

Weighted burden analysis of exome-sequenced case-control sample implicates synaptic genes in schizophrenia aetiology

Supplementary table S1

The table shows the weight accorded to each type of variant as annotated by VEP (McLaren et al., 2016). 10 was added to this weight if the variant was annotated by Polyphen as possibly or probably damaging and 10 was added if SIFT annotated it as deleterious (Adzhubei et al., 2013; Kumar et al., 2009).

VEP annotation	Weight
intergenic_variant	1
feature_truncation	3
regulatory_region_variant	3
feature_elongation	3
regulatory_region_amplification	3
regulatory_region_ablation	3
TF_binding_site_variant	3
TFBS_amplification	3
TFBS_ablation	3
downstream_gene_variant	3
upstream_gene_variant	3
non_coding_transcript_variant	3
NMD_transcript_variant	3
intron_variant	3
non_coding_transcript_exon_variant	3
3_prime_UTR_variant	5
5_prime_UTR_variant	5
mature_miRNA_variant	5
coding_sequence_variant	5
synonymous_variant	5
stop_retained_variant	5
incomplete_terminal_codon_variant	5
splice_region_variant	5
protein_altering_variant	10
missense_variant	10
inframe_deletion	15
inframe_insertion	15
transcript_amplification	15
start_lost	15
stop_lost	15
frameshift_variant	20
stop_gained	20
splice_donor_variant	20
splice_acceptor_variant	20

transcript_ablation	20
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Supplementary table 2. Table shows the SLP obtained using PATHWAYASSOC for each of 1454 GO gene sets.

GO gene set	SLP
NUCLEOPLASM	1.884471
EXTRINSIC_TO_PLASMA_MEMBRANE	0.269964
ORGANELLE_PART	1.913687
CELL_PROJECTION_PART	0.106021
CYTOPLASMIC_VESICLE_MEMBRANE	0.021462
GOLGI_MEMBRANE	1.575715
MITOCHONDRIAL_OUTER_MEMBRANE	0.653169
ORGANELLAR_RIBOSOME	0.18273
ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	0.45033
INTRINSIC_TO_ENDOPLASMIC_RETICULUM_MEMBRANE	-0.03002
BRUSH_BORDER	-0.16222
MITOCHONDRIAL_SMALL_RIBOSOMAL_SUBUNIT	0.45033
PROTEINACEOUS_EXTRACELLULAR_MATRIX	1.028111
INTRINSIC_TO_PLASMA_MEMBRANE	2.744129
ORGANELLE_INNER_MEMBRANE	0.579486
OLIGOSACCHARYL_TRANSFERASE_COMPLEX	0.360879
ADHERENS_JUNCTION	0.298689
PEROXISOMAL_MEMBRANE	0.053127
SARCOMERE	0.075244
EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	1.145736
EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX	0.364883
VESICULAR_FRACTION	0.604011
EXTRACELLULAR_MATRIX_PART	0.946965
CELL_SURFACE	2.568675
CELL_JUNCTION	-0.04417
MITOCHONDRIAL_PART	0.343306
PROTEIN_SERINE_THREONINE_PHOSPHATASE_COMPLEX	-0.0744
AXON	-0.20664
RIBONUCLEOPROTEIN_COMPLEX	0.846111
COATED_VESICLE	1.247626
MICROTUBULE_ASSOCIATED_COMPLEX	0.196453

CHROMATIN	0.45111
SYNAPSE_PART	0.627222
INTERMEDIATE_FILAMENT_CYTOSKELETON	0.365859
MEMBRANE_BOUND_VESICLE	0.730042
NUCLEAR_REPLICATION_FORK	0.447109
MICROTUBULE_CYTOSKELETON	0.570866
EXTRACELLULAR_REGION	1.483205
SPINDLE_POLE	1.221359
LATE_ENDOSOME	0.491574
INTRINSIC_TO_MEMBRANE	3.100734
CYTOPLASMIC_PART	2.70031
VESICLE_COAT	0.562705
CONTRACTILE_FIBER	0.094636
MYOFIBRIL	0.17292
MITOCHONDRIAL_MEMBRANE	0.186654
INTEGRAL_TO_GOLGI_MEMBRANE	0.007168
SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	1.656961
NUCLEAR_CHROMOSOME	0.53292
MEMBRANE_PART	2.878147
GOLGI_APPARATUS	1.258195
CHROMATIN_REMODELING_COMPLEX	2.282135
TIGHT_JUNCTION	-0.10672
INTEGRAL_TO_ENDOPLASMIC_RETICULUM_MEMBRANE	-0.03002
BASEMENT_MEMBRANE	1.30123
INTERCELLULAR_JUNCTION	-0.09162
LYTIC_VACUOLE	1.216882
MICROTUBULE_ORGANIZING_CENTER_PART	0.557366
MEMBRANE	3.063178
CORNIFIED_ENVELOPE	0.070026
NUCLEAR_PART	2.003577
CYTOPLASM	3.997382
NADH_DEHYDROGENASE_COMPLEX	-0.2195
ORGANELLE_LUMEN	1.617821

UBIQUITIN_LIGASE_COMPLEX	-1.60019
BASAL_LAMINA	0.70948
ENDOPLASMIC_RETICULUM_MEMBRANE	0.400437
ENDOPLASMIC_RETICULUM	0.349948
NUCLEAR_LUMEN	1.730692
KINESIN_COMPLEX	-0.26799
NON_MEMBRANE_BOUND_ORGANELLE	1.7642
DNA_DIRECTED_RNA_POLYMERASE_COMPLEX	0.037879
INSOLUBLE_FRACTION	0.615033
VESICLE	0.840141
CYTOSOLIC_PART	0.056345
CYTOSKELETAL_PART	0.435632
GOLGI_APPARATUS_PART	0.842394
PROTEASOME_COMPLEX	1.40679
PORE_COMPLEX	0.097116
NUCLEUS	2.580285
SPINDLE	1.039571
INTERCALATED_DISC	-0.94101
VACUOLE	1.100653
CELL_FRACTION	1.141823
CYTOSOL	0.851322
ORGANELLE_MEMBRANE	1.641427
CYTOSKELETON	1.477831
LAMELLIPODIUM	0.234314
SYNAPTIC_VESICLE	0.16786
NUCLEAR_MATRIX	0.472356
NUCLEAR_ENVELOPE_ENDOPLASMIC_RETICULUM_NETWORK	0.267718
ENDOCYTIC_VESICLE	0.219552
IMMUNOLOGICAL_SYNAPSE	0.000593
PEROXISOMAL_PART	0.014027
CYTOPLASMIC_VESICLE	0.802748
CHROMOSOMEPERICENTRIC_REGION	0.36548
VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	0.237068

ANCHORED_TO_MEMBRANE	0.164292
MEDIATOR_COMPLEX	0.105929
MITOCHONDRIAL_MATRIX	0.41037
VACUOLAR_PART	-0.17653
INTEGRATOR_COMPLEX	1.262876
VOLTAGE_GATED_POTASSIUM_CHANNEL_COMPLEX	-0.07128
MICROSOME	0.5828
OUTER_MEMBRANE	0.260153
DYSTROPHIN_ASSOCIATED_GLYCOPROTEIN_COMPLEX	-0.0234
HISTONE_DEACETYLASE_COMPLEX	0.517331
EXTRACELLULAR_REGION_PART	1.161367
APICAL_JUNCTION_COMPLEX	-0.44081
CELL_CORTEX_PART	-0.0901
ENVELOPE	0.767125
MICROBODY_MEMBRANE	0.053127
MITOCHONDRIAL_LUMEN	0.41037
EARLY_ENDOSOME	1.882108
PERINUCLEAR_REGION_OF_CYTOPLASM	0.511032
CYTOPLASMIC_VESICLE_PART	0.021462
CELL_CORTEX	0.140072
INTEGRAL_TO_MEMBRANE	3.148602
SPINDLE_MICROTUBULE	0.377752
CELL_SUBSTRATE_ADHERENS_JUNCTION	-0.35263
ENDOMEMBRANE_SYSTEM	1.764215
HETEROGENEOUS_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	0.579862
LYSOSOMAL_MEMBRANE	0.096341
DNA_DIRECTED_RNA_POLYMERASEII_CORE_COMPLEX	0.251511
INTERMEDIATE_FILAMENT	0.365859
MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I	-0.2195
CONDENSED_NUCLEAR_CHROMOSOME	0.050111
NUCLEAR_BODY	0.1705
CELL_MATRIX_JUNCTION	-0.68486
MYOSIN_COMPLEX	0.159553

CONTRACTILE_FIBER_PART	0.054069
MICROTUBULE	-0.34889
ORGANELLE_OUTER_MEMBRANE	0.120038
ORGANELLE_ENVELOPE	0.767125
LIPID_RAFT	-0.83708
INTEGRAL_TO_PLASMA_MEMBRANE	2.73386
CELL_PROJECTION	0.566449
SPLICEOSOME	0.385128
NUCLEAR_UBIQUITIN_LIGASE_COMPLEX	-1.91018
VACUOLAR_MEMBRANE	-0.04901
ACTIN_FILAMENT	-0.00062
RUFFLE	0.966377
RIBOSOME	0.355294
ENDOSOME	2.346034
NUCLEAR_ENVELOPE	0.813665
MEMBRANE_ENCLOSED_LUMEN	1.6178
DNA_DIRECTED_RNA_POLYMERASEII_HOLOENZYME	1.010816
MITOCHONDRIAL_INNER_MEMBRANE	0.210778
APICAL_PART_OF_CELL	-0.25634
CLATHRIN_COATED_VESICLE	1.00607
MICROTUBULE_ORGANIZING_CENTER	0.168152
COATED_VESICLE_MEMBRANE	0.460168
NICOTINIC_ACETYLCHOLINE_GATED_RECEPTOR_CHANNEL_COMPLEX	0.177499
TRANSPORT_VESICLE	1.362677
CELL_SOMA	0.173763
REPLICATION_FORK	1.234879
ACTIN_CYTOSKELETON	0.812669
U12_DEPENDENT_SPLICEOSOME	1.005432
RNA_POLYMERASE_COMPLEX	0.037879
CYTOPLASMIC_MEMBRANE_BOUND_VESICLE	0.680951
NUCLEAR_DNA_DIRECTED_RNA_POLYMERASE_COMPLEX	0.037879
MICROBODY_PART	0.014027
DENDRITE	-0.25929

MEMBRANE_FRACTION	0.53014
KINETOCHORE	0.412498
NUCLEAR_CHROMATIN	1.579205
NUCLEOPLASM_PART	2.064897
RECEPTOR_COMPLEX	1.593598
SECRETORY_GRANULE	0.858014
BASOLATERAL_PLASMA_MEMBRANE	-0.498
INTEGRAL_TO_ORGANELLE_MEMBRANE	0.205003
EXTRACELLULAR_SPACE	0.579223
MITOCHONDRIAL_RESPIRATORY_CHAIN	-0.81357
GOLGI_STACK	0.132862
FOCAL_ADHESION	0.313517
ER_GOLGI_INTERMEDIATE_COMPARTMENT	0.474922
INTRACELLULAR_NON_MEMBRANE_BOUND_ORGANELLE	1.7642
MEMBRANE_COAT	0.620567
CENTROSOME	-0.13984
PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	-0.15498
NUCLEAR_MEMBRANE	0.830014
INTRACELLULAR_ORGANELLE_PART	1.866861
MACROMOLECULAR_COMPLEX	2.063472
NUCLEAR_PORE	0.625261
NUCLEOLAR_PART	0.418532
MITOCHONDRION	1.32989
MITOCHONDRIAL_ENVELOPE	0.100275
CORTICAL_CYTOSKELETON	-0.07433
TRANS_GOLGI_NETWORK	0.053983
RESPIRATORY_CHAIN_COMPLEX_I	-0.2195
EXTRACELLULAR_MATRIX	1.017022
SMALL_RIBOSOMAL_SUBUNIT	0.45033
TRANSCRIPTION_FACTOR_TFIID_COMPLEX	-0.12461
MITOCHONDRIAL_RIBOSOME	0.18273
APICAL_PLASMA_MEMBRANE	0.01816
MICROBODY	0.802875

CHROMOSOMAL_PART	1.48678
APICOLATERAL_PLASMA_MEMBRANE	-0.44081
CONDENSED_CHROMOSOME	0.187001
NUCLEAR_MEMBRANE_PART	0.660648
GOLGI_ASSOCIATED_VESICLE	-0.02532
TRANSCRIPTION_FACTOR_COMPLEX	0.156341
LEADING_EDGE	1.697669
LYSOSOME	1.216882
PROTEIN_COMPLEX	1.808867
EXTRINSIC_TO_MEMBRANE	0.503521
SYNAPSE	1.13886
INTRINSIC_TO_ORGANELLE_MEMBRANE	0.148992
ANCHORED_TO_PLASMA_MEMBRANE	0.164292
INTRINSIC_TO_GOLGI_MEMBRANE	0.311279
SITE_OF_POLARIZED_GROWTH	0.006425
NUCLEAR_SPECK	0.354052
PML_BODY	0.20886
RIBOSOMAL_SUBUNIT	0.411122
CORTICAL_ACTIN_CYTOSKELETON	0.061111
ENDOPLASMIC_RETICULUM_LUMEN	-0.18387
COLLAGEN	0.200159
MITOCHONDRIAL_MEMBRANE_PART	0.043042
MICROVILLUS	-0.04998
COATED_MEMBRANE	0.620567
INTEGRIN_COMPLEX	0.676217
GROWTH_CONE	-0.05747
TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	0.360073
ENDOPLASMIC_RETICULUM_PART	0.209426
PLASMA_MEMBRANE_PART	2.415019
NEURON_PROJECTION	-0.22655
PLASMA_MEMBRANE	2.372154
PEROXISOME	0.802875
NUCLEOLUS	0.470712

SOLUBLE_FRACTION	1.44422
VESICLE_MEMBRANE	0.073644
CHROMOSOME	0.793755
NUCLEAR_CHROMOSOME_PART	1.720852
TRNA_PROCESSING	0.340231
REGULATION_OF_BIOLOGICAL_QUALITY	1.446038
DNA_METABOLIC_PROCESS	0.766469
AMINO_SUGAR_METABOLIC_PROCESS	0.103656
BIOPOLYMER_CATABOLIC_PROCESS	1.005146
RNA_METABOLIC_PROCESS	1.592583
GLUCAN_METABOLIC_PROCESS	0.05662
PROTEIN_POLYUBIQUITINATION	0.284924
PROTEIN_OLIGOMERIZATION	1.260672
REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING	-0.19853
DNA_REPAIR	0.044984
POSITIVE_REGULATION_OF_TRANSLATION	0.493901
RESPONSE_TO_VIRUS	0.338444
MUSCLE_DEVELOPMENT	0.441015
POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	0.321188
MITOTIC_CELL_CYCLE_CHECKPOINT	0.479272
ACTIN_FILAMENT_ORGANIZATION	-0.11005
PROTEIN_FOLDING	-0.09268
REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	-0.10448
AXON_GUIDANCE	0.456309
LIPID_CATABOLIC_PROCESS	0.614526
PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	-0.63055
NEGATIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_	0.839249
CYTOKINESIS	-0.74608
SPLICEOSOME_ASSEMBLY	-0.37573
GLYCEROPHOSPHOLIPID_BIOSYNTHETIC_PROCESS	-0.3998
NUCLEOBASENUCLEOSIDE_AND_NUCLEOTIDE_METABOLIC_PROCESS	-0.29938
NUCLEAR_IMPORT	1.335328
POSITIVE_REGULATION_OF_PHOSPHATE_METABOLIC_PROCESS	1.800608

NEGATIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	1.658965
REGULATION_OF_HYDROLASE_ACTIVITY	1.16701
PROTEIN_AUTOPROCESSING	0.455431
POSITIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	0.037717
REGULATION_OF_CELLULAR_PH	0.260881
NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.435618
REGULATION_OF_SECRETION	0.72023
SYSTEM_DEVELOPMENT	2.284832
BIOGENIC_AMINE_METABOLIC_PROCESS	0.545581
POSITIVE_REGULATION_OF_SIGNAL_TRANSDUCTION	1.58998
ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	0.703986
HEMOSTASIS	0.129611
G_PROTEIN_SIGNALING_ADENYLATE_CYCLASE_INHIBITING_PATHWAY	1.064149
ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	-0.5475
GLUCOSE_METABOLIC_PROCESS	2.658731
REGULATION_OF_DEFENSE_RESPONSE	-0.09671
LYSOSOME_ORGANIZATION_AND_BIOGENESIS	-0.78542
POSITIVE_REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	1.438368
TISSUE_MORPHOGENESIS	1.319484
G_PROTEIN_SIGNALING_COUPLED_TO_IP3_SECOND_MESSENGERPHOSPHOLIPASE_C	2.647683
ONE_CARBON_COMPOUND_METABOLIC_PROCESS	0.73762
NEGATIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	-0.08996
GLYCOLIPID_METABOLIC_PROCESS	0.380311
MULTI_ORGANISM_PROCESS	0.06243
INORGANIC_ANION_TRANSPORT	0.038936
POSITIVE_REGULATION_OF_CELL_PROLIFERATION	2.231534
REGULATION_OF_DNA_BINDING	-0.07859
CHROMATIN_REMODELING	0.304317
SYNAPTOGENESIS	0.805595
JAK_STAT_CASCADE	1.805255
NERVOUS_SYSTEM_DEVELOPMENT	1.105296
GLYCOPROTEIN_METABOLIC_PROCESS	0.253973
CELL_DEVELOPMENT	4.089915

INSULIN_RECEPTOR_SIGNALING_PATHWAY	-0.41391
NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS	2.185835
NEGATIVE_REGULATION_OF_APOPTOSIS	1.956072
VIRAL_GENOME_REPLICATION	-0.16431
ESTABLISHMENT_OF_LOCALIZATION	1.934831
REGULATION_OF_KINASE_ACTIVITY	1.181061
CELL_ACTIVATION	3.14954
NEURITE_DEVELOPMENT	0.239497
HORMONE_SECRETION	0.003743
REGULATION_OF_PROTEIN_KINASE_ACTIVITY	1.03015
N_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	0.041882
BIOPOLYMER_METABOLIC_PROCESS	3.020404
PROTEIN_AMINO_ACID_N_LINKED_GLYCOSYLATION	0.509326
AMINO_ACID_TRANSPORT	-0.30978
FEMALE_PREGNANCY	-0.08523
ENERGY_RESERVE_METABOLIC_PROCESS	-0.00888
CHROMATIN_ASSEMBLY	0.606583
NEGATIVE_REGULATION_OF_TRANSPORT	-0.24471
POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTI	1.021865
ISOPRENOID_METABOLIC_PROCESS	0.573758
SPERMATID_DEVELOPMENT	-0.49016
GLUTAMATE_SIGNALING_PATHWAY	1.543942
PROTEIN_TARGETING_TO_MITOCHONDRION	0.277929
TUBE_MORPHOGENESIS	-0.08748
REGULATION_OF_CYTOKINE_SECRETION	0.232061
MACROMOLECULAR_COMPLEX_ASSEMBLY	2.095296
DI__TRI_VALENT_INORGANIC_CATION_TRANSPORT	1.915403
DETECTION_OF ABIOTIC_STIMULUS	0.846348
REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	-0.13883
COFACTOR_METABOLIC_PROCESS	0.516854
REGULATION_OF_HORMONE_SECRETION	0.227063
ORGANIC_ACID_TRANSPORT	0.307865
POSITIVE_REGULATION_OF_PHOSPHORYLATION	1.634225

G2_M_TRANSITION_OF_MITOTIC_CELL_CYCLE	0.799097
T_CELL_PROLIFERATION	1.342873
FEMALE_GAMETE_GENERATION	0.201811
PROTEIN_TETRAMERIZATION	0.547137
REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	0.575573
FATTY_ACID_BETA_OXIDATION	0.592708
POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0.723787
REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	-0.15014
FOCAL_ADHESION_FORMATION	-0.02606
SECRETORY_PATHWAY	0.721578
PEROXISOME_ORGANIZATION_AND_BIOGENESIS	0.037464
MEIOSIS_I	-0.49527
MEMBRANE_LIPID_METABOLIC_PROCESS	-0.09252
REGULATION_OF_LIPID_METABOLIC_PROCESS	-0.49195
REGULATION_OF_MOLECULAR_FUNCTION	1.513446
REGULATION_OF_DNA_REPLICATION	0.315471
SIGNAL_TRANSDUCTION	4.371435
NEGATIVE_REGULATION_OF_CELLULAR_BIOSYNTHETIC_PROCESS	0.823215
DEVELOPMENTAL_MATURATION	1.463385
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1.914098
REGULATION_OF_PROTEIN_AMINO_ACID_PHOSPHORYLATION	3.218073
RESPONSE_TO_ENDOGENOUS_STIMULUS	1.213713
GLYCOPROTEIN_CATABOLIC_PROCESS	-0.26892
REPRODUCTIVE_PROCESS	0.616743
SECRETION_BY_CELL	0.290372
PATTERN_SPECIFICATION_PROCESS	1.868765
PHOSPHOLIPASE_C_ACTIVATION	1.851028
CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	1.17919
LYMPHOCYTE_DIFFERENTIATION	1.701631
CELL_STRUCTURE_DISASSEMBLY_DURING_APOPTOSIS	0.291528
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_TRANSPORT	0.608331
CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	-0.27821
DETECTION_OF_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	0.406161

RESPONSE_TO_NUTRIENT	0.158579
ACTIVATION_OF_JNK_ACTIVITY	-0.04066
REGULATION_OF_SYNAPSE_STRUCTURE_AND_ACTIVITY	-0.12379
SULFUR_METABOLIC_PROCESS	-0.22933
NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	0.599112
BIOSYNTHETIC_PROCESS	0.889941
TRANSCRIPTION_DNA_DEPENDENT	1.195099
STRIATED_MUSCLE_DEVELOPMENT	0.181208
M_PHASE	0.514543
REGULATION_OF_CELL_MIGRATION	-0.23996
PROTEIN_MATURATION	-0.34671
COENZYME_METABOLIC_PROCESS	0.969831
CYTOPLASM_ORGANIZATION_AND_BIOGENESIS	0.113928
REGULATION_OF_TRANSFERASE_ACTIVITY	1.181724
MYOBLAST_DIFFERENTIATION	0.226238
SENSORY_PERCEPTION_OF_TASTE	1.196462
GLUCOSE_CATABOLIC_PROCESS	0.690315
INTRACELLULAR_TRANSPORT	0.824561
INTRACELLULAR_PROTEIN_TRANSPORT	1.707017
PROGRAMMED_CELL_DEATH	2.437629
CENTROSOME_ORGANIZATION_AND_BIOGENESIS	-0.45842
HEMOPOIESIS	2.638229
MICROTUBULE_BASED_PROCESS	0.519067
REGULATION_OF_AXONOGENESIS	-0.14029
RESPONSE_TO_EXTRACELLULAR_STIMULUS	1.591308
APOPTOTIC_NUCLEAR_CHANGES	0.31807
INDUCTION_OF_APOPTOSIS_BY_EXTRACELLULAR_SIGNALS	0.009756
SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	0.306531
GAMETE_GENERATION	3.095868
RESPONSE_TO_TOXIN	-0.59856
POSITIVE_REGULATION_OF_BINDING	-0.03346
CELLULAR_COMPONENT_DISASSEMBLY	0.185035
IMMUNE_SYSTEM_DEVELOPMENT	2.10302

POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	1.105628
TRANSLATIONAL_INITIATION	0.274287
PHOTOTRANSDUCTION	0.399287
REGIONALIZATION	1.487052
ORGANELLE_ORGANIZATION_AND_BIOGENESIS	2.801792
NEGATIVE_REGULATION_OF_CELL_CYCLE	1.916834
HETEROPHILIC_CELL_ADHESION	0.028653
DNA_INTEGRITY_CHECKPOINT	0.18313
STEROID_METABOLIC_PROCESS	0.298212
ESTABLISHMENT_OF_CELLULAR_LOCALIZATION	1.007255
AEROBIC_RESPIRATION	0.00066
SKELETAL_DEVELOPMENT	2.521087
POSITIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_A	2.067108
REGULATION_OF_GROWTH	0.242332
NUCLEAR_TRANSPORT	0.822908
NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.521916
REGULATION_OF_PROTEIN_POLYMERIZATION	0.413499
LIPID_TRANSPORT	0.118476
ANATOMICAL_STRUCTURE_MORPHOGENESIS	1.961294
CELLULAR_RESPONSE_TO_STRESS	1.859456
POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	1.43004
CELLULAR_PROTEIN_CATABOLIC_PROCESS	0.293055
REGULATION_OF_MUSCLE_CONTRACTION	-0.0359
RESPONSE_TO_LIGHT_STIMULUS	0.337341
POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	1.019255
REGULATION_OF_TRANSLATIONAL_INITIATION	-0.07201
NEGATIVE_REGULATION_OF_TRANSCRIPTION_DNA_DEPENDENT	0.370462
PROTEIN_TARGETING	1.401258
MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	-0.16167
VIRAL_INFECTIOUS_CYCLE	0.27043
REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	2.492741
VIRAL_REPRODUCTIVE_PROCESS	0.209856
REGULATION_OF_MITOSIS	0.7403

CARBOXYLIC_ACID_METABOLIC_PROCESS	1.323613
AXONOGENESIS	0.234087
HOMOPHILIC_CELL_ADHESION	0.739214
REGULATION_OF_MAPKKK_CASCADE	-0.16277
PROTEIN_AMINO_ACID_AUTOPHOSPHORYLATION	0.396415
INTERCELLULAR_JUNCTION_ASSEMBLY	0.403303
MAINTENANCE_OF_CELLULAR_LOCALIZATION	0.026771
MICROTUBULE_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	0.101177
NUCLEAR_ORGANIZATION_AND_BIOGENESIS	0.583296
PURINE_NUCLEOTIDE_METABOLIC_PROCESS	-0.58919
PROTEIN_IMPORT	0.94121
POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	0.738618
GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	0.233797
REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	0.292829
SEXUAL_REPRODUCTION	3.335302
INTERPHASE	0.326135
NEGATIVE_REGULATION_OF_ANGIOGENESIS	-0.09947
MONOCARBOXYLIC_ACID_TRANSPORT	1.887932
EPITHELIAL_CELL_DIFFERENTIATION	0.046827
TISSUE_DEVELOPMENT	0.873909
CARBOHYDRATE_TRANSPORT	-0.19992
RESPONSE_TO_STEROID_HORMONE_STIMULUS	0.013528
MUSCLE_CELL_DIFFERENTIATION	0.302292
CYTOKINE_METABOLIC_PROCESS	2.739428
SUPEROXIDE_METABOLIC_PROCESS	0.170676
REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	0.192564
REGULATION_OF_TRANSLATION	1.681298
AMINO_ACID_METABOLIC_PROCESS	0.621847
PHOTORECEPTOR_CELL_MAINTENANCE	0.278867
RESPONSE_TO_XENOBIOTIC_STIMULUS	-0.10692
INTERLEUKIN_8_BIOSYNTHETIC_PROCESS	0.032494
DEFENSE_RESPONSE	1.659199
FATTY_ACID_BIOSYNTHETIC_PROCESS	-0.40495

CALCIUM_MEDIATED_SIGNALING	-0.13291
I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	0.874698
NUCLEOSOME_ASSEMBLY	1.681097
ACTIN_FILAMENT_BASED_PROCESS	0.458429
TUBE_DEVELOPMENT	0.005039
CELL_CYCLE_PROCESS	0.304695
FATTY_ACID_OXIDATION	0.192941
PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	-0.9935
SPHINGOLIPID_METABOLIC_PROCESS	-0.07031
NEGATIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	0.234709
INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	0.498387
BEHAVIOR	1.894978
REGULATION_OF_PROTEIN_METABOLIC_PROCESS	2.234904
REGULATION_OF_SIGNAL_TRANSDUCTION	1.433748
MITOTIC_SISTER_CHROMATID_SEGREGATION	1.88251
POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	0.086493
NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	2.312621
VITAMIN_TRANSPORT	0.054945
REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	2.026644
REGULATION_OF_GENE_SPECIFIC_TRANSCRIPTION	0.036602
POSITIVE_REGULATION_OF_TRANSPORT	0.88168
TRANSCRIPTION_INITIATION	-0.29588
AMINO_ACID_DERIVATIVE_METABOLIC_PROCESS	0.672919
PHAGOCYTOSIS	0.027161
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	3.010576
PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	0.106111
REGULATION_OF_DNA_METABOLIC_PROCESS	1.118382
LOCOMOTORY_BEHAVIOR	1.259088
RNA_ELONGATION	0.095022
REGULATION_OF_CELL_ADHESION	0.179723
T_CELL_DIFFERENTIATION	1.585927
REGULATION_OF_DEVELOPMENTAL_PROCESS	3.094667
RESPONSE_TO_HEAT	-0.01575

ACTIVATION_OF_MAPK_ACTIVITY	0.116874
GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	0.490507
DEPHOSPHORYLATION	0.176619
MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	-0.42477
PROTEIN_DNA_COMPLEX_ASSEMBLY	0.270327
CALCIUM_ION_TRANSPORT	1.492977
REGULATION_OF_T_CELL_ACTIVATION	1.416612
CELLULAR_MORPHOGENESIS_DURING_DIFFERENTIATION	0.443575
REGULATION_OF_BODY_FLUID_LEVELS	0.325362
COENZYME_BIOSYNTHETIC_PROCESS	0.854741
NEGATIVE_REGULATION_OF_GROWTH	1.138036
EPITHELIAL_TO_MESENCHYMAL_TRANSITION	1.670905
GENERATION_OF_NEURONS	1.3451
N_ACETYLGUCOSAMINE_METABOLIC_PROCESS	0.106751
RESPONSE_TO_CARBOHYDRATE_STIMULUS	0.349345
MEIOTIC_CELL_CYCLE	-0.00827
RNA_BIOSYNTHETIC_PROCESS	1.114059
DETECTION_OF_STIMULUS	0.53079
SPERM_MOTILITY	0.009357
CYTOKINE_PRODUCTION	0.700598
CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	0.048413
CELLULAR_CATABOLIC_PROCESS	1.71801
MITOTIC_CELL_CYCLE	0.600401
REGULATION_OF_PHOSPHORYLATION	3.125448
LIPOPROTEIN_METABOLIC_PROCESS	-0.39242
MESODERM_DEVELOPMENT	0.518773
LIPID_METABOLIC_PROCESS	0.742638
CELLULAR_BIOSYNTHETIC_PROCESS	1.163344
ORGANIC_ACID_METABOLIC_PROCESS	1.310699
POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	0.949507
ACTIVATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR	0.054374
BLOOD_COAGULATION	0.320124
REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	0.329397

PURINE_RIBONUCLEOTIDE_METABOLIC_PROCESS	-0.65661
COFACTOR_CATABOLIC_PROCESS	-0.00809
RAS_PROTEIN_SIGNAL_TRANSDUCTION	0.130411
MYELOID_CELL_DIFFERENTIATION	0.269641
CELL_CYCLE_PHASE	0.504019
LEUKOCYTE_DIFFERENTIATION	1.005917
JNK_CASCADE	-0.39575
POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	0.669771
CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	-0.08633
REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	-0.33071
RHYTHMIC_PROCESS	0.151812
NITROGEN_COMPOUND_METABOLIC_PROCESS	0.88189
VIRAL_REPRODUCTION	0.079058
MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	1.073402
REGULATION_OF_ACTIN_FILAMENT_LENGTH	0.413518
LEUKOCYTE_CHEMOTAXIS	0.700442
REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-0.18727
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	2.623044
BRAIN_DEVELOPMENT	0.745388
ANATOMICAL_STRUCTURE_FORMATION	0.492657
IMMUNE_EFFECTOR_PROCESS	-0.23533
RESPONSE_TO_NUTRIENT_LEVELS	1.264667
CELL_CELL_SIGNALING	1.165126
LIPID_BIOSYNTHETIC_PROCESS	-0.83181
ORGAN_MORPHOGENESIS	1.683584
DETECTION_OF_CHEMICAL_STIMULUS	0.306167
POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	1.793578
S_PHASE	0.314416
POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	0.184682
AMINO_ACID_CATABOLIC_PROCESS	0.093679
CELL_CYCLE_CHECKPOINT_GO_0000075	0.72582
MITOCHONDRIAL_MEMBRANE_ORGANIZATION_AND_BIOGENESIS	0.163077
POSITIVE_REGULATION_OF_CASPASE_ACTIVITY	1.238583

REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	1.134167
POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	1.345012
POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS	0.799693
CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	1.10909
REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	-0.10767
CELL_RECOGNITION	0.047245
PROTEOGLYCAN_METABOLIC_PROCESS	0.025462
DNA_REPLICATION_INITIATION	-0.36779
PEPTIDE_METABOLIC_PROCESS	0.312423
REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.156946
DEFENSE_RESPONSE_TO_VIRUS	-0.03847
REGULATION_OF_PH	-0.0908
CELL_SUBSTRATE_ADHESION	0.258794
MYELOID_LEUKOCYTE_DIFFERENTIATION	0.116131
CHROMOSOME_SEGREGATION	1.026704
REGULATION_OF_CHROMOSOME_ORGANIZATION_AND_BIOGENESIS	0.870267
ANION_TRANSPORT	-0.01994
PROTEIN_POLYMERIZATION	1.389458
LEUKOCYTE_ACTIVATION	2.350565
INTERLEUKIN_1_SECRETION	0.135798
ALCOHOL_METABOLIC_PROCESS	2.371962
FEEDING_BEHAVIOR	3.222166
TRNA_METABOLIC_PROCESS	0.671673
ELECTRON_TRANSPORT_GO_0006118	0.121104
ADAPTIVE_IMMUNE_RESPONSE_GO_0002460	-0.26002
INTERLEUKIN_2_PRODUCTION	-0.32022
POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	-0.20556
B_CELL_DIFFERENTIATION	0.396094
REGULATION_OF_HOMEOSTATIC_PROCESS	-1.73073
METAL_ION_TRANSPORT	2.257991
ENDOTHELIAL_CELL_PROLIFERATION	-0.92535
NEUROPEPTIDE_SIGNALING_PATHWAY	0.766578
ACTIN_POLYMERIZATION_AND_OR_DEPOLYMERIZATION	2.588231

INFLAMMATORY_RESPONSE	1.182546
NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	-1.4063
PROTEIN_EXPORT_FROM_NUCLEUS	-0.19803
PROTEIN_STABILIZATION	0.742076
ACTIVATION_OF_IMMUNE_RESPONSE	0.207477
RESPONSE_TO_STRESS	1.537685
RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS_AND_ASSEMBLY	0.332042
CELLULAR_CATION_HOMEOSTASIS	1.687123
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	4.112882
PROTEIN_COMPLEX_DISASSEMBLY	-0.13176
MITOCHONDRION_ORGANIZATION_AND_BIOGENESIS	0.953466
CIRCADIAN_RHYTHM	0.178925
RNA_PROCESSING	0.506351
B_CELL_ACTIVATION	0.732695
EXTRACELLULAR_STRUCTURE_ORGANIZATION_AND_BIOGENESIS	1.484626
INTERLEUKIN_8_PRODUCTION	0.128092
DNA_CATABOLIC_PROCESS	0.285955
RESPONSE_TO_CHEMICAL_STIMULUS	1.081774
PROTEIN_IMPORT_INTO_NUCLEUS	1.351207
REGULATION_OF_NEUROTRANSMITTER_LEVELS	0.543988
REGULATION_OF_GENE_EXPRESSION	2.973339
REGULATION_OF_CELL_DIFFERENTIATION	0.825107
SENSORY_PERCEPTION	1.231839
NEGATIVE_REGULATION_OF_DNA_BINDING	-0.02896
POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	0.979758
PROTEIN_RNA_COMPLEX_ASSEMBLY	-0.07816
POST_TRANSLATIONAL_PROTEIN_MODIFICATION	1.742068
VACUOLE_ORGANIZATION_AND_BIOGENESIS	-0.79539
POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	-0.08788
ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	0.930766
VACUOLAR_TRANSPORT	0.277654
CALCIUM_INDEPENDENT_CELL_CELL_ADHESION	-0.35382
PHOSPHOINOSITIDE_MEDIATED_SIGNALING	2.195185

PROTEIN_TARGETING_TO_MEMBRANE	0.595203
NUCLEAR_EXPORT	0.050506
REGULATION_OF_ORGANELLE_ORGANIZATION_AND_BIOGENESIS	0.166915
MORPHOGENESIS_OF_AN_EPITHELIUM	0.05901
NEUTRAL_AMINO_ACID_TRANSPORT	0.064405
AMINE_CATABOLIC_PROCESS	0.133967
CELLULAR_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	0.1452
RESPONSE_TO_BACTERIUM	-0.07301
CELLULAR_COMPONENT_ASSEMBLY	2.035334
IMMUNE_RESPONSE	0.59094
HEMOPOIETIC_OR_LYMPHOID_ORGAN_DEVELOPMENT	2.605916
REGULATION_OF_JNK_CASCADE	0.108339
PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION	-0.59738
REGULATION_OF_CATABOLIC_PROCESS	0.015229
BIOPOLYMER_BIOSYNTHETIC_PROCESS	0.878097
GROWTH	1.404231
EXCRETION	-0.01414
ANGIOGENESIS	0.148893
NEGATIVE_REGULATION_OF_PHOSPHORYLATION	1.77901
POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	-0.00661
PROTEIN_UBIQUITINATION	-0.70612
CARBOXYLIC_ACID_TRANSPORT	0.390309
NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	0.377
DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	1.01245
PROTEIN_CATABOLIC_PROCESS	0.142125
AGING	0.567539
NEGATIVE_REGULATION_OF_CELL_ADHESION	0.255573
EMBRYO_IMPLANTATION	0.00426
PROTEOLYSIS	1.116951
SECONDARY_METABOLIC_PROCESS	0.58402
PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	0.010178
VITAMIN_METABOLIC_PROCESS	0.162943
MEMBRANE_ORGANIZATION_AND_BIOGENESIS	1.315432

MAINTENANCE_OF_LOCALIZATION	0.132587
REGULATION_OF_ANGIOGENESIS	-0.30836
INTERCELLULAR_JUNCTION_ASSEMBLY_AND_MAINTENANCE	0.393429
ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	0.172593
SYNAPTIC_TRANSMISSION	1.035856
ACTIN_FILAMENT_POLYMERIZATION	1.566414
ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	0.676831
RESPONSE_TO_OXIDATIVE_STRESS	0.742205
POSITIVE_REGULATION_OF_METABOLIC_PROCESS	2.724621
KERATINOCYTE_DIFFERENTIATION	0.16316
AMINO_ACID_AND_DERIVATIVE_METABOLIC_PROCESS	1.135469
SYNAPSE_ORGANIZATION_AND_BIOGENESIS	1.074551
BILE_ACID_METABOLIC_PROCESS	0.432127
REGULATION_OF_CYTOKINE_PRODUCTION	-0.29338
RESPONSE_TO_TEMPERATURE_STIMULUS	0.524743
REGULATION_OF_ACTIN_POLYMERIZATION_AND_OR_DEPOLYMERIZATION	0.896841
OLIGOSACCHARIDE_METABOLIC_PROCESS	0.139826
REGULATION_OF_HEART_CONTRACTION	2.808922
COVALENT_CHROMATIN_MODIFICATION	2.327146
REGULATION_OF_ACTION_POTENTIAL	-0.62807
CELLULAR_PROTEIN_METABOLIC_PROCESS	2.461419
LIPID_HOMEOSTASIS	0.118827
RRNA_PROCESSING	0.899244
XENOBIOTIC_METABOLIC_PROCESS	-0.13208
ESTABLISHMENT_OF_VESICLE_LOCALIZATION	0.410241
HEME_BIOSYNTHETIC_PROCESS	-0.01858
UNFOLDED_PROTEIN_RESPONSE	-0.61492
CELL_DIVISION	-0.57059
RESPONSE_TO ABIOTIC_STIMULUS	0.695061
HOMEOSTASIS_OF_NUMBER_OF_CELLS	0.431444
REGULATED_SECRETORY_PATHWAY	0.469212
RNA_3END_PROCESSING	0.256239
RESPONSE_TO BIOTIC_STIMULUS	-0.19587

G_PROTEIN_SIGNALING_COUPLED_TO_CAMP_NUCLEOTIDE_SECOND_MESSENGER	0.322123
PROTEIN_SECRETION	-0.24837
PROTEIN_KINASE_CASCADE	2.075831
PROTEIN_AMINO_ACID_LIPIDATION	-0.37103
NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	0.155089
MACROMOLECULE_LOCALIZATION	1.563429
SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	1.846533
CELLULAR_RESPONSE_TO_STIMULUS	1.815841
MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION_AND_BIOGENESIS	-0.49682
G1_PHASE_OF_MITOTIC_CELL_CYCLE	-0.06837
GLYCOSPHINGOLIPID_METABOLIC_PROCESS	0.208945
REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	1.810691
INTERACTION_WITH_HOST	-0.0219
REGULATION_OF_RHO_GTPASE_ACTIVITY	-0.2152
MRNA_PROCESSING_GO_0006397	-0.22066
MACROMOLECULE_BIOSYNTHETIC_PROCESS	1.916748
G_PROTEIN_SIGNALING_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY	0.049021
RESPONSE_TO_OTHER_ORGANISM	0.01141
RNA_EXPORT_FROM_NUCLEUS	0.507767
LYSOSOMAL_TRANSPORT	0.112839
MACROMOLECULE_CATABOLIC_PROCESS	1.384703
AMINE_BIOSYNTHETIC_PROCESS	0.072845
POSITIVE_REGULATION_OF_T_CELL_ACTIVATION	1.107222
NEUROLOGICAL_SYSTEM_PROCESS	1.740388
REGULATION_OF_CELL_SHAPE	-0.01581
EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-0.2279
AMINO_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	0.123469
STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	1.420606
CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	2.020475
POSITIVE_REGULATION_OF_PROTEIN_SECRETION	-0.11079
REGULATION_OF_MITOTIC_CELL_CYCLE	0.536058
RIBONUCLEOTIDE_METABOLIC_PROCESS	-0.43699
BIOPOLYMER_MODIFICATION	1.854768

TRANSPORT	1.971533
CELLULAR_LIPID_CATABOLIC_PROCESS	0.769791
EPIDERMIS_DEVELOPMENT	1.733049
REGULATION_OF_RESPONSE_TO_STIMULUS	0.126106
REGULATION_OF_MAP_KINASE_ACTIVITY	0.345963
NEGATIVE_REGULATION_OF_TRANSCRIPTION	1.120016
HOMEOSTATIC_PROCESS	0.650511
SODIUM_ION_TRANSPORT	0.919774
POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	0.815213
VASCULATURE_DEVELOPMENT	0.325931
CELLULAR_HOMEOSTASIS	1.144307
STRIATED_MUSCLE_CONTRACTION_GO_0006941	-0.04148
GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	0.501468
ICOSANOID_METABOLIC_PROCESS	0.559597
PHOSPHOINOSITIDE_BIOSYNTHETIC_PROCESS	-0.42944
SECRETION	0.369226
DNA_REPLICATION	1.364662
APOPTOTIC_MITOCHONDRIAL_CHANGES	-0.05655
POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENE	-0.01632
GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	0.413935
CELL_CELL_ADHESION	-0.18633
NEGATIVE_REGULATION_OF_CELL_PROLIFERATION	0.721263
POSITIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.287983
DNA_DAMAGE_RESPONSESIGNAL_TRANSDUCTION	0.592094
EMBRYONIC_MORPHOGENESIS	0.29373
NLS_BEARING_SUBSTRATE_IMPORT_INTO_NUCLEUS	0.614138
DIGESTION	0.83529
COFACTOR_TRANSPORT	-0.11439
NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMO	0.197896
REGULATION_OF_CATALYTIC_ACTIVITY	1.720274
NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.23627
GLIOGENESIS	0.155133
NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	0.185109

LIPOPROTEIN_BIOSYNTHETIC_PROCESS	-0.43399
DNA_DAMAGE_RESPONSESIGNAL_TRANSDUCTION_RESULTING_IN_INDUCTION_OF_	-0.02486
VESICLE_LOCALIZATION	0.024504
ADAPTIVE_IMMUNE_RESPONSE	-0.19126
ANTI_APOPTOSIS	1.616065
MAINTENANCE_OF_CELLULAR_PROTEIN_LOCALIZATION	0.046326
INTRACELLULAR_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	1.636791
NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	0.24084
DNA_DAMAGE_CHECKPOINT	0.572743
REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	0.668448
GOLGI_VESICLE_TRANSPORT	0.177517
PEPTIDYL_TYROSINE_PHOSPHORYLATION	0.979198
NEGATIVE_REGULATION_OF_SECRETION	0.699322
PROTEIN_PROCESSING	0.840387
OXYGEN_AND_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	0.575102
PROTEIN_COMPLEX_ASSEMBLY	2.834494
CELLULAR_LIPID_METABOLIC_PROCESS	0.441477
REGULATION_OF_CELL_MORPHOGENESIS	-0.06003
DEFENSE_RESPONSE_TO_BACTERIUM	-0.05694
VESICLE_MEDIATED_TRANSPORT	0.800625
DOUBLE_STRAND_BREAK_REPAIR	-1.7519
PROTEIN_METABOLIC_PROCESS	3.384837
NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	2.796314
GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	-0.45335
CELLULAR_MACROMOLECULE_CATABOLIC_PROCESS	1.524181
MRNA_SPLICE_SITE_SELECTION	-0.51176
EXOCYTOSIS	0.191162
SECOND_MESSENGER_MEDIATED_SIGNALING	1.293909
G_PROTEIN_SIGNALING_COUPLED_TO_CYCLIC_NUCLEOTIDE_SECOND_MESSENGER	0.203216
REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	0.588298
REGULATION_OF_INTRACELLULAR_TRANSPORT	0.016784
SMOOTH_MUSCLE_CONTRACTION_GO_0006939	0.263773
SKELETAL_MUSCLE_DEVELOPMENT	-0.17473

ENDOSOME_TRANSPORT	0.113884
PROTEIN_AMINO_ACID_ADP_RIBOSYLATION	-0.25365
BONE_REMODELING	-0.3178
REGULATION_OF_CELLULAR_COMPONENT_SIZE	0.43822
PEPTIDYL_AMINO_ACID_MODIFICATION	1.155962
EMBRYONIC_DEVELOPMENT	1.227544
POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	-0.07178
PROTEIN_AMINO_ACID_O_LINKED_GLYCOSYLATION	-0.40271
REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	-0.00255
CELL_PROLIFERATION_GO_0008283	1.978555
REGULATION_OF_BLOOD_PRESSURE	0.226437
ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CELL_POLARITY	-0.36144
NUCLEOTIDE_EXCISION_REPAIR	0.182946
NEGATIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	0.31877
NEGATIVE_REGULATION_OF_DNA_REPLICATION	-0.32152
REGULATION_OF_ENDOCYTOSIS	0.427061
IMMUNE_SYSTEM_PROCESS	2.044088
TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	-0.61297
ANATOMICAL_STRUCTURE_DEVELOPMENT	2.581543
REGULATION_OF_T_CELL_PROLIFERATION	1.832882
RNA_SPLICINGVIA_TRANSESTERIFICATION_REACTIONS	-0.24412
DNA_RECOMBINATION	-1.60654
CELL_MATRIX_ADHESION	0.014082
PEPTIDYL_TYROSINE_MODIFICATION	0.821167
T_CELL_ACTIVATION	2.014686
G1_PHASE	-0.03056
CYTOKINE_BIOSYNTHETIC_PROCESS	2.706465
POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	0.701248
ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	0.284927
HISTONE_MODIFICATION	2.222109
TRANSCRIPTION	1.501086
POSITIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	2.939955
LEARNING_AND_OR_MEMORY	-0.51306

S_PHASE_OF_MITOTIC_CELL_CYCLE	0.227043
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	3.857432
RESPONSE_TO_EXTERNAL_STIMULUS	2.895701
MITOTIC_SPINDLE_ORGANIZATION_AND_BIOGENESIS	-0.00856
AMINE_METABOLIC_PROCESS	0.918551
INACTIVATION_OF_MAPK_ACTIVITY	1.341707
CERAMIDE_METABOLIC_PROCESS	-0.26077
WOUND_HEALING	0.535746
REGULATION_OF_NEUROGENESIS	-0.61222
TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	-0.52124
CARBOHYDRATE_METABOLIC_PROCESS	0.968346
COAGULATION	0.355733
BODY_FLUID_SECRETION	0.60428
MACROMOLECULAR_COMPLEX_DISASSEMBLY	-0.0349
RESPONSE_TO_UV	0.390771
RESPIRATORY_GASEOUS_EXCHANGE	0.19674
NEGATIVE_REGULATION_OF_BINDING	-0.00267
NEGATIVE_REGULATION_OF_METABOLIC_PROCESS	1.570197
PHOSPHOLIPID_METABOLIC_PROCESS	-0.18393
RESPONSE_TO_IONIZING_RADIATION	0.367287
POSITIVE_REGULATION_OF_JNK_ACTIVITY	0.158074
REGULATION_OF_JAK_STAT_CASCADE	0.687624
TRANSITION_METAL_ION_TRANSPORT	1.185201
NEUROGENESIS	1.508263
RESPONSE_TO_RADIATION	0.625659
REGULATION_OF_CELL_CELL_ADHESION	-0.01005
POSITIVE_REGULATION_OF_CELL_MIGRATION	0.688791
GLAND_DEVELOPMENT	0.245939
REGULATION_OF_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	-0.04996
CHEMICAL_HOMEOSTASIS	0.902681
REGULATION_OF_METABOLIC_PROCESS	3.98587
OVULATION_CYCLE	0.10825
MEIOTIC_RECOMBINATION	-1.01106

PROTEIN_HOMOOIGOMERIZATION	2.878231
CYTOKINE_AND_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	-0.39676
HEART_DEVELOPMENT	-0.16728
CELLULAR_LOCALIZATION	0.703098
DEVELOPMENTAL_GROWTH	1.429567
POSITIVE_REGULATION_OF_CELL_ADHESION	0.29611
POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	0.522741
SPHINGOID_METABOLIC_PROCESS	-0.30121
MAPKKK_CASCADE_GO_0000165	0.112661
CELL_CYCLE_ARREST_GO_0007050	1.304213
ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	0.395163
MITOSIS	0.883247
PIGMENT_BIOSYNTHETIC_PROCESS	0.779891
PIGMENT_METABOLIC_PROCESS	0.595186
REGULATION_OF_JNK_ACTIVITY	0.078551
CELL_CYCLE_GO_0007049	1.079334
ER_NUCLEAR_SIGNALING_PATHWAY	-0.26927
ION_HOMEOSTASIS	1.050704
DNA_MODIFICATION	0.846174
REGULATION_OF_TRANSPORT	0.661192
RECEPTOR_MEDIATED_ENDOCYTOSIS	0.369505
POSITIVE_REGULATION_OF_ANGIOGENESIS	0.259592
NOTCH_SIGNALING_PATHWAY	0.083893
CATION_TRANSPORT	1.268486
NEURON_DIFFERENTIATION	1.809557
REGULATION_OF_LYMPHOCYTE_ACTIVATION	2.280771
ENDOTHELIAL_CELL_MIGRATION	-1.79761
NEURON_DEVELOPMENT	1.244662
ACTIN_FILAMENT_BUNDLE_FORMATION	-0.28243
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_META	2.395557
AROMATIC_COMPOUND_METABOLIC_PROCESS	1.647044
NEGATIVE_REGULATION_OF_TRANSLATION	2.731641
PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	-1.2708

REGULATION_OF_GTPASE_ACTIVITY	-0.71539
SISTER_CHROMATID_SEGREGATION	2.749482
FATTY_ACID_METABOLIC_PROCESS	0.39076
NEUROTRANSMITTER_SECRETION	0.463214
TRICARBOXYLIC_ACID_CYCLE_INTERMEDIATE_METABOLIC_PROCESS	0.177235
NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	-0.1356
CENTROSOME_CYCLE	-0.55337
POLYSACCHARIDE_METABOLIC_PROCESS	0.109
ORGANELLE_LOCALIZATION	0.258518
ACTIN_FILAMENT_BASED_MOVEMENT	-0.38377
NEGATIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	-0.13983
HETEROCYCLE_METABOLIC_PROCESS	0.37842
RIBOSOME_BIOGENESIS_AND_ASSEMBLY	0.995926
ACUTE_INFLAMMATORY_RESPONSE	0.65379
TRIACYLGLYCEROL_METABOLIC_PROCESS	-0.25737
PHOSPHOINOSITIDE_METABOLIC_PROCESS	-0.46664
POSITIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	0.594837
CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	0.333041
CDC42_PROTEIN_SIGNAL_TRANSDUCTION	-0.4149
RESPONSE_TO_HORMONE_STIMULUS	0.237831
MRNA_METABOLIC_PROCESS	0.194657
PROTEIN_MODIFICATION_PROCESS	1.827224
PROTEIN_AMINO_ACID_PHOSPHORYLATION	2.249148
NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	0.66291
AMYLOID_PRECURSOR_PROTEIN_METABOLIC_PROCESS	0.084186
MEMBRANE_FUSION	0.537658
NITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	0.065383
APOPTOTIC_PROGRAM	1.368228
INNATE_IMMUNE_RESPONSE	-0.11194
POSITIVE_REGULATION_OF_CELL_CYCLE	0.24505
NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION	0.303199
CHROMOSOME_ORGANIZATION_AND_BIOGENESIS	4.697526
CELL_PROJECTION_BIOGENESIS	1.34224

REGULATION_OF_NEURON_APOPTOSIS	-0.58981
RNA_SPLICING	-0.117
COFACTOR_BIOSYNTHETIC_PROCESS	0.54693
LYMPHOCYTE_ACTIVATION	2.214667
POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	0.811955
REGULATION_OF_RNA_METABOLIC_PROCESS	1.79238
CATION_HOMEOSTASIS	1.348145
CHROMATIN_MODIFICATION	2.136416
RESPONSE_TO_WOUNDING	1.448379
DETECTION_OF_BIOTIC_STIMULUS	-0.28396
TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	-0.87589
NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY	0.678337
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	2.579363
TISSUE_REMODELING	-0.32921
NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	0.708785
SPHINGOLIPID_BIOSYNTHETIC_PROCESS	-0.15285
ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CHROMATIN_ARCHITECTURE	3.089555
NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	1.184455
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	4.216591
DNA_DEPENDENT_DNA_REPLICATION	0.575046
MONOVALENT_INORGANIC_CATION_TRANSPORT	0.32512
TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	0.886143
TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	-1.00873
HUMORAL_IMMUNE_RESPONSE	-0.16353
MALE_GONAD_DEVELOPMENT	0.576183
DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	0.685058
NUCLEOTIDE_METABOLIC_PROCESS	-0.28201
CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	0.348871
G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	1.185806
AMINE_TRANSPORT	0.663225
INTERPHASE_OF_MITOTIC_CELL_CYCLE	0.191145
PROTEIN_TRANSPORT	1.266921
TRANSLATION	1.79091

POSITIVE_REGULATION_OF_MAPKKK_CASCADE	0.467999
CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	-0.10261
POSITIVE_REGULATION_OF_DNA_BINDING	-0.00209
PHOSPHORYLATION	2.302615
CATABOLIC_PROCESS	1.53259
PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION	0.585961
HORMONE_METABOLIC_PROCESS	-0.55569
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	3.217352
REGULATION_OF_PROTEIN_SECRETION	0.035905
POSITIVE_REGULATION_OF_SECRETION	0.146293
INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	0.328615
PROTEIN_LOCALIZATION	1.216359
CARBOHYDRATE_CATABOLIC_PROCESS	0.331649
ADENYLATE_CYCLASE_ACTIVATION	-0.4712
BASE_EXCISION_REPAIR	1.556422
NEURON_APOPTOSIS	-0.30505
DNA_PACKAGING	0.997052
CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.070063
POTASSIUM_ION_TRANSPORT	0.488256
CYTOKINE_SECRETION	0.154085
REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.990882
POSITIVE_REGULATION_OF_PROTEIN_AMINO_ACID_PHOSPHORYLATION	1.24532
REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS	0.169062
INTERFERON_GAMMA_PRODUCTION	0.397523
REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS	2.696449
MICROTUBULE_BASED_MOVEMENT	0.280495
REGULATION_OF_PROTEIN_STABILITY	0.594836
REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.302984
REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	2.991268
REGULATION_OF_APOPTOSIS	2.771962
SPINDLE_ORGANIZATION_AND_BIOGENESIS	0.010132
PROTEIN_AMINO_ACID_DEPHOSPHORYLATION	-0.06819
NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH	2.093388

TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	-0.26036
DNA_FRAGMENTATION_DURING_APOPTOSIS	0.242842
REGULATION_OF_PROGRAMMED_CELL_DEATH	2.865217
HEME_METABOLIC_PROCESS	-0.08484
CELL_MIGRATION	0.66276
CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	0.213225
STEROID_BIOSYNTHETIC_PROCESS	-0.2484
ION_TRANSPORT	1.327468
RESPONSE_TO_DNA_DAMAGE_STIMULUS	0.837962
ORGAN_DEVELOPMENT	4.637807
TRANSMISSION_OF_NERVE_IMPULSE	0.96468
GENE_SILENCING	-0.28201
TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	0.731484
INTRACELLULAR_SIGNALING_CASCADE	5.39262
REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	-0.09471
REGULATION_OF_TRANSCRIPTION	2.192996
NEGATIVE_REGULATION_OF_CELL_MIGRATION	-0.30805
MITOCHONDRIAL_TRANSPORT	1.211393
STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_PATHWAY	-0.36392
REGULATION_OF_CELL_CYCLE	2.54981
CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	1.432329
CELL_MATURATION	1.189616
SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	0.75543
CELLULAR_DEFENSE_RESPONSE	1.899815
REGULATION_OF_IMMUNE_RESPONSE	0.412867
RRNA_METABOLIC_PROCESS	1.143226
SYSTEM_PROCESS	1.910297
ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	1.243597
REGULATION_OF_RAS_GTPASE_ACTIVITY	-0.74443
SENSORY_ORGAN_DEVELOPMENT	0.583101
POSITIVE_REGULATION_OF_TRANSCRIPTION	2.307341
UBIQUITIN_CYCLE	-0.93633
GLUCOSAMINE_METABOLIC_PROCESS	0.09954

CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	0.830293
REGULATION_OF_BINDING	-0.08267
RNA_CATABOLIC_PROCESS	1.693828
APOPTOSIS_GO	2.361003
NEGATIVE_REGULATION_OF_PHOSPHATE_METABOLIC_PROCESS	2.135633
NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	0.898066
MAINTENANCE_OF_PROTEIN_LOCALIZATION	0.072327
CELLULAR_POLYSACCHARIDE_METABOLIC_PROCESS	0.136677
DETECTION_OF_EXTERNAL_STIMULUS	0.33874
CELLULAR_RESPONSE_TO_NUTRIENT_LEVELS	1.703312
NUCLEOCYTOPLASMIC_TRANSPORT	0.784501
M_PHASE_OF_MITOTIC_CELL_CYCLE	0.725912
POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	-0.34615
SPERMATID_DIFFERENTIATION	0.092462
RESPONSE_TO_ORGANIC_SUBSTANCE	-0.39451
RHO_PROTEIN_SIGNAL_TRANSDUCTION	0.27655
CHROMOSOME_CONDENSATION	-0.00668
CELL_FATE_COMMITMENT	2.193054
RESPONSE_TO_HYPOXIA	-0.18522
MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-0.04029
REPRODUCTION	2.379928
CAMP_MEDIATED_SIGNALING	0.347575
REGULATION_OF_CELL_PROLIFERATION	2.843538
NITROGEN_COMPOUND_CATABOLIC_PROCESS	0.122657
REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	1.058834
RESPONSE_TO_DRUG	1.041385
POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	1.988841
ECTODERM_DEVELOPMENT	1.626252
LEUKOCYTE_MIGRATION	1.659153
REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	-0.75464
REGULATION_OF_MEMBRANE_POTENTIAL	-0.04287
REGULATION_OF_CELL_GROWTH	-0.05166
REGULATION_OF_VIRAL_REPRODUCTION	0.206861

G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	-0.09784
CASPASE_ACTIVATION	2.469277
CELLULAR_RESPIRATION	-0.01397
INDUCTION_OF_APOPTOSIS_BY_INTRACELLULAR_SIGNALS	0.088957
INTEGRIN_BINDING	0.047382
CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.778763
MAP_KINASE_ACTIVITY	-0.10845
TRANSLATION_REGULATOR_ACTIVITY	0.00401
HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	2.5272
MRNA_BINDING	0.219656
PROTEIN_PHOSPHATASE_TYPE_2A_REGULATOR_ACTIVITY	0.121265
ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.734566
GLUTAMATE_RECEPTOR_ACTIVITY	2.392509
ACID_AMINO_ACID_LIGASE_ACTIVITY	-0.09763
SEROTONIN_RECEPTOR_ACTIVITY	0.031718
INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.32219
HISTONE_METHYLTRANSFERASE_ACTIVITY	1.457473
PROTEIN_DOMAIN_SPECIFIC_BINDING	0.393359
CARBOHYDRATE_BINDING	1.963267
G_PROTEIN_COUPLED_RECEPTOR_BINDING	-0.33832
GTP_BINDING	0.742256
HYDRO_LYASE_ACTIVITY	0.254166
NUCLEOTIDE_BINDING	2.181388
COPPER_ION_BINDING	0.567311
DI__TRI_VALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.620275
TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	0.325456
SYMPORTER_ACTIVITY	0.273468
TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	0.246407
ANTIporter_ACTIVITY	-2.10282
HEMATOPOIETIN_INTERFERON_CLASSD200_DOMAIN_CYTOKINE_RECEPTOR_BINDING	0.393253
MONOSACCHARIDE_BINDING	0.569099
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SULFUR_GROUP_OF_DONORS	0.248992
DNA_HELICASE_ACTIVITY	0.083657

ENDODEOXYRIBONUCLEASE_ACTIVITY	0.112576
PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	0.56467
RAS_GTPASE_ACTIVATOR_ACTIVITY	0.104739
PHOSPHORIC_MONOESTER_HYDROLASE_ACTIVITY	0.296305
DAMAGED_DNA_BINDING	1.515308
RNA_HELICASE_ACTIVITY	0.559333
LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	-0.18861
LIPID_BINDING	0.813385
KINASE_BINDING	0.325739
ALDO_KETO_REDUCTASE_ACTIVITY	0.636399
PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR	0.847517
OXIDOREDUCTASE_ACTIVITY_GO_0016705	0.08677
LIPASE_ACTIVITY	1.072037
STEROID_DEHYDROGENASE_ACTIVITY	0.37034
SUGAR_BINDING	0.412553
INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	0.377256
RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	2.746958
CATION_BINDING	2.684124
PHOSPHORUS_OXYGEN_LYASE_ACTIVITY	-0.24471
SPECIFIC_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	-0.38874
PHOSPHATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.07376
SULFOTRANSFERASE_ACTIVITY	0.046044
PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR	-0.02391
SERINE_TYPE_PEPTIDASE_ACTIVITY	0.905997
CATION_CHANNEL_ACTIVITY	1.494237
SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.00445
RAS_GTPASE_BINDING	0.763896
DRUG_BINDING	-0.06823
ATP_DEPENDENT_HELICASE_ACTIVITY	1.946422
ARYLSULFATASE_ACTIVITY	0.423081
ZINC_ION_BINDING	0.582467
PROTEIN_HOMODIMERIZATION_ACTIVITY	1.405002
HEPARIN_BINDING	0.002248

RNA_POLYMERASE_II_TRANSCRIPTION_MEDIATOR_ACTIVITY	0.317536
LIGASE_ACTIVITY	-0.59645
CALCIUM_ION_BINDING	2.762949
HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDEBONDS	0.538118
CATION_TRANSPORTING_ATPASE_ACTIVITY	1.207308
PROTEIN_TRANSPORTER_ACTIVITY	0.213959
OXIDOREDUCTASE_ACTIVITY_GO_0016616	0.37166
GTPASE_REGULATOR_ACTIVITY	1.431981
METALLOPEPTIDASE_ACTIVITY	1.676104
SOLUTE_SODIUM_SYMPORTER_ACTIVITY	0.387272
RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	-0.02011
SODIUM_CHANNEL_ACTIVITY	0.993291
RNA_SPLICING_FACTOR_ACTIVITYTRANSESTERIFICATION_MECHANISM	0.108024
METABOTROPIC_GlutamateGABA_B_LIKE_RECEPTOR_ACTIVITY	1.751311
AMINE_RECEPTOR_ACTIVITY	0.561837
STEROL_BINDING	0.14369
VITAMIN_BINDING	-0.06068
PURINE_NUCLEOTIDE_BINDING	2.311363
SH2_DOMAIN_BINDING	0.150258
VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	0.433461
SMALL_CONJUGATING_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	0.085174
HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	2.045594
ANION_CATION_SYMPORTER_ACTIVITY	-0.03842
RECEPTOR_SIGNALING_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	-0.09449
HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	0.97218
SINGLE_STRANDED_DNA_BINDING	2.63493
INTERLEUKIN_BINDING	0.40561
ENZYME_ACTIVATOR_ACTIVITY	0.411541
ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_PHOSPH	1.422541
EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	0.504889
LYASE_ACTIVITY	0.094749
TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	0.346034
MANNOSYLTRANSFERASE_ACTIVITY	-0.49305

SH3_DOMAIN_BINDING	-0.21956
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	0.32032
CARBOXY_LYASE_ACTIVITY	-0.60459
INOSITOL_OR_PHOSPHATIDYLINOSITOL_PHOSPHODIESTERASE_ACTIVITY	0.549539
MICROTUBULE_BINDING	0.390761
MICROTUBULE_MOTOR_ACTIVITY	-0.14403
LIPOPROTEIN_BINDING	0.291454
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	0.395609
PHOSPHATASE_INHIBITOR_ACTIVITY	1.640121
NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	-0.00301
THIOLESTER_HYDROLASE_ACTIVITY	1.778028
ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.13131
NEUROPEPTIDE_BINDING	1.7145
TASTE_RECEPTOR_ACTIVITY	0.377393
UDP_GLYCOSYLTRANSFERASE_ACTIVITY	0.233195
PHOSPHOLIPID_BINDING	0.58801
CARBONATE_DEHYDRATASE_ACTIVITY	-1.55172
ELECTRON_CARRIER_ACTIVITY	0.225976
AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.278508
HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	1.739012
SMALL_CONJUGATING_PROTEIN_BINDING	0.596827
LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_ACTIVITY	-0.11766
VOLTAGE_GATED_CHANNEL_ACTIVITY	0.820966
HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	1.785974
BETA_TUBULIN_BINDING	-0.49025
FUCOSYLTRANSFERASE_ACTIVITY	-0.01482
GATED_CHANNEL_ACTIVITY	1.383948
SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.10729
PROTEASE_INHIBITOR_ACTIVITY	0.076997
PROTEIN_METHYLTRANSFERASE_ACTIVITY	1.134771
N_ACETYLTRANSFERASE_ACTIVITY	0.242518
NEUROPEPTIDE_RECEPTOR_ACTIVITY	1.496524
RIBONUCLEASE_ACTIVITY	0.656011

TRANSCRIPTION_ELONGATION_REGULATOR_ACTIVITY	0.453434
POLYSACCHARIDE_BINDING	1.605534
CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.888383
HORMONE_BINDING	0.053757
VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	0.202335
IDENTICAL_PROTEIN_BINDING	1.282943
TRANSFERASE_ACTIVITY_TRANSFERRING_GLYCOSYL_GROUPS	0.758038
NEUTRAL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.32529
ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.18077
SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.60696
STRUCTURAL_CONSTITUENT_OF_RIBOSOME	0.727856
STEROID_DEHYDROGENASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONOF	0.362549
PROTEIN_KINASE_ACTIVITY	0.925747
MOLECULAR_ADAPTOR_ACTIVITY	0.171758
ADENYL_RIBONUCLEOTIDE_BINDING	1.890716
EXOPEPTIDASE_ACTIVITY	1.857426
UBIQUITIN_BINDING	0.234397
SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY	1.845234
ADENYL_NUCLEOTIDE_BINDING	2.097368
CYSTEINE_TYPE_PEPTIDASE_ACTIVITY	-0.04602
HISTONE_DEACETYLASE_BINDING	-0.59793
SMALL_GTPASE_REGULATOR_ACTIVITY	1.140752
SMAD_BINDING	1.079682
ANTIGEN_BINDING	0.270141
COFACTOR_TRANSPORTER_ACTIVITY	0.567769
S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY	0.217028
HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDESCATALYZING_TRANSMEMBRA	0.961967
AMINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.938205
CHAPERONE_BINDING	0.444635
ENZYME_REGULATOR_ACTIVITY	1.978074
RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITYENHANCER_BINDING	0.302394
CYTOCHROME_C_OXIDASE_ACTIVITY	0.326133
MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.288828

HELICASE_ACTIVITY	0.495082
OXIDOREDUCTASE_ACTIVITY	0.73188
DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	0.012356
KINASE_ACTIVITY	0.96381
PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	0.357383
SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY	1.503911
SPECIFIC_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY	-0.38627
METALLOEXOPEPTIDASE_ACTIVITY	0.449119
KINASE_REGULATOR_ACTIVITY	0.155627
OXIDOREDUCTASE_ACTIVITY_GO_0016706	-0.36499
PEPTIDE_BINDING	1.068968
ADP_BINDING	0.44248
NUCLEOTIDYLTRANSFERASE_ACTIVITY	-0.08836
CHEMOKINE_ACTIVITY	-0.08824
PROTEIN_N_TERMINUS_BINDING	0.509845
PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	0.53036
RNA_POLYMERASE_ACTIVITY	-0.60665
HISTONE_ACETYLTTRANSFERASE_ACTIVITY	0.694028
OXYGEN_BINDING	-0.1141
RNA_BINDING	0.374481
N_METHYLTRANSFERASE_ACTIVITY	0.342234
GABA_RECEPTOR_ACTIVITY	-0.01287
NEUROTRANSMITTER_BINDING	1.896455
3_5_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	-0.06191
STEROID_HORMONE_RECEPTOR_ACTIVITY	-0.08274
NUCLEOSIDE_TRIPHOSPHATASE_ACTIVITY	2.780248
CARBOXYPEPTIDASE_ACTIVITY	0.278905
NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.800862
INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	0.652156
N_ACYLTRANSFERASE_ACTIVITY	0.16788
ANION_CHANNEL_ACTIVITY	0.272109
PROTEIN_KINASE_INHIBITOR_ACTIVITY	0.573068
METHYLTRANSFERASE_ACTIVITY	0.913724

PROTEIN_COMPLEX_BINDING	0.712066
MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.14873
TELOMERIC_DNA_BINDING	2.228405
INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	-0.07698
PROTEIN_TYROSINE_KINASE_ACTIVITY	0.225282
PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	-0.54292
CARBON_OXYGEN_LYASE_ACTIVITY	0.317404
ACETYL GALACTOSAMINYLTRANSFERASE_ACTIVITY	0.045231
SULFURIC_ESTER_HYDROLASE_ACTIVITY	0.471287
TRANSCRIPTION_COACTIVATOR_ACTIVITY	-0.33064
ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS	1.285597
ATP_DEPENDENT_RNA_HELICASE_ACTIVITY	1.547435
ACETYLTRANSFERASE_ACTIVITY	0.44586
CARBOHYDRATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.113291
POTASSIUM_CHANNEL_ACTIVITY	0.223906
CHEMOKINE_RECEPTOR_BINDING	-0.13874
MONOOXYGENASE_ACTIVITY	0.270681
RHODOPSIN_LIKE_RECEPTOR_ACTIVITY	1.672043
KINASE_INHIBITOR_ACTIVITY	0.74568
TRANSCRIPTION_COREPRESSOR_ACTIVITY	0.533584
PEPTIDE_RECEPTOR_ACTIVITY	0.835465
DEOXYRIBONUCLEASE_ACTIVITY	0.111987
PHOSPHOINOSITIDE_BINDING	0.250056
HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDE BONDS IN CY	1.091353
ATPASE_ACTIVITY_COUPLED	1.143547
G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	2.076893
TRANSCRIPTION_ACTIVATOR_ACTIVITY	0.246853
COFACTOR_BINDING	0.387325
TRANSLATION_FACTOR_ACTIVITY_NUCLEIC_ACID_BINDING	0.279383
NEUROPEPTIDE_HORMONE_ACTIVITY	-1.1779
ENDORIBONUCLEASE_ACTIVITY	0.314441
VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	0.57594
DNA_POLYMERASE_ACTIVITY	-0.20519

ACTIN_BINDING	0.333726
ION_BINDING	4.3437
3_5_EXONUCLEASE_ACTIVITY	-0.19585
TRANSCRIPTION_REPRESSOR_ACTIVITY	1.487705
TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYLOTHER_THAN_METHYLGR	0.578173
COLLAGEN_BINDING	0.727504
SEQUENCE_SPECIFIC_DNA_BINDING	1.95698
CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	-0.06912
NUCLEAR_HORMONE_RECEPTOR_BINDING	0.63202
KINASE_ACTIVATOR_ACTIVITY	-0.32468
PROTEIN_DEACETYLASE_ACTIVITY	0.069166
GUANYL_NUCLEOTIDE_BINDING	0.758583
DEAMINASE_ACTIVITY	0.408309
DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	0.065574
ENZYME_INHIBITOR_ACTIVITY	1.641769
TUBULIN_BINDING	0.212419
PRIMARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.92206
PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	0.174417
RNA_DEPENDENT_ATPASE_ACTIVITY	1.534634
INOSITOL_OR_PHOSPHATIDYLINOSITOL_PHOSPHATASE_ACTIVITY	0.970427
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_TRANSMEMBRANE_TRA	-0.12951
LIPID_KINASE_ACTIVITY	-0.91125
ENDOPEPTIDASE_ACTIVITY	0.919331
MAGNESIUM_ION_BINDING	2.668485
STRUCTURAL_MOLECULE_ACTIVITY	1.757121
SIALYLTRANSFERASE_ACTIVITY	1.404702
DOUBLE_STRANDED_RNA_BINDING	0.447224
IONOTROPIC_Glutamate_RECEPTOR_ACTIVITY	1.076586
ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	0.210461
RECEPTOR_BINDING	0.753393
SERINE_HYDROLASE_ACTIVITY	0.894181
NF_KAPPAB_BINDING	-0.82937
RECEPTOR_SIGNALING_PROTEIN_ACTIVITY	0.165567

CARBON_CARBON_LYASE_ACTIVITY	-0.03094
LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	-0.32371
PROTEIN_BINDING_BRIDGING	0.230373
RECEPTOR_ACTIVITY	2.920403
DEACETYLASE_ACTIVITY	0.134645
TRANSMEMBRANE_RECEPTOR_ACTIVITY	3.36938
VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	0.632962
PROTEIN_KINASE_REGULATOR_ACTIVITY	0.235997
PHOSPHOLIPASE_C_ACTIVITY	0.736243
LIGAND_GATED_CHANNEL_ACTIVITY	1.208364
RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	4.109914
DOUBLE_STRANDED_DNA_BINDING	2.79435
SMALL_GTPASE_BINDING	0.135736
PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	0.0104
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	0.406429
ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	0.459378
TRANSCRIPTION_FACTOR_ACTIVITY	0.243786
ENDONUCLEASE_ACTIVITY	0.551849
PDZ_DOMAIN_BINDING	0.325065
TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	1.151254
EXONUCLEASE_ACTIVITY	-0.31273
ACTIN_FILAMENT_BINDING	-0.21855
CALCIUM_CHANNEL_ACTIVITY	0.439726
ACETYLCHOLINE_BINDING	0.509892
STRUCTURE_SPECIFIC_DNA_BINDING	3.691001
CYTOSKELETAL_PROTEIN_BINDING	0.34239
DNA_DEPENDENT_ATPASE_ACTIVITY	0.304626
AUXILIARY_TRANSPORT_PROTEIN_ACTIVITY	0.968009
POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	0.922906
PHOSPHOLIPASE_A2_ACTIVITY	0.980721
MOTOR_ACTIVITY	-0.12967
NUCLEOTIDE_KINASE_ACTIVITY	0.428172
AMINOPEPTIDASE_ACTIVITY	2.121992

STEROID_BINDING	-0.05318
STEROID_HORMONE_RECEPTOR_BINDING	0.359692
PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	-0.01737
EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	0.43795
HORMONE_ACTIVITY	-0.16731
SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	0.446547
PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	0.613506
TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS	1.023383
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NADH_OR_NADPH	-0.49629
CARBOHYDRATE_KINASE_ACTIVITY	1.428083
CHLORIDE_CHANNEL_ACTIVITY	0.535532
HEMATOPOIETIN_INTERFERON_CLASSD200_DOMAIN_CYTOKINE_RECEPTOR_ACTIVIT	1.370539
CARBOXYLESTERASE_ACTIVITY	0.730168
RHO_GTPASE_ACTIVATOR_ACTIVITY	0.323255
STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	0.334595
PATTERN_BINDING	1.34172
INTERLEUKIN_RECEPTOR_ACTIVITY	0.606842
TRANSCRIPTION_FACTOR_BINDING	0.593614
PROTEIN_KINASE_BINDING	0.39692
TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	0.404028
PHOSPHOLIPASE_ACTIVITY	0.956355
PROTEIN_HETERODIMERIZATION_ACTIVITY	1.273232
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DO	0.719885
ATPASE_ACTIVITY	1.942887
METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.670593
HYDROGEN_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.67977
PROTEIN_C_TERMINUS_BINDING	0.149693
GTPASE_ACTIVITY	1.538885
INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.813502
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	0.662692
NUCLEOBASENUCLEOSIDENUCLEOTIDE_KINASE_ACTIVITY	-0.01181
GTPASE_ACTIVATOR_ACTIVITY	0.180913
PEPTIDASE_ACTIVITY	1.938403

ION_CHANNEL_ACTIVITY	1.691848
SMALL_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	-0.10873
CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.108978
PROTEIN_DIMERIZATION_ACTIVITY	2.415332
CHANNEL_REGULATOR_ACTIVITY	0.951712
TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	0.398174
SIGNAL_SEQUENCE_BINDING	0.132788
MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.51216
STRUCTURAL_CONSTITUENT_OF_MUSCLE	0.274288
L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.143129
PROTEIN_PHOSPHATASE_BINDING	1.449397
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	0.227694
COENZYME_BINDING	0.339368
GTPASE_BINDING	0.093634
GROWTH_FACTOR_BINDING	-0.23904
ENZYME_BINDING	0.873112
CHROMATIN_BINDING	1.151416
LIPID_TRANSPORTER_ACTIVITY	-0.0828
PURINE_RIBONUCLEOTIDE_BINDING	2.104088
AMINE_BINDING	0.334556
ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.636608
UNFOLDED_PROTEIN_BINDING	-0.58894
TRANSITION_METAL_ION_BINDING	0.709719
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DO	1.628423
SH3_SH2_ADAPTOR_ACTIVITY	-0.03912
SMALL_CONJUGATING_PROTEIN_LIGASE_ACTIVITY	-0.07505
TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	0.015154
GLYCOSAMINOGLYCAN_BINDING	1.655877
PHOSPHATASE_BINDING	1.501107
CARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.729675
NICOTINIC_ACETYLCHOLINE_ACTIVATED_CATION_SELECTIVE_CHANNEL_ACTIVITY	0.177499
PHOSPHATASE_REGULATOR_ACTIVITY	0.744668
CALMODULIN_BINDING	0.080005

GLUTATHIONE_TRANSFERASE_ACTIVITY	0.199938
TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.027433
PYROPHOSPHATASE_ACTIVITY	2.52325
THYROID_HORMONE_RECEPTOR_BINDING	0.53951
CYTOKINE_BINDING	0.43712
HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDEBONDSIN_LIN	0.389408
SERINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.691774
TRANSLATION_INITIATION_FACTOR_ACTIVITY	0.267309
TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.285787
NUCLEASE_ACTIVITY	0.666297
SECRETIN_LIKE_RECEPTOR_ACTIVITY	0.012013
RIBONUCLEOPROTEIN_BINDING	0.129779
ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	1.021501
GENERAL_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	-0.1661
TRANSFERASE_ACTIVITY_TRANSFERRING_GROUPS_OTHER_THAN_AMINO_ACYL_GRO	0.360558
DNA_BINDING	1.214016
UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-0.07484
GALACTOSYLTRANSFERASE_ACTIVITY	-0.03757
CYCLASE_ACTIVITY	-0.24471
SINGLE_STRANDED_RNA_BINDING	0.161122
GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	1.488731
ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.47521
PHOSPHOLIPID_TRANSPORTER_ACTIVITY	-0.07907
LOW_DENSITY_LIPOPROTEIN_BINDING	0.091788
HORMONE_RECEPTOR_BINDING	0.651081
CYTOKINE_ACTIVITY	0.691595
ATP_BINDING	1.957613
METALLOENDOPEPTIDASE_ACTIVITY	0.832637
ISOMERASE_ACTIVITY	0.587997
GROWTH_FACTOR_ACTIVITY	2.401166
MAP_KINASE_KINASE_KINASE_ACTIVITY	-0.05953
CASPASE_REGULATOR_ACTIVITY	-0.10361
EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	2.171305

ANTIOXIDANT_ACTIVITY	0.143973
ENDONUCLEASE_ACTIVITY_GO_0016893	0.375894
TRANSCRIPTION_COFACTOR_ACTIVITY	0.318931
INOSITOL_OR_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	-2.33174