

ED_RNA_VS_MRNA_DC_UP, GSE14000_TRANSLATED_RNA_VS_MRNA_DC_UP

GSE14000_TRANSLATED_RNA_VS_MRNA_4H_LPS_DC_UP, GSE14000_TRANSLATED_RNA_VS_MRNA_4H_LPS_DC_UP
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY, GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY
GSE41867_NAIVE_VS_DAY30_LCMV_ARMSTRONG_MEMORY_CD8_TCELL_UP, GSE41867_NAIVE_VS_DAY30_LCMV_ARMSTRONG_MEMORY_CD8_TCELL_UP
GSE14000_UNSTIM_VS_4H_LPS_DC_TRANSLATED_RNA_UP, GSE14000_UNSTIM_VS_4H_LPS_DC_TRANSLATED_RNA_UP
GSE41867_NAIVE_VS_EFFECTOR_CD8_TCELL_UP, GSE41867_NAIVE_VS_EFFECTOR_CD8_TCELL_UP
GSE22886_IGG_IGA_MEMORY_BCELL_VS_BLOOD_PLASMA_CELL_DN, GSE22886_IGG_IGA_MEMORY_BCELL_VS_BLOOD_PLASMA_CELL_DN
GSE2770_IL12_AND_TGFB_ACT_VS_ACT_CD4_TCELL_48H_DN, GSE2770_IL12_AND_TGFB_ACT_VS_ACT_CD4_TCELL_48H_DN
GSE14000_UNSTIM_VS_16H_LPS_DC_DN, GSE14000_UNSTIM_VS_16H_LPS_DC_DN
GSE17721_LPS_VS_CPG_8H_BMDC_DN, GSE17721_LPS_VS_CPG_8H_BMDC_DN
GSE11864_UNTREATED_VS_CSF1_IN_MAC_DN, GSE11864_UNTREATED_VS_CSF1_IN_MAC_DN
GSE3982_MAST_CELL_VS_EFF_MEMORY_CD4_TCELL_UP, GSE3982_MAST_CELL_VS_EFF_MEMORY_CD4_TCELL_UP
GSE2770_IL12_AND_TGFB_VS_IL4_TREATED_ACT_CD4_TCELL_2H_UP, GSE2770_IL12_AND_TGFB_VS_IL4_TREATED_ACT_CD4_TCELL_2H_UP
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION, GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION
GGAANCGGAANY_UNKNOWN, GGAANCGGAANY_UNKNOWN
GSE39820_CTRL_VS_TGFBETA1_IL6_CD4_TCELL_UP, GSE39820_CTRL_VS_TGFBETA1_IL6_CD4_TCELL_UP
GSE2770_TGFB_AND_IL4_ACT_VS_ACT_CD4_TCELL_48H_UP, GSE2770_TGFB_AND_IL4_ACT_VS_ACT_CD4_TCELL_48H_UP
GSE37301_MULTIPOTENT_PROGENITOR_VS_RAG2_KO_NK_CELL_DN, GSE37301_MULTIPOTENT_PROGENITOR_VS_RAG2_KO_NK_CELL_DN
GSE25087_TREG_VS_TCONV_FETUS_DN, GSE25087_TREG_VS_TCONV_FETUS_DN
GSE4748_CTRL_VS_CYANOBACTERIUM_LPSLIKE_STIM_DC_1H_UP, GSE4748_CTRL_VS_CYANOBACTERIUM_LPSLIKE_STIM_DC_1H_UP
GSE21670_UNTREATED_VS_TGFB_IL6_TREATED_CD4_TCELL_DN, GSE21670_UNTREATED_VS_TGFB_IL6_TREATED_CD4_TCELL_DN
GSE5542_IFNA_VS_IFNA_AND_IFNG_TREATED_EPITHELIAL_CELLS_24H_DN, GSE5542_IFNA_VS_IFNA_AND_IFNG_TREATED_EPITHELIAL_CELLS_24H_DN
GSE18281_MEDULLARY_THYMOCYTE_VS_WHOLE_MEDULLA_THYMUS_DN, GSE18281_MEDULLARY_THYMOCYTE_VS_WHOLE_MEDULLA_THYMUS_DN
SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP, SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
GSE17721_PAM3CSK4_VS_CPG_0.5H_BMDC_UP, GSE17721_PAM3CSK4_VS_CPG_0.5H_BMDC_UP
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS, GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS
GSE37416_CTRL_VS_3H_F_TULARENSIS_LVS_NEUTROPHIL_DN, GSE37416_CTRL_VS_3H_F_TULARENSIS_LVS_NEUTROPHIL_DN
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP, TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP
GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS, GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS
BURTON_ADIPOGENESIS_12, BURTON_ADIPOGENESIS_12
GSE41176_UNSTIM_VS_ANTLIGM_STIM_TAK1_KO_BCELL_6H_UP, GSE41176_UNSTIM_VS_ANTLIGM_STIM_TAK1_KO_BCELL_6H_UP
YAGL_AML_WITH_T_9_11_TRANSLOCATION, YAGL_AML_WITH_T_9_11_TRANSLOCATION
GSE4984_UNTREATED_VS_VEHICLE_CTRL_TREATED_DC_DN, GSE4984_UNTREATED_VS_VEHICLE_CTRL_TREATED_DC_DN
GO_RNA_POLYMERASE_BINDING, GO_RNA_POLYMERASE_BINDING
GSE15624_3H_VS_6H_HALOFUGINONE_TREATED_CD4_TCELL_DN, GSE15624_3H_VS_6H_HALOFUGINONE_TREATED_CD4_TCELL_DN
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_2_OXOGLUTARATE_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_EACH_OF_OXYGEN_INTO_BOTH_DONORS, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_2_OXOGLUTARATE_AS_ONE_DONOR_AND_INCORPORATION
GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING, GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING
GO_DEMETHYLASE_ACTIVITY, GO_DEMETHYLASE_ACTIVITY
GO_SWI_SNF_SUPERFAMILY_TYPE_COMPLEX, GO_SWI_SNF_SUPERFAMILY_TYPE_COMPLEX
GO_RNA_POLYMERASE_CORE_ENZYME_BINDING, GO_RNA_POLYMERASE_CORE_ENZYME_BINDING
GSE16385_UNTREATED_VS_12H_ROSIGLITAZONE_IL4_TREATED_MACROPHAGE_DN, GSE16385_UNTREATED_VS_12H_ROSIGLITAZONE_IL4_TREATED_MACROPHAGE_DN
GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS, GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS
GSE20152_SPHK1_KO_VS_WT_HTNFA_OVERXPRESS_ANKLE_UP, GSE20152_SPHK1_KO_VS_WT_HTNFA_OVERXPRESS_ANKLE_UP
GO_TRANSLATION_INITIATION_FACTOR_BINDING, GO_TRANSLATION_INITIATION_FACTOR_BINDING
GO_CELLULAR_PIGMENTATION, GO_CELLULAR_PIGMENTATION
GO_EXOSOME_RNASE_COMPLEX, GO_EXOSOME_RNASE_COMPLEX
GSE14350_IL2RB_KO_VS_WT_TEFF_DN, GSE14350_IL2RB_KO_VS_WT_TEFF_DN
GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX, GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX
GO_DIOXYGENASE_ACTIVITY, GO_DIOXYGENASE_ACTIVITY
GO_MITOTIC_CHROMOSOME_CONDENSATION, GO_MITOTIC_CHROMOSOME_CONDENSATION
GO_RNA_POLYMERASE_II_CORE_BINDING, GO_RNA_POLYMERASE_II_CORE_BINDING
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY, GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY
GSE43955_TH0_VS_TGFB_IL6_TH17_ACT_CD4_TCELL_60H_UP, GSE43955_TH0_VS_TGFB_IL6_TH17_ACT_CD4_TCELL_60H_UP
GO_MITOCHONDRIAL_GENOME_MAINTENANCE, GO_MITOCHONDRIAL_GENOME_MAINTENANCE
GSE17721_PAM3CSK4_VS_CPG_2H_BMDC_DN, GSE17721_PAM3CSK4_VS_CPG_2H_BMDC_DN
GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT, GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT
GO_CYTOPLASMIC_EXOSOME_RNASE_COMPLEX, GO_CYTOPLASMIC_EXOSOME_RNASE_COMPLEX
GO_RNA_SURVEILLANCE, GO_RNA_SURVEILLANCE
GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION, GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION
GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING, GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING
PID_MYC_PATHWAY, PID_MYC_PATHWAY
PAX5_01, PAX5_01
GO_PSEUDOURIDINE_SYNTHESIS, GO_PSEUDOURIDINE_SYNTHESIS
GSE23505_UNTREATED_VS_4DAY_IL6_IL1_TREATED_CD4_TCELL_DN, GSE23505_UNTREATED_VS_4DAY_IL6_IL1_TREATED_CD4_TCELL_DN
GO_DEMETHYLATION, GO_DEMETHYLATION
YIH_RESPONSE_TO_ARSENITE_C1, YIH_RESPONSE_TO_ARSENITE_C1
GO_ACTIN_CYTOSKELETON_REORGANIZATION, GO_ACTIN_CYTOSKELETON_REORGANIZATION
KEGG_RNA_POLYMERASE, KEGG_RNA_POLYMERASE
GO_INO80_TYPE_COMPLEX, GO_INO80_TYPE_COMPLEX
GO_HISTONE_MONOUBIQUITINATION, GO_HISTONE_MONOUBIQUITINATION
DAIRKEE_TERT_TARGETS_DN, DAIRKEE_TERT_TARGETS_DN
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER, GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER
GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION, GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION
GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS, GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS
GO_GLUCAN_METABOLIC_PROCESS, GO_GLUCAN_METABOLIC_PROCESS
GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS, GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS
GSE21927_EL4_VS_MCA203_TUMOR_MONOCYTES_DN, GSE21927_EL4_VS_MCA203_TUMOR_MONOCYTES_DN
GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS, GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS
AKT_UP_MTOR_DN.V1_DN, AKT_UP_MTOR_DN.V1_DN
GO_SPINDLE_LOCALIZATION, GO_SPINDLE_LOCALIZATION
LI_CYTIDINE_ANALOGS_CYCTOTOXICITY, LI_CYTIDINE_ANALOGS_CYCTOTOXICITY
GO_SWI_SNF_COMPLEX, GO_SWI_SNF_COMPLEX
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY, GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS, REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
GO_POLYSACCHARIDE_METABOLIC_PROCESS, GO_POLYSACCHARIDE_METABOLIC_PROCESS
GO_GLUCAN_BIOSYNTHETIC_PROCESS, GO_GLUCAN_BIOSYNTHETIC_PROCESS
PPARG_01, PPARG_01
GO_MITOCHONDRIAL_DNA_METABOLIC_PROCESS, GO_MITOCHONDRIAL_DNA_METABOLIC_PROCESS
GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION, GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION
GO_DNA_HELICASE_COMPLEX, GO_DNA_HELICASE_COMPLEX
GO_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS, GO_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS
GO_BAF_TYPE_COMPLEX, GO_BAF_TYPE_COMPLEX
KATSANOUELAVL1_TARGETS_DN, KATSANOUELAVL1_TARGETS_DN
FIGUEROA_AML_METHYLATION_CLUSTER_2_UP, FIGUEROA_AML_METHYLATION_CLUSTER_2_UP
GSE18281_SUBCAPSULAR_VS_PERIMEDULLARY_CORTICAL_REGION_OF_THYMUS_DN, GSE18281_SUBCAPSULAR_VS_PERIMEDULLARY_CORTICAL_REGION_OF_THYMUS_DN
GO_PROTEASOME_BINDING, GO_PROTEASOME_BINDING
GO_PIGMENT GRANULE_ORGANIZATION, GO_PIGMENT GRANULE_ORGANIZATION
YUAN_ZNF143_PARTNERS, YUAN_ZNF143_PARTNERS
GO_H4_HISTONE_ACETYLTTRANSFERASE_COMPLEX, GO_H4_HISTONE_ACETYLTTRANSFERASE_COMPLEX