
GARDIQUIMOD_0.5H_BMDC_UP, GSE17721_CTRL_VS_GARDIQUIMOD_0.5H_BMDC_UP
GSE17721_LPS_VS_GARDIQUIMOD_6H_BMDC_DN, GSE17721_LPS_VS_GARDIQUIMOD_6H_BMDC_DN
GSE17721_CTRL_VS_CPG_12H_BMDC_UP, GSE17721_CTRL_VS_CPG_12H_BMDC_UP
GSE17721_CTRL_VS_PAM3CSK4_12H_BMDC_UP, GSE17721_CTRL_VS_PAM3CSK4_12H_BMDC_UP
GSE17721_POLYIC_VS_GARDIQUIMOD_16H_BMDC_DN, GSE17721_POLYIC_VS_GARDIQUIMOD_16H_BMDC_DN
GSE17721_CTRL_VS_PAM3CSK4_8H_BMDC_UP, GSE17721_CTRL_VS_PAM3CSK4_8H_BMDC_UP
GSE17721_0.5H_VS_24H_POLYIC_BMDC_DN, GSE17721_0.5H_VS_24H_POLYIC_BMDC_DN
GSE17721_POLYIC_VS_GARDIQUIMOD_0.5H_BMDC_DN, GSE17721_POLYIC_VS_GARDIQUIMOD_0.5H_BMDC_DN
GSE17721_0.5H_VS_4H_POLYIC_BMDC_DN, GSE17721_0.5H_VS_4H_POLYIC_BMDC_DN
GO_RNA_POLYMERASE_COMPLEX, GO_RNA_POLYMERASE_COMPLEX
GSE17721_CTRL_VS_LPS_2H_BMDC_UP, GSE17721_CTRL_VS_LPS_2H_BMDC_UP
GSE37534_UNTREATED_VS_ROSIGLITAZONE_TREATED_CD4_TCELL_PPARG1_AND_FOXP3_TRASDUCED_DN, GSE37534_UNTREATED_VS_ROSIGLITAZONE_TREATED_CD4_TCELL_PPARG1_AND
GSE17721_0.5H_VS_8H_POLYIC_BMDC_DN, GSE17721_0.5H_VS_8H_POLYIC_BMDC_DN
GSE37534_UNTREATED_VS_PIOGLITAZONE_TREATED_CD4_TCELL_PPARG1_AND_FOXP3_TRASDUCED_DN, GSE37534_UNTREATED_VS_PIOGLITAZONE_TREATED_CD4_TCELL_PPARG1_AND_F
GSE17721_CTRL_VS_POLYIC_1H_BMDC_UP, GSE17721_CTRL_VS_POLYIC_1H_BMDC_UP
GSE21033_CTRL_VS_POLYIC_STIM_DC_24H_UP, GSE21033_CTRL_VS_POLYIC_STIM_DC_24H_UP
GSE17721_0.5H_VS_4H_LPS_BMDC_DN, GSE17721_0.5H_VS_4H_LPS_BMDC_DN
GSE17721_CTRL_VS_GARDIQUIMOD_4H_BMDC_DN, GSE17721_CTRL_VS_GARDIQUIMOD_4H_BMDC_DN
GSE2770_IL4_ACT_VS_ACT_CD4_TCELL_48H_DN, GSE2770_IL4_ACT_VS_ACT_CD4_TCELL_48H_DN
GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY, GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY
GSE17721_PAM3CSK4_VS_CPG_4H_BMDC_DN, GSE17721_PAM3CSK4_VS_CPG_4H_BMDC_DN
GO_MITOCHONDRION_LOCALIZATION, GO_MITOCHONDRION_LOCALIZATION
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE, GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE
PID_ER_NONGENOMIC_PATHWAY, PID_ER_NONGENOMIC_PATHWAY
PID_UPA_UPAR_PATHWAY, PID_UPA_UPAR_PATHWAY
GSE37605_NOD_VS_C57BL6_IRES_GFP_TREG_UP, GSE37605_NOD_VS_C57BL6_IRES_GFP_TREG_UP
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9, YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9
TRAYNOR_RETT_SYNDROM_DN, TRAYNOR_RETT_SYNDROM_DN
PID_INTEGRIN_A9B1_PATHWAY, PID_INTEGRIN_A9B1_PATHWAY
GO_STAT_CASCADE, GO_STAT_CASCADE
GO_REGULATION_OF_B_CELL_PROLIFERATION, GO_REGULATION_OF_B_CELL_PROLIFERATION
GSE40274_IRF4_VS_FOXP3_AND_IRF4_TRANSDUCED_ACTIVATED_CD4_TCELL_DN, GSE40274_IRF4_VS_FOXP3_AND_IRF4_TRANSDUCED_ACTIVATED_CD4_TCELL_DN
ESC_V6.5_UP_LATE.V1_UP, ESC_V6.5_UP_LATE.V1_UP
HFH4_01, HFH4_01
GO_INTEGRIN_BINDING, GO_INTEGRIN_BINDING
GO_PEPTIDE_CATABOLIC_PROCESS, GO_PEPTIDE_CATABOLIC_PROCESS
WHITESIDE_CISPLATIN_RESISTANCE_UP, WHITESIDE_CISPLATIN_RESISTANCE_UP
KIM_MYCL1_AMPLIFICATION_TARGETS_DN, KIM_MYCL1_AMPLIFICATION_TARGETS_DN
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX, REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX
GO_GLYCEROPHOSPHOLIPID_CATABOLIC_PROCESS, GO_GLYCEROPHOSPHOLIPID_CATABOLIC_PROCESS
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT, GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT
GO_ENDODERMAL_CELL_DIFFERENTIATION, GO_ENDODERMAL_CELL_DIFFERENTIATION
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES, KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES
KAMIKUBO_MYELOID_MN1_NETWORK, KAMIKUBO_MYELOID_MN1_NETWORK
GO_PLASMA_MEMBRANE_FUSION, GO_PLASMA_MEMBRANE_FUSION