

2-4 nt.backtracking of Pol II complex on the template leading to elongation pausing

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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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- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
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Reactome database release: 88

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

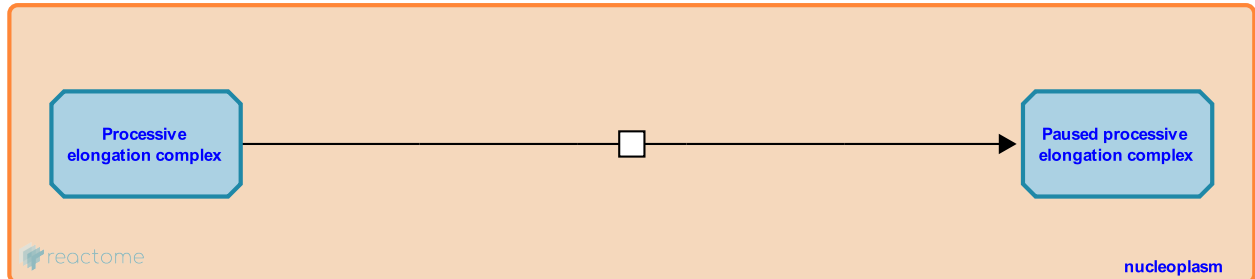
2-4 nt.backtracking of Pol II complex on the template leading to elongation pausing



Stable identifier: R-HSA-113411

Type: transition

Compartments: nucleoplasm



Pol II pausing is believed to result from reversible backtracking of the Pol II enzyme complex by ~2 to 4 nucleotides. This leads to misaligned 3'-OH terminus that is unable to be an acceptor for the incoming NTPs in synthesis of next phosphodiester bond (reviewed by Shilatifard et al., 2003).

Literature references

Conaway, JW., Shilatifard, A., Conaway, RC. (2003). The RNA polymerase II elongation complex. *Annu Rev Biochem*, 72, 693-715. [↗](#)

Editions

2004-06-23

Authored

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