3' PPT-primed initiation of plus-strand DNA synthesis

D'Eustachio, P., Gopinathrao, G., Hughes, SH.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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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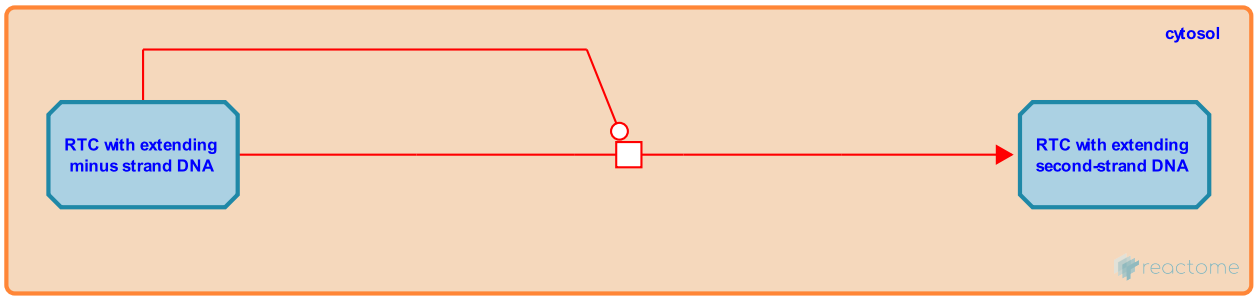
Stable identifier: R-HSA-164513

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



HIV-1 genomic RNA contains a centrally located PPT (cPPT) within the pol gene that, like 3'PPT, is spared by RNase H during minus-strand DNA synthesis and persists to prime plus-strand DNA synthesis. This ribonucleotide primes the synthesis of a plus-strand DNA extending through the U3 and R regions of the HIV sequence and terminating in the PBS region (the tRNA primer-binding site). This DNA segment is known as plus-strand strong-stop DNA (+sssDNA) (Telesnitsky and Goff 1997; Pullen et al. 1993; Huber and Richardson 1990). cPPT priming is important for efficient viral replication (Alizon et al. 1992; Rausch and Le Grice 2004). Several features of cPPT priming in vivo remain to be clarified.

Literature references

De Clercq, E., Anne, J., Jonckheere, H. (2000). The HIV-1 reverse transcription (RT) process as target for RT inhibitors. *Med Res Rev, 20*, 129-54. ↗

Pullen, KA., Champoux, JJ., Rattray, AJ. (1993). The sequence features important for plus strand priming by human immunodeficiency virus type 1 reverse transcriptase. *J Biol Chem, 268*, 6221-7. ↗

Huber, HE., Richardson, CC. (1990). Processing of the primer for plus strand DNA synthesis by human immunodeficiency virus 1 reverse transcriptase. *J Biol Chem, 265*, 10565-73. ↗

Varmus, HE., Hughes, SH., Coffin, JM. (1997). Reverse Transcriptase and the Generation of Retroviral DNA, Retroviruses. *Cold Spring Harbor Laboratory Press*, 121-160.

Editions

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