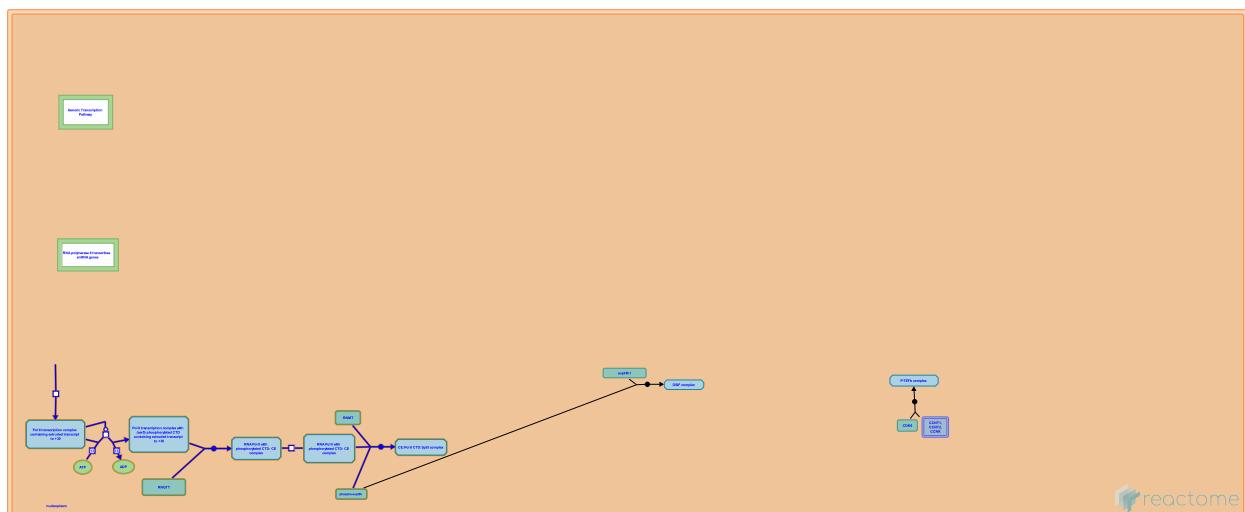


RNA Pol II CTD phosphorylation and interaction with CE



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](#).

18/05/2024

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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)

Reactome database release: 88

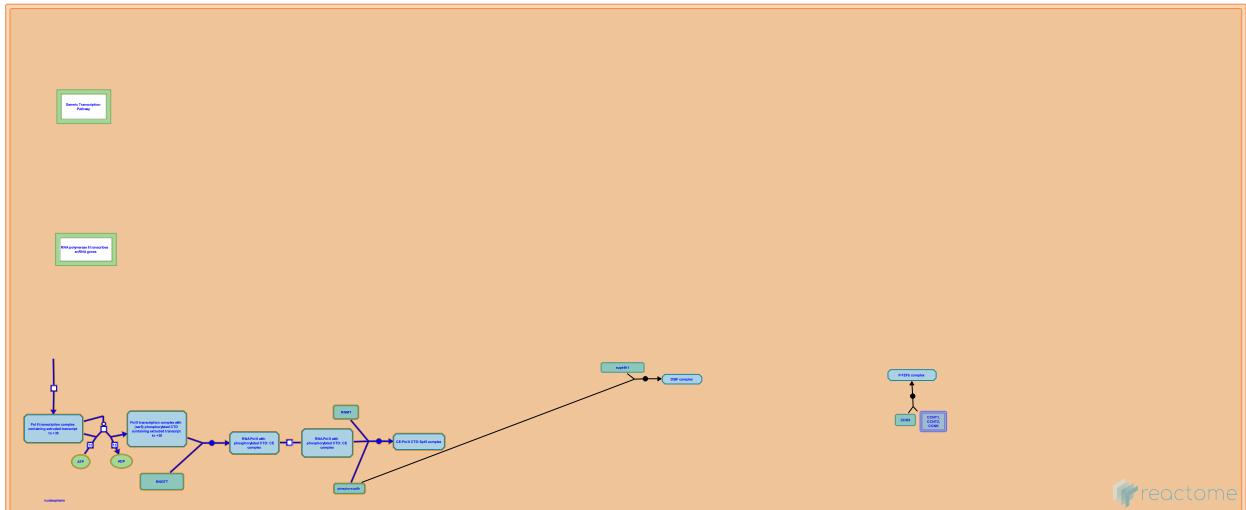
This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

RNA Pol II CTD phosphorylation and interaction with CE [↗](#)

Stable identifier: R-DRE-77075

Compartments: nucleoplasm

Inferred from: RNA Pol II CTD phosphorylation and interaction with CE (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also:
<http://www.pantherdb.org/about.jsp>

Extrusion of 5'-end of 30 nt long transcript through the pore in Pol II complex ↗

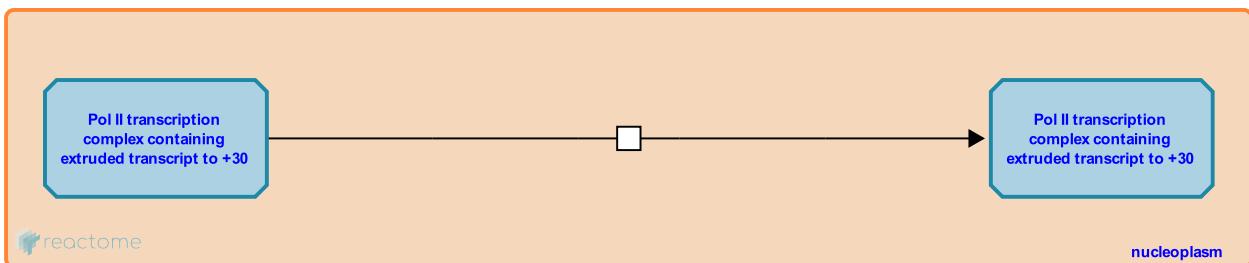
Location: RNA Pol II CTD phosphorylation and interaction with CE

Stable identifier: R-DRE-113430

Type: transition

Compartments: nucleoplasm

Inferred from: [Extrusion of 5'-end of 30 nt long transcript through the pore in Pol II complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [Phosphorylation \(Ser5\) of RNA pol II CTD](#)

Phosphorylation (Ser5) of RNA pol II CTD ↗

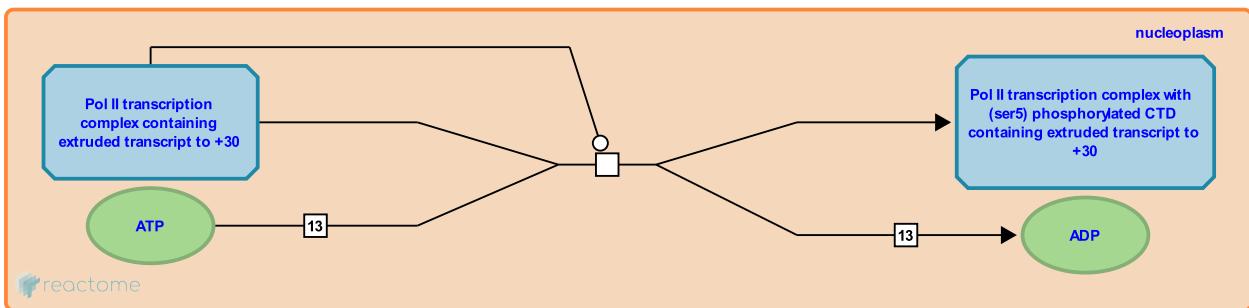
Location: RNA Pol II CTD phosphorylation and interaction with CE

Stable identifier: R-DRE-77071

Type: transition

Compartments: nucleoplasm

Inferred from: Phosphorylation (Ser5) of RNA pol II CTD (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome](#). For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: Extrusion of 5'-end of 30 nt long transcript through the pore in Pol II complex

Followed by: RNA Polymerase II CTD (phosphorylated) binds to CE

RNA Polymerase II CTD (phosphorylated) binds to CE ↗

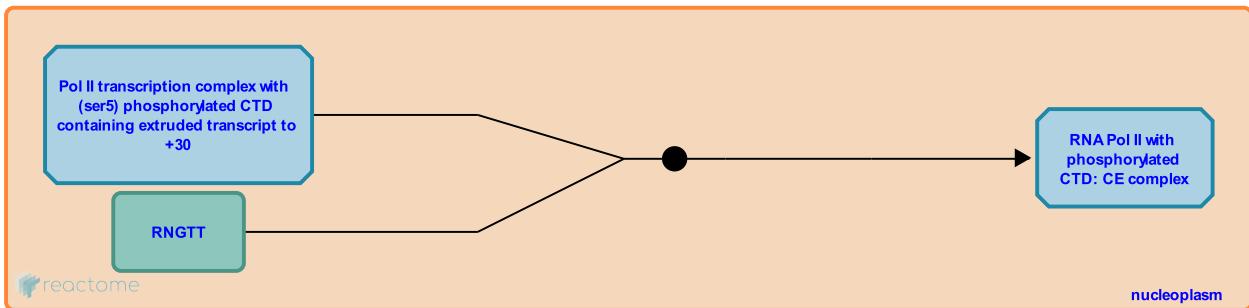
Location: RNA Pol II CTD phosphorylation and interaction with CE

Stable identifier: R-DRE-77069

Type: binding

Compartments: nucleoplasm

Inferred from: RNA Polymerase II CTD (phosphorylated) binds to CE (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome](#). For details on PANTHER see also:
<http://www.pantherdb.org/about.jsp>

Preceded by: Phosphorylation (Ser5) of RNA pol II CTD

Followed by: Activation of GT

Activation of GT ↗

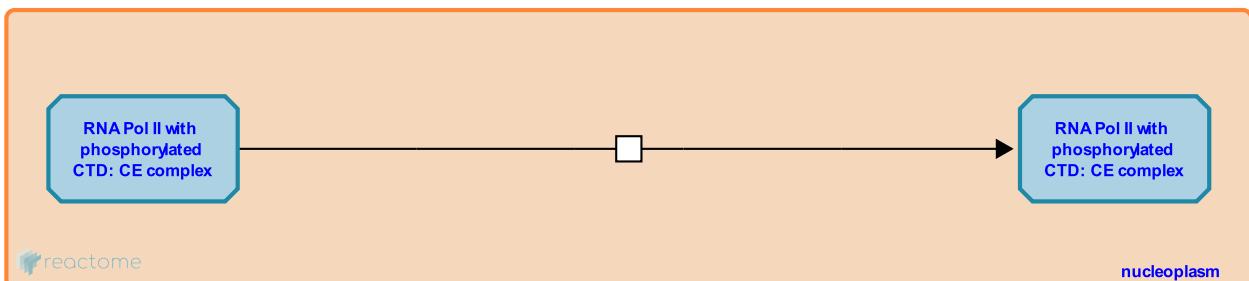
Location: RNA Pol II CTD phosphorylation and interaction with CE

Stable identifier: R-DRE-77068

Type: transition

Compartments: nucleoplasm

Inferred from: Activation of GT (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome](#). For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: RNA Polymerase II CTD (phosphorylated) binds to CE

Followed by: SPT5 subunit of Pol II binds the RNA triphosphatase (RTP)

SPT5 subunit of Pol II binds the RNA triphosphatase (RTP) ↗

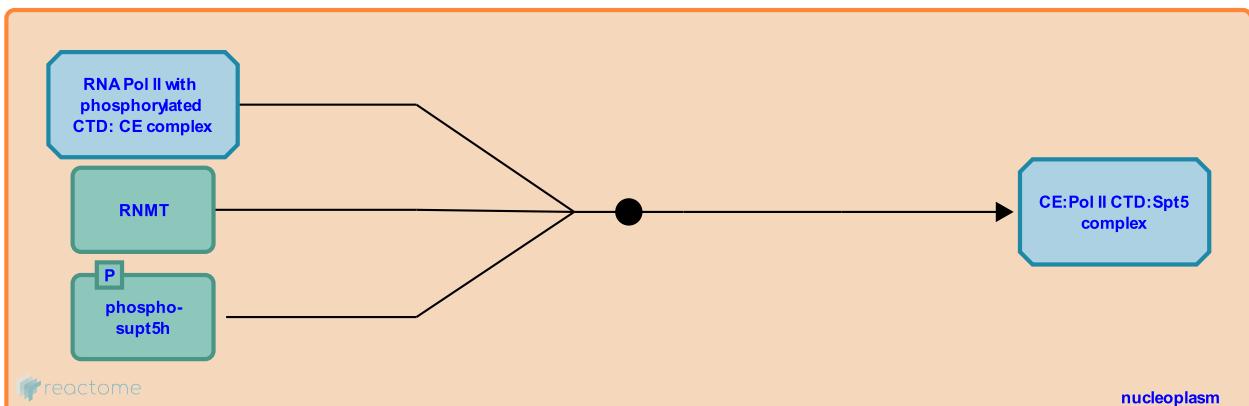
Location: RNA Pol II CTD phosphorylation and interaction with CE

Stable identifier: R-DRE-77073

Type: binding

Compartments: nucleoplasm

Inferred from: SPT5 subunit of Pol II binds the RNA triphosphatase (RTP) (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: Activation of GT

Table of Contents

Introduction	1
RNA Pol II CTD phosphorylation and interaction with CE	2
➤ Extrusion of 5'-end of 30 nt long transcript through the pore in Pol II complex	3
➤ Phosphorylation (Ser5) of RNA pol II CTD	4
➤ RNA Polymerase II CTD (phosphorylated) binds to CE	5
➤ Activation of GT	6
➤ SPT5 subunit of Pol II binds the RNA triphosphatase (RTP)	7
Table of Contents	8