# 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 |

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|---|---|
| transcript_ablation | 20 |

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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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|---|---|
| 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 |

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| 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 |

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|---|---|
| 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 |

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| 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_ACETYLGLUCOSAMINE_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 |

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| 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 |

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| 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 |

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| 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 |

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| 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_BIOGEN | 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 |

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| 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 |

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| 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 |

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| 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_PROMOT | 0.197896 |
| REGULATION_OF_CATALYTIC_ACTIVITY | 1.720274 |
| NUCLEOTIDE_BIOSYNTHETIC_PROCESS | -0.23627 |
| GLIOGENESIS | 0.155133 |
| NUCLEOTIDE_SUGAR_METABOLIC_PROCESS | 0.185109 |

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|---|---|
| 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 |

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| 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 |

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| 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 |

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| PROTEIN_HOMOOLIGOMERIZATION | 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 |

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| 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 |

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| 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_P | -1.00873 |
| HUMORAL_IMMUNE_RESPONSE | -0.16353 |
| MALE_GONAD_DEVELOPMENT | 0.576183 |
| DNA_DAMAGE_RESPONSESIGNAL_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 |

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| 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 |

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| 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 |

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| 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 |

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| 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_BINDIN | 0.393253 |
| MONOSACCHARIDE_BINDING | 0.569099 |
| OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SULFUR_GROUP_OF_DONORS | 0.248992 |
| DNA_HELICASE_ACTIVITY | 0.083657 |

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| 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 |

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| 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 |

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| 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 |

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| 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_DONO | 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 |

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| 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_ACETYLTRANSFERASE_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 |

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| 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 |
| ACETYLGALACTOSAMINYLTRANSFERASE_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_PEPTIDEBONDSIN_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 |

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| 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_METHYLGRC | 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 |

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| 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 |

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| 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 |

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| 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 |

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| 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 |

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| ANTIOXIDANT_ACTIVITY | 0.143973 |
| ENDONUCLEASE_ACTIVITY_GO_0016893 | 0.375894 |
| TRANSCRIPTION_COFACTOR_ACTIVITY | 0.318931 |
| INOSITOL_OR_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY | -2.33174 |