Addition of nucleotides leads to transcript elongation

Gopinathrao, G.

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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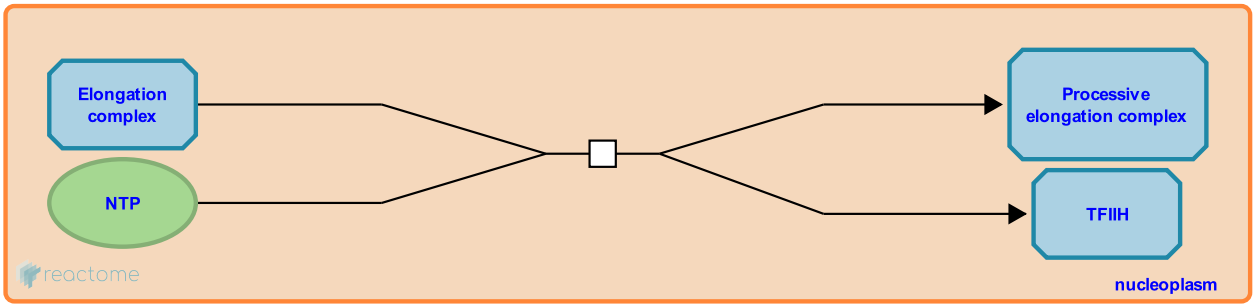
Stable identifier: R-HSA-112385

Type: transition

Compartments: nucleoplasm



High-resolution structures of free, catalytically active yeast Pol II and of an elongating form reveal that Pol II elongation complex includes features like:
- RNA-DNA hybrid, an unwound template ahead of 3'-OH terminus of growing transcript and an exit groove at the base of the CTD, possibly for dynamic interaction of processing and transcriptional factors.
- a cleft or channel created by Rpb1 and Rpb2 subunits to accommodate DNA template, extending to Mg2+ ion located deep in the enzyme core
-a 50 kDa "clamp" with open confirmation in free polymerase, allowing entry of DNA strands but closed in the processive elongation phase.
The clamp is composed of portions of Rpb1,Rpb2 and Rpb3 , five loops or "switches" that change from unfolded to well-folded structures stabilizing the elongation complex, and a long "bridging helix" that emanates from Rpb1 subunit, crossing near the Mg2+ ion. The bridging helix is thought to "bend" to push on the base pair at the 3'-end of RNA-DNA hybrid like a ratchet, translocating Pol II along the DNA (Cramer et al.,2001; Gnatt et al.,2001).In addition to its dynamic biochemical potential, Pol II possess a repertoire of functions to serve as a critical platform of recruiting and coordinating the actions of a host of additional enzyme and proteins involved in various pathways.

Literature references

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Editions

2004-06-22	Authored	Gopinathrao, G.