Synthesis of full-length duplex viral DNA with a discontinuous plus strand

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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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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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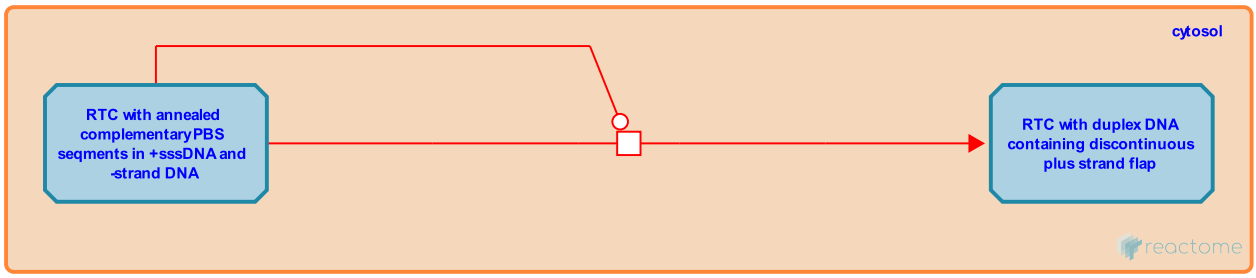
Stable identifier: R-HSA-164505

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



After the second jump, elongation of the plus and minus strands continues. The elongation process requires strand displacement, which RT can mediate, at least in vitro (Huber et al. 1989; Hottiger et al. 1994; Rausch and Le Grice 2004). The final product is a blunt-ended linear duplex DNA with a discontinuity in its "plus" strand at the site of the cPPT sequence motif.

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Editions

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