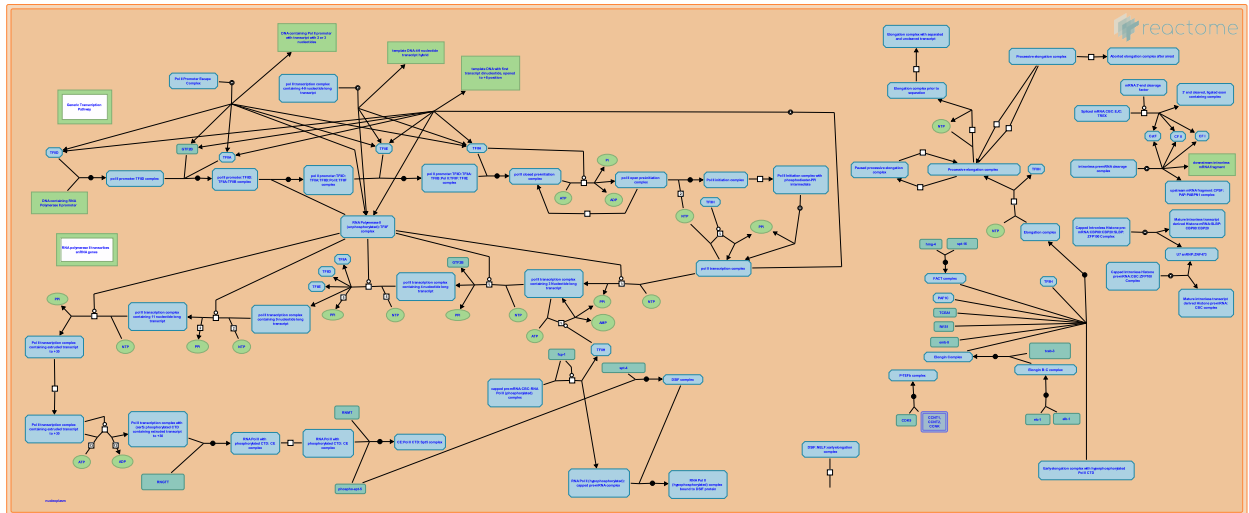


RNA Polymerase II Transcription



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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses).

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](https://reactome.org/textbook).

05/05/2024

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

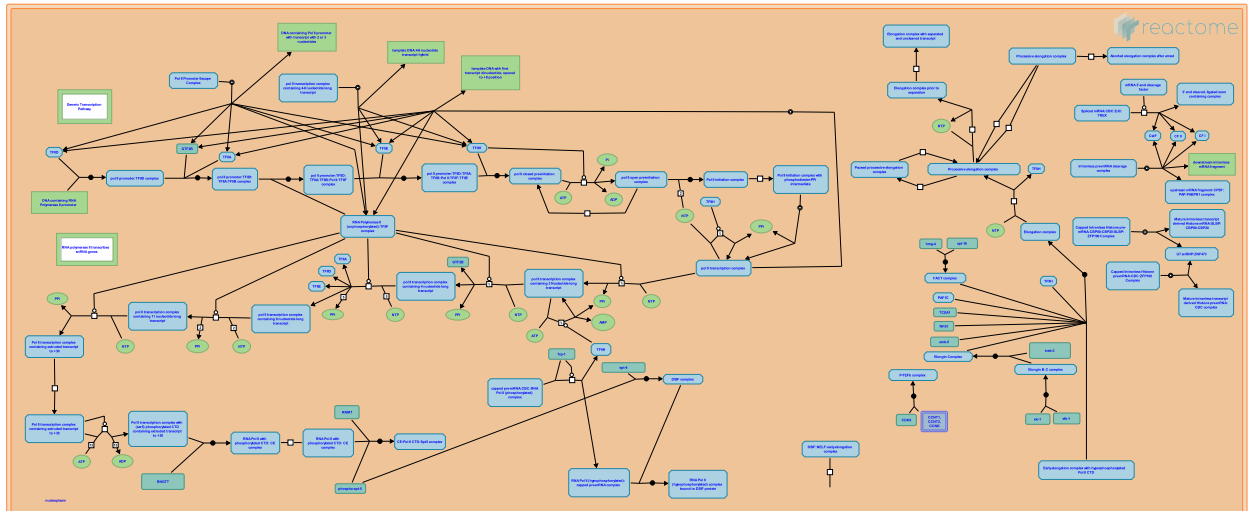
This document contains 9 pathways ([see Table of Contents](#))

RNA Polymerase II Transcription ↗

Stable identifier: R-CEL-73857

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Generic Transcription Pathway ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-212436

Inferred from: Generic Transcription Pathway (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

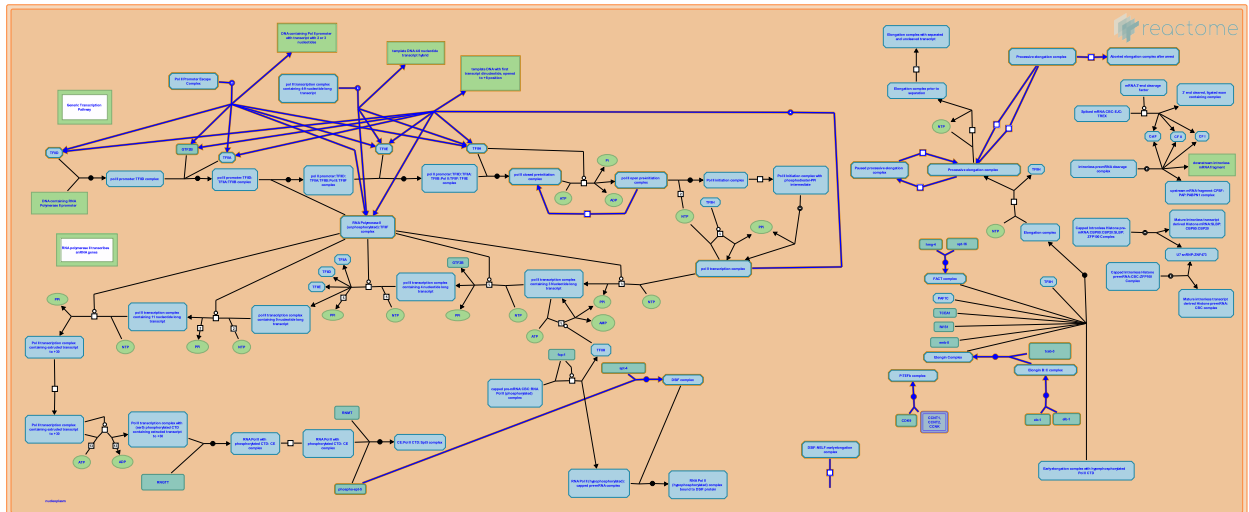
RNA Polymerase II Pre-transcription Events ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-674695

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Pre-transcription Events (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

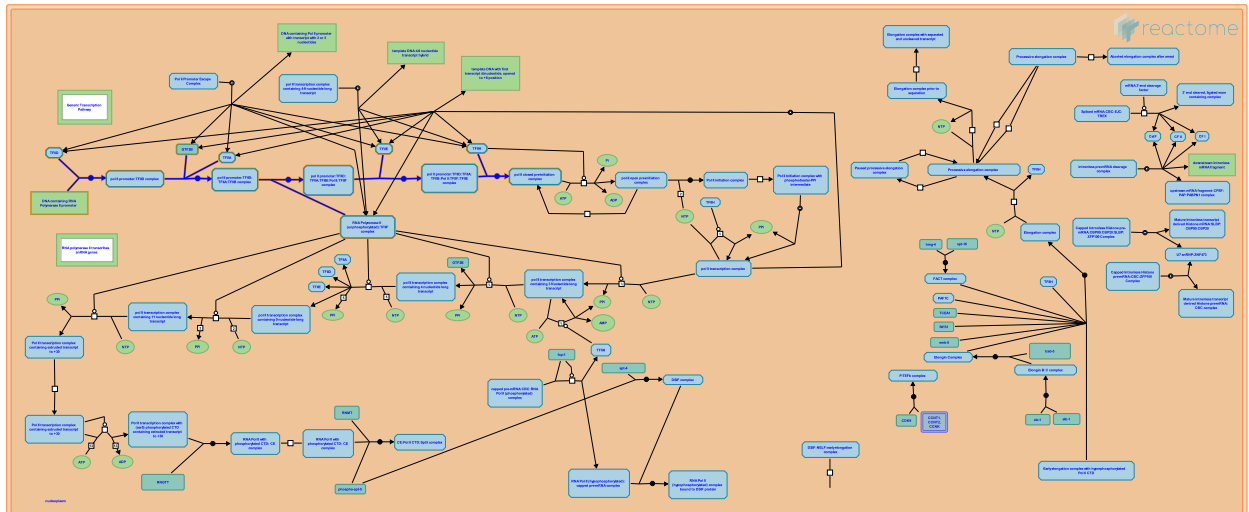
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-73779

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription Pre-Initiation And Promoter Opening (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.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

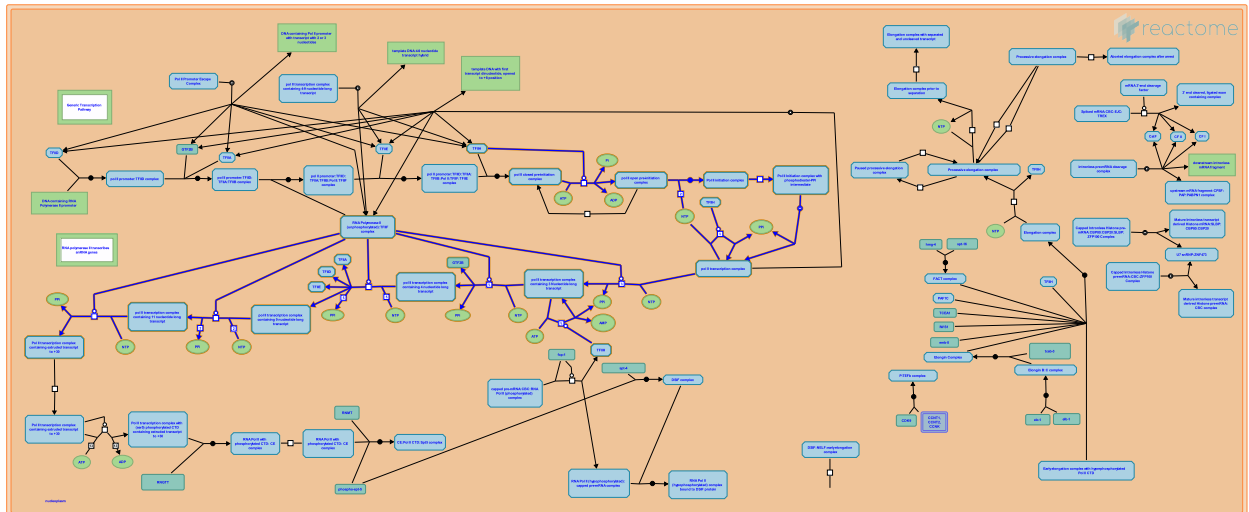
RNA Polymerase II Transcription Initiation And Promoter Clearance ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-76042

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription Initiation And Promoter Clearance (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.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

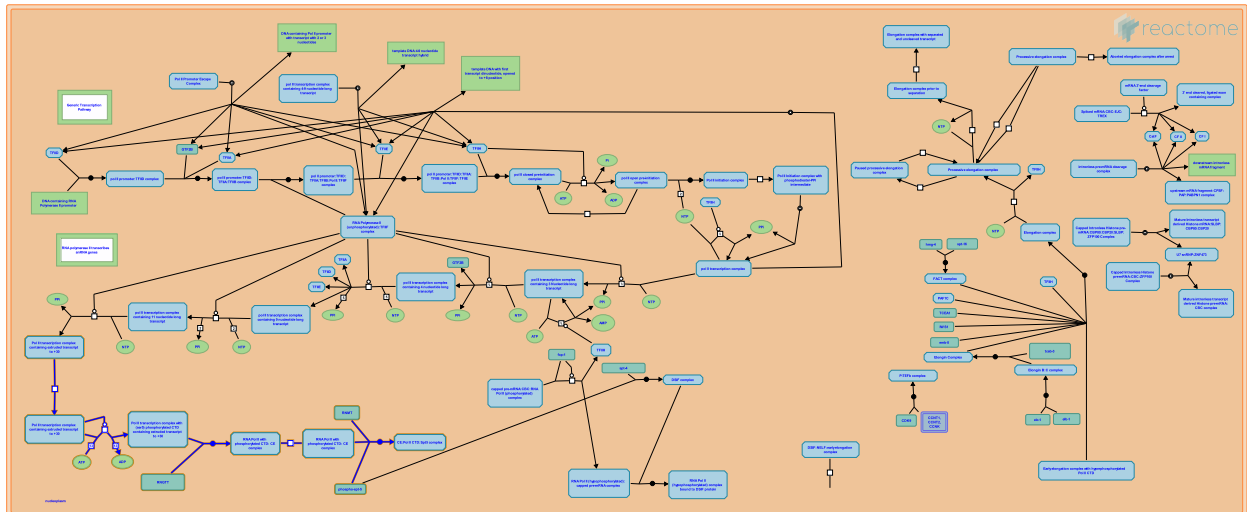
RNA Pol II CTD phosphorylation and interaction with CE ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

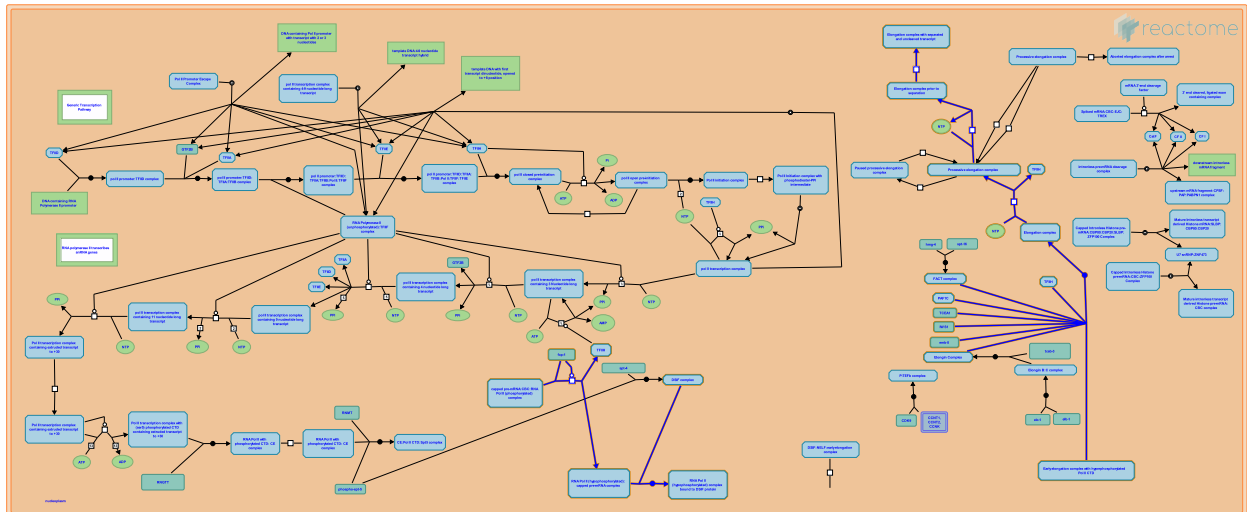
RNA Polymerase II Transcription Elongation ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-75955

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription Elongation (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

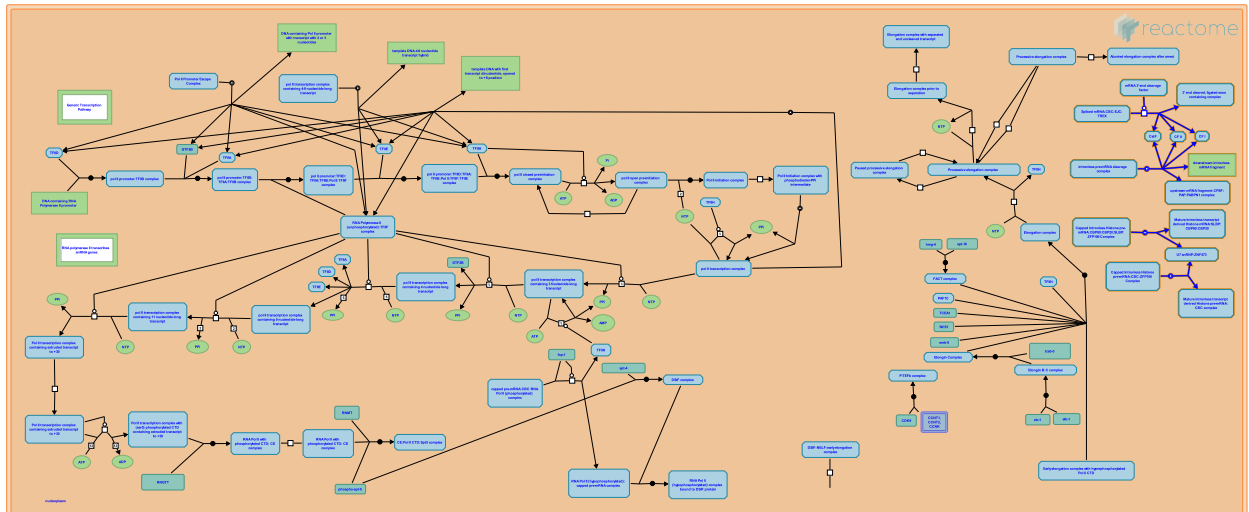
RNA Polymerase II Transcription Termination ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-73856

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription Termination (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.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

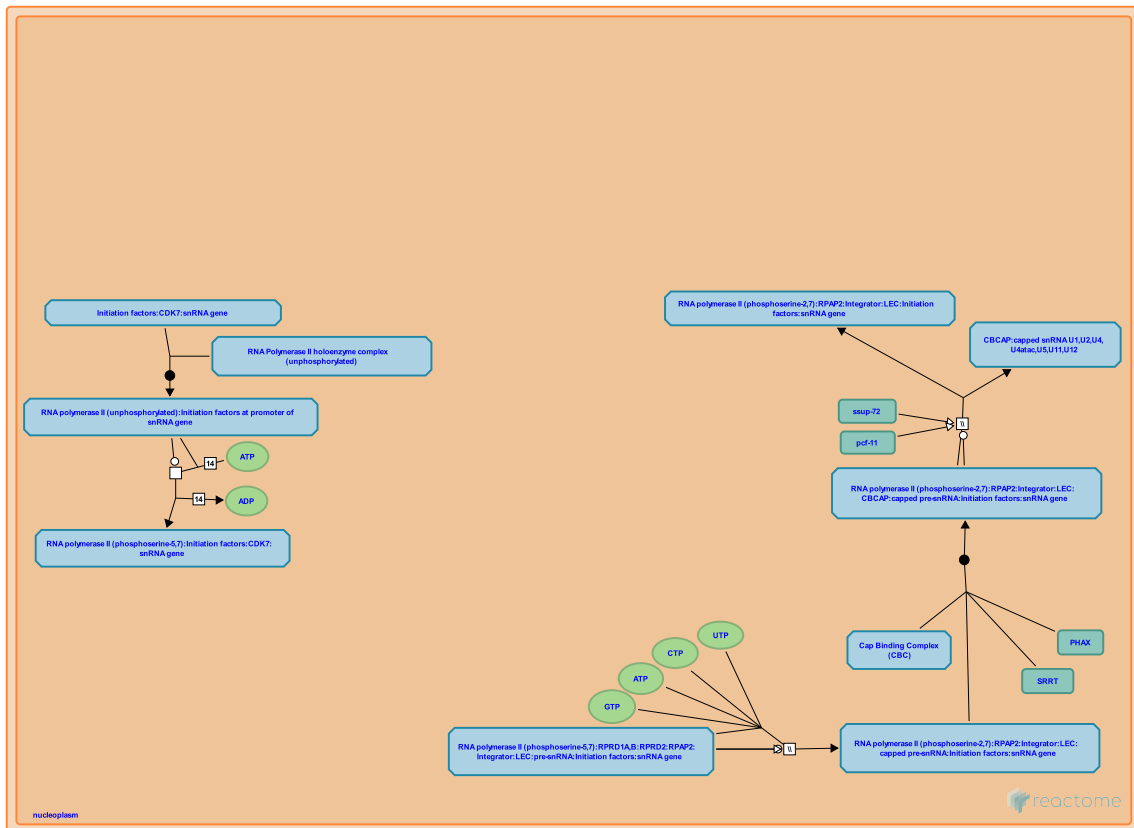
RNA polymerase II transcribes snRNA genes ↗

Location: RNA Polymerase II Transcription

Stable identifier: R-CEL-6807505

Compartments: nucleoplasm

Inferred from: RNA polymerase II transcribes snRNA genes (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Table of Contents

Introduction	1
RNA Polymerase II Transcription	2
Generic Transcription Pathway	3
RNA Polymerase II Pre-transcription Events	4
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	5
RNA Polymerase II Transcription Initiation And Promoter Clearance	6
RNA Pol II CTD phosphorylation and interaction with CE	7
RNA Polymerase II Transcription Elongation	8
RNA Polymerase II Transcription Termination	9
RNA polymerase II transcribes snRNA genes	10
Table of Contents	11