION OF REGULATED SECRETORY PATHWAY	114	-0.20	-0.96	0.5106	0.8320
POSITIVE REGULATION OF SECRETION	323	0.19	0.89	0.7712	0.8321
REGULATION OF POLYSACCHARIDE METABOLIC PROCESS	39	-0.26	-0.96	0.5087	0.8323
PROTEIN LIPID COMPLEX BINDING	22	-0.30	-0.96	0.4809	0.8326
REGULATION OF CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	316	0.19	0.89	0.7843	0.8331
MICROTUBULE CYTOSKELETON ORGANIZATION INVOLVED IN MITOSIS	33	0.27	0.89	0.6238	0.8342
HEMOSTASIS	265	-0.19	-0.96	0.6448	0.8350
DORSAL SPINAL CORD DEVELOPMENT	18	0.32	0.89	0.6170	0.8351
INTRACILIARY TRANSPORT PARTICLE	27	0.29	0.89	0.6189	0.8352
NEPHRON DEVELOPMENT	109	-0.21	-0.96	0.5401	0.8352
DEVELOPMENTAL CELL GROWTH	71	-0.23	-0.96	0.5422	0.8352
ADENYLYLATE CYCLASE INHIBITING G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY	63	-0.23	-0.96	0.5197	0.8360
FACE DEVELOPMENT	47	0.25	0.89	0.6527	0.8363
ADENYLYLATE CYCLASE MODULATING G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY	130	-0.21	-0.96	0.5677	0.8363
REGULATION OF MEMBRANE POTENTIAL	325	0.19	0.88	0.7716	0.8375
RESPONSE TO DEXAMETHASONE	30	0.28	0.88	0.6401	0.8384
PEPTIDYL LYSINE TRIMETHYLATION	17	0.32	0.88	0.6177	0.8389
REGULATION OF CELL FATE COMMITMENT	24	0.29	0.88	0.6221	0.8397
CELLULAR RESPONSE TO NUTRIENT	38	0.26	0.88	0.6633	0.8399
DNA BINDING BENDING	20	-0.31	-0.95	0.5187	0.8399
ERBB2 SIGNALING PATHWAY	35	0.27	0.88	0.6483	0.8400
UTERUS DEVELOPMENT	18	-0.31	-0.95	0.5151	0.8401

POSITIVE REGULATION OF TOLL LIKE RECEPTOR SIGNALING PATHWAY	18	0.32	0.88	0.6277	0.8401
ACTIVATION OF ADENYLYL CYCLASE ACTIVITY	35	0.27	0.88	0.6486	0.8402
REGULATION OF PLATELET AGGREGATION	15	0.33	0.88	0.6136	0.8404
POSITIVE REGULATION OF CAMP METABOLIC PROCESS	82	-0.22	-0.95	0.5537	0.8405
NEGATIVE REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	16	-0.33	-0.95	0.5406	0.8406
GANGLIOSIDE METABOLIC PROCESS	23	-0.29	-0.95	0.5263	0.8408
DEVELOPMENTAL MATURATION	168	0.20	0.88	0.7058	0.8410
REGULATION OF CATION TRANSMEMBRANE TRANSPORT	190	-0.19	-0.95	0.5859	0.8412
MATERNAL PROCESS INVOLVED IN FEMALE PREGNANCY	54	-0.24	-0.95	0.5567	0.8413
SERTOLI CELL DIFFERENTIATION	17	-0.32	-0.95	0.5024	0.8414
SYNAPTIC VESICLE LOCALIZATION	98	-0.21	-0.95	0.5531	0.8415
CELL KILLING	29	-0.28	-0.95	0.5371	0.8415
IONOTROPIC GLUTAMATE RECEPTOR COMPLEX	44	-0.25	-0.95	0.5118	0.8415
REGULATION OF EPITHELIAL CELL MIGRATION	157	-0.20	-0.95	0.6194	0.8419
NEGATIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY	91	0.22	0.88	0.6574	0.8421
POSITIVE REGULATION OF TRANSPORTER ACTIVITY	70	0.23	0.88	0.6528	0.8422
NEURAL TUBE DEVELOPMENT	138	-0.20	-0.95	0.5779	0.8422
POSITIVE REGULATION OF PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	16	-0.33	-0.95	0.5159	0.8428
NEGATIVE REGULATION OF INFLAMMATORY RESPONSE	89	0.22	0.88	0.6770	0.8438
SH3 SH2 ADAPTOR ACTIVITY	46	0.25	0.88	0.6508	0.8438
AXON PART	204	0.20	0.88	0.7522	0.8453
PANCREAS DEVELOPMENT	67	0.23	0.88	0.6641	0.8453
GLOMERULUS DEVELOPMENT	47	0.25	0.88	0.6651	0.8454
GLYCOSPHINGOLIPID METABOLIC PROCESS	58	0.24	0.88	0.6703	0.8455
ADENYLYLTRANSFERASE ACTIVITY	20	0.31	0.88	0.6170	0.8456
POSITIVE REGULATION OF RESPONSE TO BIOTIC STIMULUS	36	0.26	0.88	0.6455	0.8456

MULTIVESICULAR BODY	32	0.27	0.88	0.6512	0.8461
CELLULAR RESPONSE TO INTERLEUKIN 6	19	0.30	0.88	0.6181	0.8463
REGULATION OF PROTEIN EXIT FROM ENDOPLASMIC RETICULUM	17	0.31	0.88	0.6043	0.8464
OSSIFICATION	233	0.20	0.88	0.7686	0.8465
DEATH RECEPTOR BINDING	15	0.32	0.88	0.6293	0.8466
NEGATIVE REGULATION OF SYNAPTIC TRANSMISSION	57	0.24	0.88	0.6526	0.8472
MONOVALENT INORGANIC CATION TRANSPORT	394	0.19	0.88	0.8031	0.8472
REPLACEMENT OSSIFICATION	24	0.29	0.88	0.6728	0.8473
REGULATION OF NOTCH SIGNALING PATHWAY	58	-0.24	-0.95	0.5503	0.8480
CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	33	-0.27	-0.95	0.5402	0.8482
PLASMA MEMBRANE ORGANIZATION	183	0.20	0.87	0.7601	0.8485
REGULATION OF CELL SIZE	160	-0.20	-0.95	0.6250	0.8486
REGULATION OF OSSIFICATION	162	0.20	0.87	0.7397	0.8486
SIALYLTRANSFERASE ACTIVITY	18	-0.32	-0.95	0.5385	0.8486
HISTONE DEACETYLASE COMPLEX	55	0.24	0.87	0.6799	0.8486
INSULIN LIKE GROWTH FACTOR BINDING	25	-0.28	-0.95	0.5094	0.8487
G PROTEIN ALPHA SUBUNIT BINDING	19	0.31	0.87	0.6267	0.8489
BRANCHING INVOLVED IN URETERIC BUD MORPHOGENESIS	40	0.26	0.87	0.6388	0.8491
POSITIVE REGULATION OF ANION TRANSPORT	56	-0.24	-0.95	0.5430	0.8491
POSITIVE REGULATION OF CELL SUBSTRATE ADHESION	92	-0.21	-0.95	0.5770	0.8492
TRANSPORTER COMPLEX	295	-0.18	-0.95	0.6750	0.8497
REGULATION OF ENDOTHELIAL CELL PROLIFERATION	91	0.22	0.87	0.6869	0.8499
MEGAKARYOCYTE DIFFERENTIATION	18	0.32	0.87	0.6318	0.8504
REGULATION OF MUSCLE ADAPTATION	59	0.24	0.87	0.6733	0.8504
BONE REMODELING	33	0.27	0.87	0.6645	0.8515
REGULATION OF INTERLEUKIN 8 SECRETION	15	0.33	0.87	0.6133	0.8515
CILIARY TRANSITION ZONE	18	0.31	0.87	0.6310	0.8517
AMELOGENESIS	20	0.31	0.87	0.6373	0.8518
SCHWANN CELL DEVELOPMENT	24	0.29	0.87	0.6582	0.8522
REGULATION OF PROTEIN EXPORT FROM NUCLEUS	29	-0.28	-0.94	0.5488	0.8529

NEGATIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY VIA DEATH DOMAIN RECEPTORS	31	0.27	0.87	0.6632	0.8532
POSITIVE REGULATION OF CELLULAR RESPONSE TO INSULIN STIMULUS	20	-0.31	-0.94	0.5346	0.8533
ERBB SIGNALING PATHWAY	74	0.23	0.87	0.6957	0.8536
BLOOD VESSEL ENDOTHELIAL CELL MIGRATION	23	-0.29	-0.94	0.5467	0.8536
SARCOPLASMIC RETICULUM MEMBRANE	34	0.27	0.87	0.6738	0.8537
RESPONSE TO BACTERIUM	388	-0.18	-0.94	0.6513	0.8539
CALCIUM ION TRANSMEMBRANE IMPORT INTO CYTOSOL	35	-0.26	-0.94	0.5510	0.8547
CALCIUM ION IMPORT INTO CYTOSOL	35	-0.26	-0.94	0.5475	0.8552
GERM CELL DEVELOPMENT	175	-0.19	-0.94	0.6173	0.8555
CYTOSKELETAL ADAPTOR ACTIVITY	16	0.32	0.87	0.6471	0.8555
MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	35	0.26	0.87	0.6684	0.8556
NEGATIVE REGULATION OF GLIOGENESIS	33	0.27	0.87	0.6794	0.8558
DENDRITIC SPINE DEVELOPMENT	19	-0.30	-0.94	0.5231	0.8559
RESPONSE TO CARBOHYDRATE	155	-0.20	-0.94	0.6494	0.8559
CHROMOSOME CONDENSATION	28	-0.28	-0.94	0.5446	0.8560
PHOSPHATIDYL SERINE BINDING	31	-0.27	-0.94	0.5436	0.8561
POSITIVE REGULATION OF TRANSFORMING GROWTH FACTOR BETA PRODUCTION	15	-0.33	-0.94	0.5432	0.8565
BONE GROWTH	19	-0.31	-0.94	0.5619	0.8566
RETINA HOMEOSTASIS	52	-0.24	-0.94	0.5380	0.8567
REGULATION OF METAL ION TRANSPORT	296	-0.18	-0.94	0.6968	0.8568
RESPONSE TO MECHANICAL STIMULUS	190	-0.19	-0.94	0.6627	0.8569
REGULATION OF LEUKOCYTE DEGRANULATION	35	-0.26	-0.94	0.5620	0.8572
PHOTOPERIODISM	22	-0.30	-0.94	0.5624	0.8572
REGULATION OF ENDOTHELIAL CELL APOPTOTIC PROCESS	38	-0.25	-0.94	0.5783	0.8572
POSITIVE REGULATION OF LEUKOCYTE APOPTOTIC PROCESS	23	-0.29	-0.94	0.5314	0.8574
REGULATION OF PEPTIDYL SERINE PHOSPHORYLATION	104	0.21	0.87	0.7411	0.8576
REGULATION OF PEPTIDE TRANSPORT	228	-0.19	-0.93	0.6773	0.8577

PROSTAGLANDIN BIOSYNTHETIC PROCESS	17	-0.31	-0.93	0.5553	0.8577
SIALYLATION	18	-0.32	-0.93	0.5797	0.8578
POSITIVE REGULATION OF SMOOTH MUSCLE CONTRACTION	30	0.27	0.87	0.6527	0.8578
ATP DEPENDENT CHROMATIN REMODELING	53	0.24	0.87	0.6915	0.8578
CALCIUM ION REGULATED EXOCYTOSIS	72	-0.22	-0.94	0.5954	0.8578
PHOSPHOLIPASE C ACTIVATING G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY	75	-0.22	-0.93	0.5884	0.8578
REGULATION OF DNA RECOMBINATION	52	-0.24	-0.94	0.6021	0.8579
SYNAPTIC TRANSMISSION CHOLINERGIC	32	-0.27	-0.93	0.5729	0.8579
DETECTION OF MECHANICAL STIMULUS	38	-0.25	-0.93	0.5711	0.8579
POSITIVE REGULATION OF MYELOID CELL DIFFERENTIATION	72	-0.22	-0.94	0.5994	0.8580
MORPHOGENESIS OF EMBRYONIC EPITHELIUM	123	-0.20	-0.93	0.5926	0.8581
DETECTION OF VISIBLE LIGHT	40	-0.25	-0.93	0.5308	0.8581
ACETYLCHOLINE RECEPTOR ACTIVITY	26	-0.27	-0.93	0.5714	0.8581
POSITIVE REGULATION OF CARTILAGE DEVELOPMENT	28	-0.27	-0.93	0.5787	0.8582
POSITIVE REGULATION OF NUCLEOTIDE METABOLIC PROCESS	121	-0.20	-0.93	0.6689	0.8582
REGULATION OF BEHAVIOR	62	-0.23	-0.93	0.6169	0.8582
REGULATION OF GRANULOCYTE DIFFERENTIATION	16	-0.32	-0.94	0.5553	0.8583
POSITIVE REGULATION OF CHROMOSOME ORGANIZATION	129	-0.20	-0.93	0.6776	0.8583
REGULATION OF BODY FLUID LEVELS	445	-0.17	-0.94	0.7647	0.8583
EXTRACELLULAR LIGAND GATED ION CHANNEL ACTIVITY	69	-0.22	-0.93	0.5802	0.8585
SERINE HYDROLASE ACTIVITY	182	-0.19	-0.93	0.6638	0.8585
SUBSTRATE DEPENDENT CELL MIGRATION	24	0.29	0.87	0.6582	0.8585
FEMALE MEIOTIC DIVISION	21	0.30	0.87	0.6615	0.8585
RESPONSE TO AUDITORY STIMULUS	22	0.29	0.87	0.6427	0.8585
RESPONSE TO MOLECULE OF BACTERIAL ORIGIN	286	-0.18	-0.93	0.7413	0.8586
CELLULAR RESPONSE TO PEPTIDE	246	0.19	0.87	0.7915	0.8588
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT3 PROTEIN	41	-0.26	-0.93	0.5539	0.8588
CELL BODY	456	0.18	0.87	0.8495	0.8588

CELL ADHESION MOLECULE BINDING	172	-0.19	-0.93	0.6846	0.8589
AORTA MORPHOGENESIS	21	0.29	0.86	0.6603	0.8590
NEGATIVE REGULATION OF CELL CYCLE ARREST	16	-0.32	-0.93	0.5357	0.8590
NON MEMBRANE SPANNING PROTEIN TYROSINE KINASE ACTIVITY	38	-0.25	-0.93	0.5787	0.8590
REGULATION OF EARLY ENDOSOME TO LATE ENDOSOME TRANSPORT	15	0.32	0.87	0.6479	0.8591
GLIAL CELL DEVELOPMENT	68	0.23	0.86	0.6863	0.8591
EMBRYONIC CAMERA TYPE EYE MORPHOGENESIS	23	0.29	0.87	0.6356	0.8591
POSITIVE REGULATION OF ACTIVATED T CELL PROLIFERATION	22	-0.30	-0.93	0.5660	0.8591
HEMATOPOIETIC PROGENITOR CELL DIFFERENTIATION	85	0.22	0.87	0.7289	0.8591
CELLULAR RESPONSE TO EPIDERMAL GROWTH FACTOR STIMULUS	23	0.29	0.87	0.6761	0.8591
REGULATION OF LEUKOCYTE MEDIATED CYTOTOXICITY	45	0.25	0.87	0.6700	0.8591
PROSTANOID BIOSYNTHETIC PROCESS	17	-0.31	-0.93	0.5439	0.8592
PEPTIDYL TYROSINE AUTOPHOSPHORYLATION	34	-0.26	-0.93	0.5514	0.8592
POSITIVE REGULATION OF MULTICELLULAR ORGANISM GROWTH	27	0.27	0.86	0.6640	0.8593
MALE GENITALIA DEVELOPMENT	20	-0.30	-0.93	0.5298	0.8593
CELL CELL ADHERENS JUNCTION	50	0.24	0.87	0.6759	0.8593
ACETYLCHOLINE GATED CHANNEL COMPLEX	19	0.30	0.87	0.6353	0.8594
REGULATION OF PROTEIN ACETYLATION	54	-0.24	-0.93	0.5982	0.8595
POSITIVE REGULATION OF AXONOGENESIS	64	0.23	0.87	0.6916	0.8596
DETECTION OF ABIOTIC STIMULUS	107	-0.20	-0.93	0.6530	0.8597
REGULATION OF RUFFLE ASSEMBLY	16	-0.32	-0.93	0.5759	0.8597
MIDBRAIN DEVELOPMENT	81	0.22	0.86	0.7058	0.8598
REGULATION OF ENDOPLASMIC RETICULUM UNFOLDED PROTEIN RESPONSE	25	-0.28	-0.94	0.5526	0.8599
REGULATION OF HISTONE H3 K4 METHYLATION	24	0.29	0.86	0.6667	0.8600
POSITIVE REGULATION OF NUCLEOTIDE CATABOLIC PROCESS	16	0.32	0.86	0.6250	0.8600
ORGAN OR TISSUE SPECIFIC IMMUNE RESPONSE	21	-0.29	-0.93	0.5498	0.8604

POSITIVE REGULATION OF CELL CYCLE ARREST	73	0.23	0.86	0.7224	0.8606
REGULATION OF EPIDERMIS DEVELOPMENT	57	-0.23	-0.92	0.6145	0.8607
LAMELLIPODUM ASSEMBLY	29	0.27	0.86	0.6729	0.8609
ENDOCYTOSIS	429	0.18	0.86	0.8495	0.8610
GANGLIOSIDE BIOSYNTHETIC PROCESS	15	-0.32	-0.93	0.5481	0.8611
RESPONSE TO CAMP	96	-0.21	-0.93	0.6453	0.8611
ADRENERGIC RECEPTOR BINDING	19	0.31	0.86	0.6667	0.8612
BLOOD VESSEL MORPHOGENESIS	338	0.19	0.86	0.8225	0.8612
GLUTAMATE RECEPTOR ACTIVITY	26	-0.28	-0.93	0.5870	0.8612
NEGATIVE REGULATION OF FAT CELL DIFFERENTIATION	39	-0.25	-0.93	0.5772	0.8614
HEART MORPHOGENESIS	201	-0.18	-0.92	0.7169	0.8615
WOUND HEALING	413	-0.17	-0.93	0.8239	0.8616
OVULATION	16	-0.32	-0.93	0.5561	0.8617
REGULATION OF CARDIAC MUSCLE CELL ACTION POTENTIAL	19	0.30	0.86	0.6593	0.8617
POSITIVE REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	54	0.24	0.86	0.6972	0.8620
NEGATIVE REGULATION OF TRANSPORTER ACTIVITY	62	0.23	0.86	0.6948	0.8624
CELLULAR RESPONSE TO DRUG	62	0.23	0.86	0.7190	0.8624
DORSAL VENTRAL AXIS SPECIFICATION	18	0.30	0.86	0.6172	0.8626
NEGATIVE REGULATION OF CALCIUM ION IMPORT	21	0.30	0.86	0.6615	0.8626
ANGIOGENESIS	273	0.19	0.86	0.8239	0.8627
NEGATIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	116	0.21	0.86	0.7717	0.8635
REGULATION OF GLIAL CELL DIFFERENTIATION	55	0.24	0.86	0.7143	0.8635
REGULATION OF TISSUE REMODELING	59	0.23	0.86	0.7132	0.8639
NEURAL CREST CELL DIFFERENTIATION	73	0.23	0.86	0.7034	0.8641
FIBROBLAST GROWTH FACTOR RECEPTOR BINDING	26	0.27	0.86	0.6752	0.8642
NEGATIVE REGULATION OF OXIDOREDUCTASE ACTIVITY	22	0.29	0.86	0.6855	0.8642
RESPONSE TO GROWTH FACTOR	443	0.18	0.86	0.8546	0.8643
VIRAL GENOME REPLICATION	17	0.31	0.86	0.6373	0.8644
NEGATIVE REGULATION OF STEM CELL DIFFERENTIATION	41	-0.26	-0.92	0.5698	0.8645
RESPONSE TO ZINC ION	40	0.25	0.86	0.6937	0.8650

EMBRYONIC HEART TUBE MORPHOGENESIS	58	0.23	0.86	0.6953	0.8650
HYPOTHALAMUS DEVELOPMENT	24	0.28	0.86	0.6807	0.8653
SERINE TYPE ENDOPEPTIDASE INHIBITOR ACTIVITY	75	0.22	0.86	0.7353	0.8653
NEUROEPITHELIAL CELL DIFFERENTIATION	58	0.23	0.86	0.7228	0.8658
SENSORY PERCEPTION OF TEMPERATURE STIMULUS	20	0.29	0.86	0.6903	0.8662
NEGATIVE REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	33	0.27	0.86	0.6571	0.8663
MICROVILLUS MEMBRANE	16	0.31	0.86	0.6705	0.8665
T CELL HOMEOSTASIS	29	0.27	0.86	0.6922	0.8668
RESPONSE TO AMPHETAMINE	27	0.27	0.86	0.6759	0.8669
POSITIVE REGULATION OF INTERLEUKIN 6 SECRETION	15	-0.31	-0.92	0.5753	0.8672
NEGATIVE REGULATION OF NEUROLOGICAL SYSTEM PROCESS	15	-0.32	-0.92	0.5386	0.8679
POST EMBRYONIC DEVELOPMENT	79	0.22	0.85	0.7259	0.8683
POSITIVE REGULATION OF ERYTHROCYTE DIFFERENTIATION	21	0.29	0.85	0.6509	0.8684
ENDOPLASMIC RETICULUM LUMEN	179	0.20	0.85	0.8016	0.8686
TUBE FORMATION	122	0.21	0.85	0.7621	0.8688
CARDIAC MYOFIBRIL ASSEMBLY	16	0.31	0.85	0.6402	0.8689
EXCRETION	40	0.25	0.85	0.6855	0.8694
ENTRAINMENT OF CIRCADIAN CLOCK	23	0.29	0.85	0.6650	0.8697
TRANSFERASE ACTIVITY TRANSFERRING PENTOSYL GROUPS	43	0.25	0.85	0.7105	0.8698
CELLULAR RESPONSE TO CAMP	47	0.24	0.85	0.6878	0.8699
RESPONSE TO PEPTIDE	368	0.18	0.85	0.9038	0.8700
CHONDROITIN SULFATE PROTEOGLYCAN BIOSYNTHETIC PROCESS	28	-0.27	-0.92	0.5659	0.8701
REGULATION OF ANOIKIS	22	0.29	0.85	0.6549	0.8703
MULTICELLULAR ORGANISM METABOLIC PROCESS	84	0.22	0.85	0.7400	0.8704
PHOSPHATIDYLINOSITOL 3 KINASE ACTIVITY	67	0.23	0.85	0.7469	0.8704
REGULATION OF STEROID BIOSYNTHETIC PROCESS	45	-0.24	-0.92	0.6228	0.8706
REGULATION OF RENAL SODIUM EXCRETION	20	-0.30	-0.92	0.5700	0.8708
REGULATION OF NON CANONICAL WNT SIGNALING PATHWAY	19	-0.30	-0.92	0.5585	0.8708

REGULATION OF NUCLEOTIDE METABOLIC PROCESS	193	-0.19	-0.92	0.7450	0.8713
VITAMIN BINDING	70	-0.22	-0.92	0.6543	0.8715
NEURON DEATH	37	-0.25	-0.92	0.5960	0.8716
DIVALENT INORGANIC CATION TRANSPORT	244	-0.18	-0.92	0.6820	0.8716
POSITIVE REGULATION OF ENDOCYTOSIS	101	-0.21	-0.92	0.6585	0.8716
ACETYLCHOLINE BINDING	20	0.29	0.85	0.6602	0.8718
CATION TRANSPORTING ATPASE COMPLEX	16	-0.32	-0.92	0.5674	0.8719
EXCITATORY EXTRACELLULAR LIGAND GATED ION CHANNEL ACTIVITY	50	-0.24	-0.92	0.5944	0.8721
ADHERENS JUNCTION ORGANIZATION	66	0.23	0.85	0.7365	0.8721
REGULATION OF VIRAL GENOME REPLICATION	58	0.23	0.85	0.7296	0.8722
REGULATION OF BLOOD CIRCULATION	277	0.19	0.85	0.8497	0.8722
PROTEIN TYROSINE KINASE ACTIVITY	161	0.20	0.85	0.7926	0.8723
PROTEIN COMPLEX SCAFFOLD	55	-0.23	-0.92	0.6274	0.8725
REGULATION OF DELAYED RECTIFIER POTASSIUM CHANNEL ACTIVITY	18	-0.31	-0.92	0.5357	0.8727
LAMELLIPOD IUM MEMBRANE	18	-0.30	-0.92	0.5953	0.8728
DEFENSE RESPONSE TO GRAM POSITIVE BACTERIUM	50	0.24	0.85	0.7299	0.8730
NEGATIVE REGULATION OF CELLULAR RESPONSE TO GROWTH FACTOR STIMULUS	107	0.21	0.85	0.7699	0.8732
PEPTIDYL ASPARAGINE MODIFICATION	35	0.26	0.85	0.6883	0.8732
HORMONE BIOSYNTHETIC PROCESS	42	0.25	0.85	0.7056	0.8733
CELLULAR EXTRAVASATION	23	-0.29	-0.91	0.5952	0.8754
AUDITORY RECEPTOR CELL DEVELOPMENT	16	-0.31	-0.91	0.5660	0.8757
RESPONSE TO LITHIUM ION	26	0.27	0.85	0.6877	0.8758
POSITIVE REGULATION OF PURINE NUCLEOTIDE METABOLIC PROCESS	121	-0.20	-0.91	0.6523	0.8760
HYDROGEN PEROXIDE METABOLIC PROCESS	24	0.28	0.85	0.7053	0.8760
REGULATION OF MAST CELL ACTIVATION	33	-0.26	-0.91	0.6263	0.8764
EPITHELIAL CELL MORPHOGENESIS	40	-0.25	-0.91	0.6178	0.8765
POSITIVE REGULATION OF MUSCLE CELL DIFFERENTIATION	78	0.22	0.85	0.7604	0.8765
SPINDLE MIDZONE	24	0.28	0.85	0.6952	0.8773

CARDIAC CHAMBER MORPHOGENESIS	99	-0.21	-0.91	0.6625	0.8774
SINGLE FERTILIZATION	92	0.21	0.85	0.7655	0.8781
REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER IN RESPONSE TO HYPOXIA	29	0.27	0.84	0.7116	0.8781
VOLTAGE GATED CALCIUM CHANNEL COMPLEX	36	0.26	0.84	0.7089	0.8782
NEGATIVE REGULATION OF ENDOCYTOSIS	36	0.25	0.84	0.6991	0.8790
PROTEIN ADP RIBOSYLATION	15	0.31	0.84	0.6583	0.8792
REGULATION OF CIRCADIAN SLEEP WAKE CYCLE	24	0.28	0.84	0.7029	0.8793
FIBRIL ORGANIZATION	18	0.30	0.84	0.6876	0.8794
MYOTUBE CELL DEVELOPMENT	24	0.28	0.84	0.6776	0.8796
REGULATION OF CELLULAR RESPONSE TO TRANSFORMING GROWTH FACTOR BETA STIMULUS	85	0.21	0.84	0.7799	0.8796
PHOTORECEPTOR CELL DEVELOPMENT	35	0.26	0.84	0.7114	0.8796
LYSOSOME ORGANIZATION	42	0.24	0.84	0.6861	0.8797
NEGATIVE REGULATION OF CHEMOTAXIS	48	0.24	0.84	0.7200	0.8798
HISTONE METHYLTRANSFERASE ACTIVITY H3 K4 SPECIFIC	16	0.30	0.84	0.6774	0.8799
POSITIVE REGULATION OF TELOMERASE ACTIVITY	26	0.28	0.84	0.7031	0.8800
MULTICELLULAR ORGANISMAL WATER HOMEOSTASIS	45	0.25	0.84	0.7348	0.8801
RAB GTPASE BINDING	111	0.21	0.84	0.7703	0.8802
CELLULAR RESPONSE TO GONADOTROPIN STIMULUS	15	0.31	0.84	0.6865	0.8804
NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	15	0.31	0.84	0.6667	0.8804
NONRIBOSOMAL PEPTIDE BIOSYNTHETIC PROCESS	15	0.31	0.84	0.6753	0.8814
VASCULOGENESIS	53	-0.23	-0.91	0.6519	0.8815
OXYGEN BINDING	20	-0.30	-0.91	0.5687	0.8818
ENDOTHELIAL CELL PROLIFERATION	22	0.28	0.84	0.6848	0.8818
EPHRIN RECEPTOR SIGNALING PATHWAY	78	-0.21	-0.91	0.6719	0.8823
DIVALENT INORGANIC CATION HOMEOSTASIS	315	0.18	0.84	0.8630	0.8825
EPITHELIAL TUBE BRANCHING INVOLVED IN LUNG MORPHOGENESIS	24	-0.28	-0.91	0.5754	0.8828

CERAMIDE BIOSYNTHETIC PROCESS	33	0.25	0.84	0.6969	0.8829
VASCULATURE DEVELOPMENT	437	0.18	0.84	0.9022	0.8829
NITRIC OXIDE MEDIATED SIGNAL TRANSDUCTION	18	0.30	0.84	0.7059	0.8832
NEGATIVE REGULATION OF GTPASE ACTIVITY	37	0.26	0.84	0.7013	0.8848
NEGATIVE REGULATION OF LOCOMOTION	239	0.19	0.84	0.8727	0.8851
NEGATIVE REGULATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	77	0.22	0.84	0.7590	0.8851
REGULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR SIGNALING PATHWAY	85	0.21	0.84	0.7700	0.8852
RESPONSE TO PROSTAGLANDIN	29	0.26	0.84	0.7286	0.8852
POSITIVE REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORT	26	0.27	0.84	0.7186	0.8865
DNA MODIFICATION	66	-0.22	-0.91	0.6607	0.8868
DNA SYNTHESIS INVOLVED IN DNA REPAIR	57	-0.23	-0.91	0.6541	0.8872
POSITIVE REGULATION OF GLYCOPROTEIN METABOLIC PROCESS	15	0.31	0.84	0.6636	0.8875
PIGMENT GRANULE	93	0.21	0.83	0.7809	0.8880
CELLULAR RESPONSE TO GAMMA RADIATION	18	0.30	0.83	0.6805	0.8883
MIDBODY	115	0.20	0.83	0.7994	0.8887
MULTICELLULAR ORGANISMAL HOMEOSTASIS	225	0.19	0.83	0.8555	0.8894
CATION CATION ANTIPORTER ACTIVITY	23	0.28	0.83	0.7110	0.8895
ADENYLYLATE CYCLASE ACTIVATING G PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY	65	0.22	0.83	0.7835	0.8896
BICARBONATE TRANSPORT	26	0.27	0.83	0.7109	0.8896
PROTEIN O LINKED GLYCOSYLATION	82	-0.21	-0.91	0.6687	0.8897
KIDNEY MORPHOGENESIS	78	0.22	0.83	0.7564	0.8898
EXTRINSIC COMPONENT OF MEMBRANE	219	0.19	0.83	0.8514	0.8899
EMBRYONIC SKELETAL SYSTEM MORPHOGENESIS	85	-0.20	-0.90	0.6667	0.8902
POSITIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER IN RESPONSE TO STRESS	20	-0.29	-0.91	0.5658	0.8903
RESPONSE TO WOUNDING	495	0.17	0.83	0.9394	0.8906
CARDIAC CELL DEVELOPMENT	47	0.24	0.83	0.7483	0.8909

WATER HOMEOSTASIS	55	0.23	0.83	0.7539	0.8913
RETINA LAYER FORMATION	20	-0.29	-0.90	0.5586	0.8913
GAMETE GENERATION	468	0.17	0.83	0.9244	0.8924
MEMBRANE LIPID CATABOLIC PROCESS	22	0.28	0.83	0.6782	0.8924
METENCEPHALON DEVELOPMENT	94	0.21	0.83	0.7815	0.8925
REGULATION OF FATTY ACID TRANSPORT	24	0.28	0.83	0.6979	0.8930
MUSCLE SYSTEM PROCESS	267	0.18	0.83	0.8876	0.8933
DENDRITE	419	0.17	0.83	0.9263	0.8934
LYTIC VACUOLE ORGANIZATION	42	0.24	0.83	0.7330	0.8936
NEUROTRANSMITTER BINDING	25	-0.27	-0.90	0.6020	0.8942
UROGENITAL SYSTEM DEVELOPMENT	272	0.18	0.83	0.8745	0.8950
AORTA DEVELOPMENT	39	0.25	0.83	0.7164	0.8951
SIGNALING ADAPTOR ACTIVITY	68	0.22	0.83	0.7684	0.8970
REGULATION OF EPIDERMAL CELL DIFFERENTIATION	40	-0.25	-0.90	0.6267	0.8972
HOMOPHILIC CELL ADHESION VIA PLASMA MEMBRANE ADHESION MOLECULES	111	-0.20	-0.90	0.6962	0.8978
CYTOKINE BINDING	84	-0.21	-0.90	0.7200	0.8979
NEGATIVE REGULATION OF INTERFERON GAMMA PRODUCTION	27	-0.27	-0.90	0.6381	0.8984
AUDITORY RECEPTOR CELL DIFFERENTIATION	26	0.27	0.83	0.7188	0.8987
REGULATION OF TRANSCRIPTION INVOLVED IN G1 S TRANSITION OF MITOTIC CELL CYCLE	22	0.28	0.82	0.7005	0.8997
NEGATIVE REGULATION OF PEPTIDASE ACTIVITY	195	0.19	0.82	0.8619	0.8999
CELLULAR RESPONSE TO NITROGEN COMPOUND	461	0.17	0.82	0.9266	0.9002
RESPIRATORY SYSTEM DEVELOPMENT	185	0.19	0.82	0.8652	0.9014
PROTEIN COMPLEX LOCALIZATION	44	-0.24	-0.90	0.6234	0.9017
TELENCEPHALON DEVELOPMENT	214	-0.18	-0.90	0.7764	0.9021
NEURONAL CELL BODY MEMBRANE	20	-0.29	-0.90	0.6139	0.9022
SEX DIFFERENTIATION	231	-0.18	-0.90	0.7845	0.9024
ALDO KETO REDUCTASE NADP ACTIVITY	16	-0.31	-0.90	0.6147	0.9028
POSITIVE REGULATION OF PROTEIN SERINE THREONINE KINASE ACTIVITY	260	0.18	0.82	0.8935	0.9028
CELLULAR RESPONSE TO ALCOHOL	103	0.21	0.82	0.8133	0.9029
INORGANIC ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	114	-0.20	-0.90	0.7252	0.9029
GTP METABOLIC PROCESS	18	0.29	0.82	0.7226	0.9033

MESENCHYMAL CELL DIFFERENTIATION	129	0.20	0.82	0.8272	0.9040
REGULATION OF URINE VOLUME	18	0.29	0.82	0.6767	0.9047
AMIDE TRANSPORT	89	-0.20	-0.90	0.7034	0.9051
LIGAND GATED CHANNEL ACTIVITY	132	-0.19	-0.89	0.7463	0.9059
POSITIVE REGULATION OF PROTEIN MATURATION	15	-0.32	-0.89	0.5845	0.9059
MEMORY	91	-0.20	-0.89	0.6909	0.9062
PHOTORECEPTOR CELL MAINTENANCE	32	0.25	0.82	0.7685	0.9064
RECEPTOR COMPLEX	304	0.18	0.82	0.9102	0.9068
ENDOCYTIC VESICLE	212	0.19	0.82	0.8838	0.9068
SYNTAXIN BINDING	83	0.21	0.82	0.8219	0.9069
REGULATION OF MULTICELLULAR ORGANISMAL METABOLIC PROCESS	32	-0.25	-0.89	0.6168	0.9069
MALE GAMETE GENERATION	377	0.17	0.82	0.9249	0.9070
REGULATION OF VOLTAGE GATED CALCIUM CHANNEL ACTIVITY	24	0.27	0.82	0.7367	0.9070
PROTEIN DEACETYLASE ACTIVITY	40	0.24	0.82	0.7615	0.9071
REGULATION OF TYPE I INTERFERON PRODUCTION	100	0.20	0.82	0.8394	0.9073
POSITIVE REGULATION OF INTERFERON BETA PRODUCTION	30	0.26	0.82	0.7125	0.9074
REGULATION OF TRANSPORTER ACTIVITY	185	0.19	0.82	0.8570	0.9082
INTEGRIN BINDING	98	-0.20	-0.89	0.7059	0.9088
RESPONSE TO CORTICOSTEROID	164	0.19	0.82	0.8768	0.9089
VESICLE MEDIATED TRANSPORT BETWEEN ENDOSOMAL COMPARTMENTS	17	0.30	0.82	0.7133	0.9090
ANTIMICROBIAL HUMORAL RESPONSE	26	-0.27	-0.89	0.6073	0.9094
POSITIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	15	-0.32	-0.89	0.5962	0.9094
T CELL DIFFERENTIATION IN THYMUS	42	-0.23	-0.89	0.6620	0.9097
NEGATIVE REGULATION OF MYELOID CELL DIFFERENTIATION	72	-0.21	-0.89	0.7309	0.9098
CONNEXON COMPLEX	17	0.30	0.81	0.7158	0.9099
REGULATION OF ION HOMEOSTASIS	178	-0.18	-0.89	0.7953	0.9101
RESPONSE TO FIBROBLAST GROWTH FACTOR	104	-0.20	-0.89	0.7294	0.9101
POSITIVE REGULATION OF ION TRANSPORT	219	-0.18	-0.89	0.7768	0.9102
PRESYNAPTIC ACTIVE ZONE	29	0.26	0.81	0.7409	0.9103
FOREBRAIN NEURON DEVELOPMENT	32	-0.25	-0.89	0.6235	0.9105
EATING BEHAVIOR	30	-0.25	-0.89	0.6044	0.9106

MICROTUBULE MOTOR ACTIVITY	53	-0.22	-0.89	0.6747	0.9108
REGULATION OF NATURAL KILLER CELL MEDIATED IMMUNITY	26	-0.26	-0.89	0.6145	0.9111
PLATELET ALPHA GRANULE LUMEN	52	0.23	0.81	0.7793	0.9115
NEUROTROPHIN SIGNALING PATHWAY	22	-0.28	-0.89	0.6310	0.9116
EMBRYONIC PLACENTA DEVELOPMENT	82	0.21	0.81	0.8072	0.9118
REGULATION OF PROTEIN SECRETION	332	-0.17	-0.88	0.9021	0.9119
REGULATION OF SUPEROXIDE METABOLIC PROCESS	20	0.29	0.81	0.7196	0.9122
CARDIAC MUSCLE TISSUE MORPHOGENESIS	52	-0.22	-0.88	0.6783	0.9122
REGULATION OF LIPASE ACTIVITY	80	0.21	0.81	0.8169	0.9123
REGULATION OF ACTION POTENTIAL	38	0.24	0.81	0.7600	0.9125
POSITIVE REGULATION OF INSULIN SECRETION	58	-0.22	-0.88	0.7075	0.9126
GRANULOCYTE ACTIVATION	18	-0.30	-0.88	0.6197	0.9128
POSITIVE REGULATION OF VASODILATION	31	0.26	0.81	0.7446	0.9128
REGULATION OF HEMATOPOIETIC PROGENITOR CELL DIFFERENTIATION	29	0.25	0.81	0.7554	0.9128
GLUTAMATE SECRETION	28	0.26	0.81	0.7471	0.9128
TRANSFERASE ACTIVITY TRANSFERRING AMINO ACYL GROUPS	18	-0.29	-0.88	0.6222	0.9129
APICOLATERAL PLASMA MEMBRANE	15	-0.31	-0.89	0.6227	0.9130
REGULATION OF PROTEIN OLIGOMERIZATION	29	0.25	0.81	0.7443	0.9130
HINDBRAIN DEVELOPMENT	127	0.20	0.81	0.8484	0.9130
POSITIVE REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORT	55	-0.22	-0.88	0.7033	0.9130
MESENCHYME DEVELOPMENT	176	-0.18	-0.88	0.8312	0.9131
REGULATION OF NITRIC OXIDE SYNTHASE ACTIVITY	44	-0.24	-0.89	0.6585	0.9132
MAMMARY GLAND DUCT MORPHOGENESIS	28	-0.25	-0.88	0.6441	0.9132
VENTRICULAR CARDIAC MUSCLE CELL DIFFERENTIATION	18	-0.30	-0.89	0.6194	0.9133
ASTROCYTE DEVELOPMENT	17	-0.30	-0.88	0.5911	0.9133
REGULATION OF CELL PROJECTION ASSEMBLY	133	0.19	0.81	0.8577	0.9133
CILIARY PART	236	-0.18	-0.88	0.8465	0.9134
RESPONSE TO VITAMIN A	19	-0.29	-0.88	0.6441	0.9135
HMG BOX DOMAIN BINDING	17	-0.30	-0.88	0.6241	0.9136
LEUKOTRIENE METABOLIC PROCESS	21	-0.28	-0.88	0.6237	0.9136

RESPONSE TO AXON INJURY	42	-0.23	-0.88	0.6821	0.9136
MONOVALENT INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	333	0.17	0.81	0.9322	0.9136
CEREBELLAR CORTEX DEVELOPMENT	44	-0.23	-0.88	0.6712	0.9137
REGULATION OF G PROTEIN COUPLED RECEPTOR PROTEIN SIGNALING PATHWAY	117	-0.20	-0.89	0.7647	0.9138
VISUAL BEHAVIOR	47	-0.23	-0.88	0.6898	0.9138
CIRCULATORY SYSTEM PROCESS	338	-0.17	-0.88	0.8865	0.9140
NEGATIVE REGULATION OF VIRAL GENOME REPPLICATION	36	-0.24	-0.88	0.6731	0.9140
REGULATION OF SYNAPTIC TRANSMISSION DOPAMINERGIC	16	-0.30	-0.88	0.6232	0.9141
RESPONSE TO ETHANOL	123	-0.19	-0.88	0.7645	0.9142
VENTRAL SPINAL CORD INTERNEURON DIFFERENTIATION	16	-0.30	-0.88	0.6062	0.9143
POSITIVE REGULATION OF HISTONE H3 K4 METHYLATION	15	-0.30	-0.87	0.6315	0.9144
ATP DEPENDENT MICROTUBULE MOTOR ACTIVITY	16	-0.30	-0.88	0.6316	0.9144
NOTCH BINDING	17	-0.30	-0.88	0.6179	0.9144
NEGATIVE REGULATION OF CELLULAR RESPONSE TO INSULIN STIMULUS	29	-0.25	-0.87	0.6877	0.9144
MUSCLE ADAPTATION	28	-0.26	-0.89	0.6576	0.9145
MALE SEX DIFFERENTIATION	128	-0.19	-0.88	0.7559	0.9146
NEGATIVE REGULATION OF ENDOTHELIAL CELL PROLIFERATION	30	-0.26	-0.88	0.6551	0.9147
REGULATION OF INFLAMMATORY RESPONSE	257	-0.17	-0.88	0.9031	0.9149
KERATAN SULFATE BIOSYNTHETIC PROCESS	24	-0.26	-0.88	0.6372	0.9150
REGULATION OF CELL SUBSTRATE ADHESION	157	-0.18	-0.88	0.7760	0.9150
REGULATION OF OSTEOBLAST DIFFERENTIATION	103	-0.19	-0.88	0.7287	0.9151
GLYCOSPHINGOLIPID BIOSYNTHETIC PROCESS	21	-0.28	-0.88	0.6194	0.9152
POSITIVE REGULATION OF IMMUNE RESPONSE	447	0.17	0.81	0.9502	0.9159
REGULATION OF BONE RESORPTION	31	0.25	0.81	0.7650	0.9159
INOSITOL LIPID MEDIATED SIGNALING	114	-0.19	-0.87	0.7695	0.9161
CARRECEPTOR ACTIVITY	58	0.22	0.81	0.7892	0.9162
POSITIVE CHEMOTAXIS	31	-0.25	-0.87	0.6569	0.9163

CELLULAR RESPONSE TO ACID CHEMICAL	159	-0.18	-0.87	0.8073	0.9166
CHLORIDE TRANSPORT	88	-0.20	-0.87	0.7468	0.9167
THYMOCYTE AGGREGATION	42	-0.23	-0.87	0.7016	0.9167
MAMMARY GLAND EPITHELIUM DEVELOPMENT	51	0.23	0.81	0.7658	0.9168
BONE DEVELOPMENT	146	-0.18	-0.87	0.8095	0.9174
REGULATION OF HEART RATE	81	0.21	0.81	0.8192	0.9176
REGULATION OF SYSTEM PROCESS	477	0.17	0.81	0.9574	0.9177
ANATOMICAL STRUCTURE HOMEOSTASIS	232	0.18	0.81	0.8885	0.9177
GTP DEPENDENT PROTEIN BINDING	17	-0.29	-0.87	0.6465	0.9178
GLUTATHIONE DERIVATIVE METABOLIC PROCESS	16	0.29	0.81	0.6989	0.9178
NEGATIVE REGULATION OF TUMOR NECROSIS FACTOR SUPERFAMILY CYTOKINE PRODUCTION	40	-0.24	-0.87	0.6657	0.9179
PHOSPHATASE BINDING	138	0.19	0.81	0.8578	0.9181
REGULATION OF NOREPINEPHRINE SECRETION	17	-0.29	-0.87	0.6209	0.9184
APICAL JUNCTION COMPLEX	117	0.20	0.81	0.8534	0.9188
DESMOSOME	24	-0.27	-0.87	0.6908	0.9188
POSTSYNAPSE	348	0.17	0.80	0.9504	0.9189
POSITIVE REGULATION OF ENDOTHELIAL CELL MIGRATION	65	-0.21	-0.87	0.7423	0.9198
REGULATION OF MEIOTIC CELL CYCLE	38	0.24	0.80	0.7546	0.9200
CELL SUBSTRATE JUNCTION	365	0.17	0.80	0.9515	0.9202
PLATELET DENSE GRANULE	18	0.29	0.80	0.7326	0.9203
PLASMA MEMBRANE PROTEIN COMPLEX	455	0.17	0.80	0.9693	0.9204
REGULATION OF SEQUESTERING OF CALCIUM ION	93	-0.19	-0.87	0.7626	0.9205
POSITIVE REGULATION OF TRANSCRIPTION FACTOR IMPORT INTO NUCLEUS	45	-0.23	-0.87	0.7028	0.9211
CIRCADIAN REGULATION OF GENE EXPRESSION	52	-0.22	-0.87	0.7131	0.9212
POSITIVE REGULATION OF PROTEIN IMPORT	95	0.20	0.80	0.8356	0.9212
TRANSFERASE ACTIVITY TRANSFERRING NITROGENOUS GROUPS	22	0.27	0.80	0.7323	0.9214
PHOSPHATIDYLINOSITOL 3 PHOSPHATE BIOSYNTHETIC PROCESS	47	0.23	0.80	0.7925	0.9215
PROTEIN AUTOPHOSPHORYLATION	175	0.18	0.80	0.8919	0.9216

REGULATION OF GLIOGENESIS	83	0.21	0.80	0.8323	0.9216
ENDODERM DEVELOPMENT	67	-0.21	-0.87	0.7568	0.9218
TISSUE MORPHOGENESIS	496	-0.16	-0.87	0.9609	0.9225
MICROVILLUS	67	0.21	0.80	0.7925	0.9230
REGULATION OF INTERLEUKIN 17 PRODUCTION	19	-0.28	-0.87	0.6463	0.9233
CARBOXYPEPTIDASE ACTIVITY	38	0.24	0.80	0.7806	0.9235
POSITIVE REGULATION OF MITOTIC NUCLEAR DIVISION	44	-0.23	-0.87	0.7157	0.9235
ERYTHROCYTE HOMEOSTASIS	60	-0.21	-0.86	0.7808	0.9236
AMINOGLYCAN METABOLIC PROCESS	148	0.19	0.80	0.8942	0.9236
RESPONSE TO ESTROGEN	198	0.18	0.80	0.9044	0.9236
SYNAPTIC VESICLE RECYCLING	23	0.26	0.80	0.7240	0.9237
NEUROTRANSMITTER SODIUM SYMPORTER ACTIVITY	17	0.29	0.80	0.7177	0.9238
POSITIVE REGULATION OF LIPASE ACTIVITY	63	-0.21	-0.86	0.7213	0.9238
NEGATIVE REGULATION OF PEPTIDYL TYROSINE PHOSPHORYLATION	35	0.24	0.80	0.7708	0.9239
MEIOTIC CHROMOSOME SEGREGATION	52	-0.22	-0.86	0.7313	0.9240
REGULATION OF TELOMERE CAPPING	21	0.27	0.80	0.7333	0.9241
SH3 DOMAIN BINDING	106	-0.19	-0.86	0.7508	0.9242
PLATELET DERIVED GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	31	0.25	0.80	0.7439	0.9245
PEPTIDE SECRETION	55	-0.22	-0.86	0.7003	0.9246
POSITIVE REGULATION OF CYTOKINE SECRETION	73	-0.20	-0.86	0.7761	0.9257
REPRODUCTIVE SYSTEM DEVELOPMENT	365	-0.16	-0.86	0.9379	0.9257
MOTILE CILIUM	86	0.20	0.80	0.8361	0.9263
POSITIVE REGULATION OF PROTEIN KINASE B SIGNALING	70	0.21	0.80	0.8293	0.9268
CELLULAR RESPONSE TO OXYGEN LEVELS	126	0.19	0.80	0.8754	0.9269
SULFUR COMPOUND BINDING	209	0.18	0.79	0.9099	0.9280
PROSTAGLANDIN METABOLIC PROCESS	23	-0.27	-0.86	0.6721	0.9282
CARDIAC MUSCLE TISSUE DEVELOPMENT	135	0.19	0.79	0.8826	0.9282
CHRONIC INFLAMMATORY RESPONSE	15	-0.30	-0.86	0.6531	0.9283
ACTIVATION OF MAPK ACTIVITY	124	0.19	0.79	0.8782	0.9285
RAS PROTEIN SIGNAL TRANSDUCTION	127	-0.18	-0.86	0.8384	0.9285
REGULATION OF GASTRULATION	34	0.24	0.79	0.7827	0.9287
POSITIVE REGULATION OF PROTEIN SECRETION	175	-0.17	-0.86	0.8715	0.9288

ACTIN FILAMENT BINDING	108	0.19	0.79	0.8874	0.9289
BICELLULAR TIGHT JUNCTION ASSEMBLY	28	-0.25	-0.86	0.6822	0.9292
POSITIVE REGULATION OF OXIDOREDUCTASE ACTIVITY	42	0.23	0.79	0.7745	0.9292
POSITIVE REGULATION OF CATION CHANNEL ACTIVITY	36	0.24	0.79	0.7855	0.9293
TRANSMEMBRANE RECEPTOR PROTEIN PHOSPHATASE ACTIVITY	17	-0.29	-0.86	0.6423	0.9294
CARDIAC CHAMBER DEVELOPMENT	136	0.19	0.79	0.8715	0.9295
REGULATION OF INTERLEUKIN 6 PRODUCTION	92	0.20	0.79	0.8423	0.9296
POSITIVE REGULATION OF STRIATED MUSCLE CONTRACTION	15	0.30	0.79	0.7274	0.9313
NUCLEOSIDE TRANSPORT	15	0.29	0.79	0.7635	0.9314
REGULATION OF EXOCYTOSIS	165	0.18	0.79	0.8984	0.9328
ACTIN BASED CELL PROJECTION	164	0.18	0.79	0.9008	0.9330
MEMBRANE ASSEMBLY	23	0.26	0.79	0.7453	0.9332
NEGATIVE REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORT	27	0.25	0.79	0.8034	0.9332
REGULATION OF MACROPHAGE ACTIVATION	25	0.26	0.79	0.7483	0.9333
COPPER ION TRANSPORT	18	-0.29	-0.86	0.6522	0.9334
REGULATION OF POTASSIUM ION TRANSPORT	78	0.21	0.79	0.8453	0.9334
BENZENE CONTAINING COMPOUND METABOLIC PROCESS	22	0.27	0.79	0.7750	0.9335
POTASSIUM ION IMPORT	28	-0.26	-0.85	0.6502	0.9335
REGULATION OF HISTONE METHYLATION	50	0.22	0.79	0.8323	0.9336
POSITIVE REGULATION OF JUN KINASE ACTIVITY	57	0.22	0.79	0.8396	0.9336
REGULATION OF SODIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	34	0.24	0.79	0.7885	0.9337
RECEPTOR MEDIATED ENDOCYTOSIS	186	0.18	0.79	0.9223	0.9338
ACETYLGLACTOSAMINYLTRANSFERASE ACTIVITY	30	0.25	0.79	0.7781	0.9338
POSITIVE REGULATION OF PEPTIDE SECRETION	82	-0.20	-0.85	0.7813	0.9340
GLUTATHIONE DERIVATIVE BIOSYNTHETIC PROCESS	16	0.29	0.79	0.7345	0.9341
NEGATIVE REGULATION OF GLIAL CELL DIFFERENTIATION	24	-0.26	-0.85	0.6870	0.9342

PROSTANOID METABOLIC PROCESS	23	-0.27	-0.86	0.6675	0.9344
CENTRAL NERVOUS SYSTEM NEURON DEVELOPMENT	64	-0.21	-0.85	0.7566	0.9345
PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	48	0.22	0.79	0.8150	0.9348
REGULATION OF EXTENT OF CELL GROWTH	94	-0.20	-0.85	0.7876	0.9350
ANCHORING JUNCTION	448	-0.16	-0.85	0.9929	0.9352
CENTROSOME LOCALIZATION	16	-0.29	-0.85	0.6838	0.9352
CARDIAC VENTRICLE DEVELOPMENT	98	0.20	0.78	0.8746	0.9363
REGULATION OF ANTIGEN RECEPTOR MEDIATED SIGNALING PATHWAY	38	0.24	0.78	0.8192	0.9364
POSITIVE REGULATION OF ERBB SIGNALING PATHWAY	31	0.25	0.78	0.7892	0.9365
CELL CELL JUNCTION	352	0.17	0.78	0.9642	0.9365
NEURONAL STEM CELL POPULATION MAINTENANCE	19	0.28	0.78	0.7517	0.9365
SUBSTRATE ADHESION DEPENDENT CELL SPREADING	33	0.24	0.78	0.8036	0.9366
NEGATIVE REGULATION OF TOLL LIKE RECEPTOR SIGNALING PATHWAY	24	0.26	0.78	0.7709	0.9366
NEUROTRANSMITTER TRANSPORTER ACTIVITY	23	0.26	0.78	0.7655	0.9367
BLASTODERM SEGMENTATION	15	0.29	0.78	0.7436	0.9368
SMOOTHENED SIGNALING PATHWAY	65	-0.21	-0.85	0.7578	0.9376
REGULATION OF ALCOHOL BIOSYNTHETIC PROCESS	42	-0.23	-0.85	0.7416	0.9379
O GLYCAN PROCESSING	48	0.22	0.78	0.8175	0.9384
POSITIVE REGULATION OF LIPID KINASE ACTIVITY	28	0.25	0.78	0.7863	0.9390
ANION CHANNEL ACTIVITY	78	0.20	0.78	0.8567	0.9391
PROTEIN HOMOTRIMERIZATION	19	-0.27	-0.85	0.6611	0.9391
RAS GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	199	0.18	0.78	0.9387	0.9392
INORGANIC ANION EXCHANGER ACTIVITY	17	0.28	0.78	0.7620	0.9393
REGULATION OF RAS PROTEIN SIGNAL TRANSDUCTION	156	0.18	0.78	0.9243	0.9393
KINASE ACTIVATOR ACTIVITY	55	0.22	0.78	0.8311	0.9393
SOMATIC STEM CELL POPULATION MAINTENANCE	63	0.21	0.78	0.8447	0.9394
ACTIN FILAMENT POLYMERIZATION	19	0.28	0.78	0.7629	0.9394

REGULATION OF STEROID HORMONE SECRETION	18	0.28	0.78	0.7861	0.9394
MYELOID CELL DIFFERENTIATION	167	0.18	0.78	0.9271	0.9396
LUNG EPITHELIUM DEVELOPMENT	33	0.24	0.78	0.7997	0.9397
REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS	21	0.26	0.78	0.7560	0.9397
KIDNEY EPITHELIUM DEVELOPMENT	118	0.19	0.78	0.8946	0.9397
DNA BIOSYNTHETIC PROCESS	94	0.20	0.78	0.8748	0.9398
NEGATIVE REGULATION OF NUCLEOSIDE METABOLIC PROCESS	18	0.27	0.78	0.7739	0.9398
REGULATION OF GLUCOSE IMPORT	49	0.22	0.78	0.8270	0.9399
CELL CELL RECOGNITION	48	0.22	0.78	0.8281	0.9400
NEGATIVE REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	34	0.24	0.78	0.7810	0.9401
EPIDERMAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	53	0.22	0.78	0.8297	0.9401
REGULATION OF VESICLE FUSION	56	0.21	0.77	0.8632	0.9410
NEGATIVE REGULATION OF ATP METABOLIC PROCESS	18	0.27	0.77	0.7853	0.9410
NEGATIVE REGULATION OF HISTONE MODIFICATION	31	0.24	0.77	0.7939	0.9412
TUBE MORPHOGENESIS	302	0.17	0.77	0.9791	0.9417
VASCULAR PROCESS IN CIRCULATORY SYSTEM	152	-0.18	-0.85	0.8617	0.9418
CATECHOLAMINE BINDING	15	0.29	0.77	0.7606	0.9424
MORPHOGENESIS OF AN ENDOTHELIUM	15	-0.29	-0.85	0.6587	0.9425
POSITIVE REGULATION OF HORMONE SECRETION	107	0.19	0.77	0.8963	0.9426
POSITIVE REGULATION OF NOTCH SIGNALING PATHWAY	31	-0.24	-0.85	0.6885	0.9427
EMBRYONIC DIGESTIVE TRACT MORPHOGENESIS	16	-0.29	-0.85	0.6544	0.9428
RESPONSE TO NICOTINE	47	0.22	0.77	0.8500	0.9428
BLOOD MICROPARTICLE	89	0.20	0.77	0.8985	0.9428
CELL CELL SIGNALING INVOLVED IN CARDIAC CONDUCTION	21	-0.27	-0.84	0.6925	0.9428
METALLOENDOPEPTIDASE ACTIVITY	98	-0.19	-0.85	0.7860	0.9429
ACTIN POLYMERIZATION OR DEPOLYMERIZATION	33	-0.24	-0.85	0.7156	0.9429
CYCLASE ACTIVITY	21	0.26	0.77	0.7929	0.9430

POSITIVE REGULATION OF NATURAL KILLER CELL MEDIATED IMMUNITY	17	-0.28	-0.84	0.7280	0.9432
REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	39	0.23	0.77	0.7844	0.9433
REGULATION OF HAIR CYCLE	21	-0.27	-0.85	0.7067	0.9437
CHEMOREPELLENT ACTIVITY	27	-0.25	-0.84	0.7077	0.9438
CILIUM	373	-0.16	-0.84	0.9657	0.9439
ACTIN FILAMENT ORGANIZATION	152	-0.18	-0.84	0.8504	0.9440
CELLULAR PROCESS INVOLVED IN REPRODUCTION IN MULTICELLULAR ORGANISM	213	-0.17	-0.84	0.9033	0.9441
PRODUCTION OF SMALL RNA INVOLVED IN GENE SILENCING BY RNA	20	-0.27	-0.84	0.7026	0.9443
DETECTION OF BIOTIC STIMULUS	17	-0.28	-0.84	0.7197	0.9444
REGULATION OF MYELOID LEUKOCYTE DIFFERENTIATION	98	-0.19	-0.84	0.8404	0.9445
REGULATION OF ADENYLYLATE CYCLASE ACTIVITY	65	-0.20	-0.84	0.7867	0.9446
POSITIVE REGULATION OF MUSCLE CONTRACTION	44	-0.22	-0.84	0.7628	0.9446
ASTROCYTE DIFFERENTIATION	37	-0.23	-0.84	0.7245	0.9446
POSITIVE REGULATION OF HISTONE METHYLATION	29	-0.25	-0.84	0.7215	0.9447
MEIOTIC CELL CYCLE PROCESS	124	-0.18	-0.84	0.8596	0.9447
MORPHOGENESIS OF AN EPITHELIUM	370	-0.16	-0.84	0.9600	0.9448
DSRNA FRAGMENTATION	20	-0.27	-0.84	0.6767	0.9452
NEGATIVE REGULATION OF ION TRANSPORT	117	0.19	0.77	0.8983	0.9453
POSITIVE REGULATION OF ADENYLYLATE CYCLASE ACTIVITY	44	0.22	0.77	0.8228	0.9453
DEOXYRIBOSE PHOSPHATE CATABOLIC PROCESS	18	0.27	0.77	0.7837	0.9454
LENS MORPHOGENESIS IN CAMERA TYPE EYE	19	0.27	0.77	0.7792	0.9454
BRANCHING INVOLVED IN SALIVARY GLAND MORPHOGENESIS	16	0.28	0.77	0.7787	0.9457
CALMODULIN DEPENDENT PROTEIN KINASE ACTIVITY	26	0.25	0.77	0.7892	0.9457
SENSORY PERCEPTION OF LIGHT STIMULUS	192	-0.17	-0.84	0.9156	0.9458
CILIARY PLASM	53	0.21	0.77	0.8404	0.9464
RESPONSE TO ALCOHOL	330	-0.16	-0.84	0.9500	0.9465

REGULATION OF REPRODUCTIVE PROCESS	121	0.18	0.77	0.9231	0.9471
BAF TYPE COMPLEX	21	-0.27	-0.84	0.6989	0.9476
STRIATED MUSCLE CONTRACTION	94	0.19	0.76	0.8688	0.9480
REGULATION OF POTASSIUM ION TRANSMEMBRANE TRANSPORT	59	-0.21	-0.84	0.7644	0.9480
POSITIVE REGULATION OF INTERLEUKIN 12 PRODUCTION	31	0.24	0.76	0.8283	0.9480
POSTSYNAPTIC MEMBRANE ORGANIZATION	25	0.25	0.76	0.7987	0.9481
RESPONSE TO VITAMIN	93	-0.19	-0.84	0.8055	0.9484
MODULATION OF SYNAPTIC TRANSMISSION	283	0.17	0.76	0.9723	0.9485
NEGATIVE REGULATION OF HISTONE METHYLATION	16	-0.28	-0.83	0.6435	0.9491
SECRETORY GRANULE	316	-0.16	-0.83	0.9524	0.9493
RETINA DEVELOPMENT IN CAMERA TYPE EYE	121	0.18	0.76	0.9130	0.9495
REGULATION OF RENAL SYSTEM PROCESS	33	-0.23	-0.83	0.7532	0.9495
TELOMERE CAPPING	19	-0.27	-0.83	0.7070	0.9496
PEPTIDASE INHIBITOR ACTIVITY	134	-0.18	-0.83	0.9011	0.9499
DIGESTIVE SYSTEM PROCESS	57	0.21	0.76	0.8707	0.9499
PHOSPHATIDYLSERINE ACYL CHAIN REMODELING	16	0.28	0.76	0.7784	0.9507
MEIOTIC CELL CYCLE	152	0.18	0.76	0.9426	0.9508
REGULATION OF STEM CELL DIFFERENTIATION	104	0.19	0.76	0.9170	0.9508
NEGATIVE REGULATION OF ACTIN FILAMENT BUNDLE ASSEMBLY	18	0.27	0.76	0.8094	0.9512
SENSORY PERCEPTION OF PAIN	72	0.20	0.76	0.8649	0.9518
EMBRYONIC HEART TUBE DEVELOPMENT	69	0.20	0.76	0.8794	0.9521
REGULATION OF JUN KINASE ACTIVITY	72	0.20	0.76	0.8849	0.9523
REGULATION OF EXECUTION PHASE OF APOPTOSIS	20	0.26	0.76	0.8055	0.9526
AXIS ELONGATION	27	-0.24	-0.83	0.7203	0.9527
EPHRIN RECEPTOR BINDING	24	-0.25	-0.83	0.7147	0.9531
PEPTIDE HORMONE BINDING	35	-0.23	-0.83	0.7352	0.9534
REGULATION OF CALCIUM ION DEPENDENT EXOCYTOSIS	76	-0.20	-0.83	0.8233	0.9537
REGULATION OF LAMELLIPOD IUM ASSEMBLY	23	0.25	0.76	0.8112	0.9537
SALIVARY GLAND DEVELOPMENT	31	0.24	0.76	0.8137	0.9538

REGULATION OF RHO PROTEIN SIGNAL TRANSDUCTION	92	-0.19	-0.83	0.8125	0.9539
NEGATIVE REGULATION OF EPITHELIAL TO MESENCHYMAL TRANSITION	22	-0.26	-0.83	0.7120	0.9541
ENZYME ACTIVATOR ACTIVITY	413	0.16	0.76	0.9905	0.9541
CELLULAR RESPONSE TO MECHANICAL STIMULUS	73	0.20	0.76	0.8795	0.9541
REGULATION OF ACTIN FILAMENT DEPOLYMERIZATION	37	-0.23	-0.83	0.7519	0.9543
SMOOTH ENDOPLASMIC RETICULUM	32	-0.24	-0.83	0.7476	0.9546
CATECHOLAMINE METABOLIC PROCESS	34	0.23	0.75	0.8574	0.9548
REGULATION OF CELLULAR RESPONSE TO GROWTH FACTOR STIMULUS	206	0.17	0.75	0.9482	0.9550
ESTABLISHMENT OR MAINTENANCE OF APICAL BASAL CELL POLARITY	31	0.24	0.75	0.8342	0.9551
POSITIVE REGULATION OF REGULATED SECRETORY PATHWAY	44	0.22	0.75	0.8616	0.9551
CATECHOL CONTAINING COMPOUND METABOLIC PROCESS	34	0.23	0.75	0.8459	0.9551
RESPONSE TO GROWTH HORMONE	24	-0.25	-0.83	0.6923	0.9553
REGULATION OF OXIDOREDUCTASE ACTIVITY	81	0.19	0.75	0.8918	0.9554
CELL RECOGNITION	110	0.18	0.75	0.9201	0.9554
MUSCLE CONTRACTION	220	0.17	0.75	0.9613	0.9556
REGULATION OF COLLATERAL SPROUTING	16	0.28	0.75	0.8179	0.9558
NEGATIVE REGULATION OF CHROMATIN MODIFICATION	40	0.22	0.75	0.8539	0.9558
T CELL RECEPTOR COMPLEX	17	-0.28	-0.83	0.6930	0.9559
NOTCH SIGNALING PATHWAY	103	0.19	0.75	0.9299	0.9560
NEGATIVE REGULATION OF MUSCLE ORGAN DEVELOPMENT	31	0.24	0.75	0.8341	0.9560
ALDEHYDE DEHYDROGENASE NAD ACTIVITY	18	0.27	0.75	0.8225	0.9562
AMINO ACID BINDING	95	0.19	0.75	0.9196	0.9563
POSITIVE REGULATION OF MESENCHYMAL CELL PROLIFERATION	23	0.25	0.75	0.8166	0.9564
MODIFIED AMINO ACID BINDING	57	0.20	0.75	0.8662	0.9565
REGULATION OF BONE DEVELOPMENT	15	-0.28	-0.82	0.6843	0.9567
PHAGOCYTOSIS	142	0.18	0.75	0.9451	0.9567
POSITIVE REGULATION OF TISSUE REMODELING	24	0.24	0.75	0.8429	0.9569

POSITIVE REGULATION OF MAP KINASE ACTIVITY	188	-0.17	-0.82	0.9109	0.9571
ESTABLISHMENT OR MAINTENANCE OF BIPOLAR CELL POLARITY	31	0.24	0.75	0.8163	0.9572
CELL PROJECTION ASSEMBLY	215	0.17	0.75	0.9688	0.9573
CAMP MEDIATED SIGNALING	36	0.23	0.75	0.8451	0.9573
PROTEIN TYROSINE SERINE THREONINE PHOSPHATASE ACTIVITY	43	0.22	0.75	0.8505	0.9575
MYELOID DENDRITIC CELL DIFFERENTIATION	18	-0.28	-0.82	0.7072	0.9576
POSITIVE REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY VIA DEATH DOMAIN RECEPTORS	15	0.28	0.74	0.8139	0.9576
REGULATION OF LIPOPOLYSACCHARIDE MEDIATED SIGNALING PATHWAY	16	0.27	0.74	0.7784	0.9578
PLASMA MEMBRANE FUSION	22	-0.26	-0.82	0.7543	0.9579
CYCLIC NUCLEOTIDE BINDING	35	0.23	0.74	0.8542	0.9579
POST ANAL TAIL MORPHOGENESIS	17	-0.27	-0.82	0.7116	0.9579
DNA REPLICATION INITIATION	21	0.25	0.75	0.8295	0.9580
ARACHIDONIC ACID METABOLIC PROCESS	31	0.23	0.75	0.8586	0.9581
SECONDARY METABOLIC PROCESS	33	0.23	0.75	0.8515	0.9581
DNA DIRECTED DNA POLYMERASE ACTIVITY	25	-0.25	-0.82	0.7401	0.9584
REGULATION OF MONOOXYGENASE ACTIVITY	55	-0.21	-0.82	0.7698	0.9585
CELLULAR RESPONSE TO AMINO ACID STIMULUS	47	-0.21	-0.82	0.7943	0.9586
PEPTIDE HORMONE PROCESSING	29	-0.24	-0.82	0.7375	0.9587
POSITIVE REGULATION OF PROTEIN AUTOPHOSPHORYLATION	20	-0.26	-0.82	0.7188	0.9590
AMINOGLYCAN BIOSYNTHETIC PROCESS	97	0.18	0.74	0.9099	0.9591
BONE MINERALIZATION	35	-0.23	-0.82	0.7354	0.9591
BRANCHING INVOLVED IN MAMMARY GLAND DUCT MORPHOGENESIS	20	0.25	0.74	0.8151	0.9593
PATTERNING OF BLOOD VESSELS	30	-0.24	-0.82	0.7364	0.9593
BRANCHING MORPHOGENESIS OF AN EPITHELIAL TUBE	124	0.18	0.74	0.9402	0.9595
GLUTAMINE FAMILY AMINO ACID BIOSYNTHETIC PROCESS	17	-0.28	-0.82	0.7342	0.9595
ION CHANNEL BINDING	104	0.18	0.74	0.9325	0.9597

REGULATION OF INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	52	-0.21	-0.82	0.7920	0.9599
LENS DEVELOPMENT IN CAMERA TYPE EYE	61	0.20	0.74	0.8937	0.9605
REGULATION OF FILOPODIUM ASSEMBLY	33	-0.23	-0.82	0.7592	0.9605
ENDODERMAL CELL DIFFERENTIATION	38	0.22	0.74	0.8646	0.9606
IMMUNOGLOBULIN PRODUCTION INVOLVED IN IMMUNOGLOBULIN MEDIATED IMMUNE RESPONSE	15	0.28	0.74	0.8242	0.9607
REGULATION OF ERAD PATHWAY	24	0.25	0.74	0.8536	0.9607
POSITIVE REGULATION OF NIK NF KAPPAB SIGNALING	24	0.25	0.74	0.8484	0.9607
SPECIFICATION OF SYMMETRY	104	0.18	0.74	0.9343	0.9608
APOPTOTIC NUCLEAR CHANGES	22	0.25	0.74	0.8316	0.9609
NEURON APOPTOTIC PROCESS	27	0.24	0.74	0.8393	0.9611
REGULATION OF RELEASE OF SEQUESTERED CALCIUM ION INTO CYTOSOL	68	-0.20	-0.82	0.8192	0.9611
GLUTATHIONE PEROXIDASE ACTIVITY	16	0.27	0.74	0.8182	0.9611
ADULT LOCOMOTORY BEHAVIOR	72	-0.19	-0.81	0.8300	0.9612
PERIKARYON	98	0.18	0.74	0.9207	0.9613
REGULATION OF LYASE ACTIVITY	80	-0.19	-0.82	0.8722	0.9613
REGULATION OF NEURONAL SYNAPTIC PLASTICITY	44	0.21	0.74	0.8509	0.9614
RESPONSE TO COPPER ION	27	0.24	0.74	0.8281	0.9615
CLATHRIN BINDING	56	0.21	0.74	0.8833	0.9616
MESENCHYME MORPHOGENESIS	37	0.22	0.73	0.8744	0.9617
NERVE DEVELOPMENT	59	0.20	0.73	0.8936	0.9617
FORMATION OF PRIMARY GERM LAYER	102	0.18	0.73	0.9367	0.9618
ERROR PRONE TRANSLATION SYNTHESIS	15	-0.29	-0.81	0.7043	0.9618
GLUTATHIONE METABOLIC PROCESS	47	0.21	0.73	0.9029	0.9619
CHANNEL REGULATOR ACTIVITY	122	0.18	0.73	0.9508	0.9621
RESPONSE TO FOOD	17	-0.27	-0.81	0.7528	0.9621
REGULATION OF NEUROTRANSMITTER TRANSPORT	59	0.20	0.73	0.8901	0.9622
CARBOHYDRATE BINDING	212	0.17	0.74	0.9775	0.9622
POTASSIUM ION BINDING	15	0.27	0.73	0.8149	0.9624
REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY VIA DEATH DOMAIN RECEPTORS	50	0.21	0.73	0.9081	0.9627

TUMOR NECROSIS FACTOR RECEPTOR BINDING	27	0.23	0.73	0.8553	0.9629
REGULATION OF PHOSPHOLIPID METABOLIC PROCESS	55	0.20	0.73	0.8934	0.9630
POSITIVE REGULATION OF ALCOHOL BIOSYNTHETIC PROCESS	21	0.25	0.73	0.8287	0.9630
POSITIVE REGULATION OF ENDOTHELIAL CELL DIFFERENTIATION	15	-0.27	-0.81	0.7423	0.9630
DENDRITIC SHAFT	35	0.22	0.73	0.8593	0.9630
REGULATION OF MEMBRANE DEPOLARIZATION	39	0.22	0.73	0.8869	0.9630
MICROTUBULE END	21	0.25	0.73	0.8443	0.9631
NEGATIVE CHEMOTAXIS	39	0.22	0.73	0.8767	0.9631
CALMODULIN BINDING	162	-0.17	-0.81	0.9560	0.9631
MODULATION OF TRANSCRIPTION IN OTHER ORGANISM INVOLVED IN SYMBIOTIC INTERACTION	19	0.25	0.73	0.8108	0.9632
PHOSPHATIDYLINOSITOL KINASE ACTIVITY	47	0.21	0.73	0.8952	0.9633
PHENOL CONTAINING COMPOUND BIOSYNTHETIC PROCESS	31	-0.23	-0.81	0.7696	0.9634
INTERCELLULAR BRIDGE	35	-0.23	-0.81	0.7751	0.9639
ATPASE ACTIVITY COUPLED TO TRANSMEMBRANE MOVEMENT OF IONS PHOSPHORYLATIVE MECHANISM	33	0.22	0.73	0.8756	0.9641
POSITIVE REGULATION OF ORGANIC ACID TRANSPORT	28	-0.24	-0.81	0.7469	0.9653
POSITIVE REGULATION OF AXON EXTENSION	33	0.22	0.73	0.8787	0.9657
RESPONSE TO TESTOSTERONE	36	0.22	0.73	0.8663	0.9660
GENITALIA DEVELOPMENT	40	0.21	0.73	0.8989	0.9661
HORMONE TRANSPORT	73	0.19	0.72	0.9204	0.9669
STEM CELL DIFFERENTIATION	179	0.17	0.72	0.9808	0.9671
PURINE NUCLEOBASE METABOLIC PROCESS	18	-0.27	-0.81	0.7424	0.9672
CILIARY TIP	40	0.21	0.72	0.8847	0.9672
SIN3 TYPE COMPLEX	15	0.27	0.72	0.8198	0.9672
SKELETAL MUSCLE TISSUE REGENERATION	24	0.24	0.72	0.8503	0.9673
NEUROPEPTIDE RECEPTOR BINDING	25	0.24	0.72	0.8771	0.9674
POSITIVE REGULATION OF EPITHELIAL CELL APOPTOTIC PROCESS	21	0.24	0.72	0.8441	0.9674

POSITIVE REGULATION OF RECEPTOR MEDIATED ENDOCYTOSIS	41	0.21	0.72	0.8738	0.9674
REGULATED EXOCYTOSIS	202	0.16	0.72	0.9830	0.9675
MUSCLE CELL PROLIFERATION	18	0.26	0.72	0.8336	0.9675
SPINAL CORD PATTERNING	22	-0.25	-0.80	0.7472	0.9676
BODY MORPHOGENESIS	40	0.21	0.72	0.8869	0.9677
MYELOID CELL HOMEOSTASIS	72	0.19	0.72	0.9313	0.9677
BONE CELL DEVELOPMENT	20	0.25	0.72	0.8452	0.9678
NEGATIVE REGULATION OF ANOIKIS	15	-0.29	-0.81	0.7329	0.9678
EYE PHOTORECEPTOR CELL DIFFERENTIATION	38	0.21	0.72	0.8951	0.9680
RESPONSE TO ELECTRICAL STIMULUS	41	0.21	0.72	0.8925	0.9680
CELLULAR RESPONSE TO GROWTH HORMONE STIMULUS	16	-0.27	-0.80	0.7289	0.9682
PEPTIDYL TYROSINE MODIFICATION	170	0.17	0.72	0.9755	0.9682
REGULATION OF PROTEIN TYROSINE KINASE ACTIVITY	57	-0.20	-0.81	0.8329	0.9683
MISMATCH REPAIR	24	0.24	0.72	0.8526	0.9683
INTRACELLULAR ESTROGEN RECEPTOR SIGNALING PATHWAY	15	0.26	0.72	0.8351	0.9683
HOMEOSTASIS OF NUMBER OF CELLS WITHIN A TISSUE	26	0.24	0.72	0.8564	0.9684
FC GAMMA RECEPTOR SIGNALING PATHWAY	67	-0.19	-0.80	0.8665	0.9685
RESPONSE TO MERCURY ION	15	0.26	0.72	0.8300	0.9685
NAD DEPENDENT PROTEIN DEACETYLASE ACTIVITY	16	0.27	0.72	0.8502	0.9686
TRACHEA DEVELOPMENT	18	0.25	0.71	0.8420	0.9690
ASYMMETRIC PROTEIN LOCALIZATION	18	-0.26	-0.80	0.7529	0.9691
REGULATION OF SODIUM ION TRANSMEMBRANE TRANSPORT	41	0.21	0.71	0.9044	0.9694
REGULATION OF PHOSPHATIDYLINOSITOL 3 KINASE SIGNALING	129	-0.17	-0.80	0.9075	0.9695
NEGATIVE REGULATION OF ORGAN GROWTH	17	-0.27	-0.81	0.7240	0.9696
POSITIVE REGULATION OF PROTEIN DEPOLYMERIZATION	18	-0.27	-0.81	0.7153	0.9697
POSITIVE REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	35	0.21	0.71	0.8951	0.9699
ACYLGLYCEROL HOMEOSTASIS	26	0.23	0.71	0.8556	0.9699

1 PHOSPHATIDYLINOSITOL 3 KINASE ACTIVITY	41	0.20	0.71	0.9100	0.9700
NEGATIVE REGULATION OF DEPHOSPHORYLATION	64	0.19	0.71	0.9146	0.9701
LIPOPOLYSACCHARIDE MEDIATED SIGNALING PATHWAY	30	0.22	0.71	0.8843	0.9701
FERTILIZATION	123	0.17	0.71	0.9635	0.9701
PLACENTA BLOOD VESSEL DEVELOPMENT	27	0.23	0.71	0.8577	0.9702
PALLIUM DEVELOPMENT	145	0.17	0.71	0.9847	0.9703
TRIGLYCERIDE HOMEOSTASIS	26	0.23	0.71	0.8711	0.9703
REGULATION OF MESENCHYMAL CELL PROLIFERATION	29	0.22	0.71	0.8915	0.9703
REGULATION OF CALCIUM ION TRANSPORT INTO CYTOSOL	84	0.18	0.71	0.9481	0.9704
LABYRINTHINE LAYER DEVELOPMENT	44	0.20	0.71	0.9038	0.9704
NEGATIVE REGULATION OF TRANSMEMBRANE TRANSPORT	80	0.18	0.71	0.9527	0.9704
CARBOHYDRATE PHOSPHORYLATION	20	0.25	0.71	0.8611	0.9705
RNA POLYMERASE II TRANSCRIPTION COREPRESSOR ACTIVITY	22	0.24	0.71	0.8659	0.9705
NEGATIVE REGULATION OF LIPID BIOSYNTHETIC PROCESS	38	-0.22	-0.80	0.8127	0.9711
GMP METABOLIC PROCESS	17	0.25	0.71	0.8776	0.9712
SECRETORY VESICLE	416	-0.15	-0.80	1.0000	0.9717
ESTROUS CYCLE	18	0.25	0.70	0.8657	0.9719
REGULATION OF EXTRINSIC APOPTOTIC SIGNALING PATHWAY IN ABSENCE OF LIGAND	42	-0.22	-0.80	0.8005	0.9720
REGULATION OF INTERLEUKIN 1 SECRETION	23	-0.25	-0.80	0.7794	0.9721
DIGESTION	112	-0.18	-0.80	0.9179	0.9722
NEURON RECOGNITION	32	-0.23	-0.80	0.7722	0.9725
POSITIVE REGULATION OF PROTEIN ACETYLATION	33	-0.23	-0.80	0.7934	0.9726
FEAR RESPONSE	26	-0.24	-0.80	0.7940	0.9727
CARBOHYDRATE KINASE ACTIVITY	18	-0.27	-0.80	0.7664	0.9729
ADRENAL GLAND DEVELOPMENT	21	-0.25	-0.80	0.7700	0.9729
ESTABLISHMENT OR MAINTENANCE OF CELL POLARITY	125	0.17	0.70	0.9813	0.9729
CELLULAR MODIFIED AMINO ACID CATABOLIC PROCESS	15	0.26	0.70	0.8463	0.9731

POSITIVE REGULATION OF CYCLASE ACTIVITY	56	0.19	0.70	0.9258	0.9731
STEROID CATABOLIC PROCESS	20	-0.26	-0.80	0.7683	0.9732
ACTIN CYTOSKELETON	390	0.15	0.70	0.9988	0.9732
SCHWANN CELL DIFFERENTIATION	29	0.22	0.70	0.9058	0.9734
RHO GTPASE BINDING	69	-0.19	-0.80	0.8452	0.9734
REGULATION OF PHOSPHATIDYLINOSITOL 3 KINASE ACTIVITY	35	0.21	0.70	0.9025	0.9735
GLYCOPROTEIN COMPLEX	19	0.25	0.70	0.8777	0.9735
NEGATIVE REGULATION OF MULTI ORGANISM PROCESS	124	0.17	0.70	0.9764	0.9735
NEURON NEURON SYNAPTIC TRANSMISSION	52	0.19	0.70	0.9320	0.9736
POSITIVE REGULATION OF NUCLEAR DIVISION	55	0.19	0.70	0.9315	0.9736
CILIARY BASE	20	0.24	0.70	0.8731	0.9737
REGULATION OF ARF PROTEIN SIGNAL TRANSDUCTION	15	0.26	0.70	0.8591	0.9737
ACTIN BINDING	342	-0.15	-0.79	0.9944	0.9737
NEGATIVE REGULATION OF VIRAL ENTRY INTO HOST CELL	16	0.25	0.69	0.8569	0.9737
DEFENSE RESPONSE TO FUNGUS	24	0.23	0.70	0.8950	0.9739
PEPTIDASE REGULATOR ACTIVITY	167	0.16	0.70	0.9890	0.9739
APOPTOTIC CELL CLEARANCE	23	0.23	0.70	0.8605	0.9740
ALPHA ACTinin BINDING	19	0.24	0.69	0.8752	0.9741
CELL FATE COMMITMENT INVOLVED IN FORMATION OF PRIMARY GERM LAYER	28	0.22	0.70	0.8854	0.9742
ESTABLISHMENT OF TISSUE POLARITY	15	0.26	0.69	0.8574	0.9748
PROSTATE GLAND DEVELOPMENT	39	-0.21	-0.79	0.8191	0.9748
SECRETION BY CELL	440	0.15	0.69	1.0000	0.9749
STRIATED MUSCLE CELL DIFFERENTIATION	162	0.16	0.69	0.9931	0.9749
REGULATION OF T CELL DIFFERENTIATION IN THYMUS	23	0.22	0.69	0.8841	0.9750
OUTFLOW TRACT MORPHOGENESIS	55	0.19	0.69	0.9303	0.9750
VACUOLAR LUMEN	95	-0.18	-0.79	0.9421	0.9750
MODULATION OF EXCITATORY POSTSYNAPTIC POTENTIAL	29	0.22	0.69	0.8767	0.9750
CYTOKINE SECRETION	30	0.22	0.69	0.9037	0.9751
REGULATION OF PROTEIN MATURATION	68	-0.19	-0.79	0.8716	0.9751
ESTABLISHMENT OF CELL POLARITY	79	0.18	0.69	0.9630	0.9751

POLYOL BIOSYNTHETIC PROCESS	23	0.23	0.69	0.8932	0.9751
NEGATIVE REGULATION OF CELL JUNCTION ASSEMBLY	18	0.24	0.69	0.8713	0.9751
MUSCLE CELL DEVELOPMENT	117	0.17	0.69	0.9822	0.9752
CHANNEL INHIBITOR ACTIVITY	33	0.21	0.69	0.9179	0.9752
SOLUTE CATION ANTIPORTER ACTIVITY	28	0.22	0.69	0.9089	0.9753
SECRETORY GRANULE LUMEN	73	0.18	0.69	0.9475	0.9754
AUTONOMIC NERVOUS SYSTEM DEVELOPMENT	37	-0.22	-0.79	0.8187	0.9754
REGULATION OF HEART RATE BY CARDIAC CONDUCTION	29	-0.23	-0.79	0.7819	0.9754
SEX CHROMOSOME	27	0.22	0.69	0.9067	0.9756
SUBSTANTIA NIGRA DEVELOPMENT	38	0.20	0.68	0.9408	0.9756
MUCOPOLYSACCHARIDE METABOLIC PROCESS	95	-0.18	-0.79	0.9323	0.9757
REGULATION OF INTERLEUKIN 2 PRODUCTION	44	0.20	0.69	0.9241	0.9757
FATTY ACID DERIVATIVE METABOLIC PROCESS	64	-0.19	-0.79	0.8712	0.9757
ACTIN FILAMENT BUNDLE ORGANIZATION	45	0.19	0.68	0.9285	0.9757
SKIN EPIDERMIS DEVELOPMENT	65	-0.19	-0.79	0.8787	0.9757
REGULATION OF CALCIUM ION TRANSPORT	191	-0.16	-0.79	0.9502	0.9757
NEURAL PRECURSOR CELL PROLIFERATION	66	-0.19	-0.79	0.8678	0.9757
CARDIAC CONDUCTION	77	-0.19	-0.79	0.8954	0.9758
GLIAL CELL DIFFERENTIATION	128	0.17	0.68	0.9849	0.9759
ASPARTIC TYPE PEPTIDASE ACTIVITY	17	-0.26	-0.79	0.7754	0.9760
FILOPODIA	89	-0.18	-0.79	0.9103	0.9760
POSITIVE REGULATION OF LYASE ACTIVITY	56	0.19	0.68	0.9495	0.9761
REGULATION OF STEM CELL POPULATION MAINTENANCE	15	-0.28	-0.79	0.7466	0.9761
PLATELET ACTIVATION	132	-0.17	-0.79	0.9585	0.9762
HYDROLASE ACTIVITY HYDROLYZING N GLYCOSYL COMPOUNDS	18	-0.26	-0.79	0.7815	0.9764
ICOSANOID METABOLIC PROCESS	64	-0.19	-0.78	0.8778	0.9764
NAD ADP RIBOSYLTRANSFERASE ACTIVITY	19	-0.26	-0.79	0.7635	0.9766
REGULATION OF CHROMATIN SILENCING	20	-0.25	-0.78	0.7780	0.9767
INTRACELLULAR LIGAND GATED ION CHANNEL ACTIVITY	28	-0.23	-0.78	0.8325	0.9768

INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	483	-0.14	-0.78	1.0000	0.9769
PROSTATE GLAND MORPHOGENESIS	22	-0.24	-0.78	0.7838	0.9769
POSITIVE REGULATION OF TELOMERE CAPPING	15	0.25	0.68	0.8571	0.9770
MECHANORECEPTOR DIFFERENTIATION	46	0.20	0.68	0.9387	0.9770
NEGATIVE REGULATION OF EXOCYTOSIS	24	0.22	0.68	0.8962	0.9771
ACTIN FILAMENT BASED MOVEMENT	87	-0.18	-0.78	0.8895	0.9771
MYOBLAST FUSION	19	-0.25	-0.78	0.7899	0.9772
REGULATION OF RECEPTOR RECYCLING	18	-0.26	-0.78	0.7973	0.9772
PLACENTA DEVELOPMENT	129	0.16	0.68	0.9903	0.9773
MACROPHAGE ACTIVATION	29	0.22	0.68	0.9215	0.9773
INSULIN SECRETION	37	0.20	0.68	0.9206	0.9774
TELOMERE MAINTENANCE VIA RECOMBINATION	30	-0.22	-0.78	0.8147	0.9775
REGULATION OF PROTEIN TARGETING TO MEMBRANE	23	-0.24	-0.78	0.7980	0.9776
POSITIVE REGULATION OF MONOOXYGENASE ACTIVITY	25	0.23	0.68	0.8770	0.9780
SYNCYTIA FORMATION	23	0.22	0.67	0.8986	0.9780
OLIGODENDROCYTE DIFFERENTIATION	56	0.19	0.67	0.9624	0.9781
ROUGH ENDOPLASMIC RETICULUM	66	0.18	0.67	0.9617	0.9781
GAP JUNCTION	26	0.22	0.68	0.9171	0.9781
CENTRIOLE ASSEMBLY	16	0.24	0.66	0.8907	0.9783
REGULATION OF THYMOCYTE AGGREGATION	23	0.22	0.67	0.9085	0.9783
GTP RHO BINDING	15	0.25	0.67	0.8741	0.9783
MRNA TRANSCRIPTION	20	0.23	0.67	0.9034	0.9784
REGULATION OF POSTTRANSCRIPTIONAL GENE SILENCING	20	0.22	0.66	0.9099	0.9784
CORTICAL CYTOSKELETON ORGANIZATION	30	0.21	0.67	0.9103	0.9784
MYELOID LEUKOCYTE MEDIATED IMMUNITY	37	0.20	0.67	0.9252	0.9785
PEPTIDASE ACTIVATOR ACTIVITY INVOLVED IN APOPTOTIC PROCESS	17	0.24	0.67	0.8791	0.9785
RESPONSE TO FUNGUS	36	0.20	0.66	0.9210	0.9786
CELLULAR RESPONSE TO CORTICOSTEROID STIMULUS	52	0.19	0.67	0.9540	0.9787
CELLULAR RESPONSE TO RETINOIC ACID	61	0.18	0.67	0.9501	0.9788
DEVELOPMENTAL INDUCTION	27	0.21	0.67	0.9086	0.9790
CELLULAR RESPONSE TO VITAMIN	25	0.22	0.67	0.9134	0.9790

NUCLEAR OUTER MEMBRANE	21	0.23	0.67	0.9031	0.9791
MORPHOGENESIS OF AN EPITHELIAL SHEET	41	0.20	0.67	0.9421	0.9794
B CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	31	0.21	0.67	0.9351	0.9794
NEGATIVE REGULATION OF CATION CHANNEL ACTIVITY	32	0.20	0.67	0.9289	0.9796
REGULATION OF TOLL LIKE RECEPTOR SIGNALING PATHWAY	43	-0.21	-0.78	0.8401	0.9797
REGULATION OF NUCLEAR TRANSCRIBED mRNA CATABOLIC PROCESS DEADENYLATION DEPENDENT DECAY	15	0.24	0.67	0.9000	0.9798
DNA CATABOLIC PROCESS ENDONUCLEOLYTIC	17	0.24	0.66	0.8991	0.9803
ESTABLISHMENT OF SPINDLE ORIENTATION	24	0.22	0.66	0.9212	0.9805
HEAD MORPHOGENESIS	33	0.21	0.66	0.9173	0.9807
ACROSOMAL MEMBRANE	21	0.22	0.66	0.9063	0.9807
REGULATION OF NEUROTRANSMITTER LEVELS	171	0.15	0.66	0.9972	0.9807
MITOTIC RECOMBINATION	36	0.20	0.66	0.9301	0.9808
CELLULAR RESPONSE TO DSRNA	35	0.20	0.66	0.9370	0.9809
PHOSPHATIDYLINOSITOL 3 KINASE BINDING	27	0.21	0.66	0.9321	0.9809
MESODERMAL CELL DIFFERENTIATION	25	0.21	0.65	0.9155	0.9816
CELLULAR RESPONSE TO OSMOTIC STRESS	18	0.23	0.65	0.9078	0.9816
POSITIVE REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	15	0.24	0.65	0.8929	0.9818
EXOCRINE SYSTEM DEVELOPMENT	42	0.19	0.65	0.9551	0.9820
NEURON PROJECTION MEMBRANE	33	-0.22	-0.77	0.8199	0.9830
CELLULAR RESPONSE TO ACETYLCHOLINE	18	-0.26	-0.77	0.7588	0.9838
NEGATIVE REGULATION OF VIRAL PROCESS	69	-0.18	-0.77	0.9153	0.9840
REGULATION OF INTRACELLULAR ESTROGEN RECEPTOR SIGNALING PATHWAY	23	0.22	0.65	0.9247	0.9841
POSITIVE REGULATION OF NUCLEAR TRANSCRIBED mRNA CATABOLIC PROCESS DEADENYLATION DEPENDENT DECAY	15	0.24	0.64	0.9056	0.9844

INNER EAR RECEPTOR CELL DEVELOPMENT	32	-0.22	-0.77	0.8469	0.9845
CYTOPLASMIC SIDE OF MEMBRANE	145	-0.16	-0.77	0.9804	0.9845
CRANIAL SKELETAL SYSTEM DEVELOPMENT	53	0.18	0.64	0.9581	0.9846
ADULT WALKING BEHAVIOR	28	-0.22	-0.77	0.8262	0.9846
RESPONSE TO ACETYLCHOLINE	18	-0.26	-0.77	0.7945	0.9847
MUSCLE MYOSIN COMPLEX	17	-0.26	-0.77	0.7986	0.9847
NUCLEOTIDE KINASE ACTIVITY	21	0.22	0.64	0.9519	0.9847
EXOCYST	15	-0.27	-0.76	0.8160	0.9847
NEGATIVE REGULATION OF INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	28	0.21	0.64	0.9426	0.9848
SIGNAL TRANSDUCTION INVOLVED IN CELLULAR RESPONSE TO AMMONIUM ION	18	-0.26	-0.76	0.8333	0.9848
EMBRYONIC SKELETAL SYSTEM DEVELOPMENT	112	-0.17	-0.77	0.9486	0.9849
ACID SECRETION	65	-0.19	-0.76	0.9218	0.9849
GLIAL CELL MIGRATION	33	-0.22	-0.76	0.8555	0.9850
POSITIVE REGULATION OF OSTEOBLAST DIFFERENTIATION	54	-0.19	-0.77	0.8740	0.9850
LYMPH NODE DEVELOPMENT	17	-0.26	-0.77	0.7973	0.9850
REGULATION OF CELL SHAPE	119	-0.17	-0.77	0.9431	0.9851
REGULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	25	-0.23	-0.76	0.8305	0.9852
MATURE B CELL DIFFERENTIATION	16	-0.27	-0.77	0.7653	0.9852
G PROTEIN COUPLED ACETYLCHOLINE RECEPTOR SIGNALING PATHWAY	18	-0.26	-0.76	0.8133	0.9853
CELL SUBSTRATE ADHESION	150	-0.16	-0.76	0.9665	0.9855
POSTSYNAPTIC SIGNAL TRANSDUCTION	18	-0.26	-0.77	0.7459	0.9857
WATER TRANSPORT	18	0.22	0.64	0.8973	0.9857
COSTAMERE	17	-0.26	-0.77	0.7920	0.9863
FILAMENTOUS ACTIN	20	0.22	0.64	0.9333	0.9865
ACETYLCHOLINE RECEPTOR SIGNALING PATHWAY	18	-0.26	-0.76	0.8182	0.9866
DEFENSE RESPONSE TO GRAM NEGATIVE BACTERIUM	31	-0.22	-0.77	0.8272	0.9866
WALKING BEHAVIOR	28	-0.22	-0.76	0.8377	0.9868
BASE EXCISION REPAIR	31	0.19	0.63	0.9583	0.9873
RESPONSE TO SALT	16	0.23	0.63	0.9235	0.9874

REGULATION OF GENE SILENCING BY RNA	20	0.22	0.63	0.9226	0.9876
CATECHOLAMINE BIOSYNTHETIC PROCESS	18	-0.25	-0.76	0.7916	0.9876
VESICLE DOCKING INVOLVED IN EXOCYTOSIS	33	0.19	0.63	0.9595	0.9876
LATERAL PLASMA MEMBRANE	45	0.18	0.63	0.9772	0.9877
CRANIAL NERVE DEVELOPMENT	38	0.19	0.63	0.9607	0.9877
BIOMINERAL TISSUE DEVELOPMENT	68	0.17	0.63	0.9741	0.9877
STRUCTURAL CONSTITUENT OF EYE LENS	19	0.22	0.63	0.9201	0.9877
NEGATIVE REGULATION OF EMBRYONIC DEVELOPMENT	25	0.21	0.63	0.9371	0.9879
IMMUNOLOGICAL SYNAPSE	31	0.20	0.63	0.9548	0.9879
EPHRIN RECEPTOR ACTIVITY	18	-0.25	-0.76	0.8242	0.9883
CALCIUM DEPENDENT CELL CELL ADHESION VIA PLASMA MEMBRANE CELL ADHESION MOLECULES	24	0.21	0.62	0.9508	0.9883
MORPHOGENESIS OF A BRANCHING STRUCTURE	158	0.15	0.62	1.0000	0.9883
REGULATION OF MEIOTIC NUCLEAR DIVISION	29	0.20	0.62	0.9479	0.9886
SULFUR COMPOUND TRANSPORT	27	0.20	0.62	0.9399	0.9886
MOLTING CYCLE	73	0.16	0.62	0.9791	0.9887
METANEPHRIC EPITHELIUM DEVELOPMENT	20	0.22	0.62	0.9277	0.9887
ARGININE METABOLIC PROCESS	15	0.24	0.62	0.9228	0.9888
NEGATIVE REGULATION OF PROTEIN LOCALIZATION TO CELL PERIPHERY	17	0.22	0.62	0.9203	0.9891
NEGATIVE REGULATION OF CALCIUM ION TRANSPORT	43	0.18	0.62	0.9759	0.9894
CALCIUM ACTIVATED CATION CHANNEL ACTIVITY	27	-0.23	-0.76	0.8474	0.9894
CGMP BIOSYNTHETIC PROCESS	15	-0.26	-0.75	0.8067	0.9894
HAIR CYCLE	73	0.16	0.62	0.9910	0.9894
MESODERM DEVELOPMENT	100	-0.17	-0.75	0.9439	0.9896
EPIBOLY	22	-0.24	-0.75	0.7986	0.9899
VASOCONSTRICITION	27	-0.23	-0.75	0.8409	0.9904
CARDIAC SEPTUM MORPHOGENESIS	49	-0.20	-0.75	0.8911	0.9906
ACTOMYOSIN STRUCTURE ORGANIZATION	71	0.16	0.61	0.9893	0.9908
STRUCTURAL CONSTITUENT OF MUSCLE	38	0.18	0.61	0.9662	0.9909
REGULATION OF CALCIUM ION TRANSMEMBRANE TRANSPORT	108	0.15	0.60	0.9958	0.9909

SARCOPLASM	62	0.16	0.60	0.9909	0.9910
HISTONE KINASE ACTIVITY	18	0.21	0.60	0.9371	0.9910
PROTEIN TRIMERIZATION	34	-0.21	-0.75	0.8551	0.9910
PHOSPHATIDYLINOSITOL 3 4 5 TRISPHOSPHATE BINDING	31	0.19	0.61	0.9537	0.9911
RESPONSE TO RETINOIC ACID	95	0.15	0.61	0.9928	0.9912
MESODERM MORPHOGENESIS	60	0.16	0.60	0.9955	0.9912
REGULATION OF SYNAPTIC PLASTICITY	134	0.15	0.61	0.9986	0.9912
NEGATIVE REGULATION OF PROTEIN LOCALIZATION TO PLASMA MEMBRANE	17	0.22	0.60	0.9503	0.9913
HYALURONIC ACID BINDING	19	0.21	0.60	0.9304	0.9913
REGULATION OF B CELL DIFFERENTIATION	20	0.20	0.60	0.9661	0.9916
ACTIVATION OF GTPASE ACTIVITY	70	0.16	0.59	0.9953	0.9916
CYTOKINE METABOLIC PROCESS	17	-0.25	-0.74	0.8103	0.9918
LUNG MORPHOGENESIS	43	-0.20	-0.73	0.9003	0.9918
PROTEIN PHOSPHATASE 1 BINDING	16	0.22	0.60	0.9696	0.9918
PSEUDOPODIUM	16	0.21	0.60	0.9556	0.9919
REGULATION OF GENE SILENCING	42	0.17	0.59	0.9811	0.9920
RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC DNA BINDING	60	0.16	0.59	0.9938	0.9921
NEGATIVE REGULATION OF REGULATED SECRETORY PATHWAY	18	-0.24	-0.74	0.8349	0.9922
POSITIVE REGULATION OF LYMPHOCYTE APOPTOTIC PROCESS	16	-0.26	-0.73	0.8420	0.9923
REGULATION OF CHEMOKINE PRODUCTION	58	-0.18	-0.74	0.9182	0.9923
ESTABLISHMENT OF MITOTIC SPINDLE ORIENTATION	19	0.21	0.59	0.9564	0.9924
MATING	31	-0.21	-0.74	0.8575	0.9925
CHONDROITIN SULFATE PROTEOGLYCAN METABOLIC PROCESS	39	-0.20	-0.73	0.8985	0.9926
SYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	17	0.21	0.59	0.9549	0.9926
MATERNAL PLACENTA DEVELOPMENT	28	-0.22	-0.73	0.8320	0.9927
HEXOSE CATABOLIC PROCESS	43	0.17	0.58	0.9754	0.9927
CATECHOL CONTAINING COMPOUND BIOSYNTHETIC PROCESS	18	-0.25	-0.74	0.8163	0.9928
MIDDLE EAR MORPHOGENESIS	20	-0.24	-0.73	0.8469	0.9928
REGULATION OF LIPID KINASE ACTIVITY	42	0.17	0.59	0.9837	0.9929
REGULATION OF CHOLESTEROL EFFLUX	17	-0.25	-0.75	0.8140	0.9929

POSITIVE REGULATION OF EPIDERMAL CELL DIFFERENTIATION	17	-0.25	-0.75	0.8299	0.9929
NEURAL RETINA DEVELOPMENT	47	-0.20	-0.74	0.9030	0.9929
SYNAPSIS	28	-0.21	-0.73	0.8689	0.9930
NEGATIVE REGULATION OF ACTIN FILAMENT DEPOLYMERIZATION	25	-0.23	-0.74	0.8627	0.9932
POSITIVE REGULATION OF CHEMOKINE PRODUCTION	42	-0.20	-0.74	0.8966	0.9932
GLUCOSE 6 PHOSPHATE METABOLIC PROCESS	19	-0.24	-0.74	0.8342	0.9933
DETECTION OF STIMULUS	194	-0.15	-0.73	0.9796	0.9934
CELL MATRIX ADHESION	111	-0.17	-0.75	0.9439	0.9934
POSITIVE REGULATION OF PHOSPHOLIPID METABOLIC PROCESS	37	-0.20	-0.74	0.8972	0.9935
REGULATION OF INTERLEUKIN 13 PRODUCTION	15	-0.26	-0.74	0.8122	0.9935
FEMALE GENITALIA DEVELOPMENT	15	-0.26	-0.74	0.8248	0.9935
SPERMATID NUCLEUS DIFFERENTIATION	15	-0.27	-0.75	0.7831	0.9936
HEPARAN SULFATE PROTEOGLYCAN BINDING	16	-0.26	-0.74	0.8288	0.9937
MUSCLE CELL DIFFERENTIATION	219	-0.15	-0.74	0.9919	0.9938
REGULATION OF ERYTHROCYTE DIFFERENTIATION	32	-0.21	-0.74	0.8915	0.9942
POSITIVE REGULATION OF OSSIFICATION	77	-0.18	-0.75	0.9466	0.9942
HISTONE PHOSPHORYLATION	24	-0.23	-0.73	0.8679	0.9944
SPERM FLAGELLUM	48	-0.19	-0.75	0.9195	0.9944
REGULATION OF INTERFERON BETA PRODUCTION	42	-0.19	-0.72	0.9229	0.9946
NEURON PROJECTION REGENERATION	29	0.18	0.57	0.9778	0.9947
DENDRITE CYTOPLASM	15	-0.25	-0.71	0.8401	0.9947
FOCAL ADHESION ASSEMBLY	21	0.20	0.57	0.9602	0.9947
REGULATION OF ADHERENS JUNCTION ORGANIZATION	45	-0.19	-0.71	0.9321	0.9947
A BAND	32	-0.20	-0.71	0.9131	0.9948
SPECTRIN BINDING	18	-0.24	-0.73	0.8689	0.9949
RHYTHMIC BEHAVIOR	16	0.20	0.56	0.9626	0.9949
NEUROBLAST PROLIFERATION	29	0.18	0.57	0.9748	0.9949
EMBRYONIC EYE MORPHOGENESIS	31	0.17	0.56	0.9802	0.9950
NEGATIVE REGULATION OF GENE SILENCING	19	0.20	0.57	0.9653	0.9950

POSITIVE REGULATION OF INTERLEUKIN 8 PRODUCTION	38	-0.19	-0.72	0.9280	0.9950
EXOCYTIC VESICLE MEMBRANE	53	-0.18	-0.72	0.9319	0.9951
NEGATIVE REGULATION OF BIOMINERAL TISSUE DEVELOPMENT	18	0.19	0.56	0.9579	0.9951
SOMATIC STEM CELL DIVISION	22	-0.23	-0.72	0.8935	0.9951
CELL SUBSTRATE ADHERENS JUNCTION ASSEMBLY	21	0.20	0.57	0.9688	0.9952
RESPONSE TO ESTRADIOL	135	-0.15	-0.72	0.9853	0.9952
MUSCLE FIBER DEVELOPMENT	40	0.17	0.57	0.9819	0.9952
NEGATIVE REGULATION OF MYELOID LEUKOCYTE DIFFERENTIATION	41	0.17	0.56	0.9836	0.9952
DNA POLYMERASE ACTIVITY	32	-0.21	-0.71	0.9142	0.9953
HOMOLOGOUS CHROMOSOME SEGREGATION	36	-0.20	-0.71	0.9323	0.9953
NEGATIVE REGULATION OF TYPE I INTERFERON PRODUCTION	34	-0.20	-0.71	0.9182	0.9954
GLIOGENESIS	163	-0.15	-0.71	0.9926	0.9954
POSITIVE REGULATION OF SYNAPTIC TRANSMISSION GLUTAMATERGIC	16	-0.25	-0.73	0.8529	0.9955
AMINOGLYCAN CATABOLIC PROCESS	60	-0.17	-0.72	0.9547	0.9955
PEPTIDYL GLUTAMIC ACID MODIFICATION	25	-0.22	-0.72	0.8412	0.9955
ACUTE PHASE RESPONSE	34	-0.21	-0.72	0.9028	0.9955
NEUROTRANSMITTER TRANSPORT	143	-0.15	-0.72	0.9829	0.9956
POSITIVE REGULATION OF CYTOKINESIS	30	-0.21	-0.72	0.9091	0.9956
REGULATION OF MITOCHONDRIAL DEPOLARIZATION	16	-0.23	-0.67	0.9062	0.9957
STEM CELL PROLIFERATION	58	-0.18	-0.72	0.9133	0.9957
REGULATION OF NEUROTRANSMITTER SECRETION	48	-0.18	-0.71	0.9413	0.9957
GLUTAMATE RECEPTOR SIGNALING PATHWAY	38	-0.19	-0.71	0.9319	0.9957
LYMPH VESSEL DEVELOPMENT	19	-0.22	-0.68	0.8998	0.9958
REGULATION OF SMOOTH MUSCLE CELL DIFFERENTIATION	18	-0.24	-0.71	0.8616	0.9958
NEGATIVE REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	25	-0.19	-0.61	0.9661	0.9959
REGULATION OF TOLL LIKE RECEPTOR 4 SIGNALING PATHWAY	15	-0.25	-0.71	0.8408	0.9959
NUCLEOTIDE EXCISION REPAIR DNA GAP FILLING	20	-0.23	-0.71	0.8732	0.9959
GOLGI LUMEN	78	-0.17	-0.73	0.9482	0.9960

CELLULAR RESPONSE TO GLUCAGON STIMULUS	33	-0.16	-0.55	0.9946	0.9960
POSITIVE REGULATION OF NEUROLOGICAL SYSTEM PROCESS	21	0.19	0.55	0.9863	0.9961
EMBRYONIC CAMERA TYPE EYE DEVELOPMENT	34	-0.19	-0.67	0.9293	0.9961
ENHANCER BINDING	86	-0.16	-0.72	0.9719	0.9962
ENDODERM FORMATION	48	-0.19	-0.72	0.9195	0.9962
POSITIVE REGULATION OF FILOPODIUM ASSEMBLY	22	-0.19	-0.61	0.9672	0.9962
NEGATIVE REGULATION OF REPRODUCTIVE PROCESS	51	-0.17	-0.67	0.9699	0.9962
TRANSLATION SYNTHESIS	30	-0.21	-0.72	0.9074	0.9962
PARAXIAL MESODERM DEVELOPMENT	15	-0.24	-0.68	0.8858	0.9963
SECONDARY METABOLITE BIOSYNTHETIC PROCESS	18	-0.24	-0.70	0.8698	0.9964
ERK1 AND ERK2 CASCADE	22	-0.18	-0.58	0.9730	0.9965
CELLULAR RESPONSE TO FLUID SHEAR STRESS	17	-0.21	-0.62	0.9236	0.9965
ACTIVIN RECEPTOR SIGNALING PATHWAY	22	-0.23	-0.73	0.8544	0.9965
GLYCOPROTEIN BINDING	91	-0.16	-0.67	0.9910	0.9966
RESPONSE TO PAIN	25	-0.17	-0.55	0.9924	0.9966
CRANIAL NERVE MORPHOGENESIS	20	-0.22	-0.68	0.8680	0.9966
NEGATIVE REGULATION OF MEIOTIC CELL CYCLE	18	-0.20	-0.59	0.9513	0.9967
REGULATION OF EMBRYONIC DEVELOPMENT	109	-0.16	-0.70	0.9794	0.9967
MICROFILAMENT MOTOR ACTIVITY	20	-0.17	-0.53	0.9739	0.9967
NEGATIVE REGULATION OF STRESS FIBER ASSEMBLY	15	-0.25	-0.70	0.8633	0.9967
POSITIVE REGULATION OF PROTEIN COMPLEX DISASSEMBLY	23	-0.19	-0.61	0.9551	0.9968
POSITIVE REGULATION OF CALCIUM MEDIATED SIGNALING	36	-0.17	-0.62	0.9718	0.9968
RECIPROCAL DNA RECOMBINATION	33	-0.18	-0.62	0.9658	0.9968
M BAND	19	-0.19	-0.59	0.9597	0.9968
ORGAN FORMATION	29	-0.21	-0.72	0.8750	0.9968
AXONAL FASCICULATION	19	-0.22	-0.68	0.9135	0.9969
CARDIAC MUSCLE CELL ACTION POTENTIAL	36	-0.16	-0.56	0.9950	0.9969
ACTIN FILAMENT BUNDLE	52	-0.14	-0.57	0.9971	0.9969
GABA RECEPTOR ACTIVITY	22	-0.22	-0.69	0.8884	0.9969

PHOTORECEPTOR CELL DIFFERENTIATION	46	0.16	0.55	0.9921	0.9969
DERMATAN SULFATE PROTEOGLYCAN METABOLIC PROCESS	16	-0.23	-0.67	0.9009	0.9970
DETECTION OF LIGHT STIMULUS INVOLVED IN SENSORY PERCEPTION	16	-0.24	-0.68	0.8635	0.9970
FRIZZLED BINDING	35	-0.16	-0.57	0.9900	0.9970
GABA RECEPTOR COMPLEX	18	-0.22	-0.67	0.9145	0.9970
NEGATIVE REGULATION OF OSTEOCLAST DIFFERENTIATION	22	-0.18	-0.58	0.9672	0.9970
RESPONSE TO THYROID HORMONE	17	-0.20	-0.58	0.9638	0.9971
ANATOMICAL STRUCTURE ARRANGEMENT	16	-0.20	-0.59	0.9509	0.9971
MITOTIC SPINDLE	46	-0.18	-0.68	0.9583	0.9971
NEURAL NUCLEUS DEVELOPMENT	57	-0.15	-0.59	0.9948	0.9971
RECIPROCAL MEIOTIC RECOMBINATION	33	-0.18	-0.62	0.9537	0.9971
ANKYRIN BINDING	16	-0.19	-0.55	0.9669	0.9972
PHOTOTRANSDUCTION VISIBLE LIGHT	20	-0.17	-0.53	0.9868	0.9972
SPERM PART	125	-0.15	-0.70	0.9966	0.9972
HYPEROSMOTIC RESPONSE	19	-0.19	-0.57	0.9714	0.9972
POSITIVE REGULATION OF INTERFERON ALPHA PRODUCTION	16	-0.20	-0.56	0.9652	0.9972
LYSOSOMAL LUMEN	75	-0.17	-0.69	0.9550	0.9973
LIPASE INHIBITOR ACTIVITY	16	-0.21	-0.61	0.9633	0.9973
CELLULAR RESPONSE TO VIRUS	20	0.19	0.54	0.9775	0.9973
IONOTROPIC GLUTAMATE RECEPTOR SIGNALING PATHWAY	22	-0.22	-0.70	0.8859	0.9974
XY BODY	15	-0.22	-0.62	0.9341	0.9974
POSITIVE REGULATION OF LEUKOCYTE DEGRANULATION	15	-0.20	-0.59	0.9615	0.9974
POSITIVE REGULATION OF ACTIN NUCLEATION	15	-0.20	-0.60	0.9529	0.9974
ACTIN FILAMENT	67	-0.13	-0.54	1.0000	0.9975
ACTION POTENTIAL	90	-0.16	-0.69	0.9783	0.9975
CYTOSOLIC CALCIUM ION TRANSPORT	46	-0.18	-0.70	0.9492	0.9975
KERATAN SULFATE METABOLIC PROCESS	29	-0.20	-0.70	0.9145	0.9975
NEGATIVE REGULATION OF AXON GUIDANCE	27	-0.20	-0.67	0.9430	0.9975
NEGATIVE REGULATION OF CATION TRANSMEMBRANE TRANSPORT	57	-0.15	-0.60	0.9915	0.9975
DETECTION OF LIGHT STIMULUS INVOLVED IN VISUAL PERCEPTION	16	-0.24	-0.68	0.9031	0.9975

STEM CELL DIVISION	29	-0.16	-0.55	0.9851	0.9975
AXON REGENERATION	20	-0.20	-0.61	0.9688	0.9976
ECTODERM DEVELOPMENT	20	-0.20	-0.59	0.9510	0.9976
MYOSIN BINDING	56	0.15	0.54	0.9969	0.9976
MYOFIBRIL ASSEMBLY	45	-0.18	-0.68	0.9658	0.9976
REGULATION OF INTERFERON ALPHA PRODUCTION	19	-0.17	-0.52	0.9810	0.9976
REGULATION OF PROTEIN AUTOPHOSPHORYLATION	32	-0.20	-0.69	0.9188	0.9978
CHONDROITIN SULFATE BIOSYNTHETIC PROCESS	24	-0.19	-0.62	0.9529	0.9978
REGULATION OF LONG TERM NEURONAL SYNAPTIC PLASTICITY	21	-0.22	-0.69	0.8769	0.9978
REGULATION OF CARDIAC MUSCLE CELL MEMBRANE REPOLARIZATION	20	-0.16	-0.51	0.9924	0.9978
REGULATION OF LONG TERM SYNAPTIC POTENTIATION	18	-0.18	-0.54	0.9861	0.9979
POSITIVE REGULATION OF EPIDERMIS DEVELOPMENT	28	-0.18	-0.61	0.9653	0.9979
PHOSPHATIDYLINOSITOL 3 KINASE SIGNALING	23	-0.19	-0.60	0.9584	0.9979
FLUID TRANSPORT	25	-0.18	-0.60	0.9758	0.9979
OSTEOBLAST DEVELOPMENT	17	-0.23	-0.69	0.9067	0.9979
KINESIN BINDING	26	-0.21	-0.68	0.9242	0.9980
ACROSOMAL VESICLE	84	-0.16	-0.70	0.9732	0.9980
BRANCH ELONGATION OF AN EPITHELIUM	17	-0.23	-0.69	0.8708	0.9981
REGULATION OF NEURON PROJECTION REGENERATION	18	-0.23	-0.68	0.8947	0.9981
MYOTUBE DIFFERENTIATION	50	-0.18	-0.69	0.9553	0.9982
BASEMENT MEMBRANE	84	0.14	0.53	0.9970	0.9982
REGULATION OF KERATINOCYTE DIFFERENTIATION	23	-0.19	-0.62	0.9455	0.9984
POSITIVE REGULATION OF INTERLEUKIN 1 SECRETION	16	0.19	0.53	0.9799	0.9984
PROTEIN SERINE THREONINE TYROSINE KINASE ACTIVITY	34	-0.20	-0.69	0.9177	0.9985
NEGATIVE REGULATION OF STEM CELL PROLIFERATION	15	-0.16	-0.45	0.9955	0.9987
DEFINITIVE HEMOPOIESIS	16	-0.23	-0.66	0.9071	0.9987
MEMBRANE REPOLARIZATION	15	-0.24	-0.69	0.8732	0.9987

PROTEIN SERINE THREONINE KINASE ACTIVATOR ACTIVITY	18	0.17	0.47	1.0000	0.9987
TISSUE HOMEOSTASIS	140	-0.15	-0.69	1.0000	0.9989
SYNAPTONEMAL COMPLEX	29	0.16	0.51	0.9983	0.9990
HORMONE BINDING	62	0.13	0.48	0.9984	0.9990
REGULATION OF MEMBRANE REPOLARIZATION	29	0.15	0.47	0.9951	0.9990
POSITIVE REGULATION OF EXTRACELLULAR MATRIX ORGANIZATION	16	-0.22	-0.62	0.9365	0.9990
POSITIVE REGULATION OF INTERLEUKIN 4 PRODUCTION	20	-0.15	-0.45	0.9974	0.9991
ACTIN CYTOSKELETON REORGANIZATION	51	0.13	0.49	0.9984	0.9991
RESPONSE TO MAGNESIUM ION	22	0.17	0.49	0.9886	0.9991
ESTABLISHMENT OF MITOTIC SPINDLE LOCALIZATION	22	0.16	0.48	0.9965	0.9991
STRIATED MUSCLE ADAPTATION	23	0.17	0.51	0.9898	0.9992
CELL COMMUNICATION INVOLVED IN CARDIAC CONDUCTION	35	-0.18	-0.66	0.9427	0.9992
MUSCLE CELL MIGRATION	18	-0.16	-0.48	0.9951	0.9992
REGULATION OF MYELOID CELL APOPTOTIC PROCESS	19	-0.22	-0.66	0.9115	0.9992
GLUTATHIONE TRANSFERASE ACTIVITY	27	0.16	0.50	0.9895	0.9992
OXIDOREDUCTASE ACTIVITY ACTING ON PEROXIDE AS ACCEPTOR	35	0.15	0.49	0.9984	0.9994
MORPHOGENESIS OF A POLARIZED EPITHELIUM	24	-0.21	-0.69	0.8875	0.9994
SPINDLE LOCALIZATION	35	0.15	0.50	0.9902	0.9995
REGULATION OF NITRIC OXIDE SYNTHASE BIOSYNTHETIC PROCESS	17	-0.22	-0.66	0.9113	0.9995
CARDIAC MUSCLE CELL CONTRACTION	29	0.14	0.45	0.9967	0.9995
POSITIVE REGULATION OF EPITHELIAL TO MESENCHYMAL TRANSITION	29	0.16	0.51	0.9850	0.9995
MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE BINDING	16	-0.22	-0.63	0.9397	0.9995
RESPONSE TO GLUCAGON	43	-0.18	-0.66	0.9676	0.9995
NEGATIVE REGULATION OF PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	15	-0.16	-0.46	0.9957	0.9995
P53 BINDING	55	0.14	0.50	1.0000	0.9995
GLUCOSE CATABOLIC PROCESS	27	-0.19	-0.63	0.9589	0.9996

REGULATION OF INTERLEUKIN 4 PRODUCTION	25	-0.15	-0.48	0.9948	0.9996
EXTRACELLULAR GLUTAMATE GATED ION CHANNEL ACTIVITY	19	-0.20	-0.62	0.9578	0.9997
EMBRYONIC CRANIAL SKELETON MORPHOGENESIS	44	-0.17	-0.66	0.9423	0.9997
CALCIUM ACTIVATED POTASSIUM CHANNEL ACTIVITY	16	0.19	0.51	0.9892	0.9997
NEGATIVE REGULATION OF EPITHELIAL CELL PROLIFERATION	105	-0.15	-0.66	0.9965	0.9997
MULTICELLULAR ORGANISM AGING	24	0.14	0.43	0.9982	0.9998
MELANOCYTE DIFFERENTIATION	17	0.14	0.37	1.0000	0.9999
POSITIVE REGULATION OF EXCITATORY POSTSYNAPTIC POTENTIAL	21	-0.20	-0.63	0.9487	0.9999
POSITIVE REGULATION OF STEM CELL DIFFERENTIATION	44	-0.17	-0.62	0.9839	0.9999
LIGAND GATED CALCIUM CHANNEL ACTIVITY	16	0.14	0.39	1.0000	1.0000
SULFUR COMPOUND TRANSMEMBRANE TRANSPORTER ACTIVITY	23	-0.20	-0.66	0.9299	1.0000
PROTEIN SECRETION	103	-0.15	-0.65	0.9968	1.0000
GAMMA AMINOBUTYRIC ACID SIGNALING PATHWAY	23	-0.20	-0.65	0.9316	1.0000
PROTEIN DEPOLYMERIZATION	22	-0.20	-0.65	0.9515	1.0000
MEMBRANE INVAGINATION	24	-0.20	-0.64	0.9514	1.0000
REGULATION OF ANDROGEN RECEPTOR SIGNALING PATHWAY	20	-0.21	-0.64	0.9420	1.0000
REGULATION OF INTERLEUKIN 8 PRODUCTION	51	-0.16	-0.64	0.9751	1.0000
HETEROTRIMERIC G PROTEIN COMPLEX	29	-0.19	-0.64	0.9460	1.0000
MULTICELLULAR ORGANISMAL RESPONSE TO STRESS	61	-0.16	-0.64	0.9947	1.0000
POSITIVE REGULATION OF COLLAGEN METABOLIC PROCESS	19	-0.21	-0.64	0.9545	1.0000
ENDOCHONDRAL BONE MORPHOGENESIS	41	-0.17	-0.64	0.9614	1.0000
REGULATION OF EXTRACELLULAR MATRIX ORGANIZATION	27	-0.19	-0.64	0.9398	1.0000
MYOSIN II COMPLEX	23	-0.20	-0.64	0.9457	1.0000
STEREOCILIUM BUNDLE	35	-0.18	-0.63	0.9699	1.0000
MEIOSIS I	68	-0.15	-0.63	0.9917	1.0000
ACTOMYOSIN	58	-0.16	-0.63	0.9887	1.0000

TONGUE DEVELOPMENT	19	-0.21	-0.63	0.9467	1.0000
POSITIVE REGULATION OF MULTICELLULAR ORGANISMAL METABOLIC PROCESS	19	-0.21	-0.63	0.9426	1.0000
REGULATION OF CELL JUNCTION ASSEMBLY	63	-0.16	-0.63	0.9897	1.0000