Assembly of an Active Transcription Complex

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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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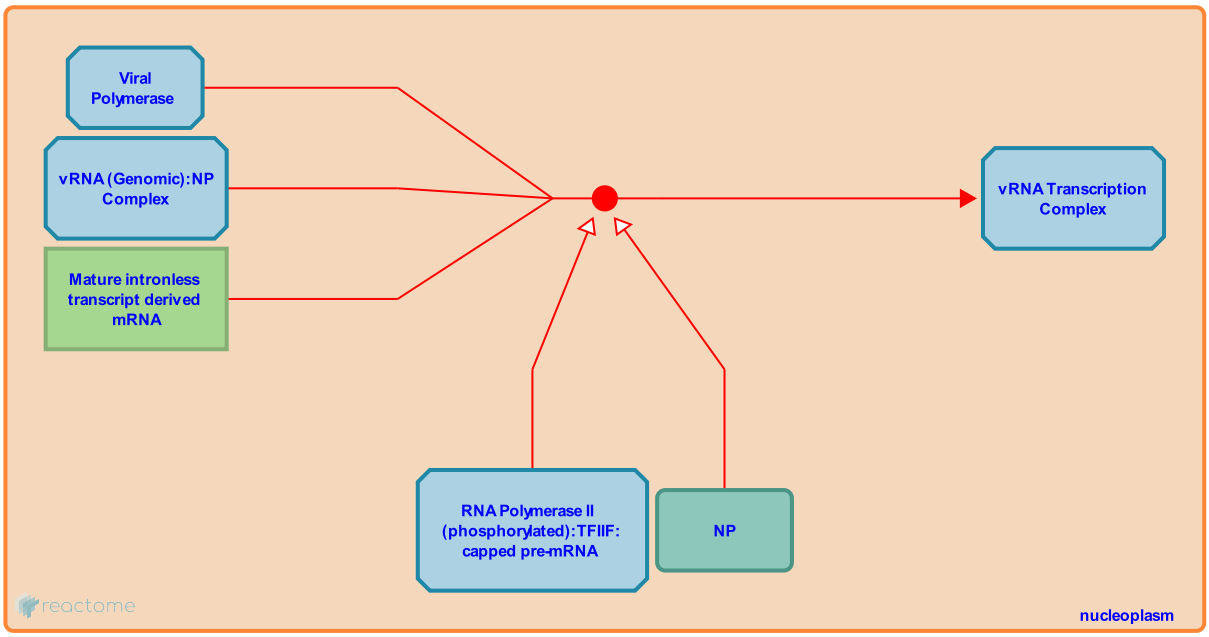
Stable identifier: R-HSA-168326

Type: binding

Compartments: nucleoplasm

Diseases: influenza



The 5' end of the vRNA associates with a binding site on the PB1 subunit of the viral RNA polymerase, distinct from the 3' vRNA binding site, which is subsequenty bound forming a loop. These binding events set off allosteric conformational changes in the trimeric polymerase complex that induce PB2 binding of the methylated cap on a host pre-mRNA (Plotch, 1981; Cianci, 1995; Li, 1998; Brownlee, 2002; Kolpashchikov, 2004). PB2 amino acids 242-282 and 538-577 are involved in cap binding (Honda, 1999). Direct or indirect interaction with active, transcribing host RNA polymerase II is thought to supply host mRNA for the caps (Bouloy, 1978; Engelhardt, 2005).

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Editions

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