Phosphorylation (Ser5) of RNA pol II CTD

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02/03/2021

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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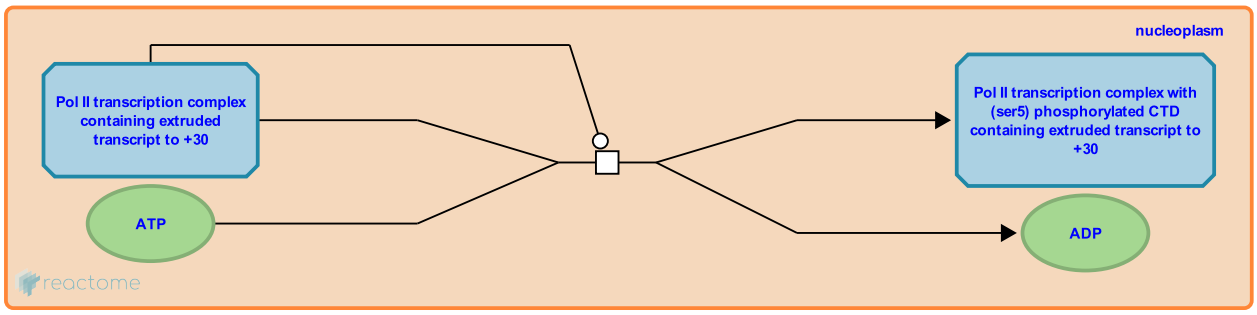
Stable identifier: R-HSA-77071

Type: transition

Compartments: nucleoplasm



Phosphorylation of serine 5 residue at the CTD of pol II largest subunit is an important step signaling the end of initiation and escape into processive elongation processes. Cdk7 protein subunit of TFIIH phosphorylates RNA Pol II CTD serine 5 residues on its heptad repeats (Buratowski 2009).

Literature references

Buratowski, S. (2009). Progression through the RNA polymerase II CTD cycle. *Mol. Cell, 36*, 541-6. ↗

Editions

2003-10-15	Authored	Buratowski, S.