E_PHOSPHORYLATION, HALLMARK_OXIDATIVE_PHOSPHORYLATION
GSE21360_SECONDARY_VS_TERTIARY_MEMORY_CD8_TCELL_UP, GSE21360_SECONDARY_VS_TERTIARY_MEMORY_CD8_TCELL_UP
GSE16266_CTRL_VS_HEATSHOCK_AND_LPS_STIM_MEF_UP, GSE16266_CTRL_VS_HEATSHOCK_AND_LPS_STIM_MEF_UP
GSE21927_GMCSF_IL6_VS_GMCSF_GCSF_TREATED_BONE_MARROW_DN, GSE21927_GMCSF_IL6_VS_GMCSF_GCSF_TREATED_BONE_MARROW_DN
GSE9006_HEALTHY_VS_TYPE_2_DIABETES_PBMC_AT_DX_UP, GSE9006_HEALTHY_VS_TYPE_2_DIABETES_PBMC_AT_DX_UP
GSE22432_PDC_VS_TGFB1_TREATEDCOMMON_DC_PROGENITOR_UP, GSE22432_PDC_VS_TGFB1_TREATEDCOMMON_DC_PROGENITOR_UP
GSE42021_CD24INT_TREG_VS_CD24INT_TCONV_THYMUS_UP, GSE42021_CD24INT_TREG_VS_CD24INT_TCONV_THYMUS_UP
KAECH_DAY8_EFF_VS_DAY15_EFF_CD8_TCELL_UP, KAECH_DAY8_EFF_VS_DAY15_EFF_CD8_TCELL_UP
GSE22886_CTRL_VS_LPS_24H_DC_UP, GSE22886_CTRL_VS_LPS_24H_DC_UP
GSE22886_DAY1_VS_DAY7_MONOCYTE_IN_CULTURE_DN, GSE22886_DAY1_VS_DAY7_MONOCYTE_IN_CULTURE_DN
MORF_PPP6C, MORF_PPP6C
GSE22140_HEALTHY_VS_ARTHRITIC_GERMFREE_MOUSE_CD4_TCELL_UP, GSE22140_HEALTHY_VS_ARTHRITIC_GERMFREE_MOUSE_CD4_TCELL_UP
GSE1432_6H_VS_24H_IFNG_MICROGLIA_DN, GSE1432_6H_VS_24H_IFNG_MICROGLIA_DN
GSE24634_NAIVE_CD4_TCELL_VS_DAY10_IL4_CONV_TREG_DN, GSE24634_NAIVE_CD4_TCELL_VS_DAY10_IL4_CONV_TREG_DN
GSE22886_NAIVE_CD4_TCELL_VS_DC_DN, GSE22886_NAIVE_CD4_TCELL_VS_DC_DN
GSE25087_FETAL_VS_ADULT_TCONV_UP, GSE25087_FETAL_VS_ADULT_TCONV_UP
GSE42021_CD24LO_TREG_VS_CD24LO_TCONV_THYMUS_DN, GSE42021_CD24LO_TREG_VS_CD24LO_TCONV_THYMUS_DN
CAMP_UP.V1_UP, CAMP_UP.V1_UP
GSE37605_FOXP3_FUSION_GFP_VS_IRES_GFP_TREG_NOD_UP, GSE37605_FOXP3_FUSION_GFP_VS_IRES_GFP_TREG_NOD_UP
GSE36888_UNTREATED_VS_IL2_TREATED_STAT5_AB_KNOCKIN_TCELL_6H_DN, GSE36888_UNTREATED_VS_IL2_TREATED_STAT5_AB_KNOCKIN_TCELL_6H_DN
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13, YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
GSE45365_WT_VS_IFNAR_KO_CD8A_DC_UP, GSE45365_WT_VS_IFNAR_KO_CD8A_DC_UP
GSE12845_IGD_POS_VS_NEG_BLOOD_BCELL_DN, GSE12845_IGD_POS_VS_NEG_BLOOD_BCELL_DN
GO_MITOCHONDRIAL_TRANSLATION, GO_MITOCHONDRIAL_TRANSLATION
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT, REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
GSE23505_IL6_IL1_VS_IL6_IL1_TGFB_TREATED_CD4_TCELL_DN, GSE23505_IL6_IL1_VS_IL6_IL1_TGFB_TREATED_CD4_TCELL_DN
GSE41867_DAY8_VS_DAY15_LCMV_CLONE13_EFFECTOR_CD8_TCELL_DN, GSE41867_DAY8_VS_DAY15_LCMV_CLONE13_EFFECTOR_CD8_TCELL_DN
GSE22886_NAIVE_CD8_TCELL_VS_DC_DN, GSE22886_NAIVE_CD8_TCELL_VS_DC_DN
GSE17721_POLYIC_VS_PAM3CSK4_16H_BMDC_DN, GSE17721_POLYIC_VS_PAM3CSK4_16H_BMDC_DN
GSE17322_CD103_POS_VS_CD11B_HIGH_LUNG_DC_DN, GSE17322_CD103_POS_VS_CD11B_HIGH_LUNG_DC_DN
GSE22886_NAIVE_BCELL_VS_DC_DN, GSE22886_NAIVE_BCELL_VS_DC_DN
GSE23308_CTRL_VS_CORTICOSTERONE_TREATED_MACROPHAGE_MINERALCORTICOID_REC_KO_DN, GSE23308_CTRL_VS_CORTICOSTERONE_TREATED_MACROPHAGE_MINERALCORTICOID_REC_KO_DN
GSE17721_POLYIC_VS_PAM3CSK4_12H_BMDC_DN, GSE17721_POLYIC_VS_PAM3CSK4_12H_BMDC_DN
GSE22886_DAY0_VS_DAY7_MONOCYTE_IN_CULTURE_DN, GSE22886_DAY0_VS_DAY7_MONOCYTE_IN_CULTURE_DN
GSE23505_UNTREATED_VS_4DAY_IL6_IL1_TREATED_CD4_TCELL_UP, GSE23505_UNTREATED_VS_4DAY_IL6_IL1_TREATED_CD4_TCELL_UP
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY, GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY
GO_MITOCHONDRIAL_TRANSPORT, GO_MITOCHONDRIAL_TRANSPORT
GSE19401_UNSTIM_VS_PAM2CSK4_STIM_FOLLICULAR_DC_DN, GSE19401_UNSTIM_VS_PAM2CSK4_STIM_FOLLICULAR_DC_DN
GSE3982_DC_VS_NEUTROPHIL_LPS_STIM_UP, GSE3982_DC_VS_NEUTROPHIL_LPS_STIM_UP
GSE14769_20MIN_VS_360MIN_LPS_BMDM_UP, GSE14769_20MIN_VS_360MIN_LPS_BMDM_UP
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_, REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTI
GSE3982_DC_VS_NEUTROPHIL_UP, GSE3982_DC_VS_NEUTROPHIL_UP
GSE12845_PRE_GC_VS_DARKZONE_GC_TONSIL_BCELL_DN, GSE12845_PRE_GC_VS_DARKZONE_GC_TONSIL_BCELL_DN
MODULE_152, MODULE_152
GSE17721_PAM3CSK4_VS_CPG_12H_BMDC_UP, GSE17721_PAM3CSK4_VS_CPG_12H_BMDC_UP
GO_MITOCHONDRIAL_MEMBRANE_PART, GO_MITOCHONDRIAL_MEMBRANE_PART
GSE2706_2H_VS_8H_R848_AND_LPS_STIM_DC_UP, GSE2706_2H_VS_8H_R848_AND_LPS_STIM_DC_UP
GSE17721_POLYIC_VS_PAM3CSK4_24H_BMDC_DN, GSE17721_POLYIC_VS_PAM3CSK4_24H_BMDC_DN
KEGG_OXIDATIVE_PHOSPHORYLATION, KEGG_OXIDATIVE_PHOSPHORYLATION
GSE19198_CTRL_VS_IL21_TREATED_TCELL_6H_UP, GSE19198_CTRL_VS_IL21_TREATED_TCELL_6H_UP
GSE17721_CTRL_VS_CPG_12H_BMDC_UP, GSE17721_CTRL_VS_CPG_12H_BMDC_UP
GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_HET_2H_DN, GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_HET_2H_DN
GSE360_DC_VS_MAC_B_MALAYI_HIGH_DOSE_UP, GSE360_DC_VS_MAC_B_MALAYI_HIGH_DOSE_UP
GSE16385_IFNG_TNF_VS_IL4_STIM_MACROPHAGE_ROSIGLITAZONE_TREATED_DN, GSE16385_IFNG_TNF_VS_IL4_STIM_MACROPHAGE_ROSIGLITAZONE_TREATED_DN
GSE3982_MAC_VS_EFF_MEMORY_CD4_TCELL_UP, GSE3982_MAC_VS_EFF_MEMORY_CD4_TCELL_UP
GO_TRANSLATIONAL_TERMINATION, GO_TRANSLATIONAL_TERMINATION
GSE37301_COMMON_LYMPHOID_PROGENITOR_VS_PRO_BCELL_DN, GSE37301_COMMON_LYMPHOID_PROGENITOR_VS_PRO_BCELL_DN
GSE24726_WT_VS_E2-2_KO_PDC_DAY4_POST_DELETION_DN, GSE24726_WT_VS_E2-2_KO_PDC_DAY4_POST_DELETION_DN
GSE22886_NAIVE_TCELL_VS_DC_DN, GSE22886_NAIVE_TCELL_VS_DC_DN
GSE17721_0.5H_VS_12H_GARDIQUIMOD_BMDC_UP, GSE17721_0.5H_VS_12H_GARDIQUIMOD_BMDC_UP
GSE22886_NAIVE_VS_IGM_MEMORY_BCELL_DN, GSE22886_NAIVE_VS_IGM_MEMORY_BCELL_DN
GSE17721_0.5H_VS_8H_PAM3CSK4_BMDC_UP, GSE17721_0.5H_VS_8H_PAM3CSK4_BMDC_UP
GSE17721_12H_VS_24H_GARDIQUIMOD_BMDC_DN, GSE17721_12H_VS_24H_GARDIQUIMOD_BMDC_DN
GSE26030_TH1_VS_TH17_RESTIMULATED_DAY15_POST_POLARIZATION_DN, GSE26030_TH1_VS_TH17_RESTIMULATED_DAY15_POST_POLARIZATION_DN
GSE3982_MAST_CELL_VS_CENT_MEMORY_CD4_TCELL_UP, GSE3982_MAST_CELL_VS_CENT_MEMORY_CD4_TCELL_UP
MORF_RAB5A, MORF_RAB5A
GSE41087_WT_VS_FOXP3_MUT_ANTI_CD3_CD28_STIM_CD4_TCELL_DN, GSE41087_WT_VS_FOXP3_MUT_ANTI_CD3_CD28_STIM_CD4_TCELL_DN
GSE5589_LPS_VS_LPS_AND_IL10_STIM_IL6_KO_MACROPHAGE_180MIN_DN, GSE5589_LPS_VS_LPS_AND_IL10_STIM_IL6_KO_MACROPHAGE_180MIN_DN
GSE26030_TH1_VS_TH17_DAY15_POST_POLARIZATION_DN, GSE26030_TH1_VS_TH17_DAY15_POST_POLARIZATION_DN
GSE3982_EOSINOPHIL_VS_BCELL_DN, GSE3982_EOSINOPHIL_VS_BCELL_DN
GO_MITOCHONDRIAL_PROTEIN_COMPLEX, GO_MITOCHONDRIAL_PROTEIN_COMPLEX
MODULE_62, MODULE_62
GSE14000_4H_VS_16H_LPS_DC_UP, GSE14000_4H_VS_16H_LPS_DC_UP
GSE23984_CTRL_VS_HYPOCALEMIC_VITAMIND_ANALOG_TCELL_UP, GSE23984_CTRL_VS_HYPOCALEMIC_VITAMIND_ANALOG_TCELL_UP
GO_TRANSLATIONAL_ELONGATION, GO_TRANSLATIONAL_ELONGATION
GSE17580_UNINFECTED_VS_S_MANSONI_INF_TREG_DN, GSE17580_UNINFECTED_VS_S_MANSONI_INF_TREG_DN
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT, REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
KEGG_ALZHEIMERS_DISEASE, KEGG_ALZHEIMERS_DISEASE
GO_CELLULAR_RESPIRATION, GO_CELLULAR_RESPIRATION
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX, GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX
GO_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS, GO_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS
GSE17721_12H_VS_24H_LPS_BMDC_DN, GSE17721_12H_VS_24H_LPS_BMDC_DN
GSE17721_CTRL_VS_CPG_4H_BMDC_UP, GSE17721_CTRL_VS_CPG_4H_BMDC_UP
GSE22886_NAIVE_VS_IGG_IGA_MEMORY_BCELL_DN, GSE22886_NAIVE_VS_IGG_IGA_MEMORY_BCELL_DN
GSE41176_UNSTIM_VS_ANTI_IGM_STIM_TAK1_KO_BCELL_24H_UP, GSE41176_UNSTIM_VS_ANTI_IGM_STIM_TAK1_KO_BCELL_24H_UP
GSE360_CTRL_VS_T_GONDII_MAC_UP, GSE360_CTRL_VS_T_GONDII_MAC_UP
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_MARK, WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_MARK
GSE411_100MIN_VS_400MIN_IL6_STIM_SOCS3_KO_MACROPHAGE_UP, GSE411_100MIN_VS_400MIN_IL6_STIM_SOCS3_KO_MACROPHAGE_UP
GSE43955_1H_VS_10H_ACT_CD4_TCELL_UP, GSE43955_1H_VS_10H_ACT_CD4_TCELL_UP
KEGG_PARKINSONS_DISEASE, KEGG_PARKINSONS_DISEASE
GSE3982_MAC_VS_BASOPHIL_UP, GSE3982_MAC_VS_BASOPHIL_UP
KEGG_HUNTINGTONS_DISEASE, KEGG_HUNTINGTONS_DISEASE
GSE22140_HEALTHY_VS_ARTHRITIC_MOUSE_CD4_TCELL_UP, GSE22140_HEALTHY_VS_ARTHRITIC_MOUSE_CD4_TCELL_UP
GSE3039_CD4_TCELL_VS_B2_BCELL_DN, GSE3039_CD4_TCELL_VS_B2_BCELL_DN
GSE27786_LIN_NEG_VS_ERYTHROBLAST_UP, GSE27786_LIN_NEG_VS_ERYTHROBLAST_UP
HALLMARK_ADIPOGENESIS, HALLMARK_ADIPOGENESIS
GSE17721_12H_VS_24H_PAM3CSK4_BMDC_DN, GSE17721_12H_VS_24H_PAM3CSK4_BMDC_DN
GSE3982_MAC_VS_NKCELL_UP, GSE3982_MAC_VS_NKCELL_UP
GO_ORGANELLAR_RIBOSOME, GO_ORGANELLAR_RIBOSOME
GSE43955_1H_VS_42H_ACT_CD4_TCELL_WITH_TGFB_IL6_UP, GSE43955_1H_VS_42H_ACT_CD4_TCELL_WITH_TGFB_IL6_UP
GSE3982_MAC_VS_CENT_MEMORY_CD4_TCELL_UP, GSE3982_MAC_VS_CENT_MEMORY_CD4_TCELL_UP
BURTON_ADIPOGENESIS_5, BURTON_ADIPOGENESIS_5
GSE9006_HEALTHY_VS_TYPE_1_DIABETES_PBMC_AT_DX_UP, GSE9006_HEALTHY_VS_TYPE_1_DIABETES_PBMC_AT_DX_UP
GSE17721_CTRL_VS_PAM3CSK4_12H_BMDC_UP, GSE17721_CTRL_VS_PAM3CSK4_12H_BMDC_UP
GSE43955_1H_VS_60H_ACT_CD4_TCELL_UP, GSE43955_1H_VS_60H_ACT_CD4_TCELL_UP
GSE17721_4H_VS_24H_POLYIC_BMDC_UP, GSE17721_4H_VS_24H_POLYIC_BMDC_UP
GSE360_L_MAJOR_VS_B_MALAYI_LOW_DOSE_DC_DN, GSE360_L_MAJOR_VS_B_MALAYI_LOW_DOSE_DC_DN
GSE26030_TH1_VS_TH17_RESTIMULATED_DAY5_POST_POLARIZATION_UP, GSE26030_TH1_VS_TH17_RESTIMULATED_DAY5_POST_POLARIZATION_UP
LI_DCP2_BOUND_MRNA, LI_DCP2_BOUND_MRNA
MCBRYAN_PUBERTAL_BREAST_4_5WK_DN, MCBRYAN_PUBERTAL_BREAST_4_5WK_DN
GSE43955_1H_VS_10H_ACT_CD4_TCELL_WITH_TGFB_IL6_UP, GSE43955_1H_VS_10H_ACT_CD4_TCELL_WITH_TGFB_IL6_UP
GSE360_DC_VS_MAC_B_MALAYI_LOW_DOSE_UP, GSE360_DC_VS_MAC_B_MALAYI_LOW_DOSE_UP
GSE360_CTRL_VS_L_DONOVANI_MAC_UP, GSE360_CTRL_VS_L_DONOVANI_MAC_UP
MODULE_22, MODULE_22
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR, WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR
GSE360_L_MAJOR_VS_B_MALAYI_LOW_DOSE_MAC_DN, GSE360_L_MAJOR_VS_B_MALAYI_LOW_DOSE_MAC_DN
MOOTHA_VOXPHOS, MOOTHA_VOXPHOS
GSE37605_TREG_VS_TCONV_C57BL6_FOXP3_IRES_GFP_DN, GSE37605_TREG_VS_TCONV_C57BL6_FOXP3_IRES_GFP_DN
GO_OXIDATIVE_PHOSPHORYLATION, GO_OXIDATIVE_PHOSPHORYLATION
GSE27241_WT_VS_RORGT_KO_TH17_POLARIZED_CD4_TCELL_DN, GSE27241_WT_VS_RORGT_KO_TH17_POLARIZED_CD4_TCELL_DN
GSE19401_UNSTIM_VS_RETINOIC_ACID_STIM_FOLLICULAR_DC_UP, GSE19401_UNSTIM_VS_RETINOIC_ACID_STIM_FOLLICULAR_DC_UP
GSE17721_0.5H_VS_12H_LPS_BMDC_UP, GSE17721_0.5H_VS_12H_LPS_BMDC_UP
GO_COFACTOR_BIOSYNTHETIC_PROCESS, GO_COFACTOR_BIOSYNTHETIC_PROCESS
GO_COENZYME_BINDING, GO_COENZYME_BINDING
GSE360_T_GONDII_VS_B_MALAYI_LOW_DOSE_MAC_DN, GSE360_T_GONDII_VS_B_MALAYI_LOW_DOSE_MAC_DN
PECE_MAMMARY_STEM_CELL_UP, PECE_MAMMARY_STEM_CELL_UP
GSE5542_IFNG_VS_IFNA_AND_IFNG_TREATED_EPITHELIAL_CELLS_6H_DN, GSE5542_IFNG_VS_IFNA_AND_IFNG_TREATED_EPITHELIAL_CELLS_6H_DN
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY, GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
GO_OUTER_MEMBRANE, GO_OUTER_MEMBRANE
GSE360_DC_VS_MAC_L_DONOVANI_UP, GSE360_DC_VS_MAC_L_DONOVANI_UP
GSE37301_MULTIPOTENT_PROGENITOR_VS_CD4_TCELL_DN, GSE37301_MULTIPOTENT_PROGENITOR_VS_CD4_TCELL_DN
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT, GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT
GSE1460_DP_VS_CD4_THYMOCYTE_UP, GSE1460_DP_VS_CD4_THYMOCYTE_UP
GSE15330_HSC_VS_LYMPHOID_PRIMED_MULTIPOTENT_PROGENITOR_IKAROS_KO_UP, GSE15330_HSC_VS_LYMPHOID_PRIMED_MULTIPOTENT_PROGENITOR_IKAROS_KO_UP
GO_RESPIRATORY_CHAIN, GO_RESPIRATORY_CHAIN
GO_ELECTRON_TRANSPORT_CHAIN, GO_ELECTRON_TRANSPORT_CHAIN
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM, REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM
GO_METAL_CLUSTER_BINDING, GO_METAL_CLUSTER_BINDING
GO_NUCLEOID, GO_NUCLEOID
MORF_PPP2R4, MORF_PPP2R4
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT, REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
GSE22886_DC_VS_MONOCYTE_UP, GSE22886_DC_VS_MONOCYTE_UP
GSE360_L_DONOVANI_VS_B_MALAYI_HIGH_DOSE_MAC_DN, GSE360_L_DONOVANI_VS_B_MALAYI_HIGH_DOSE_MAC_DN
GSE21546_WT_VS_SAP1A_KO_ANTI_CD3_STIM_DP_THYMOCYTES_UP, GSE21546_WT_VS_SAP1A_KO_ANTI_CD3_STIM_DP_THYMOCYTES_UP
GSE13411_NAIVE_VS_IGM_MEMORY_BCELL_DN, GSE13411_NAIVE_VS_IGM_MEMORY_BCELL_DN
GSE5589_UNSTIM_VS_45MIN_LPS_AND_IL10_STIM_MACROPHAGE_DN, GSE5589_UNSTIM_VS_45MIN_LPS_AND_IL10_STIM_MACROPHAGE_DN
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS, GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS
HALLMARK_GLYCOLYSIS, HALLMARK_GLYCOLYSIS
GSE360_L_MAJOR_VS_B_MALAYI_HIGH_DOSE_DC_DN, GSE360_L_MAJOR_VS_B_MALAYI_HIGH_DOSE_DC_DN
GSE4748_CTRL_VS_LPS_AND_CYANOBACTERIUM_LPSLIKE_STIM_DC_3H_DN, GSE4748_CTRL_VS_LPS_AND_CYANOBACTERIUM_LPSLIKE_STIM_DC_3H_DN
GSE18281_SUBCAPSULAR_CORTICAL_REGION_VS_WHOLE_CORTEX_THYMUS_UP, GSE18281_SUBCAPSULAR_CORTICAL_REGION_VS_WHOLE_CORTEX_THYMUS_UP
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION, GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION
GO_ORGANELLE_ENVELOPE_LUMEN, GO_ORGANELLE_ENVELOPE_LUMEN
GO_HYDROGEN_TRANSPORT, GO_HYDROGEN_TRANSPORT
GO_OXIDOREDUCTASE_COMPLEX, GO_OXIDOREDUCTASE_COMPLEX
GSE30971_2H_VS_4H_LPS_STIM_MACROPHAGE_WBP7_HET_UP, GSE30971_2H_VS_4H_LPS_STIM_MACROPHAGE_WBP7_HET_UP
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT, GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT
GSE36888_UNTREATED_VS_IL2_TREATED_TCELL_2H_DN, GSE36888_UNTREATED_VS_IL2_TREATED_TCELL_2H_DN
MORF_XPC, MORF_XPC
MODULE_116, MODULE_116
GO_AEROBIC_RESPIRATION, GO_AEROBIC_RESPIRATION
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT, GO_PROTEIN_TRANSMEMBRANE_TRANSPORT
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS, GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS
GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION, GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION
GSE26030_UNSTIM_VS_RESTIM_TH17_DAY5_POST_POLARIZATION_DN, GSE26030_UNSTIM_VS_RESTIM_TH17_DAY5_POST_POLARIZATION_DN
OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP, OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS, GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS
BURTON_ADIPOGENESIS_6, BURTON_ADIPOGENESIS_6
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX
GO_COENZYME_BIOSYNTHETIC_PROCESS, GO_COENZYME_BIOSYNTHETIC_PROCESS
MODULE_93, MODULE_93
HALLMARK_FATTY_ACID_METABOLISM, HALLMARK_FATTY_ACID_METABOLISM
SIRNA_EIF4GI_UP, SIRNA_EIF4GI_UP
GSE17721_0.5H_VS_12H_PAM3CSK4_BMDC_UP, GSE17721_0.5H_VS_12H_PAM3CSK4_BMDC_UP
GO_PROTEIN_TARGETING_TO_MITOCHONDRION, GO_PROTEIN_TARGETING_TO_MITOCHONDRION
GSE5960_TH1_VS_ANERGIC_TH1_DN, GSE5960_TH1_VS_ANERGIC_TH1_DN
GSE16385_MONOCYTE_VS_12H_ROSIGLITAZONE_TREATED_MACROPHAGE_UP, GSE16385_MONOCYTE_VS_12H_ROSIGLITAZONE_TREATED_MACROPHAGE_UP
MODULE_307, MODULE_307
NATSUME_RESPONSE_TO_INTERFERON_BETA_DN, NATSUME_RESPONSE_TO_INTERFERON_BETA_DN
GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE, GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE
GSE32901_TH1_VS_TH17_ENRICHED_CD4_TCELL_DN, GSE32901_TH1_VS_TH17_ENRICHED_CD4_TCELL_DN
GSE32423_IL7_VS_IL7_IL4_MEMORY_CD8_TCELL_DN, GSE32423_IL7_VS_IL7_IL4_MEMORY_CD8_TCELL_DN
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR, REACTOME_SIGNALING_BY_INSULIN_RECEPTOR
GSE360_L_MAJOR_VS_B_MALAYI_HIGH_DOSE_MAC_DN, GSE360_L_MAJOR_VS_B_MALAYI_HIGH_DOSE_MAC_DN
GSE339_CD8POS_VS_CD4CD8DN_DC_DN, GSE339_CD8POS_VS_CD4CD8DN_DC_DN
GO_NADH_DEHYDROGENASE_COMPLEX, GO_NADH_DEHYDROGENASE_COMPLEX
GO_HEXOSE_METABOLIC_PROCESS, GO_HEXOSE_METABOLIC_PROCESS
GO_CHAPERONE_BINDING, GO_CHAPERONE_BINDING
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT, GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT
DITTMER_PTHLH_TARGETS_DN, DITTMER_PTHLH_TARGETS_DN
GO_FATTY_ACID_CATABOLIC_PROCESS, GO_FATTY_ACID_CATABOLIC_PROCESS
GSE17721_LPS_VS_GARDIQUIMOD_24H_BMDC_UP, GSE17721_LPS_VS_GARDIQUIMOD_24H_BMDC_UP
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS, GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS
GSE17721_PAM3CSK4_VS_CPG_24H_BMDC_UP, GSE17721_PAM3CSK4_VS_CPG_24H_BMDC_UP
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS, GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS
GO_PHAGOCYTIC_VESICLE_MEMBRANE, GO_PHAGOCYTIC_VESICLE_MEMBRANE
NUTT_GBM_VS_AO_GLIOMA_DN, NUTT_GBM_VS_AO_GLIOMA_DN
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H
GO_FATTY_ACID_BETA_OXIDATION, GO_FATTY_ACID_BETA_OXIDATION
RODWELL_AGING_KIDNEY_NO_BLOOD_DN, RODWELL_AGING_KIDNEY_NO_BLOOD_DN
GO_ELECTRON_CARRIER_ACTIVITY, GO_ELECTRON_CARRIER_ACTIVITY
GSE17721_LPS_VS_POLYIC_1H_BMDC_UP, GSE17721_LPS_VS_POLYIC_1H_BMDC_UP
MODULE_273, MODULE_273
GSE360_HIGH_VS_LOW_DOSE_B_MALAYI_MAC_DN, GSE360_HIGH_VS_LOW_DOSE_B_MALAYI_MAC_DN
GSE39820_TGFBETA3_IL6_VS_TGFBETA3_IL6_IL23A_TREATED_CD4_TCELL_DN, GSE39820_TGFBETA3_IL6_VS_TGFBETA3_IL6_IL23A_TREATED_CD4_TCELL_DN
GALLUZZI_PERMEABILIZE_MITOCHONDRIA, GALLUZZI_PERMEABILIZE_MITOCHONDRIA
GSE17721_CPG_VS_GARDIQUIMOD_0.5H_BMDC_UP, GSE17721_CPG_VS_GARDIQUIMOD_0.5H_BMDC_UP
CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN, CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
GO_NAD_BINDING, GO_NAD_BINDING
GSE24574_BCL6_LOW_TFH_VS_NAIVE_CD4_TCELL_UP, GSE24574_BCL6_LOW_TFH_VS_NAIVE_CD4_TCELL_UP
GSE17721_LPS_VS_GARDIQUIMOD_0.5H_BMDC_UP, GSE17721_LPS_VS_GARDIQUIMOD_0.5H_BMDC_UP
GO_LYASE_ACTIVITY, GO_LYASE_ACTIVITY
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS, GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS
MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP, MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP
GO_REGULATION_OF_MEMBRANE_PERMEABILITY, GO_REGULATION_OF_MEMBRANE_PERMEABILITY
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS, GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION, KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION
RODWELL_AGING_KIDNEY_DN, RODWELL_AGING_KIDNEY_DN
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS, GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS
GSE29618_LAIV_VS_TIV_FLU_VACCINE_DAY7_MONOCYTE_DN, GSE29618_LAIV_VS_TIV_FLU_VACCINE_DAY7_MONOCYTE_DN
GO_LIPID_OXIDATION, GO_LIPID_OXIDATION
GSE21033_CTRL_VS_POLYIC_STIM_DC_24H_DN, GSE21033_CTRL_VS_POLYIC_STIM_DC_24H_DN
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_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA, GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
HOEBEKE_LYMPHOID_STEM_CELL_DN, HOEBEKE_LYMPHOID_STEM_CELL_DN
GSE39820_TGFBETA1_IL6_VS_TGFBETA1_IL6_IL23A_TREATED_CD4_TCELL_DN, GSE39820_TGFBETA1_IL6_VS_TGFBETA1_IL6_IL23A_TREATED_CD4_TCELL_DN
GO_HYDROGEN_EXPORTING_ATPASE_ACTIVITY, GO_HYDROGEN_EXPORTING_ATPASE_ACTIVITY
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR
GSE46606_IRF4HIGH_VS_WT_CD40L_IL2_IL5_DAY3_STIMULATED_BCELL_DN, GSE46606_IRF4HIGH_VS_WT_CD40L_IL2_IL5_DAY3_STIMULATED_BCELL_DN
KEGG_PEROXISOME, KEGG_PEROXISOME
GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES, GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES
GSE360_T_GONDII_VS_B_MALAYI_LOW_DOSE_DC_DN, GSE360_T_GONDII_VS_B_MALAYI_LOW_DOSE_DC_DN
GCM_BECN1, GCM_BECN1
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE, GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR
GSE360_L_MAJOR_VS_M_TUBERCULOSIS_DC_UP, GSE360_L_MAJOR_VS_M_TUBERCULOSIS_DC_UP
GSE9006_TYPE_1_DIABETES_AT_DX_VS_4MONTH_POST_DX_PBMC_DN, GSE9006_TYPE_1_DIABETES_AT_DX_VS_4MONTH_POST_DX_PBMC_DN
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT, GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT
GO_NAD_METABOLIC_PROCESS, GO_NAD_METABOLIC_PROCESS
HALLMARK_XENOBIOTIC_METABOLISM, HALLMARK_XENOBIOTIC_METABOLISM
MODULE_77, MODULE_77
GSE360_CTRL_VS_T_GONDII_DC_UP, GSE360_CTRL_VS_T_GONDII_DC_UP
RUAN_RESPONSE_TO_TNF_DN, RUAN_RESPONSE_TO_TNF_DN
GO_HEAT_SHOCK_PROTEIN_BINDING, GO_HEAT_SHOCK_PROTEIN_BINDING
GSE9316_CD4_TCELL_BALBC_VS_TH17_ENRI_CD4_TCELL_SKG_PMA_IONO_STIM_FR4NEG_UP, GSE9316_CD4_TCELL_BALBC_VS_TH17_ENRI_CD4_TCELL_SKG_PMA_IONO_STIM_FR4NEG_UP
GSE34515_CD16_NEG_VS_POS_MONOCYTE_UP, GSE34515_CD16_NEG_VS_POS_MONOCYTE_UP
HALLMARK_PEROXISOME, HALLMARK_PEROXISOME
TBK1.DN.48HRS_DN, TBK1.DN.48HRS_DN
GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY, GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY
HONMA_DOCETAXEL_RESISTANCE, HONMA_DOCETAXEL_RESISTANCE
KEGG_VIBRIO_CHOLERAE_INFECTION, KEGG_VIBRIO_CHOLERAE_INFECTION
GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING, GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING
GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_TREATED_CD4_TCELL_DN, GSE39820_TGFBETA1_VS_TGFBETA3_IN_IL6_TREATED_CD4_TCELL_DN
GO_TRIVALENT_INORGANIC_CATION_TRANSPORT, GO_TRIVALENT_INORGANIC_CATION_TRANSPORT
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX
PID_CERAMIDE_PATHWAY, PID_CERAMIDE_PATHWAY
GSE9006_TYPE_1_DIABETES_AT_DX_VS_1MONTH_POST_DX_PBMC_DN, GSE9006_TYPE_1_DIABETES_AT_DX_VS_1MONTH_POST_DX_PBMC_DN
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING, REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING
GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS, GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS, GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS
GSE6269_STAPH_AUREUS_VS_STREP_PNEUMO_INF_PBMC_UP, GSE6269_STAPH_AUREUS_VS_STREP_PNEUMO_INF_PBMC_UP
GO_ATPASE_COUPLED_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY, GO_ATPASE_COUPLED_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY
REACTOME_IRON_UPTAKE_AND_TRANSPORT, REACTOME_IRON_UPTAKE_AND_TRANSPORT
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS, GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION, KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
KEGG_APOPTOSIS, KEGG_APOPTOSIS
GO_NADP_BINDING, GO_NADP_BINDING
REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING, REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN, LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN
GO_CATION_TRANSPORTING_ATPASE_ACTIVITY, GO_CATION_TRANSPORTING_ATPASE_ACTIVITY
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN
MODY_HIPPOCAMPUS_POSTNATAL, MODY_HIPPOCAMPUS_POSTNATAL
GSE22025_UNTREATED_VS_TGFB1_TREATED_CD4_TCELL_UP, GSE22025_UNTREATED_VS_TGFB1_TREATED_CD4_TCELL_UP
GO_2_IRON_2_SULFUR_CLUSTER_BINDING, GO_2_IRON_2_SULFUR_CLUSTER_BINDING
GO_GLUCOSE_METABOLIC_PROCESS, GO_GLUCOSE_METABOLIC_PROCESS
GO_ATP_BIOSYNTHETIC_PROCESS, GO_ATP_BIOSYNTHETIC_PROCESS
GSE43700_UNTREATED_VS_IL10_TREATED_PBMC_DN, GSE43700_UNTREATED_VS_IL10_TREATED_PBMC_DN
CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP, CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
GSE11961_FOLLICULAR_BCELL_VS_MEMORY_BCELL_DAY40_UP, GSE11961_FOLLICULAR_BCELL_VS_MEMORY_BCELL_DAY40_UP
KORKOLA_SEMINOMA_UP, KORKOLA_SEMINOMA_UP
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS, GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS
GO_GLUTATHIONE_PEROXIDASE_ACTIVITY, GO_GLUTATHIONE_PEROXIDASE_ACTIVITY
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS
KEGG_CITRATE_CYCLE_TCA_CYCLE, KEGG_CITRATE_CYCLE_TCA_CYCLE
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT, GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT
GO_MITOCHONDRIAL_FUSION, GO_MITOCHONDRIAL_FUSION
MODULE_42, MODULE_42
MODULE_363, MODULE_363
GO_PHAGOSOME_MATURATION, GO_PHAGOSOME_MATURATION
GSE360_L_MAJOR_VS_M_TUBERCULOSIS_MAC_DN, GSE360_L_MAJOR_VS_M_TUBERCULOSIS_MAC_DN
GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS, GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS
KEEN_RESPONSE_TO_ROSIGLITAZONE_UP, KEEN_RESPONSE_TO_ROSIGLITAZONE_UP
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE, REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE, REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE
GSE22935_WT_VS_MYD88_KO_MACROPHAGE_48H_MBOVIS_BCG_STIM_UP, GSE22935_WT_VS_MYD88_KO_MACROPHAGE_48H_MBOVIS_BCG_STIM_UP
PID_CASPASE_PATHWAY, PID_CASPASE_PATHWAY
GO_ATP_HYDROLYSIS_COUPLED_TRANSMEMBRANE_TRANSPORT, GO_ATP_HYDROLYSIS_COUPLED_TRANSMEMBRANE_TRANSPORT
GSE1112_OT1_VS_HY_CD8AB_THYMOCYTE_RTOC_CULTURE_UP, GSE1112_OT1_VS_HY_CD8AB_THYMOCYTE_RTOC_CULTURE_UP
GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY, GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY
GO_ZYMOGEN_ACTIVATION, GO_ZYMOGEN_ACTIVATION
GO_DETOXIFICATION, GO_DETOXIFICATION
GO_NADH_METABOLIC_PROCESS, GO_NADH_METABOLIC_PROCESS
GSE24574_BCL6_HIGH_TFH_VS_TFH_CD4_TCELL_UP, GSE24574_BCL6_HIGH_TFH_VS_TFH_CD4_TCELL_UP
BIOCARTA_CERAMIDE_PATHWAY, BIOCARTA_CERAMIDE_PATHWAY
MODULE_43, MODULE_43
GO_IRON_ION_TRANSPORT, GO_IRON_ION_TRANSPORT
GO_MONOSACCHARIDE_METABOLIC_PROCESS, GO_MONOSACCHARIDE_METABOLIC_PROCESS
LANDIS_ERBB2_BREAST_TUMORS_324_DN, LANDIS_ERBB2_BREAST_TUMORS_324_DN
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN
GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY, GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS, REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
GO_CARBON_OXYGEN_LYASE_ACTIVITY, GO_CARBON_OXYGEN_LYASE_ACTIVITY
GSE360_L_DONOVANI_VS_T_GONDII_MAC_UP, GSE360_L_DONOVANI_VS_T_GONDII_MAC_UP
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE, REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE
GO_HEME_BIOSYNTHETIC_PROCESS, GO_HEME_BIOSYNTHETIC_PROCESS
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS, GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS
MOOTHA_FFA_OXYDATION, MOOTHA_FFA_OXYDATION
GO_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY, GO_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY
GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS, GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE, GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE
GO_ADP_METABOLIC_PROCESS, GO_ADP_METABOLIC_PROCESS
KEGG_CALCIUM_SIGNALING_PATHWAY, KEGG_CALCIUM_SIGNALING_PATHWAY
VERHAAK_GLIOBLASTOMA_NEURAL, VERHAAK_GLIOBLASTOMA_NEURAL
GSE9960_HEALTHY_VS_SEPSIS_PBMC_UP, GSE9960_HEALTHY_VS_SEPSIS_PBMC_UP
GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION, GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION
BIOCARTA_ETC_PATHWAY, BIOCARTA_ETC_PATHWAY
GO_OXALOACETATE_METABOLIC_PROCESS, GO_OXALOACETATE_METABOLIC_PROCESS
KEGG_FATTY_ACID_METABOLISM, KEGG_FATTY_ACID_METABOLISM
GSE32533_WT_VS_MIR17_OVEREXPRESS_ACT_CD4_TCELL_DN, GSE32533_WT_VS_MIR17_OVEREXPRESS_ACT_CD4_TCELL_DN
REACTOME_PEROXISOMAL_LIPID_METABOLISM, REACTOME_PEROXISOMAL_LIPID_METABOLISM
MOOTHA_TCA, MOOTHA_TCA
GSE31622_WT_VS_KLF3_KO_BCELL_UP, GSE31622_WT_VS_KLF3_KO_BCELL_UP
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS, GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS
KEGG_CARDIAC_MUSCLE_CONTRACTION, KEGG_CARDIAC_MUSCLE_CONTRACTION
GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS, GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS
REACTOME_GLUCOSE_METABOLISM, REACTOME_GLUCOSE_METABOLISM
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS, GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS
GALE_APL_WITH_FLT3_MUTATED_DN, GALE_APL_WITH_FLT3_MUTATED_DN
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR
MCBRYAN_PUBERTAL_BREAST_3_4WK_DN, MCBRYAN_PUBERTAL_BREAST_3_4WK_DN
GO_TRANSITION_METAL_ION_TRANSPORT, GO_TRANSITION_METAL_ION_TRANSPORT
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY_INVOLVED_IN_APOPTOTIC_PROCESS, GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY_INVOLVED_IN_APOPTOTIC_PROCESS
GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY, GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY
GSE5099_MONOCYTE_VS_CLASSICAL_M1_MACROPHAGE_UP, GSE5099_MONOCYTE_VS_CLASSICAL_M1_MACROPHAGE_UP
GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA, GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
KEGG_LYSINE_DEGRADATION, KEGG_LYSINE_DEGRADATION
GO_REGULATION_OF_BONE_DEVELOPMENT, GO_REGULATION_OF_BONE_DEVELOPMENT
GO_MITOCHONDRIAL_RNA_PROCESSING, GO_MITOCHONDRIAL_RNA_PROCESSING
GO_APOPTOTIC_MITOCHONDRIAL_CHANGES, GO_APOPTOTIC_MITOCHONDRIAL_CHANGES
GO_CYTOCHROME_COMPLEX_ASSEMBLY, GO_CYTOCHROME_COMPLEX_ASSEMBLY
GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION, GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION
GO_C_ACYLTRANSFERASE_ACTIVITY, GO_C_ACYLTRANSFERASE_ACTIVITY
GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX, GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX
GO_PHAGOSOME_ACIDIFICATION, GO_PHAGOSOME_ACIDIFICATION
BIOCARTA_DEATH_PATHWAY, BIOCARTA_DEATH_PATHWAY
KEGG_BUTANOATE_METABOLISM, KEGG_BUTANOATE_METABOLISM
GO_METALLO_SULFUR_CLUSTER_ASSEMBLY, GO_METALLO_SULFUR_CLUSTER_ASSEMBLY
GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE, GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE
MAHAJAN_RESPONSE_TO_IL1A_DN, MAHAJAN_RESPONSE_TO_IL1A_DN
NADLER_OBESITY_DN, NADLER_OBESITY_DN
GO_MITOCHONDRIAL_FISSION, GO_MITOCHONDRIAL_FISSION
GO_RESPONSE_TO_COPPER_ION, GO_RESPONSE_TO_COPPER_ION
GO_THIOESTER_METABOLIC_PROCESS, GO_THIOESTER_METABOLIC_PROCESS
MODULE_287, MODULE_287
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS, KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
GO_REGULATION_OF_SULFUR_METABOLIC_PROCESS, GO_REGULATION_OF_SULFUR_METABOLIC_PROCESS
KORKOLA_EMBRYONAL_CARCINOMA_UP, KORKOLA_EMBRYONAL_CARCINOMA_UP
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS, GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
GO_FATTY_ACID_TRANSPORT, GO_FATTY_ACID_TRANSPORT
JIANG_AGING_HYPOTHALAMUS_DN, JIANG_AGING_HYPOTHALAMUS_DN
REACTOME_INSULIN_RECEPTOR_RECYCLING, REACTOME_INSULIN_RECEPTOR_RECYCLING
PID_HIV_NEF_PATHWAY, PID_HIV_NEF_PATHWAY
GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS, GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX_COUPLING_FACTOR_F_O_, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX_COUPLING_FACTOR_F_O_
GO_ACYL_COA_DEHYDROGENASE_ACTIVITY, GO_ACYL_COA_DEHYDROGENASE_ACTIVITY
GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY, GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY
GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY, GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY
WU_HBX_TARGETS_2_UP, WU_HBX_TARGETS_2_UP
HALLMARK_BILE_ACID_METABOLISM, HALLMARK_BILE_ACID_METABOLISM
GSE16385_UNTREATED_VS_12H_IL4_TREATED_MACROPHAGE_DN, GSE16385_UNTREATED_VS_12H_IL4_TREATED_MACROPHAGE_DN
GO_XENOPHAGY, GO_XENOPHAGY
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS, REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS
GO_SINGLE_ORGANISM_MEMBRANE_FUSION, GO_SINGLE_ORGANISM_MEMBRANE_FUSION
GO_THIOESTER_BIOSYNTHETIC_PROCESS, GO_THIOESTER_BIOSYNTHETIC_PROCESS
NUTT_GBM_VS_AO_GLIOMA_UP, NUTT_GBM_VS_AO_GLIOMA_UP
GO_CELLULAR_LIPID_CATABOLIC_PROCESS, GO_CELLULAR_LIPID_CATABOLIC_PROCESS
GSE22611_NOD2_TRANSD_VS_CTRL_TRANSD_HEK293_MDP_STIM_2H_UP, GSE22611_NOD2_TRANSD_VS_CTRL_TRANSD_HEK293_MDP_STIM_2H_UP
GO_PIGMENT_BIOSYNTHETIC_PROCESS, GO_PIGMENT_BIOSYNTHETIC_PROCESS
GO_MITOCHONDRION_MORPHOGENESIS, GO_MITOCHONDRION_MORPHOGENESIS
BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP, BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP
HUMMERICH_SKIN_CANCER_PROGRESSION_DN, HUMMERICH_SKIN_CANCER_PROGRESSION_DN
GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX, GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION, REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION
MODULE_414, MODULE_414
MODULE_492, MODULE_492
GO_ATP_GENERATION_FROM_ADP, GO_ATP_GENERATION_FROM_ADP
SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP, SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY, GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY
GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA, GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION, KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS, GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS
GO_SUBSTANTIA_NIGRA_DEVELOPMENT, GO_SUBSTANTIA_NIGRA_DEVELOPMENT
GO_FATTY_ACYL_COA_BINDING, GO_FATTY_ACYL_COA_BINDING
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM, KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
DURCHDEWALD_SKIN_CARCINOGENESIS_UP, DURCHDEWALD_SKIN_CARCINOGENESIS_UP
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS, GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS, GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS
GO_GLUTAMATE_METABOLIC_PROCESS, GO_GLUTAMATE_METABOLIC_PROCESS
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17, MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17
GO_REGULATION_OF_FATTY_ACID_OXIDATION, GO_REGULATION_OF_FATTY_ACID_OXIDATION
MODULE_343, MODULE_343
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM, REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN, GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN
JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_UP, JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_UP
GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS, GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS
GO_PYRIDOXAL_PHOSPHATE_BINDING, GO_PYRIDOXAL_PHOSPHATE_BINDING
MODULE_286, MODULE_286
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS, GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS
GO_COFACTOR_TRANSPORT, GO_COFACTOR_TRANSPORT
MODULE_25, MODULE_25
GO_REGULATION_OF_ACYL_COA_BIOSYNTHETIC_PROCESS, GO_REGULATION_OF_ACYL_COA_BIOSYNTHETIC_PROCESS
KORKOLA_YOLK_SAC_TUMOR_UP, KORKOLA_YOLK_SAC_TUMOR_UP
GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS, GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS
GO_CARDIOLIPIN_METABOLIC_PROCESS, GO_CARDIOLIPIN_METABOLIC_PROCESS
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION, REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS, GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS
GSE22935_UNSTIM_VS_48H_MBOVIS_BCG_STIM_MACROPHAGE_UP, GSE22935_UNSTIM_VS_48H_MBOVIS_BCG_STIM_MACROPHAGE_UP
MODULE_103, MODULE_103
GO_MITOCHONDRION_LOCALIZATION, GO_MITOCHONDRION_LOCALIZATION
GO_FMN_BINDING, GO_FMN_BINDING