Hyperphosphorylation (Ser2) of RNA Pol II CTD by P-TEFb complex

Matthews, L., Rice, AP.

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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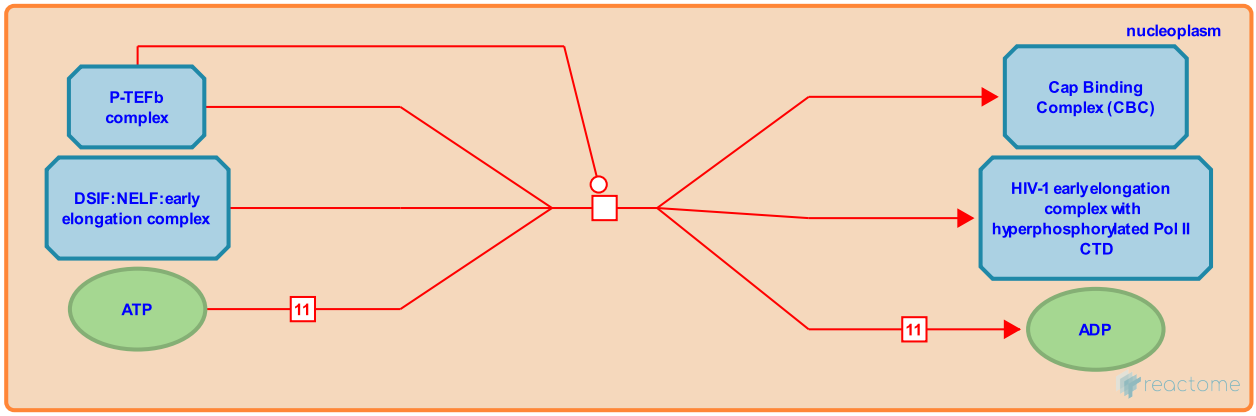
Stable identifier: R-HSA-167084

Type: transition

Compartments: nucleoplasm

Diseases: Human immunodeficiency virus infectious disease

Inferred from: Hyperphosphorylation (Ser2) of RNA Pol II CTD by P-TEFb complex (Homo sapiens)



The association between Tat, TAR and P-TEFb is believed to bring the catalytic subunit of P-TEFb(Cyclin T1:Cdk9) in close proximity to Pol II where it hyperphosphorylates the CTD of Pol II (Herrmann et al., 1995; Zhou et al. 2000). In the presence of Tat, P-TEFb(Cyclin T1:CDK9) has been shown to phosphorylate serine 5 in addition to serine 2 suggesting that modification of the substrate specificity of CDK9 may play a role in the ability of Tat to promote transcriptional elongation (Zhou et al. 2000).

Literature references

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Editions

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