First strand transfer mediated by Repeated (R) sequence

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

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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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Reactome database release: 88
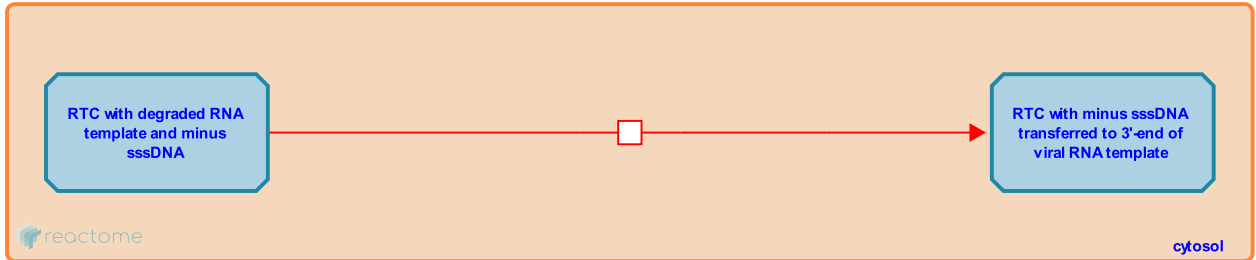
This document contains 1 reaction (see Table of Contents)

First strand transfer mediated by Repeated (R) sequence ↗

Stable identifier: R-HSA-164503

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease

The minus strand strong stop DNA (-sssDNA) is transferred to the 3' end of the HIV-1 genomic RNA, where the 3' end of the -sssDNA anneals to the viral genomic R sequence motif (Ghosh et al. 1995; Klaver and Berkhout 1994; Ohi and Clever 2000; Telesnitsky and Goff 1997). Viral NC (nucleocapsid) protein may play a role in this transfer (Driscoll and Hughes 2000).

Literature references

Klaver, B., Berkhout, B. (1994). Premature strand transfer by the HIV-1 reverse transcriptase during strong-stop DNA synthesis. *Nucleic Acids Res, 22*, 137-44. ↗

Clever, JL., Ohi, Y. (2000). Sequences in the 5' and 3' R elements of human immunodeficiency virus type 1 critical for efficient reverse transcription. *J Virol, 74*, 8324-34. ↗

Editions

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