Activation of Latent 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.

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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Reactome database release: 88
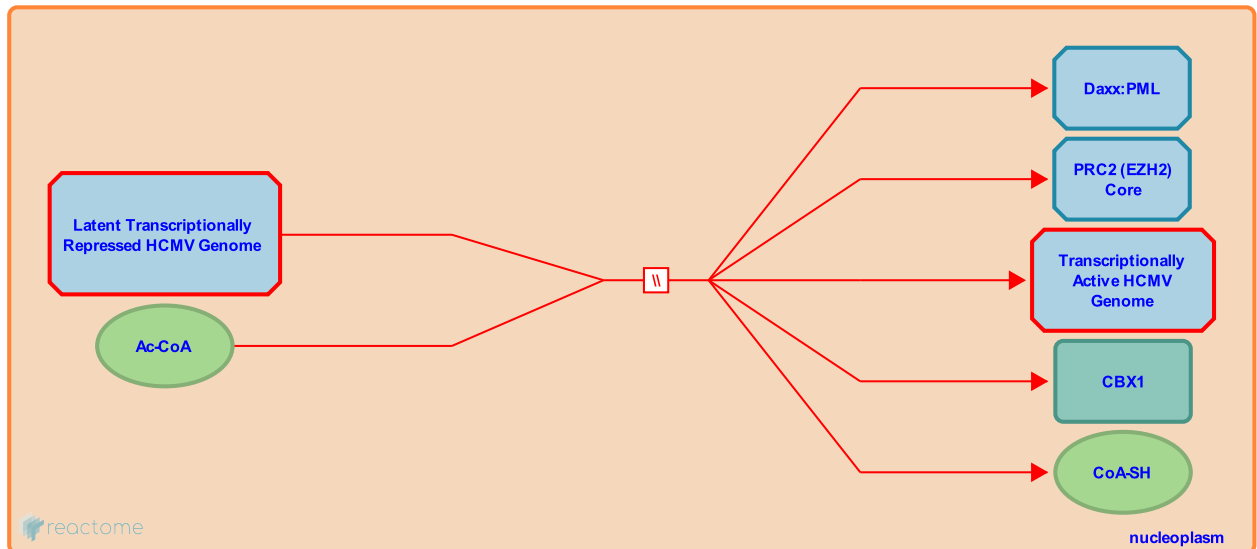
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Activation of Latent HCMV Genome ↗

Stable identifier: R-HSA-9614810

Type: omitted

Compartments: nucleoplasm

Diseases: viral infectious disease

A cell containing a repressed or latent Human Cytomegalovirus (HCMV) genome sits quietly carrying on its normal cellular functions. The HCMV silenced HCMV geneome can be activated by a number of celluar events or state changes. Reactivation of HCMV lytic infection is correlated to changes in histone modifications around the MIEP promoter resulting in a new chromatin structure conducive to transcriptional activity. These changes are intimately linked with cell differentiation, a phenomenon known to reactivate latent virus in vivo.

Literature references

Sinclair, J. (2010). Chromatin structure regulates human cytomegalovirus gene expression during latency, reactivation and lytic infection. *Biochim. Biophys. Acta, 1799*, 286-95. ↗

Knipe, DM., Howley, PM. (2013). Chapter 62 - Cytomegaloviruses, Fields Virology. *Lippincott Williams & Wilkins*.

Editions

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