RNase H-mediated digestion of tRNA, 3'PPT and cPPT RNA primers

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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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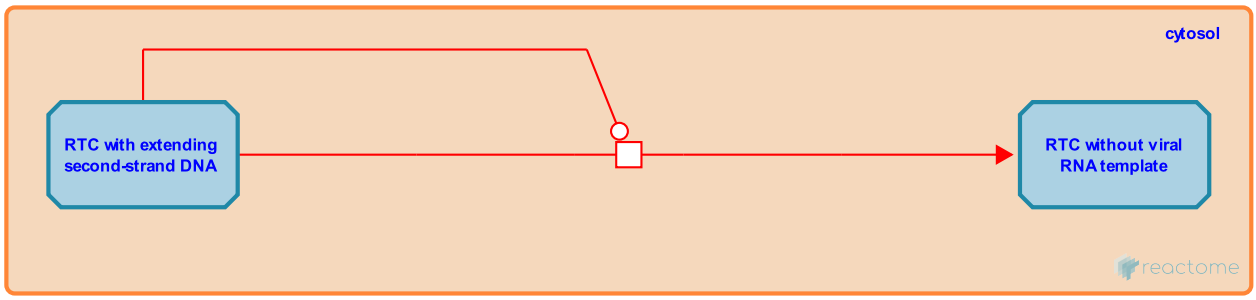
Stable identifier: R-HSA-173769

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



RNase H catalyzes the precise cleavage of the bonds linking the primer tRNA attached to the minus-strand DNA, the 3' PPT RNA primer to the plus-strand strong-stop DNA, and the cPPT primer to the stretch of plus-strand DNA whose synthesis it primed. In each case, precise cleavage near the RNA-DNA junction occurs (Pullen et al. 1992). HIV-1 RT is the only reverse transcriptase that cleaves the tRNA:DNA junction so as to leave a ribo A residue from the tRNA at the 5' end of the minus strand.

While a single RT heterodimer could in principle catalyze DNA synthesis and primer RNA:DNA bond cleavage, evidence from several in vitro systems suggests that separate RT heterodimers are likely to catalyze these two reactions (Rausch and Le Grice 2004).

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Editions

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