Packaging of Viral Genome Into C Capsids

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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

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. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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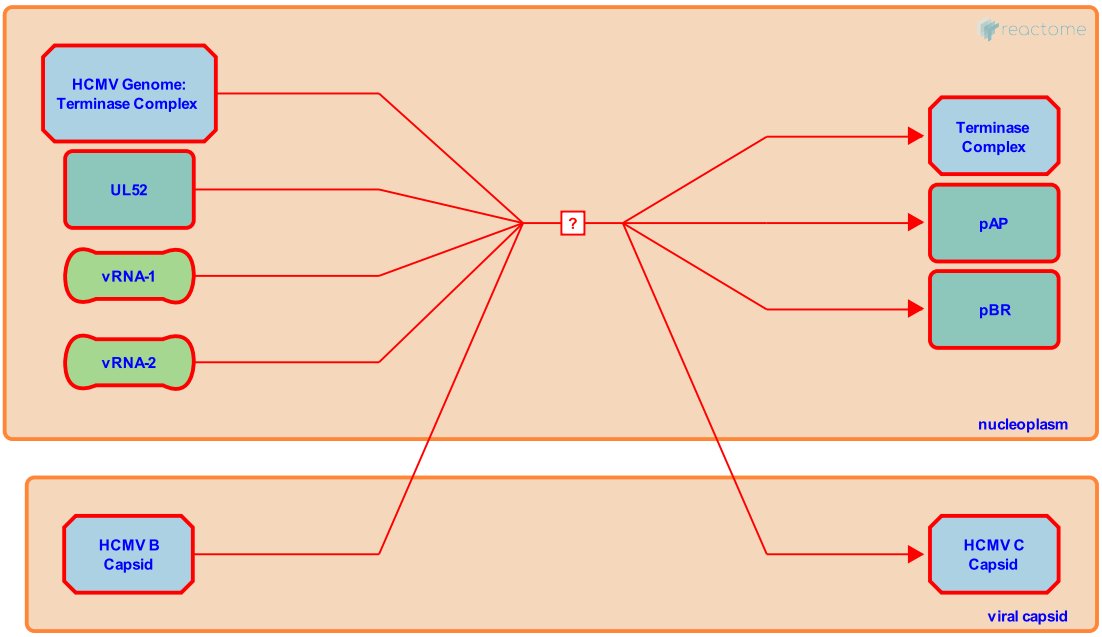
Stable identifier: R-HSA-9698925

Type: uncertain

Compartments: nucleoplasm

Diseases: viral infectious disease



The preformed procapsids are made in the nucleus proximal to DNA replication compartments. Encapsidation of unit-length viral DNA genomes depends on a terminase complex interacting with a specialized PORT penton. Terminase machinery recognizes free genomic ends and threads a single genome length of DNA through the PORT channel into each capsid. This process begins and ends at pac elements within terminal repeated a sequences, proceeding in a directional manner (S component first) on concatemeric DNA. A 129-bp region contains both cis-acting pac elements (pac1 and pac2) and is sufficient to direct cleavage and packaging leaving single-base 3′ extensions at both genomic ends.
Once the capsid has aquired the genome, it is designated a C capsid. Three capsid forms accumulate in the nucleus of herpesvirus-infected cells: A capsids that lack both scaffold and packaged viral DNA, B capsids that contain scaffold but lack viral DNA, and C capsids, contains viral DNA in place of scaffold and probably represents nucleocapsids in the process of maturation.

Literature references

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

Pari, GS., Prichard, MN., Penfold, ME., Bohlman, MC., St Jeor, S., Jairath, S. (1998). Identification of persistent RNA-DNA hybrid structures within the origin of replication of human cytomegalovirus. *J. Virol., 72*, 6997-7004. ↗

Editions

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