

	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS, REACTOME_SEPARATION_OF_SISTER_CHROMATIDS, REACTOME_MITOTIC_SPINDLE_CHECKPOINT, REACTOME_MITOTIC_SPINDLE_CHECKPOINT, REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS, REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS, REACTOME_G2_M_CHECKPOINTS, REACTOME_G2_M_CHECKPOINTS, REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION, REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION, REACTOME_DNA_REPLICATION, REACTOME_DNA_REPLICATION, WP_RETINOBLASTOMA_GENE_IN_CANCER, WP_RETINOBLASTOMA_GENE_IN_CANCER, REACTOME_MITOTIC_G2_G2_M_PHASES, REACTOME_MITOTIC_G2_G2_M_PHASES, REACTOME_HOMOLOGOY_DIRECTED_REPAIR, REACTOME_HOMOLOGOY_DIRECTED_REPAIR, REACTOME_DNA_DAMAGE_STRAND_BREAK_REPAIR, REACTOME_DNA_DAMAGE_STRAND_BREAK_REPAIR, WP_DNA_REPAIR_PATHWAYS_FULL_NETWORK, WP_DNA_REPAIR_PATHWAYS_FULL_NETWORK, REACTOME_MEIOSIS, REACTOME_MEIOSIS, REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS, REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS, REACTOME_REGULATION_OF_TP53_ACTIVITY, REACTOME_REGULATION_OF_TP53_ACTIVITY, REACTOME_PTEN_REGULATION, REACTOME_PTEN_REGULATION, REACTOME_APC_C_CDHL_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDHL_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1, REACTOME_APC_C_CDHL_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDHL_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1, KEGG_CELL_CYCLE, KEGG_CELL_CYCLE, REACTOME_CELLULAR_SENESCENCE, REACTOME_CELLULAR_SENESCENCE, REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS, REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS, REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION, REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION, REACTOME_DNA_REPLICATION_PRE_INITIATION, REACTOME_DNA_REPLICATION_PRE_INITIATION, WP_CELL_CYCLE, WP_CELL_CYCLE, REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT, REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT, REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER, REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER, REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SASP, REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SASP, REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS, REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS, REACTOME_BASE_EXCISION_REPAIR, REACTOME_BASE_EXCISION_REPAIR, REACTOME_OXIDATIVE_STRESS_SENESCENCE, REACTOME_OXIDATIVE_STRESS_SENESCENCE, REACTOME_REPRODUCTION, REACTOME_REPRODUCTION, REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY, REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY, REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE, REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE, REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS, REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS, REACTOME_CELLULAR_RESPONSE_TO_CHEMICAL_STRESS, REACTOME_CELLULAR_RESPONSE_TO_CHEMICAL_STRESS, WP_DNA_REPLICATION, WP_DNA_REPLICATION, REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFERENTIATION_OF_HSCS, REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFERENTIATION_OF_HSCS, REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR, REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR, REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE, REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE, REACTOME_CYTOPROTECTION_BY_HMOX1, REACTOME_CYTOPROTECTION_BY_HMOX1, REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX, REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX, WP_DNA_DAMAGE_STRAND_BREAK_REPAIR, WP_DNA_DAMAGE_STRAND_BREAK_REPAIR, REACTOME_CLEC7A_DECTIN_1_SIGNALING, REACTOME_CLEC7A_DECTIN_1_SIGNALING, REACTOME_DISEASES_OF_PROGRAMMED_CELL_DEATH, REACTOME_DISEASES_OF_PROGRAMMED_CELL_DEATH, REACTOME_DNA_STRAND_ELONGATION, REACTOME_DNA_STRAND_ELONGATION, REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS, REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS, REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY, REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY, REACTOME_DNA_DAMAGE_RESPONSE_IN_GG_NER, REACTOME_DNA_DAMAGE_RESPONSE_IN_GG_NER, REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER, REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER, REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR, REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR, REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS, REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS, REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME, REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME, REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR_PROTEINS, REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR_PROTEINS, REACTOME_NEGATIVE_REGULATION_OF_NOTCH1_SIGNALING, REACTOME_NEGATIVE_REGULATION_OF_NOTCH1_SIGNALING, REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX, REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX, REACTOME_REGULATION_OF_RAS_BY_GAP5, REACTOME_REGULATION_OF_RAS_BY_GAP5, WP_MIRNAS_INVOLVED_IN_DNA_DAMAGE_RESPONSE, WP_MIRNAS_INVOLVED_IN_DNA_DAMAGE_RESPONSE, KEGG_DNA_REPLICATION, KEGG_DNA_REPLICATION, REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY, REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY, REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION, REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION, REACTOME_AUFI_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA, REACTOME_AUFI_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA, REACTOME_DEGRADATION_OF_DVL, REACTOME_DEGRADATION_OF_DVL, REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX, REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX, REACTOME_REGULATION_OF_HMOX1_EXPRESSION_AND_ACTIVITY, REACTOME_REGULATION_OF_HMOX1_EXPRESSION_AND_ACTIVITY, REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA, REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA, REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING, REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING, KEGG_UBQUITIN_MEDIATED_PROTEOLYSIS, KEGG_UBQUITIN_MEDIATED_PROTEOLYSIS, PID_P53_REGULATION_PATHWAY, PID_P53_REGULATION_PATHWAY, REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE, REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE, REACTOME_DEGRADATION_OF_AXIN, REACTOME_DEGRADATION_OF_AXIN, REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY, REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY, WP_G1_TO_S_CELL_CYCLE_CONTROL, WP_G1_TO_S_CELL_CYCLE_CONTROL, REACTOME_MAPK6_MAPK4_SIGNALING, REACTOME_MAPK6_MAPK4_SIGNALING, REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES, REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES, REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER, REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER, REACTOME_SIGNALING_BY_HEDGEHOG, REACTOME_SIGNALING_BY_HEDGEHOG, REACTOME_PROTEIN_UBQUITINATION, REACTOME_PROTEIN_UBQUITINATION, REACTOME_ORC1_REMOVAL_FROM_CHROMATIN, REACTOME_ORC1_REMOVAL_FROM_CHROMATIN, REACTOME_DNA_DAMAGE_BYPASS, REACTOME_DNA_DAMAGE_BYPASS, REACTOME_UCH_PROTEINASES, REACTOME_UCH_PROTEINASES, REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21, REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21, REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS, REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION, PID_PANCREAS_PATHWAY, PID_PANCREAS_PATHWAY, REACTOME_HEDGEHOG_LIGAND_BIOGENESIS, REACTOME_HEDGEHOG_LIGAND_BIOGENESIS, REACTOME_SARS_COV_2_INFECTION, REACTOME_SARS_COV_2_INFECTION, REACTOME_APOPTOSIS, REACTOME_APOPTOSIS, REACTOME_TRANSLATION_OF_SARS_COV_2_STRUCTURAL_PROTEINS, REACTOME_TRANSLATION_OF_SARS_COV_2_STRUCTURAL_PROTEINS, REACTOME_SIGNALING_BY_NOTCH1, REACTOME_SIGNALING_BY_NOTCH1, REACTOME_PCP_CE_PATHWAY, REACTOME_PCP_CE_PATHWAY, REACTOME_EXTENSION_OF_TELOMERES, REACTOME_EXTENSION_OF_TELOMERES, PID_PLK1_PATHWAY, PID_PLK1_PATHWAY, REACTOME_HEDGEHOG_ON_STATE, REACTOME_HEDGEHOG_ON_STATE, PID_FOXM1_PATHWAY, PID_FOXM1_PATHWAY, WP_TGFBETA_SIGNALING_PATHWAY, WP_TGFBETA_SIGNALING_PATHWAY, REACTOME_METALLOPROTEASE_DUBS, REACTOME_METALLOPROTEASE_DUBS, REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS, REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS, REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNHEALING_SSA, REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNHEALING_SSA, REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS, REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS, REACTOME_G1_S_SPECIFIC_TRANSCRIPTION, REACTOME_G1_S_SPECIFIC_TRANSCRIPTION, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3, REACTOME_PANCREAS_PATHWAY, REACTOME_PANCREAS_PATHWAY, REACTOME_INTERLEUKIN_1_SIGNALING, REACTOME_INTERLEUKIN_1_SIGNALING, REACTOME_DUAL_INCISION_IN_GG_NER, REACTOME_DUAL_INCISION_IN_GG_NER, WP_PROTEASOME_DEGRADATION, WP_PROTEASOME_DEGRADATION, KEGG_OOCYTE_MEIOSIS, KEGG_OOCYTE_MEIOSIS, KEGG_NUCLEOTIDE_EXCISION_REPAIR, KEGG_NUCLEOTIDE_EXCISION_REPAIR, REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING, REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING, KEGG_PROTEASOME, KEGG_PROTEASOME, WP_NUCLEOTIDE_EXCISION_REPAIR, WP_NUCLEOTIDE_EXCISION_REPAIR, REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION, REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION, REACTOME_I3_UBQUITIN_LIGASES_UBQUITINATE_TARGET_PROTEINS, REACTOME_I3_UBQUITIN_LIGASES_UBQUITINATE_TARGET_PROTEINS, WP_SPINAL_CORD_INJURY, WP_SPINAL_CORD_INJURY, WP_DNA_DAMAGE_RESPONSE_ONLY_ATM_DEPENDENT, WP_DNA_DAMAGE_RESPONSE_ONLY_ATM_DEPENDENT, REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX, REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_E2F6, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_E2F6, REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX, REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX, REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES, REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES, REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY, REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY, REACTOME_SYNTHESIS_OF_ACTIVE_UBQUITIN, REACTOME_SYNTHESIS_OF_ACTIVE_UBQUITIN, REACTOME_SYNTHESIS_OF_ACTIVE_UBQUITIN, REACTOME_SYNTHESIS_OF_ACTIVE_UBQUITIN, REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_P107_RBL1_AND_P130_RBL2_IN_COMPLEX_WITH_HDAC1, REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_P107_RBL1_AND_P130_RBL2_IN_COMPLEX_WITH_HDAC1, REACTOME_PEROXISOMAL_PROTEIN_IMPORT, REACTOME_PEROXISOMAL_PROTEIN_IMPORT, REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT, REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT, REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERASES_BYPASSES_LESIONS_ON_DNA_TEMPLATE, REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERASES_BYPASSES_LESIONS_ON_DNA_TEMPLATE, REACTOME_UNWINDING_OF_DNA, REACTOME_UNWINDING_OF_DNA, REACTOME_CIRCADIAN_CLOCK, REACTOME_CIRCADIAN_CLOCK, WP_DNA_DAMAGE_RESPONSE, WP_DNA_DAMAGE_RESPONSE, REACTOME_LAGGING_STRAND_SYNTHESIS, REACTOME_LAGGING_STRAND_SYNTHESIS, REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT, REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT, REACTOME_ABC_TRANSPORTER_DISORDERS, REACTOME_ABC_TRANSPORTER_DISORDERS, REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS, REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS, REACTOME_DISEASES_OF_MITOTIC_CELL_CYCLE, REACTOME_DISEASES_OF_MITOTIC_CELL_CYCLE, REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT, REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT, KEGG_CHRONIC_MYELOID_LEUKEMIA, KEGG_CHRONIC_MYELOID_LEUKEMIA, REACTOME_HEDGEHOG_OFF_STATE, REACTOME_HEDGEHOG_OFF_STATE, REACTOME_E2F_ENABLED_INHIBITION_OF_PRE_REPLICATION_COMPLEX_FORMATION, REACTOME_E2F_ENABLED_INHIBITION_OF_PRE_REPLICATION_COMPLEX_FORMATION, REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS, REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS, REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RESPONSE, REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RESPONSE, REACTOME_PHOSPHORYLATION_OF_THE_APC_C, REACTOME_PHOSPHORYLATION_OF_THE_APC_C, REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B, REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B, PID_BARD1_PATHWAY, PID_BARD1_PATHWAY, PID_E2F_PATHWAY, PID_E2F_PATHWAY, REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE, REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ACETYLATION, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ACETYLATION, WP_ATR_PATHWAY, PID_ATR_PATHWAY, WP_INTEGRATED_CANCER_PATHWAY, WP_INTEGRATED_CANCER_PATHWAY, REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE, REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE, PID_FOXO_PATHWAY, PID_FOXO_PATHWAY, REACTOME_DDX58_IFFI1_MEDIATED_INDUCION_OF_INTERFERON_ALPHA_BETA, REACTOME_DDX58_IFFI1_MEDIATED_INDUCION_OF_INTERFERON_ALPHA_BETA, KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION, KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION, KEGG_MISMATCH_REPAIR, KEGG_MISMATCH_REPAIR, BIOCARTA_MCM_PATHWAY, BIOCARTA_MCM_PATHWAY, WP_DNA_MISMATCH_REPAIR, WP_DNA_MISMATCH_REPAIR, REACTOME_POLYMERASE_SWITCHING, REACTOME_POLYMERASE_SWITCHING, REACTOME_NEGATIVE_REGULATION_OF_MAPK_PATHWAY, REACTOME_NEGATIVE_REGULATION_OF_MAPK_PATHWAY, REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RB1_E2F1, REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RB1_E2F1, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2, REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2, REACTOME_TRANSLATION_SYNTHESIS_BY_POLK, REACTOME_TRANSLATION_SYNTHESIS_BY_POLK, REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A, REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A, BIOCARTA_CELL_CYCLE_PATHWAY, BIOCARTA_CELL_CYCLE_PATHWAY, REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC_ORIGIN_COMPLEX, REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC_ORIGIN_COMPLEX, REACTOME_REGULATED_NECROSIS, REACTOME_REGULATED_NECROSIS, REACTOME_TERMINATION_OF_TRANSLATION_DNA_SYNTHESIS, REACTOME_TERMINATION_OF_TRANSLATION_DNA_SYNTHESIS, WP_DNA_DOUBLE_STRAND_BREAKS_DSBS_AND_CELLULAR_RESPONSE_VIA_ATM, WP_DNA_DOUBLE_STRAND_BREAKS_DSBS_AND_CELLULAR_RESPONSE_VIA_ATM, REACTOME_BUDDING_AND_MATURATION_OF_HIV_VIRION, REACTOME_BUDDING_AND_MATURATION_OF_HIV_VIRION, KEGG_HOMOLOGOUS_RECOMBINATION, KEGG_HOMOLOGOUS_RECOMBINATION, REACTOME_G0_AND_EARLY_G1, REACTOME_G0_AND_EARLY_G1, REACTOME_TNF_SIGNALING, REACTOME_TNF_SIGNALING, WP_BASE_EXCISION_REPAIR, WP_BASE_EXCISION_REPAIR, REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND, REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND, REACTOME_METABOLISM_OF_POLYAMINES, REACTOME_METABOLISM_OF_POLYAMINES, REACTOME_FLT3_SIGNALING_IN_DISEASE, REACTOME_FLT3_SIGNALING_IN_DISEASE, REACTOME_ABERRANT_REGULATION_OF_MITOTIC_EXIT_IN_CANCER_DUE_TO_RB1_DEFECTS, REACTOME_ABERRANT_REGULATION_OF_MITOTIC_EXIT_IN_CANCER_DUE_TO_RB1_DEFECTS, REACTOME_NEGATIVE_REGULATORS_OF_DDX58_IFFI1_SIGNALING, REACTOME_NEGATIVE_REGULATORS_OF_DDX58_IFFI1_SIGNALING, REACTOME_SARS_COV_1_INFECTION, REACTOME_SARS_COV_1_INFECTION, REACTOME_REGULATION_OF_TNFR1_SIGNALING, REACTOME_REGULATION_OF_TNFR1_SIGNALING, REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_DREAM_COMPLEX, REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_DREAM_COMPLEX, WP_RIBSIN_AS_A_REGULATOR_OF_DENDAMATION, WP_RIBSIN_AS_A_REGULATOR_OF_DENDAMATION, WP_SIGNALING_PATHWAYS_IN_GLOBLASTOMA, WP_SIGNALING_PATHWAYS_IN_GLOBLASTOMA, REACTOME_TNFR1_INDUCED_NFKAPPAB_SIGNALING_PATHWAY, REACTOME_TNFR1_INDUCED_NFKAPPAB_SIGNALING_PATHWAY, BIOCARTA_PROTEASOME_PATHWAY, BIOCARTA_PROTEASOME_PATHWAY, REACTOME_FLT3_SIGNALING, REACTOME_FLT3_SIGNALING, REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDHL_IN_LATE_ANAPHASE, REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDHL_IN_LATE_ANAPHASE, REACTOME_INTRINSIC_PATHWAY_FOR_PROPORTIONATE_RESPONSE, REACTOME_INTRINSIC_PATHWAY_FOR_PROPORTIONATE_RESPONSE, REACTOME_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR, REACTOME_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR, SIG_BCR_SIGNALING_PATHWAY, SIG_BCR_SIGNALING_PATHWAY, REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER, REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER, REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1, REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1, REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE, REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE, KEGG_P53_SIGNALING_PATHWAY, KEGG_P53_SIGNALING_PATHWAY, WP_CHROMOSOMAL_AND_MICROSATELLITE_INSTABILITY_IN_COLORECTAL_CANCER, WP_CHROMOSOMAL_AND_MICROSATELLITE_INSTABILITY_IN_COLORECTAL_CANCER, REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION, REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION, PID_MYC_PATHWAY, PID_MYC_PATHWAY, REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION, REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION, PID_ATM_PATHWAY, PID_ATM_PATHWAY, REACTOME_SIGNALING_BY_CSF3_G_CSF, REACTOME_SIGNALING_BY_CSF3_G_CSF, KEGG_ERBB_SIGNALING_PATHWAY, KEGG_ERBB_SIGNALING_PATHWAY, REACTOME_RESPONSE_OF_MTB_TO_PHAGOCYTOSIS, REACTOME_RESPONSE_OF_MTB_TO_PHAGOCYTOSIS, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_METHYLATION, REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_METHYLATION, REACTOME_RIPK1_MEDIATED_REGULATED_NECROSIS, REACTOME_RIPK1_MEDIATED_REGULATED_NECROSIS, REACTOME_TICAM1_RIP1_MEDIATED_IKK_COMPLEX_RECRUITMENT, REACTOME_TICAM1_RIP1_MEDIATED_IKK_COMPLEX_RECRUITMENT, REACTOME_DNA_REPLICATION_IN_KIDNEY, REACTOME_DNA_REPLICATION_IN_KIDNEY, KEGG_ACUTE_MYELOID_LEUKEMIA, KEGG_ACUTE_MYELOID_LEUKEMIA, REACTOME_POLYMERASE_SWITCHING_ON_THE_C_STRAND_OF_THE_TELOMERE, REACTOME_POLYMERASE_SWITCHING_ON_THE_C_STRAND_OF_THE_TELOMERE, REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS, REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS, WP_REGULATION_OF_SISTER_CHROMATID_SEPARATION_AT_THE_METAPHASEANAPHASE_TRANSITION, WP_REGULATION_OF_SISTER_CHROMATID_SEPARATION_AT_THE_METAPHASEANAPHASE_TRANSITION, WP_ERBB_SIGNALING_PATHWAY, WP_ERBB_SIGNALING_PATHWAY, REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1_G1, REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1_G1, PID_AURORA_A_PATHWAY, PID_AURORA_A_PATHWAY, REACTOME_TRANSLATION_OF_SARS_COV_1_STRUCTURAL_PROTEINS, REACTOME_TRANSLATION_OF_SARS_COV_1_STRUCTURAL_PROTEINS, REACTOME_GLYCOGEN_SYNTHESIS, REACTOME_GLYCOGEN_SYNTHESIS, PID_P73PATHWAY, PID_P73PATHWAY, WP_GASTRIC_CANCER_NETWORK_2, WP_GASTRIC_CANCER_NETWORK_2, KEGG_COLORECTAL_CANCER, KEGG_COLORECTAL_CANCER, REACTOME_SUPPRESSION_OF_PHAGOSOMAL_MATURATION, REACTOME_SUPPRESSION_OF_PHAGOSOMAL_MATURATION, WP_GASTRIC_CANCER_NETWORK_1, WP_GASTRIC_CANCER_NETWORK_1, BIOCARTA_ETS_PATHWAY, BIOCARTA_ETS_PATHWAY, WP_INTEGRATED_BREAST_CANCER_PATHWAY, WP_INTEGRATED_BREAST_CANCER_PATHWAY, REACTOME_TRANSLATION_SYNTHESIS_BY_POLH, REACTOME_TRANSLATION_SYNTHESIS_BY_POLH, REACTOME_ER_QUALITY_CONTROL_COMPARTMENT_ERQC, REACTOME_ER_QUALITY_CONTROL_COMPARTMENT_ERQC, REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS, REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS, REACTOME_SIGNALING_BY_NOTCH1, REACTOME_SIGNALING_BY_NOTCH1, REACTOME_INACTIVATION_OF_CSF3_G_CSF_SIGNALING, REACTOME_INACTIVATION_OF_CSF3_G_CSF_SIGNALING, REACTOME_POLB_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR, REACTOME_POLB_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR, REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING, REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING, BIOCARTA_RACCD3_PATHWAY, BIOCARTA_RACCD3_PATHWAY, PID_HEDGEHOG_GLI1_PATHWAY, PID_HEDGEHOG_GLI1_PATHWAY, REACTOME_ALPHA_PROTEIN_KINASE_1_SIGNALING_PATHWAY, REACTOME_ALPHA_PROTEIN_KINASE_1_SIGNALING_PATHWAY, WP_EGFR_TYROSINE_KINASE_INHIBITOR_RESISTANCE, WP_EGFR_TYROSINE_KINASE_INHIBITOR_RESISTANCE, REACTOME_MITOPHAGY, REACTOME_MITOPHAGY, PID_P13CAKT_PATHWAY, PID_P13CAKT_PATHWAY, REACTOME_TCR_SIGNALING, REACTOME_TCR_SIGNALING, REACTOME_CALNEXIN_CALRETICULIN_CYCLE, REACTOME_CALNEXIN_CALRETICULIN_CYCLE, BIOCARTA_P53HYPOXIA_PATHWAY, BIOCARTA_P53HYPOXIA_PATHWAY, REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM_CSF_SIGNALING, REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM_CSF_SIGNALING, REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES, REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES, REACTOME_SIGNALING_BY_NOTCH1_PEST_DOMAIN_MUTANTS_IN_CANCER, REACTOME_SIGNALING_BY_NOTCH1_PEST_DOMAIN_MUTANTS_IN_CANCER, REACTOME_ASSEMBLY_OF_THE_HIV_VIRION, REACTOME_ASSEMBLY_OF_THE_HIV_VIRION, BIOCARTA_P53_PATHWAY, BIOCARTA_P53_PATHWAY, PID_TELOMERASE_PATHWAY, PID_TELOMERASE_PATHWAY, REACTOME_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION, REACTOME_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION, REACTOME_PEXOPHAGY, REACTOME_PEXOPHAGY, WP_ATM_SIGNALING_PATHWAY, WP_ATM_SIGNALING_PATHWAY, REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMA25, REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMA25, WP_NUCLEOTIDE_METABOLISM, WP_NUCLEOTIDE_METABOLISM, REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS, REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS, REACTOME_MITOTIC_TELOPHASE_CYTOKINESIS, REACTOME_MITOTIC_TELOPHASE_CYTOKINESIS, WP_PRADERWILLI_AND_ANGELMAN_SYNDROME, WP_PRADERWILLI_AND_ANGELMAN_SYNDROME, REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS, REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS, WP_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY, WP_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY, REACTOME_RAS_PROCESSING, REACTOME_RAS_PROCESSING, REACTOME_GLYCOGEN_STORAGE_DISEASES, REACTOME_GLYCOGEN_STORAGE_DISEASES, REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_CYCLE_ARREST, REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_CYCLE_ARREST, REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL, REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL, WP_PARKINUBIQUITIN_PROTEASOMAL_SYSTEM_PATHWAY, WP_PARKINUBIQUITIN_PROTEASOMAL_SYSTEM_PATHWAY, REACTOME_PREVENTION_OF_PHAGOSOMAL_LYSOSOMAL_FUSION, REACTOME_PREVENTION_OF_PHAGOSOMAL_LYSOSOMAL_FUSION, WP_IL5_SIGNALING_PATHWAY, WP_IL5_SIGNALING_PATHWAY, PID_BETA_CATENIN_DEG_PATHWAY, PID_BETA_CATENIN_DEG_PATHWAY, REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING, REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING, KEGG_PROSTATE_CANCER, KEGG_PROSTATE_CANCER, PID_RETINOIC_ACID_PATHWAY, PID_RETINOIC_ACID_PATHWAY, SIG_CHEMOTAXIS_SIC_CHEMOTAXIS, KEGG_PANCREATIC_CANCER, KEGG_PANCREATIC_CANCER, REACTOME_GLYCOGEN_METABOLISM, REACTOME_GLYCOGEN_METABOLISM, BIOCARTA_G2_PATHWAY, BIOCARTA_G2_PATHWAY, WP_AMPACTIVATED_PROTEIN_KINASE_AMPK_SIGNALING, WP_AMPACTIVATED_PROTEIN_KINASE_AMPK_SIGNALING, REACTOME_ACTIVATION_OF_PUMA_AND_TRANSLOCATION_TO_MITOCHONDRIA, REACTOME_ACTIVATION_OF_PUMA_AND_TRANSLOCATION_TO_MITOCHONDRIA, REACTOME_TICAM1_DEPENDENT_ACTIVATION_OF_IRF3_IRF7, REACTOME_TICAM1_DEPENDENT_ACTIVATION_OF_IRF3_IRF7, REACTOME_TICAM1_TRAF6_DEPENDENT_INDUCION_OF_TAK1_COMPLEX, REACTOME_TICAM1_TRAF6_DEPENDENT_INDUCION_OF_TAK1_COMPLEX, REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMA22_SMA23_SMA24_HETEROTRIMER, REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMA22_SMA23_SMA24_HETEROTRIMER, KEGG_GLIOMA, KEGG_GLIOMA, REACTOME_DOWNREGULATION_OF_SMA22_3_SMA24_TRANSCRIPTIONAL_ACTIVITY, REACTOME_DOWNREGULATION_OF_SMA22_3_SMA24_TRANSCRIPTIONAL_ACTIVITY, REACTOME_MAP3K8_TPL2_DEPENDENT_MAPK1_3_ACTIVATION, REACTOME_MAP3K8_TPL2_DEPENDENT_MAPK1_3_ACTIVATION
--	--