

TERTIARY_MEMORY_CD8_TCCELL_UP, GSE21360_SECONDARY_VS_TERTIARY_MEMORY_CD8_TCCELL_UP

HALLMARK_OXIDATIVE_PHOSPHORYLATION, HALLMARK_OXIDATIVE_PHOSPHORYLATION
GSE17974_CTRL_VS_ACT_IL4_AND_ANTIL_IL12_24H_CD4_TCCELL_DN, GSE17974_CTRL_VS_ACT_IL4_AND_ANTIL_IL12_24H_CD4_TCCELL_DN
GSE17974_0H_VS_12H_IN_VITRO_ACT_CD4_TCCELL_DN, GSE17974_0H_VS_12H_IN_VITRO_ACT_CD4_TCCELL_DN
GSE14867_DAY6_VS_DAY8_LCMV_ARMSTRONG_EFFECTOR_CD8_TCCELL_DN, GSE14867_DAY6_VS_DAY8_LCMV_ARMSTRONG_EFFECTOR_CD8_TCCELL_DN
GSE3286_UNSTIM_VS_GMCSF_AND_CURDLAN_HIGHDOSE_STIM_DC_UP, GSE3286_UNSTIM_VS_GMCSF_AND_CURDLAN_HIGHDOSE_STIM_DC_UP
GO_MITOCHONDRIAL_MEMBRANE_PART, GO_MITOCHONDRIAL_MEMBRANE_PART
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13, YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
GSE1891_CTRL_VS_NEWCASTLE_VIRUS_DC_4H_UP, GSE1891_CTRL_VS_NEWCASTLE_VIRUS_DC_4H_UP
GSE27786_BCELL_VS_MONO_MAC_UP, GSE27786_BCELL_VS_MONO_MAC_UP
GO_MITOCHONDRIAL_TRANSLATION, GO_MITOCHONDRIAL_TRANSLATION
GSE24634_TREG_VS_TCONV_POST_DAY10_IL4_CONVERSION_UP, GSE24634_TREG_VS_TCONV_POST_DAY10_IL4_CONVERSION_UP
GSE2203_UNTREATED_VS_ROSGILTAZONE_TREATED_MEF_UP, GSE2203_UNTREATED_VS_ROSGILTAZONE_TREATED_MEF_UP
GSE982_CENT_MEMORY_CD4_TCCELL_VS_TH1_DN, GSE982_CENT_MEMORY_CD4_TCCELL_VS_TH1_DN
GSE17794_0H_VS_48H_IN_VITRO_ACT_CD4_TCCELL_DN, GSE17794_0H_VS_48H_IN_VITRO_ACT_CD4_TCCELL_DN
GSE46606_UNSTIM_VS_CD40L_IL2_IL3_DAY3_STIMULATED_BCELL_DN, GSE46606_UNSTIM_VS_CD40L_IL2_IL3_DAY3_STIMULATED_BCELL_DN
GSE45863_TH1_VS_LV6C_LOW_CXCR3NEG_EFFECTOR_CD4_TCCELL_UP, GSE45863_TH1_VS_LV6C_LOW_CXCR3NEG_EFFECTOR_CD4_TCCELL_UP
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT, REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
GSE3982_BASOPHIL_VS_TH1_DN, GSE3982_BASOPHIL_VS_TH1_DN
GSE17721_PAM3CSK4_VS_GADIQUIMOD_8H_BMDC_UP, GSE17721_PAM3CSK4_VS_GADIQUIMOD_8H_BMDC_UP
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY, GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY
GSE27786_NKCELL_VS_MONO_MAC_UP, GSE27786_NKCELL_VS_MONO_MAC_UP
GSE1531_GRANULOCYTE_MONOCYTE_PROGENITOR_VS_PRO_BCELL_UP, GSE1531_GRANULOCYTE_MONOCYTE_PROGENITOR_VS_PRO_BCELL_UP
GSE17721_POLYIC_VS_PAM3CSK4_16H_BMDC_DN, GSE17721_POLYIC_VS_PAM3CSK4_16H_BMDC_DN
GO_TRANSLATIONAL_TERMINATION, GO_TRANSLATIONAL_TERMINATION
GO_TRANSLATIONAL_ELONGATION, GO_TRANSLATIONAL_ELONGATION
GSE1771_PAM3CSK4_VS_GADIQUIMOD_6H_BMDC_UP, GSE1771_PAM3CSK4_VS_GADIQUIMOD_6H_BMDC_UP
GO_MITOCHONDRIAL_PROTEIN_COMPLEX, GO_MITOCHONDRIAL_PROTEIN_COMPLEX
GSE1460_INTRATHYMIC_T_PROGENITOR_VS_CD4_THYMOCYTE_UP, GSE1460_INTRATHYMIC_T_PROGENITOR_VS_CD4_THYMOCYTE_UP
GSE2770_UNTREATED_VS_IL4_TREATED_ACT_CD4_TCCELL_2H_DN, GSE2770_UNTREATED_VS_IL4_TREATED_ACT_CD4_TCCELL_2H_DN
MORE_RFC1, MORE_RFC1
GSE1481_CTRL_VS_WEST_EQUINE_ENC_VIRUS_IMMATURE_NEURON_CELL_LINE_DN, GSE1481_CTRL_VS_WEST_EQUINE_ENC_VIRUS_IMMATURE_NEURON_CELL_LINE_DN
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS, REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS
GSE3982_MAST_CELL_VS_TH2_DN, GSE3982_MAST_CELL_VS_TH2_DN
IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR, IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
BURTON_ADIPONEGENESIS_5, BURTON_ADIPONEGENESIS_5
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX, GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX
GSE17721_0.5H_VS_8H_LPS_BMDC_UP, GSE17721_0.5H_VS_8H_LPS_BMDC_UP
GSE17721_LPS_VS_POLYIC_16H_BMDC_UP, GSE17721_LPS_VS_POLYIC_16H_BMDC_UP
MYC_UP_V1_UP, MYC_UP_V1_UP
GO_ORGANELLAR_RIBOSOME, GO_ORGANELLAR_RIBOSOME
GSE13522_CTRL_VS_T_CRUZLY_STRAIN_INF_SKIN_IFNG_KO_UP, GSE13522_CTRL_VS_T_CRUZLY_STRAIN_INF_SKIN_IFNG_KO_UP
GSE17721_LPS_VS_POLYIC_8H_BMDC_UP, GSE17721_LPS_VS_POLYIC_8H_BMDC_UP
IL12C2_BOUND_MRNA_IL12C2_BOUND_MRNA
GSE1771_4H_VS_24H_POLYIC_BMDC_UP, GSE1771_4H_VS_24H_POLYIC_BMDC_UP
GSE21063_WT_VS_NFATC1_KO_3H_ANTIL_ICM_STIM_BCELL_DN, GSE21063_WT_VS_NFATC1_KO_3H_ANTIL_ICM_STIM_BCELL_DN
KEGG_ALZHEIMERS_DISEASE, KEGG_ALZHEIMERS_DISEASE
GO_REPLICATION_FORK, GO_REPLICATION_FORK
GSE1930_NAIVE_VS_72H_IN_VITRO_STIM_IL12_CD8_TCCELL_DN, GSE1930_NAIVE_VS_72H_IN_VITRO_STIM_IL12_CD8_TCCELL_DN
GSE40274_CTRL_VS_FOXP3_AND_LEFLI_TRANSDUCED_ACTIVATED_CD4_TCCELL_DN, GSE40274_CTRL_VS_FOXP3_AND_LEFLI_TRANSDUCED_ACTIVATED_CD4_TCCELL_DN
GSE1925_CTRL_VS_IFNG_PRIMED_MACROPHAGE_24H_IFNG_STIM_DN, GSE1925_CTRL_VS_IFNG_PRIMED_MACROPHAGE_24H_IFNG_STIM_DN
GSE24026_PD1_LIGATION_VS_CTRL_IN_ACT_TCCELL_LINE_UP, GSE24026_PD1_LIGATION_VS_CTRL_IN_ACT_TCCELL_LINE_UP
GSE3982_MAST_CELL_VS_DC_UP, GSE3982_MAST_CELL_VS_DC_UP
GSE11924_TH1_VS_TH17_CD4_TCCELL_DN, GSE11924_TH1_VS_TH17_CD4_TCCELL_DN
GSE11924_TH1_VS_TH1_CD4_TCCELL_DN, GSE11924_TH1_VS_TH1_CD4_TCCELL_DN
GSE26030_TH1_VS_TH17_RESTIMULATED_DAYS_POST_POLARIZATION_UP, GSE26030_TH1_VS_TH17_RESTIMULATED_DAYS_POST_POLARIZATION_UP
GSE3982_MAC_VS_TH1_DN, GSE3982_MAC_VS_TH1_DN
GO_NUCLEAR_PART, GO_NUCLEAR_PART
GSE3971_2H_VS_4H_LPS_STIM_MACROPHAGE_WBP7_HET_UP, GSE3971_2H_VS_4H_LPS_STIM_MACROPHAGE_WBP7_HET_UP
KRIEG_KDMSA_TARGETS_NOT_HYPOXIA, KRIEG_KDMSA_TARGETS_NOT_HYPOXIA
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR, GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR
GSE17721_CTRL_VS_CPG_24H_BMDC_DN, GSE17721_CTRL_VS_CPG_24H_BMDC_DN
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION, GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION
COLDRIN_GEFH1NB_RESISTANCE_UP, COLDRIN_GEFH1NB_RESISTANCE_UP
HALLMARK_GLYCOLYSIS, HALLMARK_GLYCOLYSIS
TOOKER_GEMCITABINE_RESISTANCE_DN, TOOKER_GEMCITABINE_RESISTANCE_DN
GSE27786_CD8_TCCELL_VS_NKCELL_UP, GSE27786_CD8_TCCELL_VS_NKCELL_UP
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY, GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY
GSE3982_BCELL_VS_CENT_MEMORY_CD4_TCCELL_UP, GSE3982_BCELL_VS_CENT_MEMORY_CD4_TCCELL_UP
GSE40274_CTRL_VS_HELIOS_TRANSDUCED_ACTIVATED_CD4_TCCELL_DN, GSE40274_CTRL_VS_HELIOS_TRANSDUCED_ACTIVATED_CD4_TCCELL_DN
GSE1184_UNTREATED_VS_CSF1_IFNG_PAMCYS_IN_MAC_DN, GSE1184_UNTREATED_VS_CSF1_IFNG_PAMCYS_IN_MAC_DN
HALLMARK_FATTY_ACID_METABOLISM, HALLMARK_FATTY_ACID_METABOLISM
GO_PROTEIN_TETRAMERIZATION, GO_PROTEIN_TETRAMERIZATION
GO_PROTEIN_TARGETING_TO_MITOCHONDRION, GO_PROTEIN_TARGETING_TO_MITOCHONDRION
GSE1774_CD56_BRIGHT_VS_DIM_CD62L_POSITIVE_NK_CELL_DN, GSE1774_CD56_BRIGHT_VS_DIM_CD62L_POSITIVE_NK_CELL_DN
GSE27786_1SK_VS_LIN_NEG_CELL_DN, GSE27786_1SK_VS_LIN_NEG_CELL_DN
GO_NUCLEOID, GO_NUCLEOID
GSE3982_MAC_VS_BASOPHIL_UP, GSE3982_MAC_VS_BASOPHIL_UP
GSE19888_ADENOSINE_A3R_ACT_VS_A3R_ACT_WITH_A3R_INH_PRETREATMENT_IN_MAST_CELL_DN, GSE19888_ADENOSINE_A3R_ACT_VS_A3R_ACT_WITH_A3R_INH_PRETREATMENT_IN_MAST_CELL_DN
GSE21063_1H_VS_24H_POLYIC_STIM_DC_DN, GSE21063_1H_VS_24H_POLYIC_STIM_DC_DN
GSE39820_TGFBETA1_IL6_IL23A_TREATED_CD4_TCCELL_DN, GSE39820_TGFBETA1_IL6_IL23A_TREATED_CD4_TCCELL_DN
GSE2770_IL12_AND_TGFB_ACT_VS_ACT_CD4_TCCELL_48H_UP, GSE2770_IL12_AND_TGFB_ACT_VS_ACT_CD4_TCCELL_48H_UP
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT, GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT
GSE3982_MAST_CELL_VS_TH1_DN, GSE3982_MAST_CELL_VS_TH1_DN
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC, GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC
GO_ISOMERASE_ACTIVITY, GO_ISOMERASE_ACTIVITY
GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_IL23A_TREATED_CD4_TCCELL_UP, GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_IL23A_TREATED_CD4_TCCELL_UP
GSE27786_CD8_TCCELL_VS_NKCELL_UP, GSE27786_CD8_TCCELL_VS_NKCELL_UP
GO_LYASE_ACTIVITY, GO_LYASE_ACTIVITY
GSE1289_CTRL_VS_IL12_TREATED_PBMC_UP, GSE1289_CTRL_VS_IL12_TREATED_PBMC_UP
GSE19923_I2A_KO_VS_I2A_AND_HEB_KO_DP_THYMOCYTE_DN, GSE19923_I2A_KO_VS_I2A_AND_HEB_KO_DP_THYMOCYTE_DN
GSE9988_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP, GSE9988_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP
GSE11924_TH1_VS_TH2_CD4_TCCELL_DN, GSE11924_TH1_VS_TH2_CD4_TCCELL_DN
MORE_HEAB, MORE_HEAB
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS, REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS
GO_METAL_CLUSTER_BINDING, GO_METAL_CLUSTER_BINDING
GSE1891_CTRL_VS_NEWCASTLE_VIRUS_DC_2H_UP, GSE1891_CTRL_VS_NEWCASTLE_VIRUS_DC_2H_UP
GO_TRANSLATION_SYNTHESIS, GO_TRANSLATION_SYNTHESIS
GO_ORGANELLE_ENVELOPE_LUMEN, GO_ORGANELLE_ENVELOPE_LUMEN
GO_NUCLEAR_TRANSCRIPTION_FACTOR_COMPLEX, GO_NUCLEAR_TRANSCRIPTION_FACTOR_COMPLEX
GSE17721_CTRL_VS_GARDIQUIMOD_6H_BMDC_DN, GSE17721_CTRL_VS_GARDIQUIMOD_6H_BMDC_DN
GSE3982_BASOPHIL_VS_IIF_MEMORY_CD4_TCCELL_DN, GSE3982_BASOPHIL_VS_IIF_MEMORY_CD4_TCCELL_DN
GSE9988_LOW_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP, GSE9988_LOW_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP
KEGG_RNA_DEGRADATION, KEGG_RNA_DEGRADATION
GSE11102_0T1_VS_HY_CD8AB_THYMOCYTE_RTQC_CULTURE_UP, GSE11102_0T1_VS_HY_CD8AB_THYMOCYTE_RTQC_CULTURE_UP
GSE37416_CTRL_VS_2H_I_TULARENSIS_LVS_NEUTROPHIL_DN, GSE37416_CTRL_VS_3H_I_TULARENSIS_LVS_NEUTROPHIL_DN
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC, GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC
SHEPARD_CRUSH_AND_BURN_MUTANT_UP, SHEPARD_CRUSH_AND_BURN_MUTANT_UP
GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS, GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS
MARZEC_IL2_SIGNALING_UP, MARZEC_IL2_SIGNALING_UP
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS, GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT, GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT
MODULE_567, MODULE_567
GSE9988_LOW_LPS_VS_CTRL_TREATED_MONOCYTE_UP, GSE9988_LOW_LPS_VS_CTRL_TREATED_MONOCYTE_UP
GSE37533_UNTREATED_VS_PIOGLIZATONE_TREATED_CD4_TCCELL_FOXP3_TRANSDUCED_CD4_TCCELL_UP, GSE37533_UNTREATED_VS_PIOGLIZATONE_TREATED_CD4_TCCELL_FOXP3_TRANSDUCED_CD4_TCCELL_UP
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS, GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS
GSE2770_IL12_VS_IL4_TREATED_ACT_CD4_TCCELL_6H_UP, GSE2770_IL12_VS_IL4_TREATED_ACT_CD4_TCCELL_6H_UP
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM, KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM
GO_AEROBIC_RESPIRATION, GO_AEROBIC_RESPIRATION
GO_ATP_BIOSYNTHETIC_PROCESS, GO_ATP_BIOSYNTHETIC_PROCESS
GSE4848_ANTL_VALPHA2_VS_VBETA5_DP_THYMOCYTE_DN, GSE4848_ANTL_VALPHA2_VS_VBETA5_DP_THYMOCYTE_DN
GO_NADH_DEHYDROGENASE_COMPLEX, GO_NADH_DEHYDROGENASE_COMPLEX
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE, REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE
GSE17721_LPS_VS_GARDIQUIMOD_2H_BMDC_UP, GSE17721_LPS_VS_GARDIQUIMOD_2H_BMDC_UP
GSE982_CENT_MEMORY_CD4_TCCELL_VS_NKCELL_DN, GSE982_CENT_MEMORY_CD4_TCCELL_VS_NKCELL_DN
GO_REPLISOME, GO_REPLISOME
GO_OXIDOREDUCTASE_COMPLEX, GO_OXIDOREDUCTASE_COMPLEX
GO_4_IRON_4_SULFUR_CLUSTER_BINDING, GO_4_IRON_4_SULFUR_CLUSTER_BINDING
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_1SU_RRNA, GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_1SU_RRNA
GSE862_UNSTIM_VS_TH1_2_STIM_MONOCYTE_4H_DN, GSE862_UNSTIM_VS_TH1_2_STIM_MONOCYTE_4H_DN
GSE17721_LPS_VS_POLYIC_4H_BMDC_UP, GSE17721_LPS_VS_POLYIC_4H_BMDC_UP
GSE24574_BCL6_LOW_THF_VS_NAIVE_CD4_TCCELL_UP, GSE24574_BCL6_LOW_THF_VS_NAIVE_CD4_TCCELL_UP
GSE34515_CD16_NEG_VS_POS_MONOCYTE_UP, GSE34515_CD16_NEG_VS_POS_MONOCYTE_UP
KIEB_RESPONSE_TO_ROSGILTAZONE_UP, KIEB_RESPONSE_TO_ROSGILTAZONE_UP
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE, REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE
GSE1930_STIM_VS_STIM_AND_TRICHOSTATINA_72H_CD8_T_CELL_DN, GSE1930_STIM_VS_STIM_AND_TRICHOSTATINA_72H_CD8_T_CELL_DN
WILCOX_RESPONSE_TO_PROGESTERONE_UP, WILCOX_RESPONSE_TO_PROGESTERONE_UP
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY, GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY, GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY
GO_2_IRON_2_SULFUR_CLUSTER_BINDING, GO_2_IRON_2_SULFUR_CLUSTER_BINDING
GO_CARBOHYDRATE_CATABOLIC_PROCESS, GO_CARBOHYDRATE_CATABOLIC_PROCESS
GO_HEXOSE_CATABOLIC_PROCESS, GO_HEXOSE_CATABOLIC_PROCESS
GO_SRNA_PROCESSING, GO_SRNA_PROCESSING
GO_NAD_METABOLIC_PROCESS, GO_NAD_METABOLIC_PROCESS
GO_NUCLEOTIDE_PHOSPHORYLATION, GO_NUCLEOTIDE_PHOSPHORYLATION
GO_REGULATION_OF_GLUCOSE_TRANSPORT, GO_REGULATION_OF_GLUCOSE_TRANSPORT
GO_MATURATION_OF_5_8S_RRNA, GO_MATURATION_OF_5_8S_RRNA
GSE46606_BFPHIGH_VS_WT_CD40L_IL2_IL5_DAY1_STIMULATED_BCELL_DN, GSE46606_BFPHIGH_VS_WT_CD40L_IL2_IL5_DAY1_STIMULATED_BCELL_DN
GO_NUCLEAR_EXOSOME_RNASE_COMPLEX, GO_NUCLEAR_EXOSOME_RNASE_COMPLEX
GO_MONOSACCHARIDE_METABOLIC_PROCESS, GO_MONOSACCHARIDE_METABOLIC_PROCESS
GSE11861_FOLLICULAR_BCELL_VS_PLASMA_CELL_DAY7_UP, GSE11861_FOLLICULAR_BCELL_VS_PLASMA_CELL_DAY7_UP
GO_PROTEIN_HOMOTETRAMERIZATION, GO_PROTEIN_HOMOTETRAMERIZATION
MODY_HIPPOCAMPUS_POSTNATAL, MODY_HIPPOCAMPUS_POSTNATAL
GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY, GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY
GO_RNA_POLYMERASE_II_TRANSCRIPTION_COFACTOR_ACTIVITY, GO_RNA_POLYMERASE_II_TRANSCRIPTION_COFACTOR_ACTIVITY
GO_MITOCHONDRIAL_RNA_PROCESSING, GO_MITOCHONDRIAL_RNA_PROCESSING
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX
GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_IL23A_TREATED_CD4_TCCELL_DN, GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_IL23A_TREATED_CD4_TCCELL_DN
GO_PIGMENT_BIOSYNTHETIC_PROCESS, GO_PIGMENT_BIOSYNTHETIC_PROCESS
GO_BLASTOCYST_GROWTH, GO_BLASTOCYST_GROWTH
GO_REGULATION_OF_PROTEIN_SUMOYLATION, GO_REGULATION_OF_PROTEIN_SUMOYLATION
REACTOME_PEROXISOMAL_LIPID_METABOLISM, REACTOME_PEROXISOMAL_LIPID_METABOLISM
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC, GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT, GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT
GO_TRICARBONYLIC_ACID_METABOLIC_PROCESS, GO_TRICARBONYLIC_ACID_METABOLIC_PROCESS
GO_MONOSACCHARIDE_CATABOLIC_PROCESS, GO_MONOSACCHARIDE_CATABOLIC_PROCESS
EIF4E_UP, EIF4E_UP
GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS, GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS
GO_PENTOSE_PHOSPHATE_SHUNT, GO_PENTOSE_PHOSPHATE_SHUNT
GO_MITOCHONDRION_MORPHOGENESIS, GO_MITOCHONDRION_MORPHOGENESIS
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS, GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
YYCATTCAWW_UNKNOWN, YYCATTCAWW_UNKNOWN
GSE28793_CTRL_ANTI_MIR_VS_UNTREATED_ATHEROSCLEROSIS_MACROPHAGE_UP, GSE28793_CTRL_ANTI_MIR_VS_UNTREATED_ATHEROSCLEROSIS_MACROPHAGE_UP
GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP, GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP
GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY, GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY
REACTOME_PP2ARA_ACTIVATES_GENE_EXPRESSION, REACTOME_PP2ARA_ACTIVATES_GENE_EXPRESSION
MODULE_325, MODULE_325
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_1_PROMOTER, GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_1_PROMOTER
GO_SUBSTANTIA_NIGRA_DEVELOPMENT, GO_SUBSTANTIA_NIGRA_DEVELOPMENT
GO_XENOPHAGY, GO_XENOPHAGY
GO_3_5_DNA_HELICASE_ACTIVITY, GO_3_5_DNA_HELICASE_ACTIVITY
GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY, GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY
GSE4860_THF_VS_LV6C_INT_CXCR3POS_MEMORY_CD4_TCCELL_DN, GSE4860_THF_VS_LV6C_INT_CXCR3POS_MEMORY_CD4_TCCELL_DN
CNP2_CD27, CNP2_CD27
GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS, GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS
GSE41176_WT_VS_TAK1_KO_ANTL_ICM_STIM_BCELL_3H_UP, GSE41176_WT_VS_TAK1_KO_ANTL_ICM_STIM_BCELL_3H_UP
BRACHAT_RESPONSE_TO_METHOTREXATE_DN, BRACHAT_RESPONSE_TO_METHOTREXATE_DN
GO_MITOCHONDRIAL_GENOME_MAINTENANCE, GO_MITOCHONDRIAL_GENOME_MAINTENANCE
GO_NADH_METABOLIC_PROCESS, GO_NADH_METABOLIC_PROCESS
GO_ANDROGEN_RECEPTOR_BINDING, GO_ANDROGEN_RECEPTOR_BINDING
CYCLIN_D1_KE_V1_UP, CYCLIN_D1_KE_V1_UP
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS, GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS
MOOTHA_TCA, MOOTHA_TCA
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM, KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS, GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS
GO_CARBOXYLASE_ACTIVITY, GO_CARBOXYLASE_ACTIVITY
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT, GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT
GSE9316_CD4_TCCELL_BALBC_VS_TH17_ENR_CD4_TCCELL_SKG_PMA_IJONO_STIM_FRANEG_UP, GSE9316_CD4_TCCELL_BALBC_VS_TH17_ENR_CD4_TCCELL_SKG_PMA_IJONO_STIM_FRANEG_UP
WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1, WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1
GO_HEME_BIOSYNTHETIC_PROCESS, GO_HEME_BIOSYNTHETIC_PROCESS
GO_ADP_METABOLIC_PROCESS, GO_ADP_METABOLIC_PROCESS
GO_ATP_GENERATION_FROM_ADP, GO_ATP_GENERATION_FROM_ADP
REACTOME_FORMATION_OF_ATP_BY_CHEMOSMOTIC_COUPLING, REACTOME_FORMATION_OF_ATP_BY_CHEMOSMOTIC_COUPLING
GSE17721_CTRL_VS_LPS_4H_BMDC_DN, GSE17721_CTRL_VS_LPS_4H_BMDC_DN
GO_NEURAL_NUCLEUS_DEVELOPMENT, GO_NEURAL_NUCLEUS_DEVELOPMENT
GO_ENDORIBONUCLEASE_COMPLEX, GO_ENDORIBONUCLEASE_COMPLEX
JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP, JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP
GO_INTRACILIARY_TRANSPORT_PARTICLE_B, GO_INTRACILIARY_TRANSPORT_PARTICLE_B
IWANAGA_E2F1_TARGETS_INDUCED_BY_SERUM, IWANAGA_E2F1_TARGETS_INDUCED_BY_SERUM
MODULE_272, MODULE_272
GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX, GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_1SU_RRNA, GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_1SU_RRNA
GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX, GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX
GO_GLUCOSE_CATABOLIC_PROCESS, GO_GLUCOSE_CATABOLIC_PROCESS
SEIDEN_MET_SIGNALING, SEIDEN_MET_SIGNALING
NADLER_OBESITY_DN, NADLER_OBESITY_DN
GO_REGULATION_OF_CYSINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY, GO_REGULATION_OF_CYSINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY
chm923, chm923
GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS, GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS
GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY, GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS
GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION, GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION
GO_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE
KEGG_PENTOSE_PHOSPHATE_PATHWAY, KEGG_PENTOSE_PHOSPHATE_PATHWAY
GO_QUINONE_BINDING, GO_QUINONE_BINDING
GSE12707_AT16L1_HYPOMORPH_VS_WT_THYMUS_UP, GSE12707_AT16L1_HYPOMORPH_VS_WT_THYMUS_UP
HONKADO_BREAST_CANCER_BRCA1_VS_BRCA2, HONKADO_BREAST_CANCER_BRCA1_VS_BRCA2
IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_UP, IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_UP
GSE3982_DC_VS_MAC_DN, GSE3982_DC_VS_MAC_DN
GO_POSITIVE_REGULATION_OF_RNA_SPLICING, GO_POSITIVE_REGULATION_OF_RNA_SPLICING
RAY_TUMORIGENESIS_BY_ERBB2_CD25A_UP, RAY_TUMORIGENESIS_BY_ERBB2_CD25A_UP
GO_PIGMENT_METABOLIC_PROCESS, GO_PIGMENT_METABOLIC_PROCESS
BIOCARTA_GLYCOLYSIS_PATHWAY, BIOCARTA_GLYCOLYSIS_PATHWAY
MELLMAN_TUT1_TARGETS_UP, MELLMAN_TUT1_TARGETS_UP
GO_RIBONUCLEASE_P_ACTIVITY, GO_RIBONUCLEASE_P_ACTIVITY
GO_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION, GO_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION
LEE_LIVER_CANCER_MYC_E2F1_DN, LEE_LIVER_CANCER_MYC_E2F1_DN
MODULE_210, MODULE_210
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN, GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSMINATION, REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSMINATION
GO_INNER_CELL_MASS_CELL_PROLIFERATION, GO_INNER_CELL_MASS_CELL_PROLIFERATION
MODULE_539, MODULE_539
GO_NADP_METABOLIC_PROCESS, GO_NADP_METABOLIC_PROCESS
GO_CELLULAR_KETONE_METABOLIC_PROCESS, GO_CELLULAR_KETONE_METABOLIC_PROCESS
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING, GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING
REACTOME_ACTIVATION_OF_GENES_BY_AT4, REACTOME_ACTIVATION_OF_GENES_BY_AT4
GO_ALDEHYDE_CATABOLIC_PROCESS, GO_ALDEHYDE_CATABOLIC_PROCESS
GSE9946_IMMATURE_VS_LISTERIA_INF_MATURE_DC_DN, GSE9946_IMMATURE_VS_LISTERIA_INF_MATURE_DC_DN
DOANE_BREAST_CANCER_CLASSES_DN, DOANE_BREAST_CANCER_CLASSES_DN
GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM, GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM
GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION, GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION, GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE, GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE
GAUSSMANN_MLL_AFL_FUSION_TARGETS_G_DN, GAUSSMANN_MLL_AFL_FUSION_TARGETS_G_DN
GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS, GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS
GO_P53_BINDING, GO_P53_BINDING
GO_CELLULAR_RESPONSE_TO_GLUCOSE_STARVATION, GO_CELLULAR_RESPONSE_TO_GLUCOSE_STARVATION
GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY, GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY
REACTOME_RNA_POL_1_TRANSCRIPTION_INITIATION, REACTOME_RNA_POL_1_TRANSCRIPTION_INITIATION
MORE_CASP10, MORE_CASP10
GO_BETA_AMYLOID_BINDING, GO_BETA_AMYLOID_BINDING
GO_RESPONSE_TO_IRON_IJON, GO_RESPONSE_TO_IRON_IJON
REACTOME_RNA_POL_1_TRANSCRIPTION_TERMINATION, REACTOME_RNA_POL_1_TRANSCRIPTION_TERMINATION
GO_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS, GO_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS
GO_HEME_METABOLIC_PROCESS, GO_HEME_METABOLIC_PROCESS
GO_REGULATION_OF_CELLULAR_RESPIRATION, GO_REGULATION_OF_CELLULAR_RESPIRATION
ch20q11, ch20q11
DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP, DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP
GO_HEPATOCYBILIARY_SYSTEM_DEVELOPMENT, GO_HEPATOCYBILIARY_SYSTEM_DEVELOPMENT
GO_RNA_POLYMERASE_II_CARBOXY_TERMINAL_KINASE_ACTIVITY, GO_RNA_POLYMERASE_II_CARBOXY_TERMINAL_KINASE_ACTIVITY
PID_RETINOIC_ACID_PATHWAY, PID_RETINOIC_ACID_PATHWAY
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS, GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS
ZWANG_ICF_PERSISTENTLY_UP, ZWANG_ICF_PERSISTENTLY_UP
KIM_HYPOXIA, KIM_HYPOXIA
GSE17721_CPG_VS_GARDIQUIMOD_2H_BMDC_UP, GSE17721_CPG_VS_GARDIQUIMOD_2H_BMDC_UP
GO_POSITIVE_REGULATION_OF_DNA_BINDING, GO_POSITIVE_REGULATION_OF_DNA_BINDING
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE, GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE
WALLACE_JAK2_TARGETS_UP, WALLACE_JAK2_TARGETS_UP
GSE19888_ADENOSINE_A3R_INH_VS_INH_PRETREAT_AND_ACT_WITH_TCCELL_MEMBRANES_MAST_CELL_DN, GSE19888_ADENOSINE_A3R_INH_VS_INH_PRETREAT_AND_ACT_WITH_TCCELL_MEMBRANES_MAST_CELL_DN
HOLLEMAN_VINCISTINE_RESISTANCE_ALL_UP, HOLLEMAN_VINCISTINE_RESISTANCE_ALL_UP