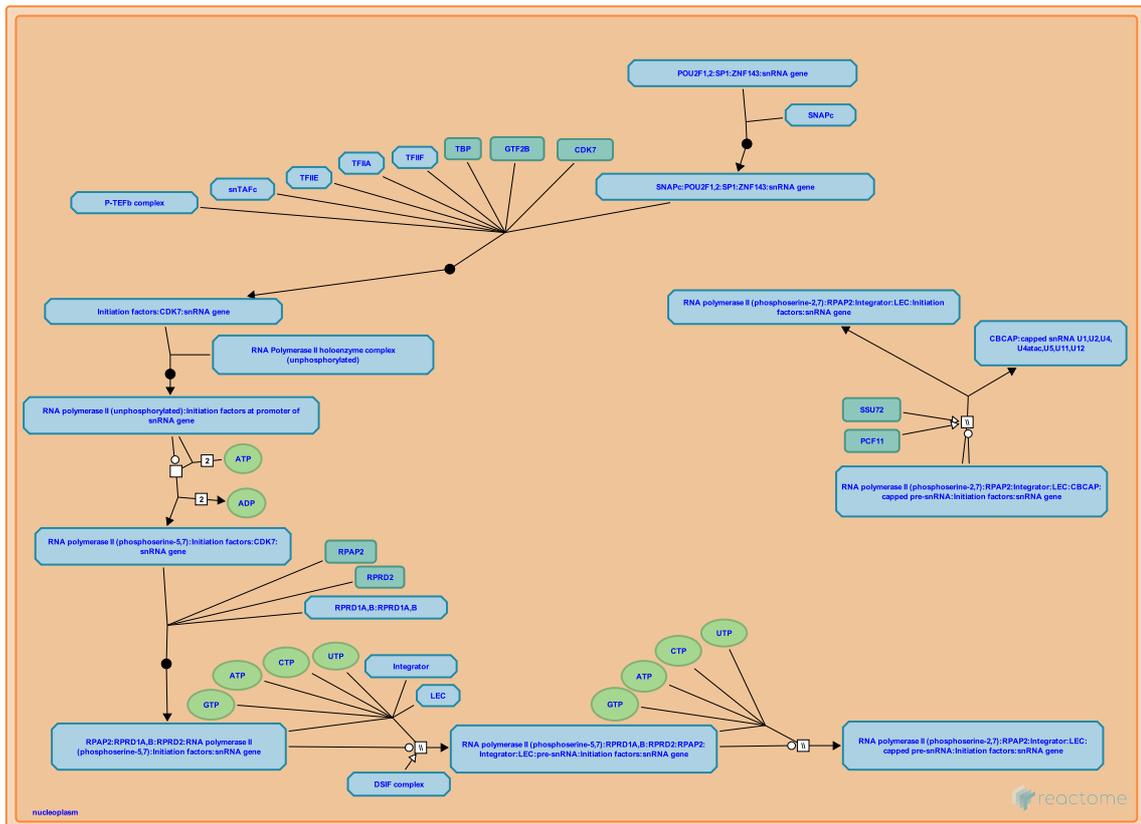


# RNA polymerase II transcribes snRNA genes



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://creativecommons.org/licenses/by/4.0/).

## 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: 70

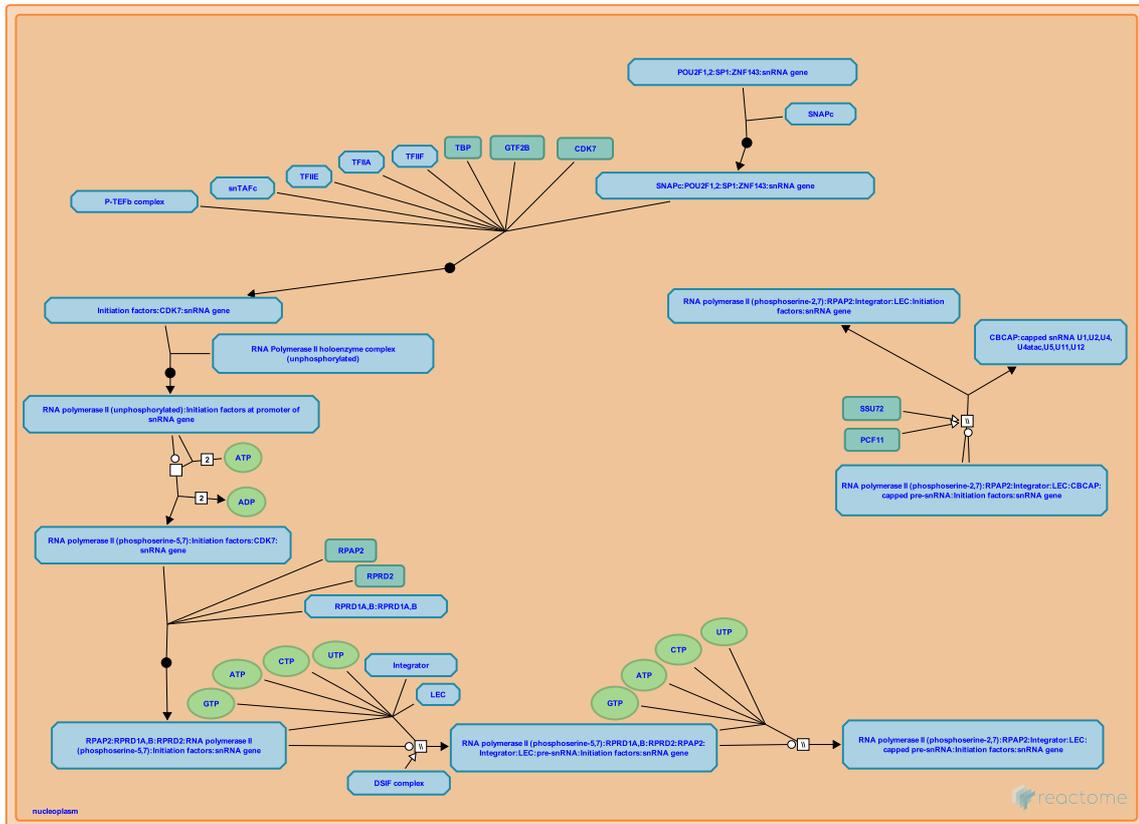
This document contains 1 pathway and 8 reactions ([see Table of Contents](#))

## RNA polymerase II transcribes snRNA genes ↗

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

## SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12) ↗

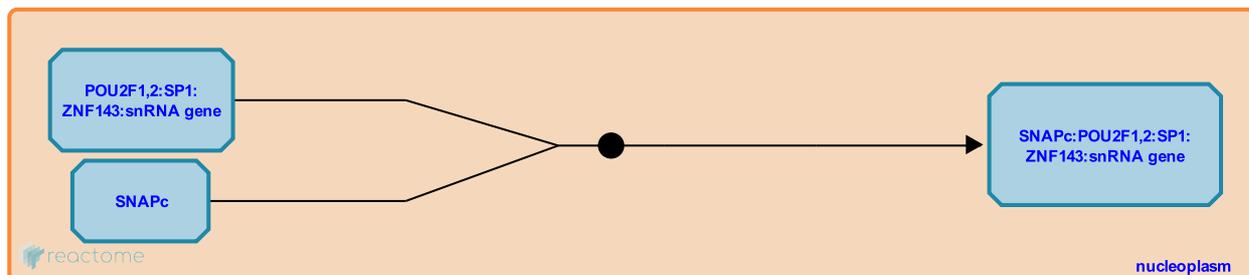
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6810239

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12) (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene](#)

## General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene ↗

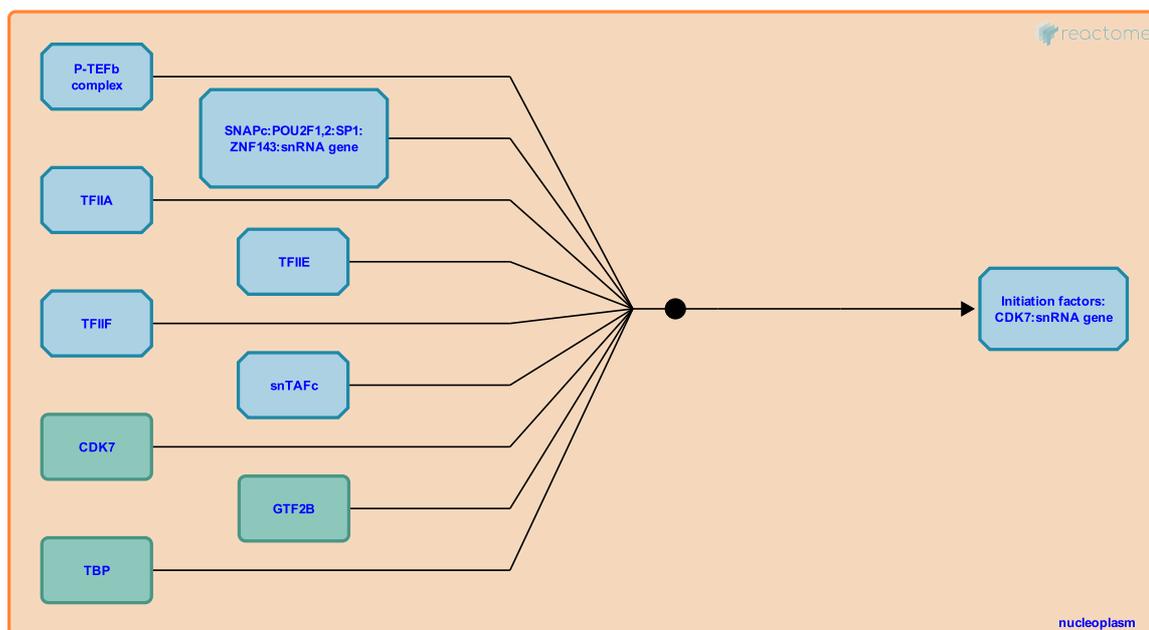
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6810234

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

**Followed by:** RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

## RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12) ↗

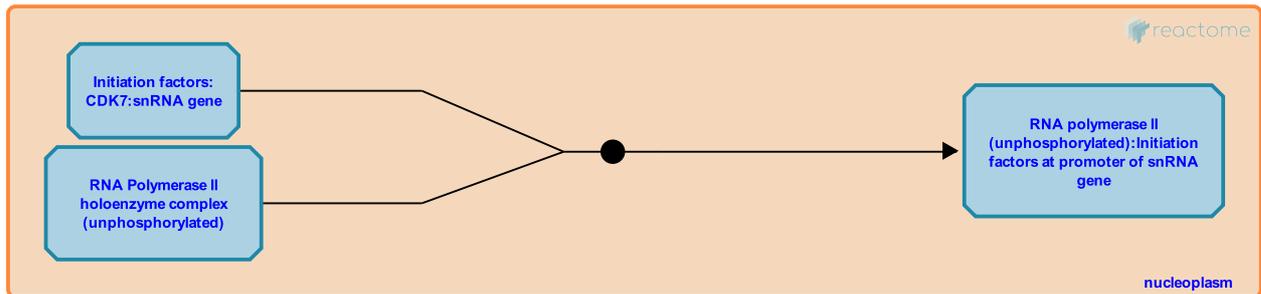
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6810238

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12) (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene

**Followed by:** CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter

## CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter ↗

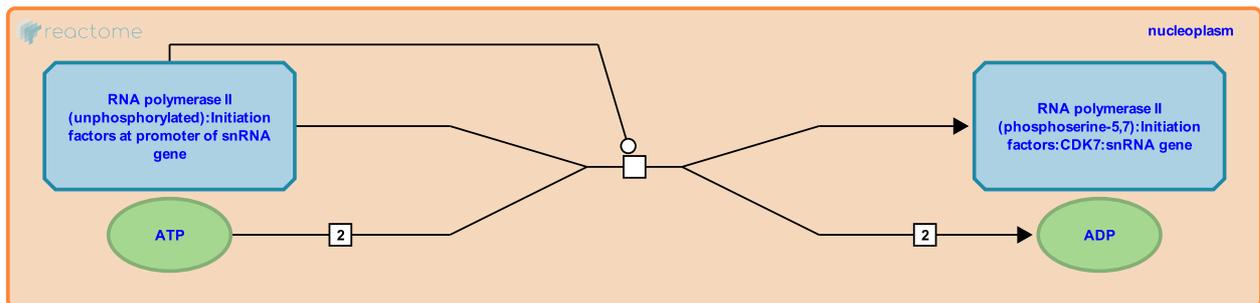
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6810233

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

**Followed by:** RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain

## RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain ↗

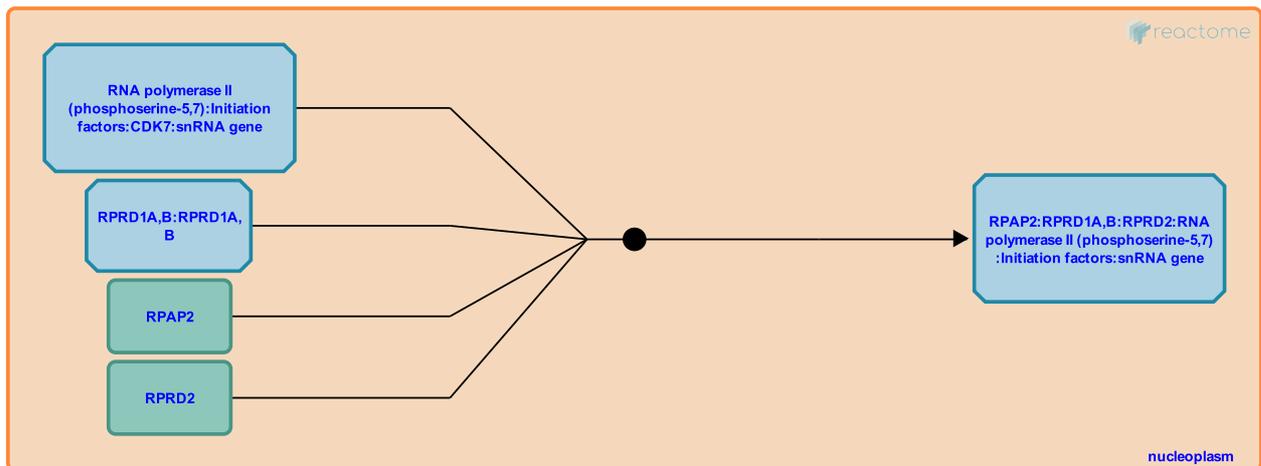
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6810235

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter

**Followed by:** Pre-snRNA transcript initiation, Integrator binding, LEC binding

## Pre-snRNA transcript initiation, Integrator binding, LEC binding ↗

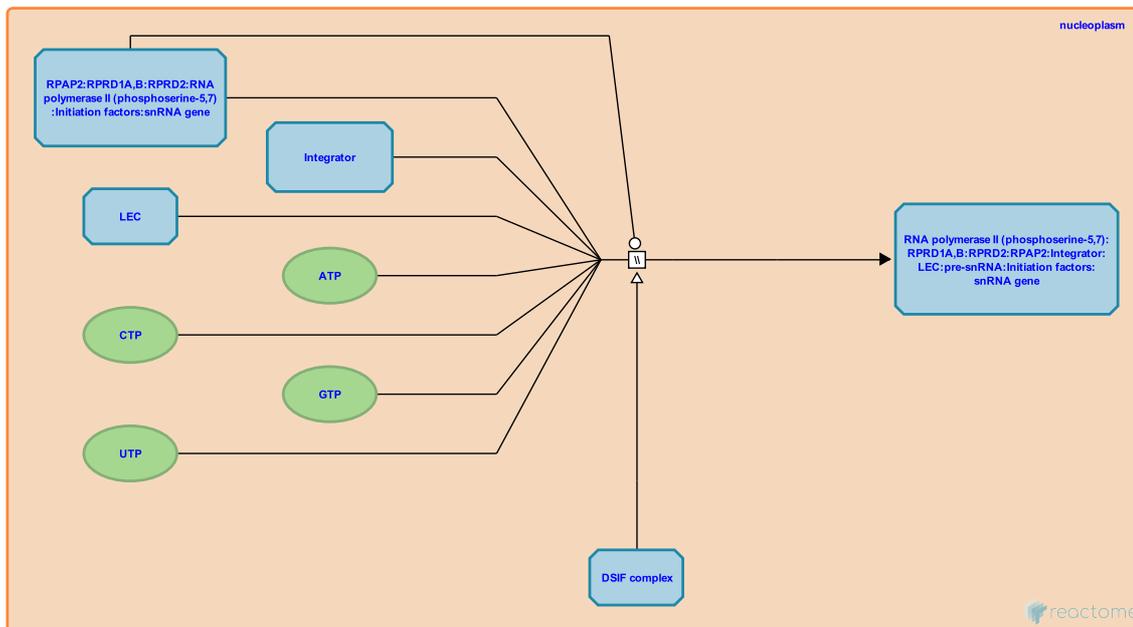
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6814549

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** Pre-snRNA transcript initiation, Integrator binding, LEC binding (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain

**Followed by:** Pre-snRNA is elongated and capped with 7-methylguanosine

## Pre-snRNA is elongated and capped with 7-methylguanosine ↗

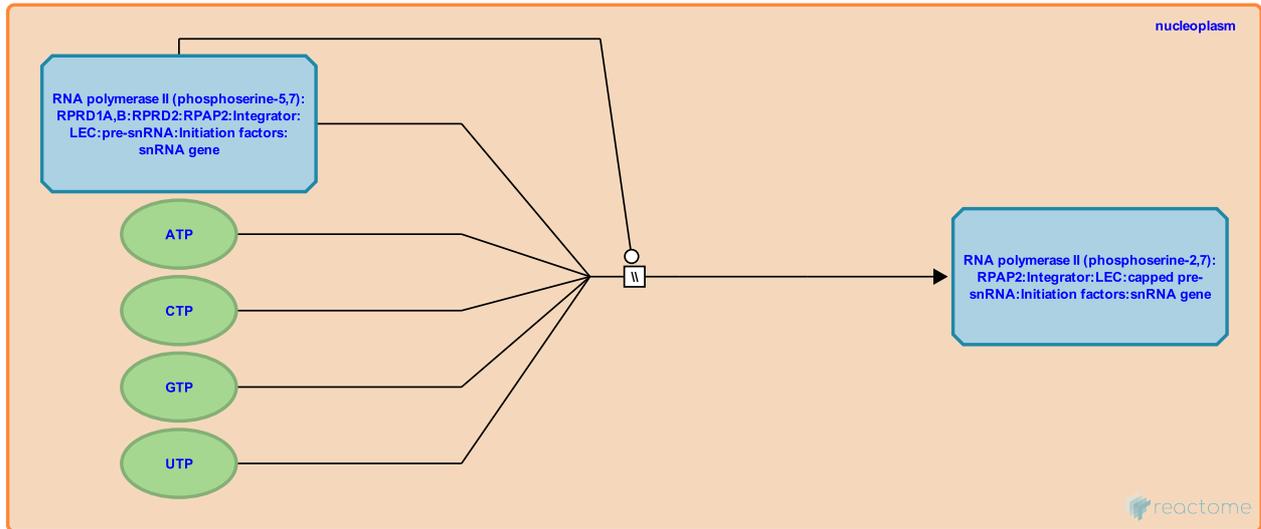
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6814559

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** Pre-snRNA is elongated and capped with 7-methylguanosine (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** Pre-snRNA transcript initiation, Integrator binding, LEC binding

## Integrator complex processes the 3' end of snRNA ↗

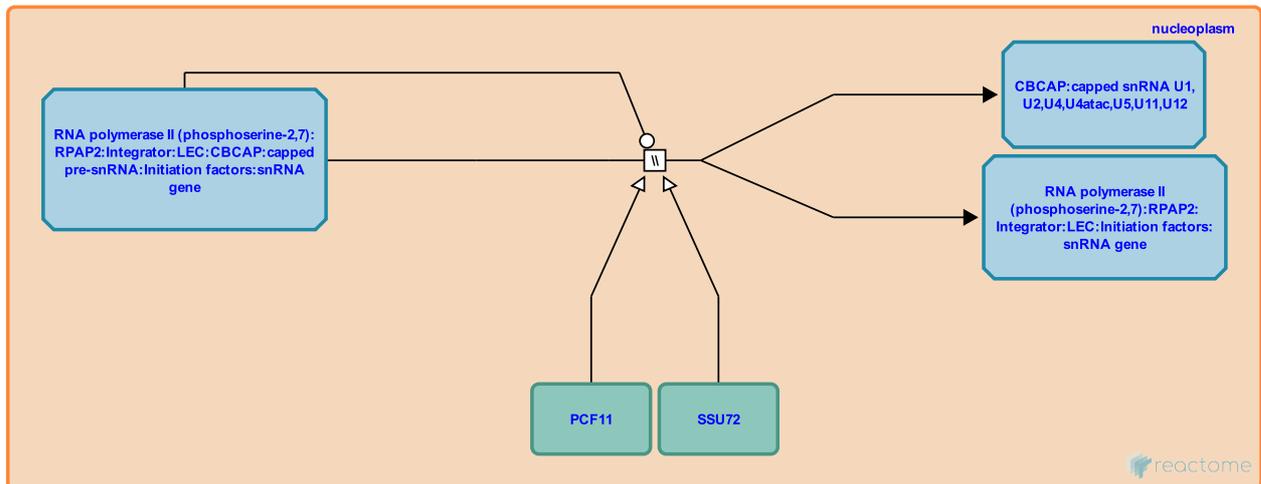
**Location:** RNA polymerase II transcribes snRNA genes

**Stable identifier:** R-DRE-6814555

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** Integrator complex processes the 3' end of snRNA (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

# Table of Contents

Introduction	1
RNA polymerase II transcribes snRNA genes	2
↳ SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)	3
↳ General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene	4
↳ RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)	5
↳ CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter	6
↳ RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain	7
↳ Pre-snRNA transcript initiation, Integrator binding, LEC binding	8
↳ Pre-snRNA is elongated and capped with 7-methylguanosine	9
↳ Integrator complex processes the 3' end of snRNA	10
Table of Contents	11