Synthesis of minus strand strong stop DNA (-sssDNA)

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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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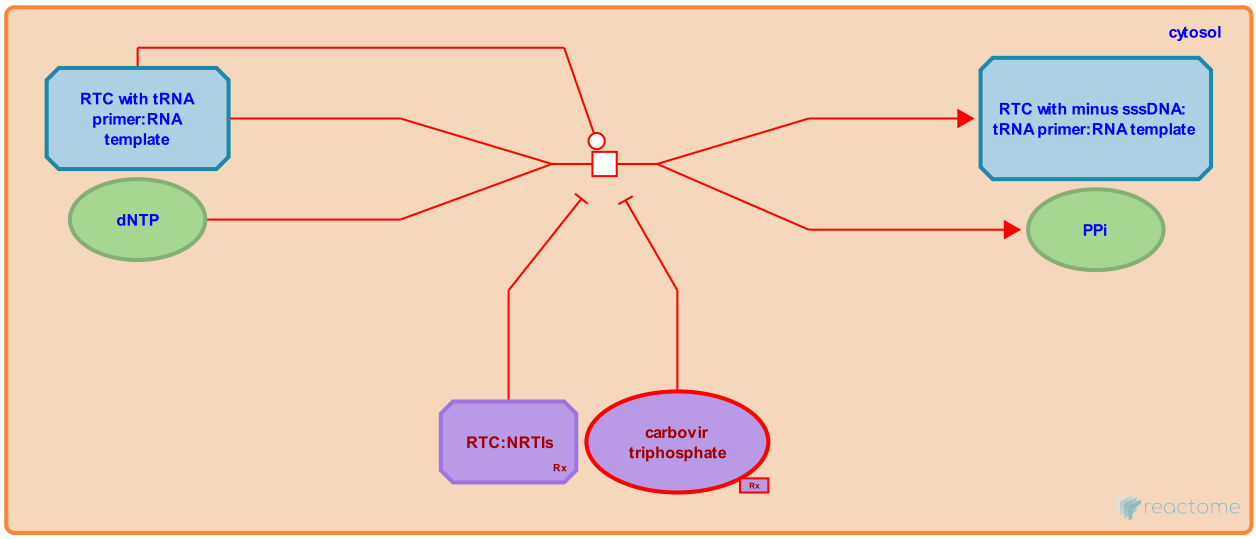
Stable identifier: R-HSA-164504

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



To catalyze DNA synthesis, retroviral reverse transcriptase requires a primer strand to extend and a template strand to copy. For HIV-1, the primer is the 3'-end of a partially unwound lysine(3) tRNA annealed to the PBS (primer binding site) 179 bases from the 5' end of the retroviral genomic RNA (Isel et al. 1995). Reverse transcription of the viral genomic RNA proceeds from the bound tRNA primer to the 5' end of the viral RNA, yielding a minus-strand strong-stop DNA (-sssDNA) complementary to the R and U5 elements of the HIV-1 viral genome, as shown in the figure below (Telesnitsky and Goff 1997; Jonckheere et al. 2000). The reaction takes place in the host cell cytosol, and is catalyzed by the reverse transcriptase activity of the HIV-1 RT heterodimer.

NucleoCapsid (NC) protein prevents self-priming by generating or stabilizing a thermodynamically favored RNA-DNA heteroduplex instead of the kinetically favored TAR hairpin seen in reverse transcription experiments in vitro (Driscoll and Hughes 2000).

Literature references

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Editions

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