

Addition of nucleotides 10 and 11 on the growing transcript: Third Transition

Joshi-Tope, G., Timmers, HTM.

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

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Reactome database release: 88

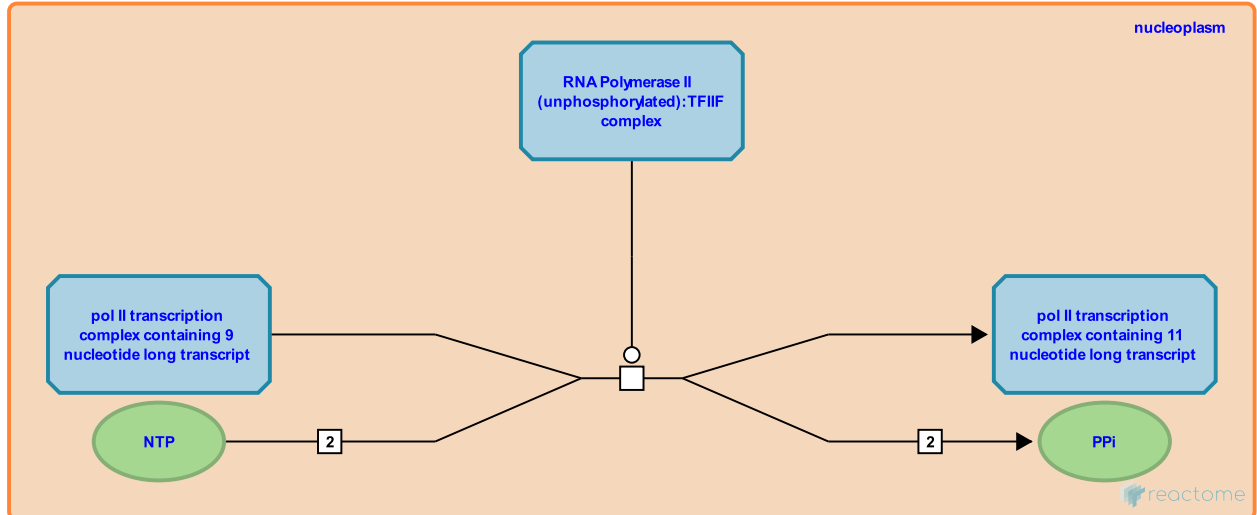
This document contains 1 reaction ([see Table of Contents](#))

Addition of nucleotides 10 and 11 on the growing transcript: Third Transition [↗](#)

Stable identifier: R-HSA-76576

Type: transition

Compartments: nucleoplasm



Formation of phosphodiester bonds nine and ten creates RNA products, which do not dissociate from the RNA pol II initiation complex. The transcription complex has entered the productive elongation phase. TFIIF and ATP-hydrolysis are required for efficient promoter escape. The open region (“transcription bubble”) expands concomitant with the site of RNA-extension. The region upstream from the transcription start site (-9 to -3) collapses to the double-stranded state. TFIIF remains associated to the RNA pol II initiation complex.

Literature references

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Fiedler, U., Timmers, HT., Holstege, FC. (1998). Three transitions in the RNA polymerase II transcription complex during initiation. *EMBO J*, 16, 7468-80. [↗](#)

Editions

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