
GSE41867_NAIVE_VS_DAY15_LCMV_EFFECTOR_CD8_TCELL_UP, GSE41867_NAIVE_VS_DAY30_LCMV_ARMSTRONG_MEMORY_CD8_TCELL_DN, GSE41867_NAIVE_VS_DAY30_LCMV_ARMSTRONG_MEMORY_CD8_TCELL_UP, GSE14908_ATOPIC_VS_NONATOPIC_PATIENT_RESTING_CD4_TCELL_DN, GSE14908_ATOPIC_VS_NONATOPIC_PATIENT_RESTING_CD4_TCELL_UP, GSE7764_IL15_TREATED_VS_CTRL_NK_CELL_24H_UP, GSE7764_IL15_TREATED_VS_CTRL_NK_CELL_24H_DN, GSE29164_UNTREATED_VS_CD8_TCELL_AND_IL12_TREATED_MELANOMA_DAY3_DN, GSE29164_UNTREATED_VS_CD8_TCELL_AND_IL12_TREATED_MELANOMA_DAY3_UP, GSE14908_ATOPIC_VS_NONATOPIC_PATIENT_HDM_STIM_CD4_TCELL_UP, GSE14908_ATOPIC_VS_NONATOPIC_PATIENT_HDM_STIM_CD4_TCELL_DN, GSE17721_CTRL_VS_PAM3CSK4_1H_BMDC_UP, GSE17721_CTRL_VS_PAM3CSK4_1H_BMDC_DN, GSE11864_CSF1_IFNG_VS_CSF1_IFNG_PAM3CYS_IN_MAC_UP, GSE11864_CSF1_IFNG_VS_CSF1_IFNG_PAM3CYS_IN_MAC_DN, GSE3982_EOSINOPHIL_VS_DC_DN, GSE3982_EOSINOPHIL_VS_DC_UP, GSE9878_CTRL_VS_EBF_TRANSDUCED_PAX5_KO_PRO_BCELL_DN, GSE9878_CTRL_VS_EBF_TRANSDUCED_PAX5_KO_PRO_BCELL_UP, GSE13485_DAY1_VS_DAY7_YF17D_VACCINE_PBMC_DN, GSE13485_DAY1_VS_DAY7_YF17D_VACCINE_PBMC_UP, GSE17721_CTRL_VS_POLYIC_1H_BMDC_UP, GSE17721_CTRL_VS_POLYIC_1H_BMDC_DN, GSE5503_MLN_DC_VS_SPLEEN_DC_ACTIVATED_ALLOGENIC_TCELL_DN, GSE5503_MLN_DC_VS_SPLEEN_DC_ACTIVATED_ALLOGENIC_TCELL_UP, GSE42724_B1_BCELL_VS_PLASMABLAST_UP, GSE42724_B1_BCELL_VS_PLASMABLAST_DN, GSE40277_GATA1_AND_SATB1_TRANSDUCED_VS_CTRL_CD4_TCELL_DN, GSE40277_GATA1_AND_SATB1_TRANSDUCED_VS_CTRL_CD4_TCELL_UP, GSE16522_MEMORY_VS_NAIVE_ANTI_CD3CD28_STIM_CD8_TCELL_DN, GSE16522_MEMORY_VS_NAIVE_ANTI_CD3CD28_STIM_CD8_TCELL_UP, IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR, IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR, GOBP_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS, GOBP_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS, GSE40274_HELIOS_VS_FOXP3_AND_HELIOS_TRANSDUCED_ACTIVATED_CD4_TCELL_DN, GSE40274_HELIOS_VS_FOXP3_AND_HELIOS_TRANSDUCED_ACTIVATED_CD4_TCELL_UP, GSE14308_TH1_VS_NATURAL_TREG_UP, GSE14308_TH1_VS_NATURAL_TREG_DN, GSE41867_NAIVE_VS_DAY8_LCMV_ARMSTRONG_EFFECTOR_CD8_TCELL_UP, GSE41867_NAIVE_VS_DAY8_LCMV_ARMSTRONG_EFFECTOR_CD8_TCELL_DN, GOBP_NUCLEUS_ORGANIZATION, GOBP_NUCLEUS_ORGANIZATION, GSE39201_UNTREATED_VS_IFNA_TREATED_FIBROBLAST_DN, GSE39201_UNTREATED_VS_IFNA_TREATED_FIBROBLAST_UP, GSE32423_CTRL_VS_IL4_MEMORY_CD8_TCELL_UP, GSE32423_CTRL_VS_IL4_MEMORY_CD8_TCELL_DN, GSE19888_NO_PRETREAT_VS_ADENOSINE_A3R_INHIBITOR_PRETREATED_MAST_CELL_TCELL_MEMBRANES_ACT_UP, GSE19888_NO_PRETREAT_VS_ADENOSINE_A3R_INHIBITOR_PRETREATED_MAST_CELL_TCELL_MEMBRANES_ACT_DN, GSE12003_4D_VS_8D_CULTURE_BM_PROGENITOR_UP, GSE12003_4D_VS_8D_CULTURE_BM_PROGENITOR_DN, GSE21670_TGFB_VS_TGFB_AND_IL6_TREATED_STAT3_KO_CD4_TCELL_UP, GSE21670_TGFB_VS_TGFB_AND_IL6_TREATED_STAT3_KO_CD4_TCELL_DN, GSE13485_CTRL_VS_DAY3_YF17D_VACCINE_PBMC_DN, GSE13485_CTRL_VS_DAY3_YF17D_VACCINE_PBMC_UP, HP_DEATH_IN_INFANCY, HP_DEATH_IN_INFANCY, GOCC_NUCLEAR_PORE, GOCC_NUCLEAR_PORE, GSE16385_UNTREATED_VS_12H_ROSIGLITAZONE_IFNG_TNF_TREATED_MACROPHAGE_DN, GSE16385_UNTREATED_VS_12H_ROSIGLITAZONE_IFNG_TNF_TREATED_MACROPHAGE_DN, GSE15930_STIM_VS_STIM_AND_IFNAB_48H_CD8_T_CELL_DN, GSE15930_STIM_VS_STIM_AND_IFNAB_48H_CD8_T_CELL_DN, HP_FETAL_ULTRASOUND_SOFT_MARKER, HP_FETAL_ULTRASOUND_SOFT_MARKER, GSE360_DC_VS_MAC_L_MAJOR_DN, GSE360_DC_VS_MAC_L_MAJOR_DN, GOBP_TRNA_TRANSPORT, GOBP_TRNA_TRANSPORT, GOCC_HOST_CELLULAR_COMPONENT, GOCC_HOST_CELLULAR_COMPONENT, GOBP_MULTI_ORGANISM_LOCALIZATION, GOBP_MULTI_ORGANISM_LOCALIZATION, MIR6501_3P, MIR6501_3P, MIR197_3P, MIR197_3P, REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRONLESS_TRANSCRIPTS, REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRONLESS_TRANSCRIPTS, GSE12505_WT_VS_E2_2_HET_PDC_DN, GSE12505_WT_VS_E2_2_HET_PDC_DN, GOBP_CHROMOSOME_SEPARATION, GOBP_CHROMOSOME_SEPARATION, GOMF_HEAT_SHOCK_PROTEIN_BINDING, GOMF_HEAT_SHOCK_PROTEIN_BINDING, REACTOME_NS1_MEDIATED_EFFECTS_ON_HOST_PATHWAYS, REACTOME_NS1_MEDIATED_EFFECTS_ON_HOST_PATHWAYS, MTOR_UP.V1_UP, MTOR_UP.V1_UP, HP_NEOPLASM_OF_THE_SKELETAL_SYSTEM, HP_NEOPLASM_OF_THE_SKELETAL_SYSTEM, GSE19888_ADENOSINE_A3R_INH_VS_ACT_WITH_INHIBITOR_PRETREATMENT_IN_MAST_CELL_UP, GSE19888_ADENOSINE_A3R_INH_VS_ACT_WITH_INHIBITOR_PRETREATMENT_IN_MAST_CELL_UP, HP_HALLUCINATIONS, HP_HALLUCINATIONS, HP_SEVERE_MUSCULAR_HYPOTONIA, HP_SEVERE_MUSCULAR_HYPOTONIA, GOBP_MATURATION_OF_SSU_RRNA, GOBP_MATURATION_OF_SSU_RRNA, HP_SKELETAL_DYSPLASIA, HP_SKELETAL_DYSPLASIA, HP_MULTIPLE_CAFE_AU_LAIT_SPOTS, HP_MULTIPLE_CAFE_AU_LAIT_SPOTS, REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA, REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA, REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLEUS, REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLEUS, GOCC_HISTONE_DEACETYLASE_COMPLEX, GOCC_HISTONE_DEACETYLASE_COMPLEX, GOBP_PROTEIN_N_LINKED_GLYCOSYLATION, GOBP_PROTEIN_N_LINKED_GLYCOSYLATION, REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN, REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN, GOBP_POSTREPLICATION_REPAIR, GOBP_POSTREPLICATION_REPAIR, GSE1448_ANTI_VALPHA2_VS_VBETA5_DP_THYMOCYTE_DN, GSE1448_ANTI_VALPHA2_VS_VBETA5_DP_THYMOCYTE_DN, GSE22443_IL2_VS_IL12_TREATED_ACT_CD8_TCELL_UP, GSE22443_IL2_VS_IL12_TREATED_ACT_CD8_TCELL_UP, GOBP_REGULATION_OF_CHROMOSOME_SEPARATION, GOBP_REGULATION_OF_CHROMOSOME_SEPARATION, HP_ABNORMALITY_OF_THE_LARYNX, HP_ABNORMALITY_OF_THE_LARYNX, GCM_DENR, GCM_DENR, GOBP_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA, GOBP_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA, GOBP_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE, GOBP_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE, GSE22611_NOD2_TRANSD_VS_CTRL_TRANSD_HEK293_MDP_STIM_6H_DN, GSE22611_NOD2_TRANSD_VS_CTRL_TRANSD_HEK293_MDP_STIM_6H_DN, HALLMARK_CHOLESTEROL_HOMEOSTASIS, HALLMARK_CHOLESTEROL_HOMEOSTASIS, HP_NEURODEGENERATION, HP_NEURODEGENERATION, HP_ICHTHYOSIS, HP_ICHTHYOSIS, GOBP_NUCLEAR_ENVELOPE_ORGANIZATION, GOBP_NUCLEAR_ENVELOPE_ORGANIZATION, GOBP_PROTEIN_K11_LINKED_UBIQUITINATION, GOBP_PROTEIN_K11_LINKED_UBIQUITINATION, REACTOME_RHOH_GTPASE_CYCLE, REACTOME_RHOH_GTPASE_CYCLE, GOCC_90S_PRERIBOSOME, GOCC_90S_PRERIBOSOME, BIOCARTA_MET_PATHWAY, BIOCARTA_MET_PATHWAY, GOCC_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX, GOCC_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX, GOBP_ENDOSOME_TO_LYSOSOME_TRANSPORT, GOBP_ENDOSOME_TO_LYSOSOME_TRANSPORT, GSE29618_LAIV_VS_TIV_FLU_VACCINE_DAY7_PDC_DN, GSE29618_LAIV_VS_TIV_FLU_VACCINE_DAY7_PDC_DN, HP_DYSPHASIA, HP_DYSPHASIA, HP_DYSGRAPHIA, HP_DYSGRAPHIA, GOMF_TAU_PROTEIN_BINDING, GOMF_TAU_PROTEIN_BINDING, HP_ABNORMALITY_OF_THE_SHOULDER_GIRDLE_MUSCULATURE, HP_ABNORMALITY_OF_THE_SHOULDER_GIRDLE_MUSCULATURE, HP_PATHOLOGIC_FRACTURE, HP_PATHOLOGIC_FRACTURE, GOBP_PEROXISOMAL_MEMBRANE_TRANSPORT, GOBP_PEROXISOMAL_MEMBRANE_TRANSPORT, HP_TRUNCAL_ATAXIA, HP_TRUNCAL_ATAXIA, HP_NEOPLASM_OF_THE_THYROID_GLAND, HP_NEOPLASM_OF_THE_THYROID_GLAND, HP_PROGRESSIVE_MUSCLE_WEAKNESS, HP_PROGRESSIVE_MUSCLE_WEAKNESS, HP_ABNORMALITY_OF_SKULL_OSSIFICATION, HP_ABNORMALITY_OF_SKULL_OSSIFICATION, MORI_PLASMA_CELL_UP, MORI_PLASMA_CELL_UP, GOBP_PROTEIN_DESTABILIZATION, GOBP_PROTEIN_DESTABILIZATION, HP_ABNORMAL_SYNAPTIC_TRANSMISSION_AT_THE_NEUROMUSCULAR_JUNCTION, HP_ABNORMAL_SYNAPTIC_TRANSMISSION_AT_THE_NEUROMUSCULAR_JUNCTION, REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION, REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION, RIZKI_TUMOR_INVASIVENESS_2D_DN, RIZKI_TUMOR_INVASIVENESS_2D_DN, STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN, STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN, HP_ABNORMAL_CIRCULATING_LONG_CHAIN_FATTY_ACID_CONCENTRATION, HP_ABNORMAL_CIRCULATING_LONG_CHAIN_FATTY_ACID_CONCENTRATION, REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURSOR_BIOSYNTHESIS, REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURSOR_BIOSYNTHESIS, WP_SEROTONIN_RECEPTOR_467_AND_NR3C_SIGNALING, WP_SEROTONIN_RECEPTOR_467_AND_NR3C_SIGNALING, HP_FLAT_OCCIPUT, HP_FLAT_OCCIPUT, MIR660_5P, MIR660_5P, GOBP_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS, GOBP_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS, GOMF_DYNEIN_COMPLEX_BINDING, GOMF_DYNEIN_COMPLEX_BINDING, MIR3155A, MIR3155B, MIR3155A, MIR3155B, GOCC_RNA_POLYMERASE_III_COMPLEX, GOCC_RNA_POLYMERASE_III_COMPLEX, REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION, REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION, HP_GLIOBLASTOMA_MULTIFORME, HP_GLIOBLASTOMA_MULTIFORME, GOBP_BLASTOCYST_GROWTH, GOBP_BLASTOCYST_GROWTH, HP_SPASTIC_GAIT, HP_SPASTIC_GAIT, GOBP_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS, GOBP_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION, GOBP_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION, HP_ABNORMALITY_OF_THE_SUPRAORBITAL_RIDGES, HP_ABNORMALITY_OF_THE_SUPRAORBITAL_RIDGES, HP_VERY_LONG_CHAIN_FATTY_ACID_ACCUMULATION, HP_VERY_LONG_CHAIN_FATTY_ACID_ACCUMULATION, GOBP_PEPTIDYL_ASPARAGINE_MODIFICATION, GOBP_PEPTIDYL_ASPARAGINE_MODIFICATION, GOBP_SNRNA_METABOLIC_PROCESS, GOBP_SNRNA_METABOLIC_PROCESS, HP_ABNORMALITY_OF_THE_CARPAL_BONES, HP_ABNORMALITY_OF_THE_CARPAL_BONES, HP_DIMINISHED_MOVEMENT, HP_DIMINISHED_MOVEMENT, GOBP_MISMATCH_REPAIR, GOBP_MISMATCH_REPAIR, HP_GENU_VARUM, HP_GENU_VARUM, REACTOME_RUNX2_REGULATES_BONE_DEVELOPMENT, REACTOME_RUNX2_REGULATES_BONE_DEVELOPMENT, HP_LIMB_GIRDLE_MUSCLE_WEAKNESS, HP_LIMB_GIRDLE_MUSCLE_WEAKNESS, GOBP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR, GOBP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR, HP_ABNORMAL_CIRCULATING_BILIRUBIN_CONCENTRATION, HP_ABNORMAL_CIRCULATING_BILIRUBIN_CONCENTRATION, REACTOME_DEFECTS_IN_VITAMIN_AND_COFACTOR_METABOLISM, REACTOME_DEFECTS_IN_VITAMIN_AND_COFACTOR_METABOLISM, GOMF_PHOSPHOTRANSFERASE_ACTIVITY_FOR_OTHER_SUBSTITUTED_PHOSPHATE_GROUPS, GOMF_PHOSPHOTRANSFERASE_ACTIVITY_FOR_OTHER_SUBSTITUTED_PHOSPHATE_GROUPS, GOBP_REGULATION_OF_CYTOPLASMIC_TRANSPORT, GOBP_REGULATION_OF_CYTOPLASMIC_TRANSPORT, GOBP_HISTONE_EXCHANGE, GOBP_HISTONE_EXCHANGE, MIR4637, MIR4637, GOMF_KINESIN_BINDING, GOMF_KINESIN_BINDING, BIOCARTA_MAL_PATHWAY, BIOCARTA_MAL_PATHWAY, GOBP_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS, GOBP_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS, GOBP_POSITIVE_REGULATION_OF_CHROMOSOME_SEPARATION, GOBP_POSITIVE_REGULATION_OF_CHROMOSOME_SEPARATION, HP_HYPOKINESIA, HP_HYPOKINESIA, HP_ABNORMALITY_OF_THE_WING_OF_THE_ILIUM, HP_ABNORMALITY_OF_THE_WING_OF_THE_ILIUM, GOMF_TRANSCRIPTION_COREPRESSOR_BINDING, GOMF_TRANSCRIPTION_COREPRESSOR_BINDING, HP_APLASIA_HYPOPLASIA_OF_THE_EYELID, HP_APLASIA_HYPOPLASIA_OF_THE_EYELID, HP_LIMB_GIRDLE_MUSCLE_ATROPHY, HP_LIMB_GIRDLE_MUSCLE_ATROPHY, HP_BRUSHFIELD_SPOTS, HP_BRUSHFIELD_SPOTS, HP_FATIGABLE_WEAKNESS_OF_BULBAR_MUSCLES, HP_FATIGABLE_WEAKNESS_OF_BULBAR_MUSCLES, HP_EPIPHYSEAL_STIPPLING, HP_EPIPHYSEAL_STIPPLING, BIOCARTA_PPARA_PATHWAY, BIOCARTA_PPARA_PATHWAY, GOMF_RNA_POLYMERASE_II_TRANSCRIPTION_COREGULATOR_BINDING, GOMF_RNA_POLYMERASE_II_TRANSCRIPTION_COREGULATOR_BINDING, SOKOLEV_PBMC_PANDEMRIX_AGE_18_64VS_7DY_DN, SOKOLEV_PBMC_PANDEMRIX_AGE_18_64VS_7DY_DN, WP_COMMON_PATHWAYS_UNDERLYING_DRUG_ADDICTION, WP_COMMON_PATHWAYS_UNDERLYING_DRUG_ADDICTION, HP_CAPILLARY_HEMANGIOMA, HP_CAPILLARY_HEMANGIOMA, HP_RECTAL_FISTULA, HP_RECTAL_FISTULA, GOBP_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION, GOBP_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION, HP_PANCREATIC_ADENOCARCINOMA, HP_PANCREATIC_ADENOCARCINOMA, GOBP_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION, GOBP_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION, HP_UNDERDEVELOPED_SUPRAORBITAL_RIDGES, HP_UNDERDEVELOPED_SUPRAORBITAL_RIDGES, HP_MILDLY_ELEVATED_CREATINE_KINASE, HP_MILDLY_ELEVATED_CREATINE_KINASE, GOBP_SNRNA_PROCESSING, GOBP_SNRNA_PROCESSING, HP_ABNORMAL_TONGUE_PHYSIOLOGY, HP_ABNORMAL_TONGUE_PHYSIOLOGY, HP_CARDIAC_DIVERTICULUM, HP_CARDIAC_DIVERTICULUM, GOBP_DOLICHOL_METABOLIC_PROCESS, GOBP_DOLICHOL_METABOLIC_PROCESS, GOBP_HISTONE_H3_DEACETYLATION, GOBP_HISTONE_H3_DEACETYLATION, GOBP_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE, GOBP_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE, HP_INCREASED_PROTEINOGENIC_AMINO_ACID_LEVEL_IN_URINE, HP_INCREASED_PROTEINOGENIC_AMINO_ACID_LEVEL_IN_URINE, HP_DEGENERATION_OF_THE_LATERAL_CORTICOSPINAL_TRACTS, HP_DEGENERATION_OF_THE_LATERAL_CORTICOSPINAL_TRACTS, KAMIKUBO_MYELOID_MN1_NETWORK, KAMIKUBO_MYELOID_MN1_NETWORK, GOBP_INNER_CELL_MASS_CELL_PROLIFERATION, GOBP_INNER_CELL_MASS_CELL_PROLIFERATION, MIR484, MIR484, MODULE_481, MODULE_481, MIR1266_3P, MIR1266_3P, GOBP_POSITIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE, GOBP_POSITIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE, GOCC_INTEGRATOR_COMPLEX, GOCC_INTEGRATOR_COMPLEX, GOCC_INTRACILIARY_TRANSPORT_PARTICLE, GOCC_INTRACILIARY_TRANSPORT_PARTICLE, GOBP_DOLICHYL_DIPHOSPHATE_BIOSYNTHETIC_PROCESS, GOBP_DOLICHYL_DIPHOSPHATE_BIOSYNTHETIC_PROCESS, HP_POSITIVE_ROMBERG_SIGN, HP_POSITIVE_ROMBERG_SIGN, MODULE_544, MODULE_544, REACTOME_RUNX2_REGULATES_OSTEOBLAST_DIFFERENTIATION, REACTOME_RUNX2_REGULATES_OSTEOBLAST_DIFFERENTIATION, GOCC_INTRACILIARY_TRANSPORT_PARTICLE_B, GOCC_INTRACILIARY_TRANSPORT_PARTICLE_B, GOBP_AUTOPHAGOSOME_MATURATION, GOBP_AUTOPHAGOSOME_MATURATION, GOBP_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION, GOBP_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION, HP_ZONULAR_CATARACT, HP_ZONULAR_CATARACT, HP_FATIGABLE_WEAKNESS_OF_SWALLOWING_MUSCLES, HP_FATIGABLE_WEAKNESS_OF_SWALLOWING_MUSCLES, GOBP_GALACTOSE_CATABOLIC_PROCESS, GOBP_GALACTOSE_CATABOLIC_PROCESS, GOBP_PLASMA_MEMBRANE_TO_ENDOSOME_TRANSPORT, GOBP_PLASMA_MEMBRANE_TO_ENDOSOME_TRANSPORT, GOCC_MRNA_EDITING_COMPLEX, GOCC_MRNA_EDITING_COMPLEX, MIR375_3P, MIR375_3P, GOBP_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL, GOBP_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL, HP_POROKERATOSIS, HP_POROKERATOSIS, GOBP_MEIOTIC_CYTOKINESIS, GOBP_MEIOTIC_CYTOKINESIS, GOBP_INCLUSION_BODY_ASSEMBLY, GOBP_INCLUSION_BODY_ASSEMBLY, HP_CLUMSINESS, HP_CLUMSINESS, GOBP_POSITIVE_REGULATION_OF_MEMBRANE_POTENTIAL, GOBP_POSITIVE_REGULATION_OF_MEMBRANE_POTENTIAL, FIGUEROA_AML_METHYLATION_CLUSTER_2_UP, FIGUEROA_AML_METHYLATION_CLUSTER_2_UP, GOBP_PROTEIN_LOCALIZATION_TO_ENDOSOME, GOBP_PROTEIN_LOCALIZATION_TO_ENDOSOME, GOBP_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY, GOBP_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY, PID_RETINOIC_ACID_PATHWAY, PID_RETINOIC_ACID_PATHWAY, MIR67608_3P, MIR67608_3P, GOCC_SCAR_COMPLEX, GOCC_SCAR_COMPLEX, HP_TONGUE_FASCICULATIONS, HP_TONGUE_FASCICULATIONS, GOBP_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY, GOBP_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY, HP_INTESTINAL_FISTULA, HP_INTESTINAL_FISTULA, HP_DEGENERATION_OF_THE_STRIATUM, HP_DEGENERATION_OF_THE_STRIATUM, SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN, SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN, HP_CSF_PLEOCYTOSIS, HP_CSF_PLEOCYTOSIS, GOMF_RNA_POLYMERASE_II_TRANSCRIPTION_COREPRESSOR_BINDING, GOMF_RNA_POLYMERASE_II_TRANSCRIPTION_COREPRESSOR_BINDING, WP_NRF2ARE_REGULATION, WP_NRF2ARE_REGULATION, HP_VAGINAL_FISTULA, HP_VAGINAL_FISTULA, HP_FATIGABLE_WEAKNESS_OF_RESPIRATORY_MUSCLES, HP_FATIGABLE_WEAKNESS_OF_RESPIRATORY_MUSCLES, GOMF_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY, GOMF_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY, GOBP_FLAVIN_CONTAINING_COMPOUND_METABOLIC_PROCESS, GOBP_FLAVIN_CONTAINING_COMPOUND_METABOLIC_PROCESS, HP_NARROW_ILIAC_WINGS, HP_NARROW_ILIAC_WINGS, GOBP_DEPYRIMIDINATION, GOBP_DEPYRIMIDINATION, GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN, GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN, WAESCH_ANAPHASE_PROMOTING_COMPLEX, WAESCH_ANAPHASE_PROMOTING_COMPLEX, REACTOME_BIOTIN_TRANSPORT_AND_METABOLISM, REACTOME_BIOTIN_TRANSPORT_AND_METABOLISM, GOBP_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_BASE_EXCISION_REPAIR_AP_SITE_FORMATION, GOBP_BASE_EXCISION_REPAIR_AP_SITE_FORMATION, 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GOCC_GEMINI_OF_COILED_BODIES, GOCC_GEMINI_OF_COILED_BODIES, HP_MULTIPLE_LENTIGINES, HP_MULTIPLE_LENTIGINES, GOBP_CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE, GOBP_CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE, HP_CORONAL_CRANIOSYNOSTOSIS, HP_CORONAL_CRANIOSYNOSTOSIS, GOMF_G_PROTEIN_BETA_SUBUNIT_BINDING, GOMF_G_PROTEIN_BETA_SUBUNIT_BINDING, GOBP_PEPTIDYL_SERINE_AUTOPHOSPHORYLATION, GOBP_PEPTIDYL_SERINE_AUTOPHOSPHORYLATION, REACTOME_DISPLACEMENT_OF_DNA_GLYCOSYLASE_BY_APEX1, REACTOME_DISPLACEMENT_OF_DNA_GLYCOSYLASE_BY_APEX1, HP_ABNORMAL_HEAD_MOVEMENTS, HP_ABNORMAL_HEAD_MOVEMENTS, GOMF_BIOTIN_BINDING, GOMF_BIOTIN_BINDING, GOBP_REGULATION_OF_AEROBIC_RESPIRATION, GOBP_REGULATION_OF_AEROBIC_RESPIRATION, GOCC_SUMO_LIGASE_COMPLEX, GOCC_SUMO_LIGASE_COMPLEX, GOMF_MTM2_5_PPPN_DIPHOSPHATASE_ACTIVITY, GOMF_MTM2_5_PPPN_DIPHOSPHATASE_ACTIVITY, HP_UROGENITAL_FISTULA, HP_UROGENITAL_FISTULA, REACTOME_GLUTATHIONE_CONJUGATION, REACTOME_GLUTATHIONE_CONJUGATION, MIR548AO_3P, MIR548AO_3P, WP_KISSPEPTINKISSPEPTIN_RECEPTOR_SYSTEM_IN_THE_OVARY, WP_KISSPEPTINKISSPEPTIN_RECEPTOR_SYSTEM_IN_THE_OVARY, REACTOME_GLUCAGON_LIKE_PEPTIDE_1_GLP1_REGULATES_INSULIN_SECRETION, REACTOME_GLUCAGON_LIKE_PEPTIDE_1_GLP1_REGULATES_INSULIN_SECRETION, REACTOME_REGULATION_OF_INSULIN_SECRETION, REACTOME_REGULATION_OF_INSULIN_SECRETION, GOBP_LEARNED_VOCALIZATION_BEHAVIOR_OR_VOCAL_LEARNING, GOBP_LEARNED_VOCALIZATION_BEHAVIOR_OR_VOCAL_LEARNING, WP_BIOTIN_METABOLISM_INCLUDING_IEMS, WP_BIOTIN_METABOLISM_INCLUDING_IEMS, HP_APLASIA_HYPOPLASIA_INVOLVING_THE_CARPAL_BONES, HP_APLASIA_HYPOPLASIA_INVOLVING_THE_CARPAL_BONES, GOBP_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATIC_MUTATION, GOBP_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATIC_MUTATION, CUI_DEVELOPING_HEART_5TH_WEEK_ATRIAL_CARDIOMYOCYTE, CUI_DEVELOPING_HEART_5TH_WEEK_ATRIAL_CARDIOMYOCYTE, REACTOME_GAP_JUNCTION_DEGRADATION, REACTOME_GAP_JUNCTION_DEGRADATION, GOBP_MEIOTIC_SPINDLE_ORGANIZATION, GOBP_MEIOTIC_SPINDLE_ORGANIZATION, GOBP_EMBRYONIC_CLEAVAGE, GOBP_EMBRYONIC_CLEAVAGE, HP_EEG_WITH_FOCAL_SPIKES, HP_EEG_WITH_FOCAL_SPIKES, GOBP_TELOMERIC_LOOP_DISASSEMBLY, GOBP_TELOMERIC_LOOP_DISASSEMBLY, HP_CARPAL_SYNOSTOSIS, HP_CARPAL_SYNOSTOSIS