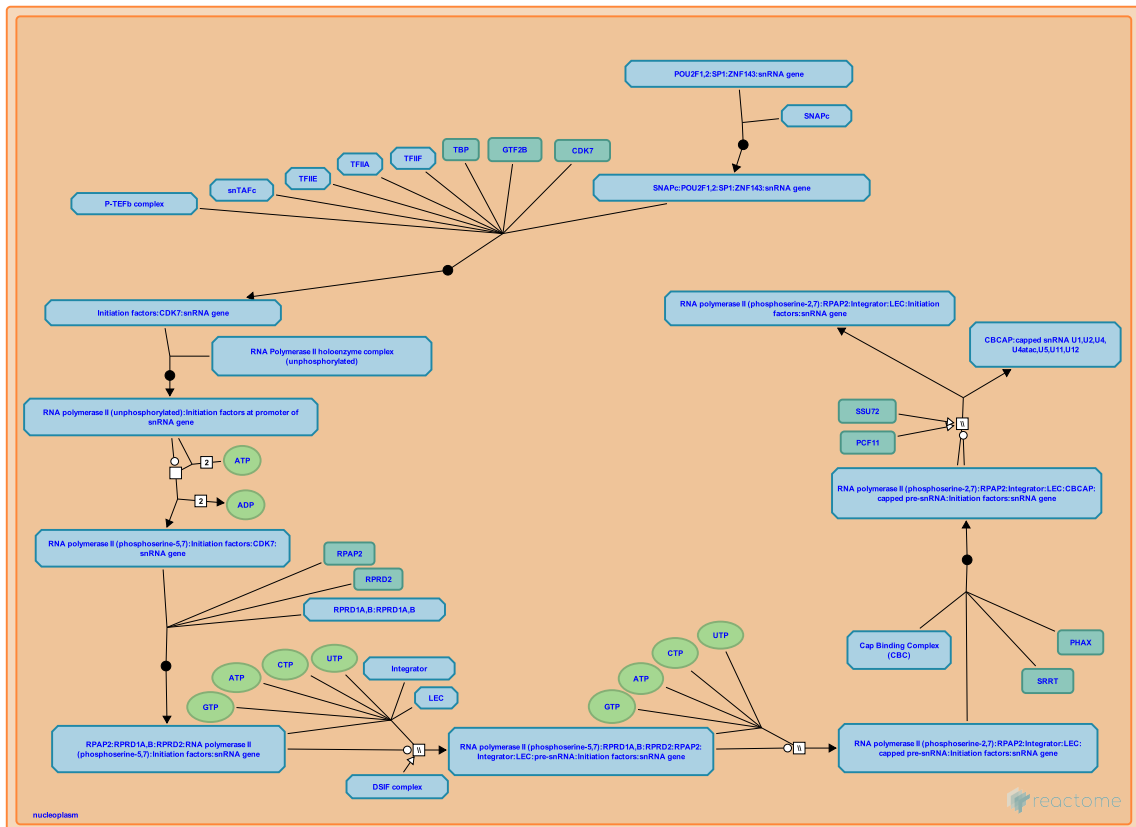


RNA polymerase II transcribes snRNA genes



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

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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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- 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 9 reactions ([see Table of Contents](#))

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

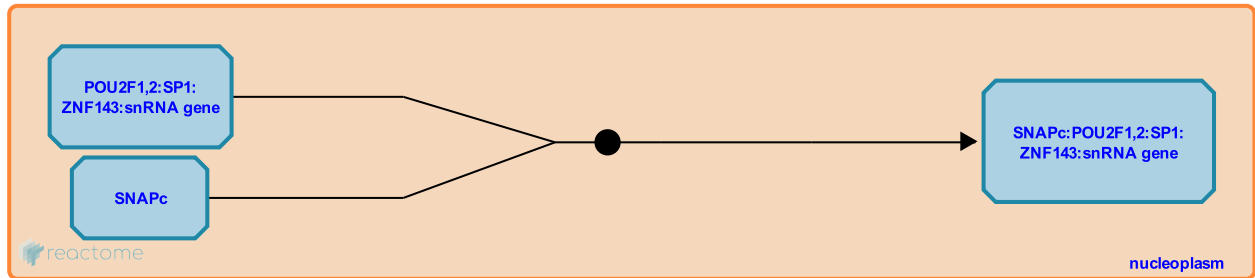
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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 ↗

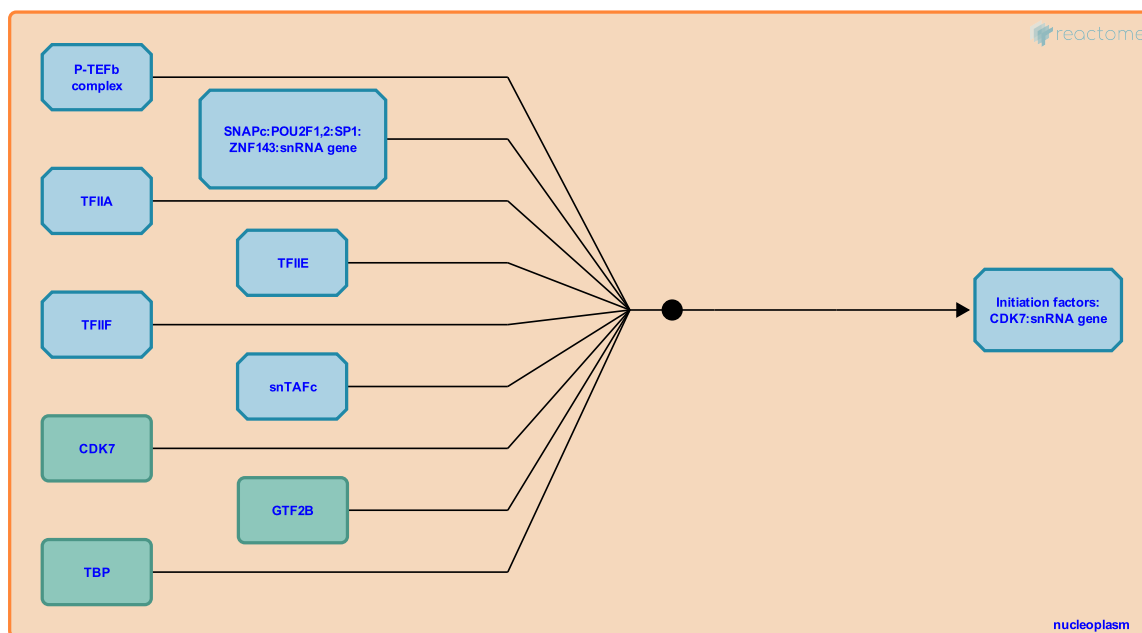
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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.

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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) ↗

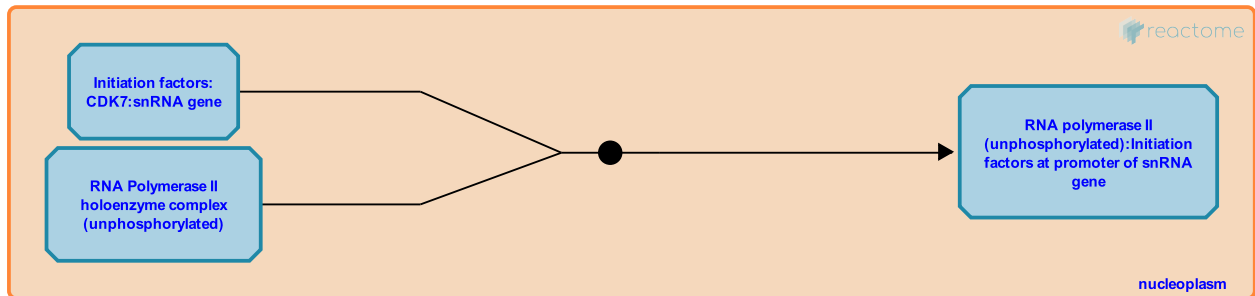
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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.

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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 ↗

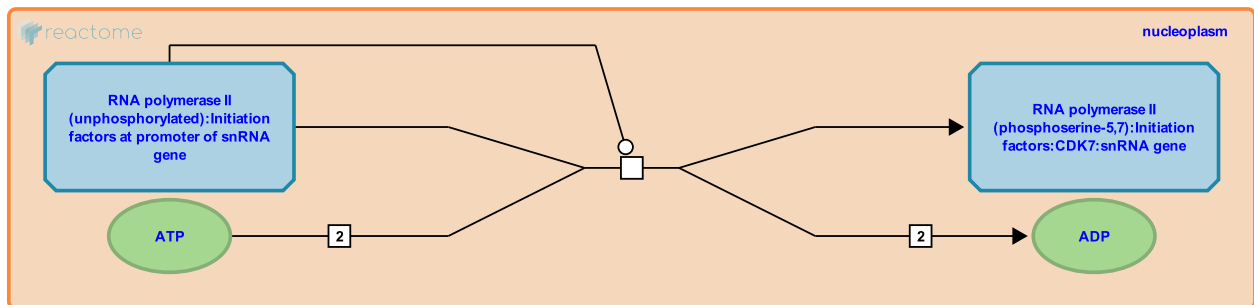
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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.

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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 ↗

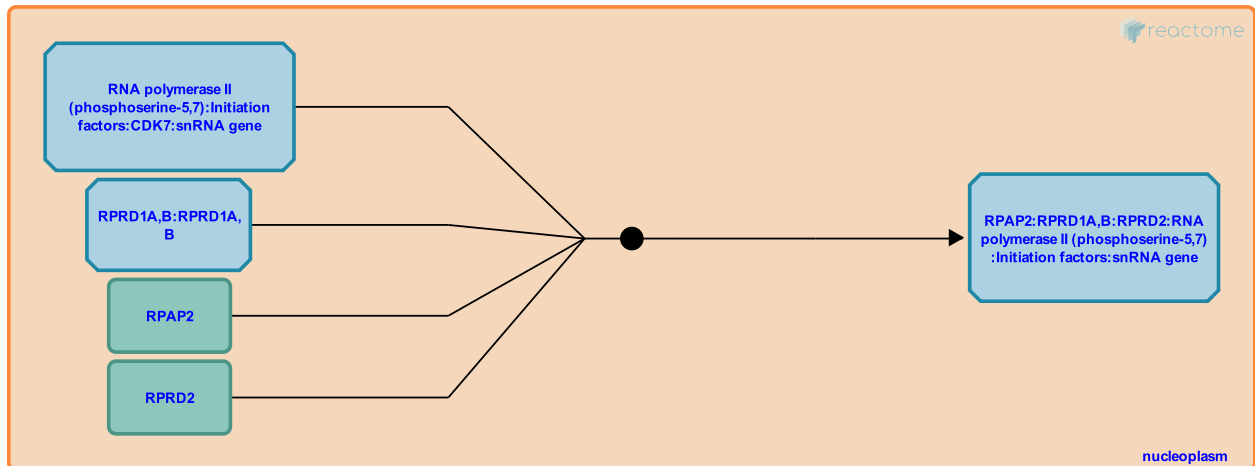
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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.

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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 ↗

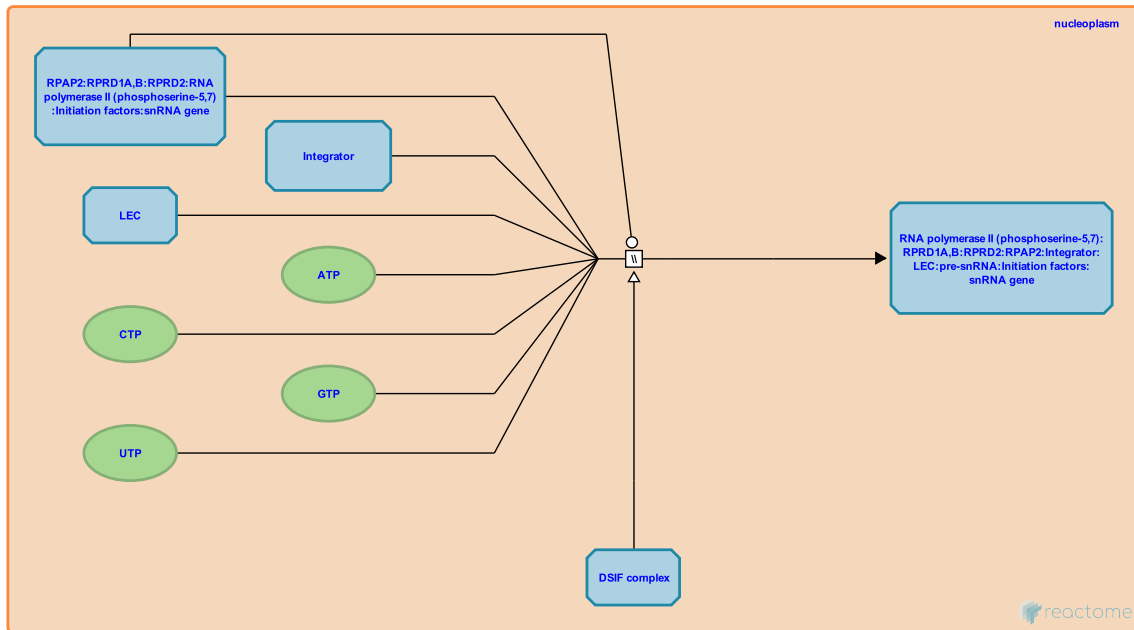
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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 ↗

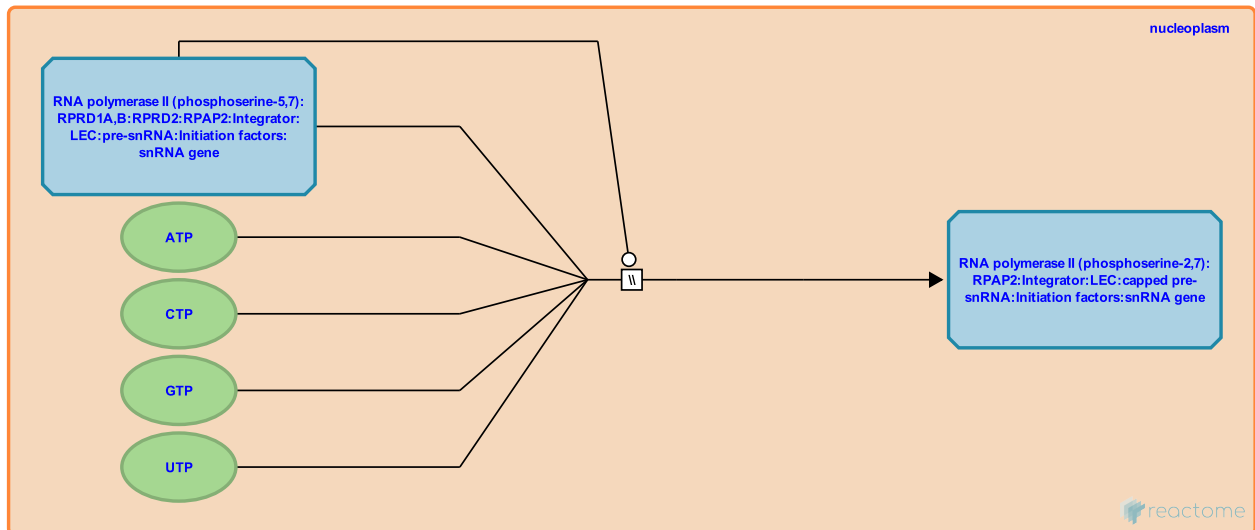
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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

Followed by: CBCAP complex binds 7-methylguanosine cap of snRNA

CBCAP complex binds 7-methylguanosine cap of snRNA ↗

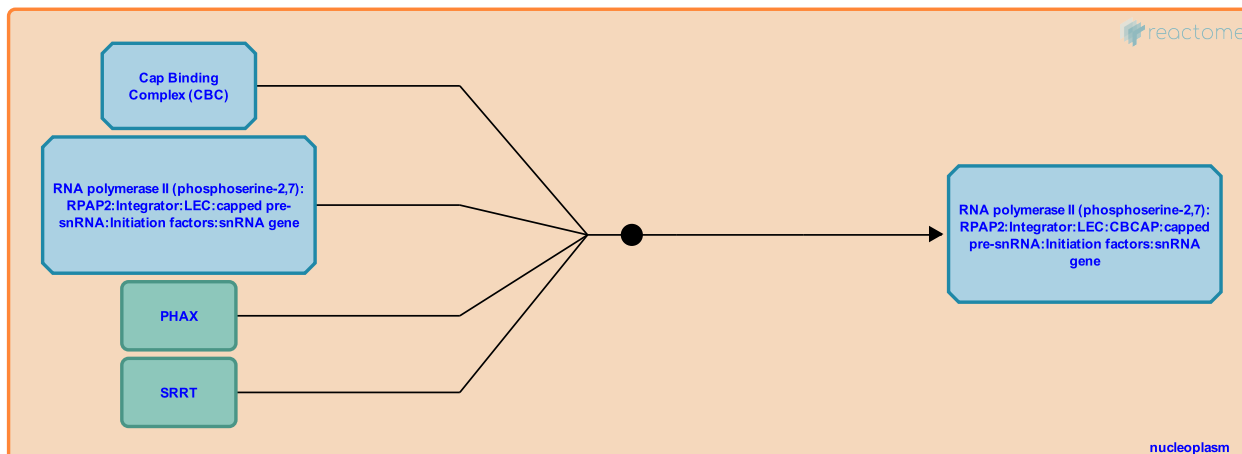
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-6814885

Type: binding

Compartments: nucleoplasm

Inferred from: CBCAP complex binds 7-methylguanosine cap 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>

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

Followed by: Integrator complex processes the 3' end of snRNA

Integrator complex processes the 3' end of snRNA ↗

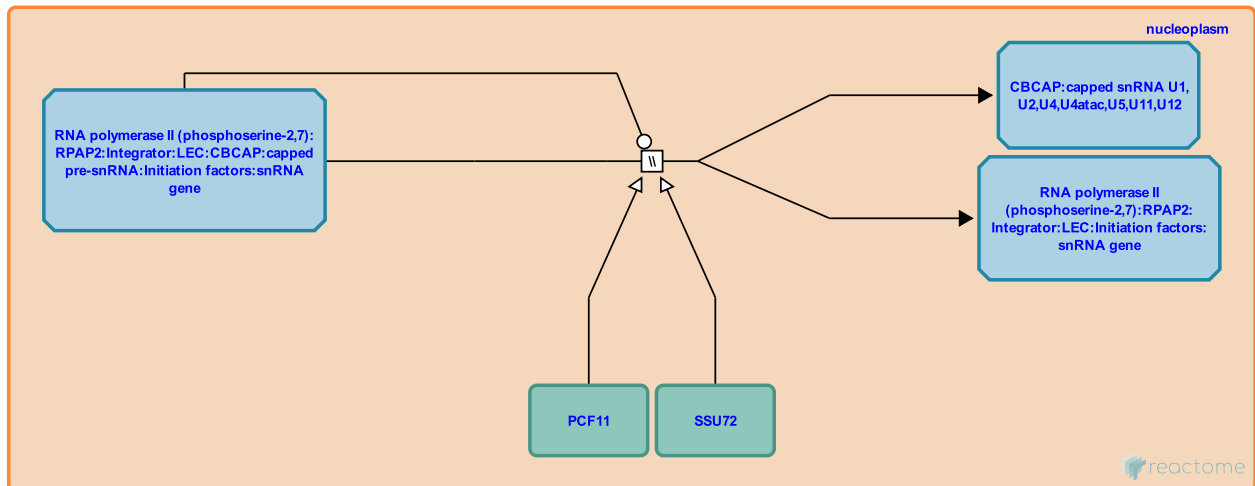
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-CFA-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>

Preceded by: [CBCAP complex binds 7-methylguanosine cap of snRNA](#)

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