Latent Transcriptinally Repressed HCMV Genome

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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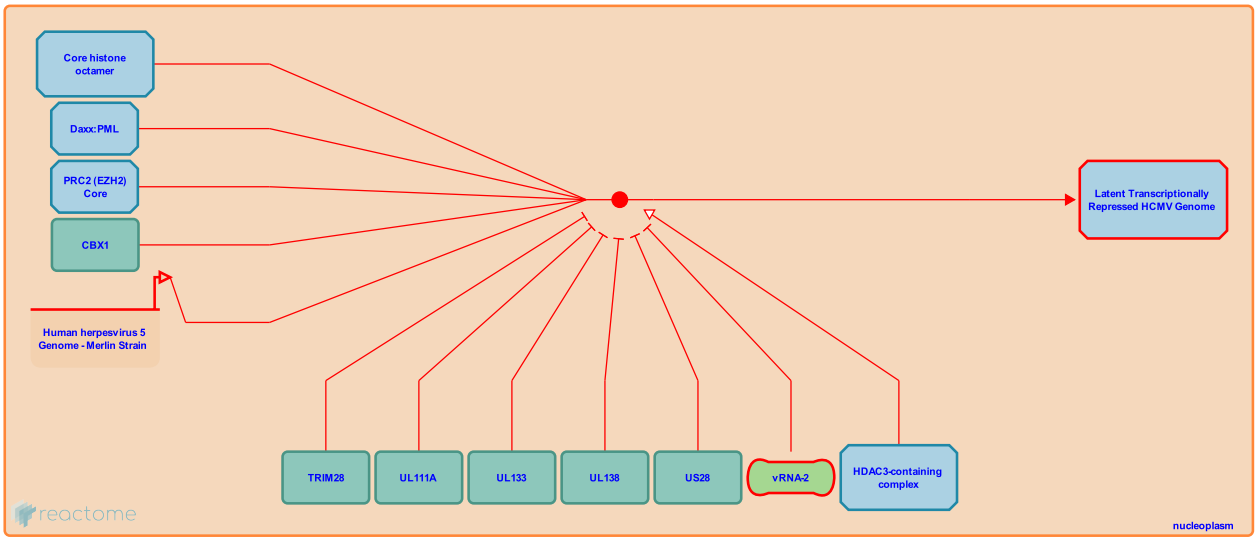
Stable identifier: R-HSA-9614816

Type: binding

Compartments: nucleoplasm

Diseases: viral infectious disease



Cells infected by with the Human Cytomegalovirus (HCMV) have two potential fates once the HCMV genome enters the nucleus. In contrast, in a latent infection the lytic transcription programme of HCMV is effectively suppressed and the cells undergo latent infection. The suppression of viral lytic gene expression observed during latency is the result from the cells inability to support robust viral immediate early (IE) gene expression; crucial genes responsible for driving the lytic cycle. The repression of IE gene expression results from specific post-translational modifications of histones associated with the viral major immediate early promoter (MIEP). The histone modifications present on the MIEP impart a repressive chromatin structure preventing transcriptional activity.
In an active infection there is extensive viral gene expression, viral DNA replication and release of progeny virus.

Literature references

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Editions

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