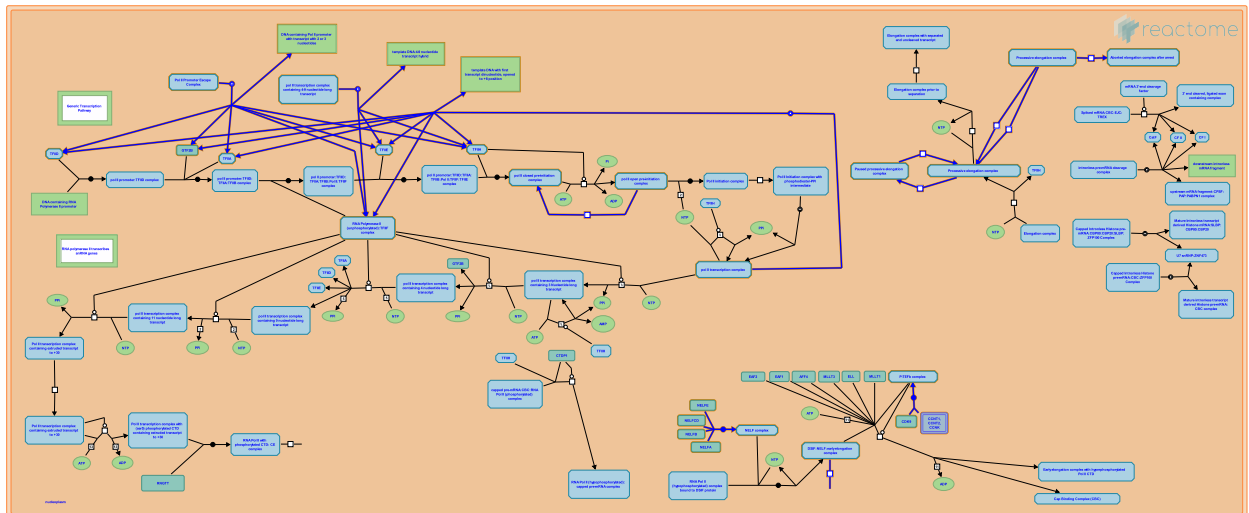


# RNA Polymerase II Pre-transcription

## Events



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

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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/about/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

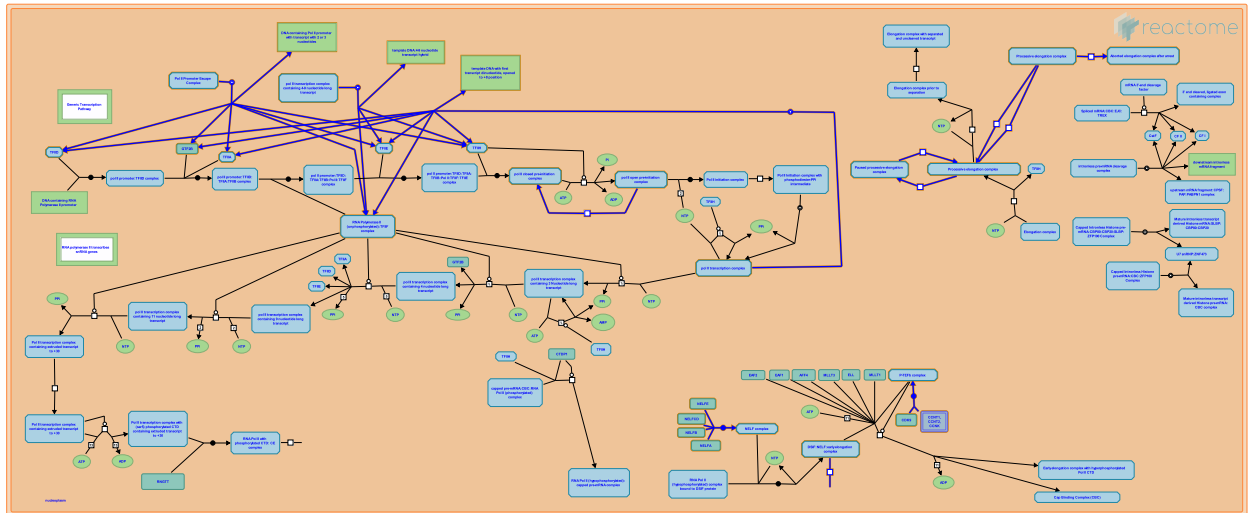
This document contains 1 pathway and 12 reactions ([see Table of Contents](#))

## RNA Polymerase II Pre-transcription Events ↗

**Stable identifier:** R-GGA-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.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Abortive initiation after formation of the first phosphodiester bond ↗

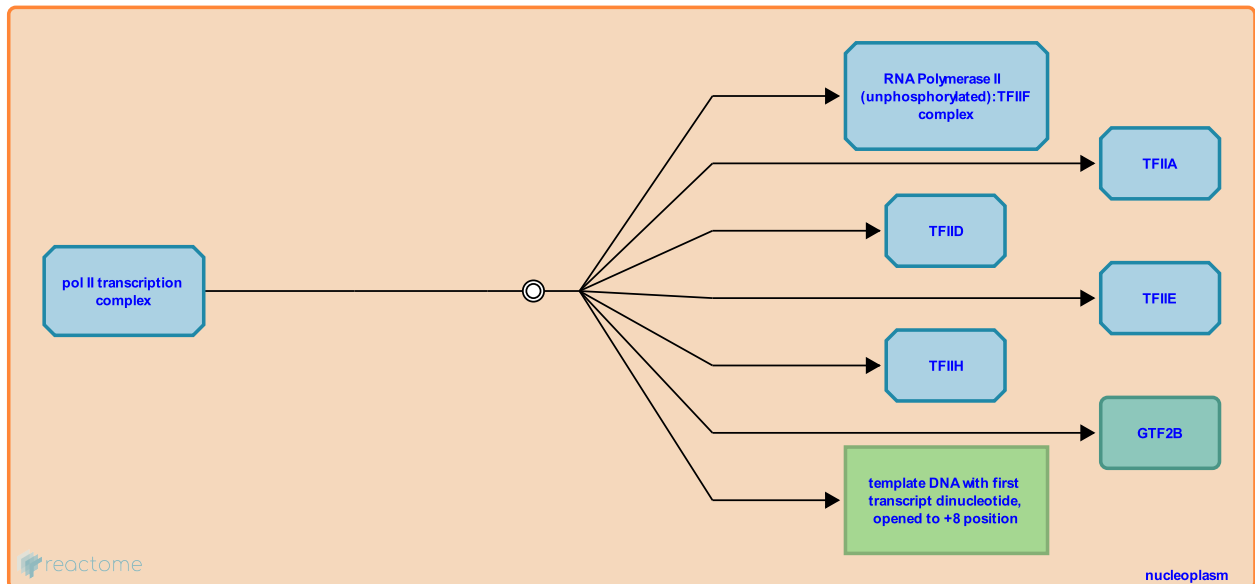
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-73946

**Type:** dissociation

**Compartments:** nucleoplasm

**Inferred from:** Abortive initiation after formation of the first phosphodiester bond (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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## Abortive Initiation After Second Transition ↗

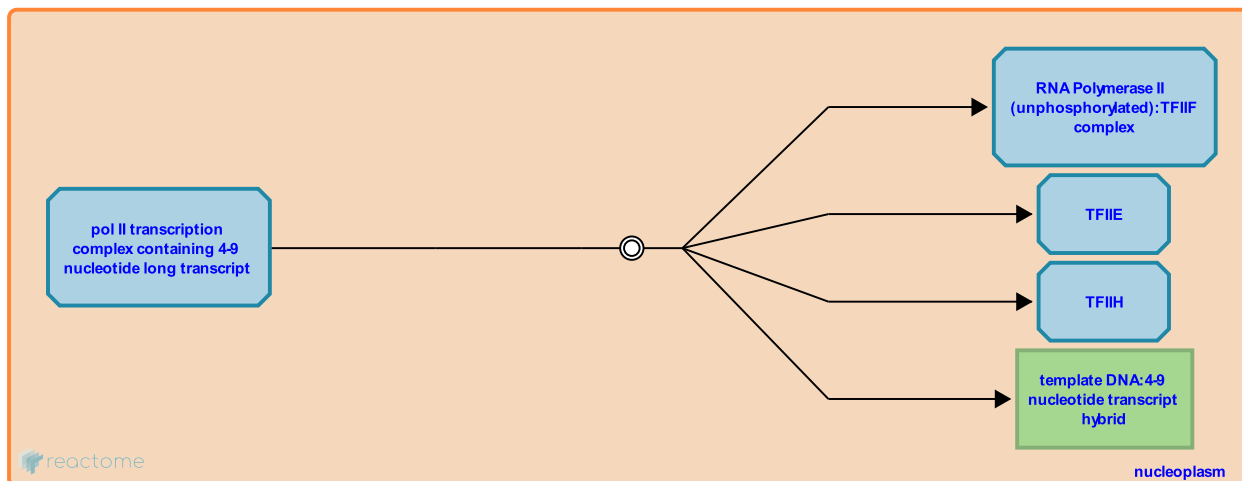
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-75891

**Type:** dissociation

**Compartments:** nucleoplasm

**Inferred from:** Abortive Initiation After Second Transition (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>

## Abortive Initiation Before Second Transition ↗

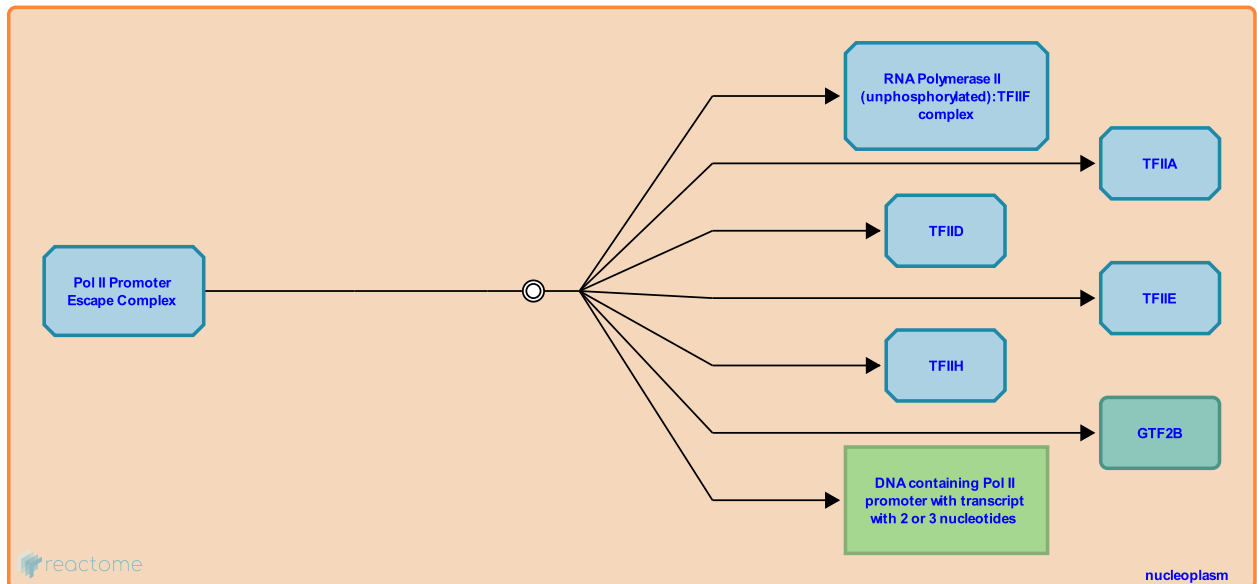
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-75856

**Type:** dissociation

**Compartments:** nucleoplasm

**Inferred from:** Abortive Initiation Before Second Transition (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>

## Formation of NELF complex ↗

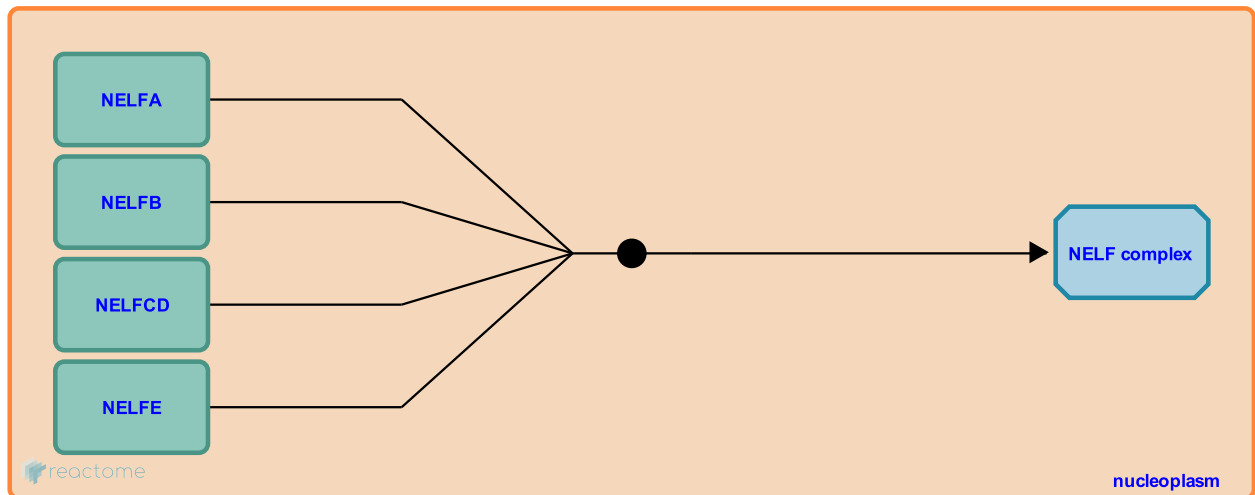
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-112437

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** Formation of NELF 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.

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## Formation of P-TEFb complex ↗

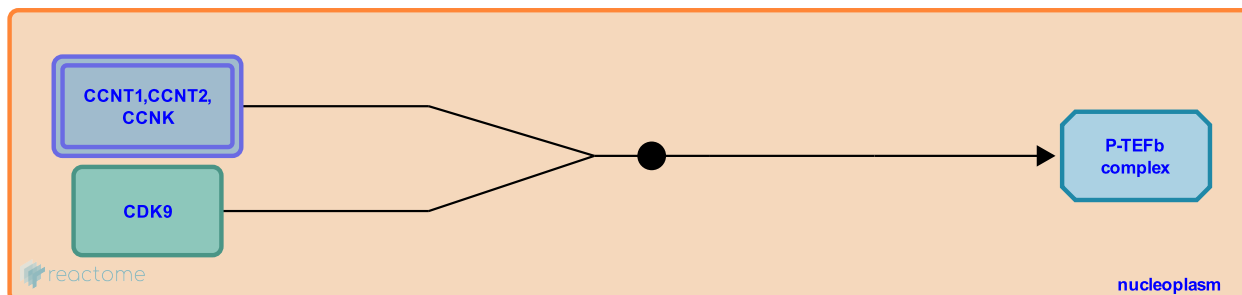
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-112430

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** Formation of P-TEFb 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>



## Resumption of elongation after recovery from pausing ↗

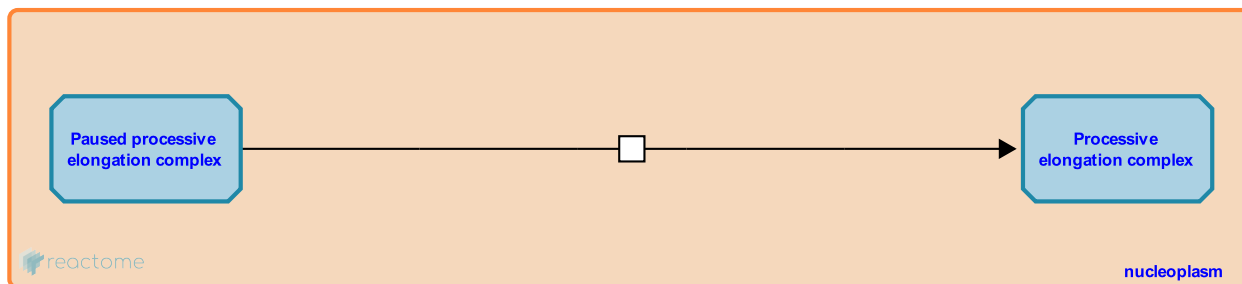
**Location:** [RNA Polymerase II Pre-transcription Events](#)

**Stable identifier:** R-GGA-112392

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [Resumption of elongation after recovery from pausing \(Homo sapiens\)](#)



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:** [2-4 nt.backtracking of Pol II complex on the template leading to elongation pausing](#)

## 2-4 nt.backtracking of Pol II complex on the template leading to elongation pausing



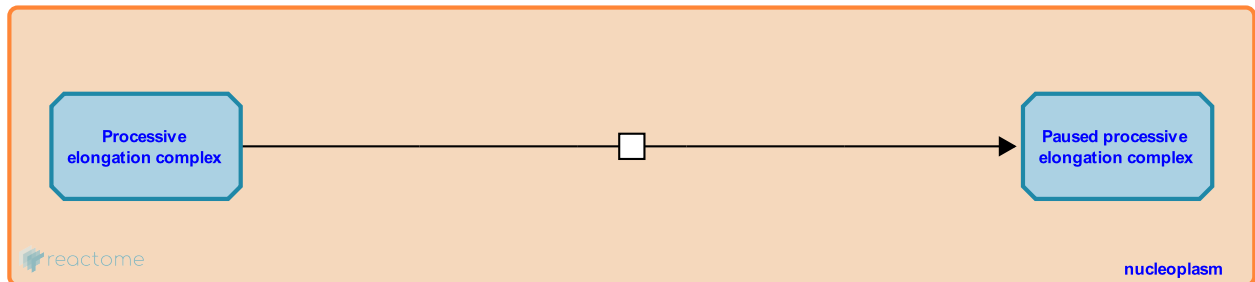
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-113411

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** 2-4 nt.backtracking of Pol II complex on the template leading to elongation pausing (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>

**Followed by:** Resumption of elongation after recovery from pausing

## 7-14 nt. Backtracking of Pol II complex on the template leading to elongation arrest



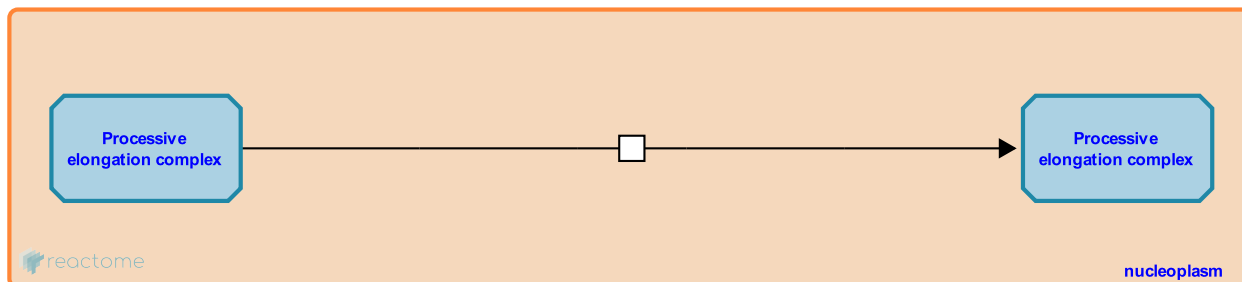
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-113414

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** 7-14 nt. Backtracking of Pol II complex on the template leading to elongation arrest (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>

**Followed by:** Abortive termination of elongation after arrest, TFIIS-mediated recovery of elongation from arrest

## TFIIS-mediated recovery of elongation from arrest ↗

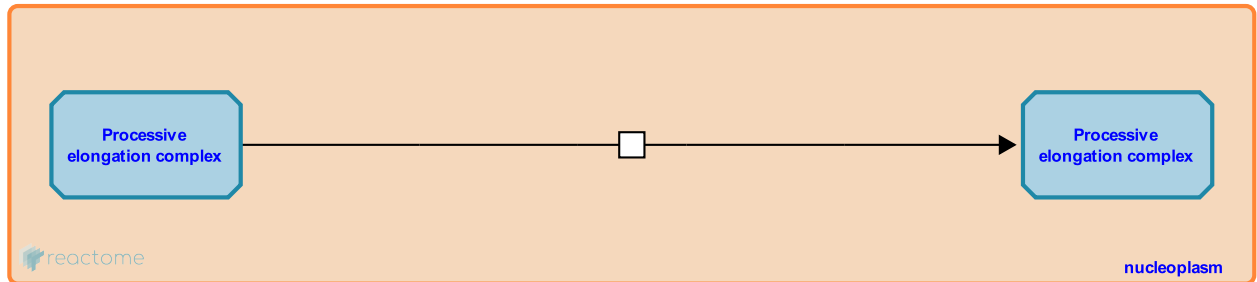
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-113413

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** TFIIS-mediated recovery of elongation from arrest (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:** 7-14 nt. Backtracking of Pol II complex on the template leading to elongation arrest

## Abortive termination of early transcription elongation by DSIF:NELF ↗

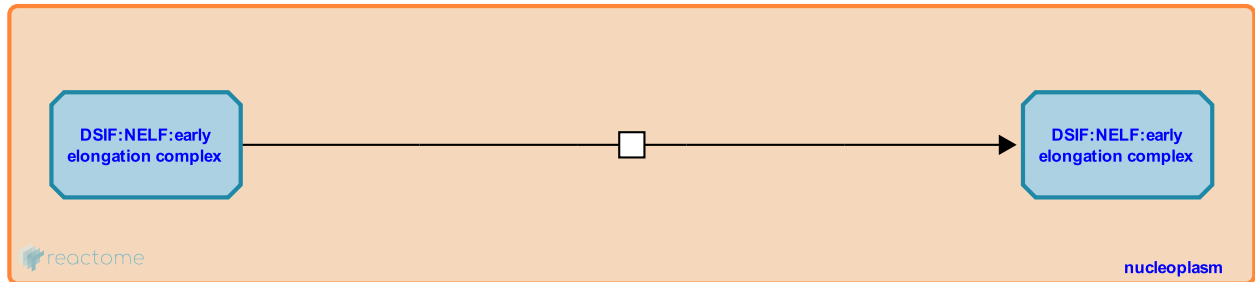
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-113409

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** Abortive termination of early transcription elongation by DSIF:NELF (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>

## Abortive termination of elongation after arrest ↗

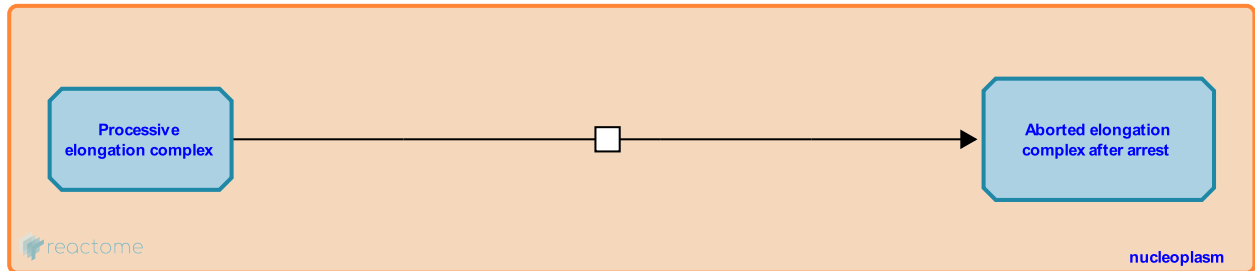
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-112395

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** Abortive termination of elongation after arrest (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>

**Preceded by:** 7-14 nt. Backtracking of Pol II complex on the template leading to elongation arrest

## Fall Back to Closed Pre-initiation Complex ↗

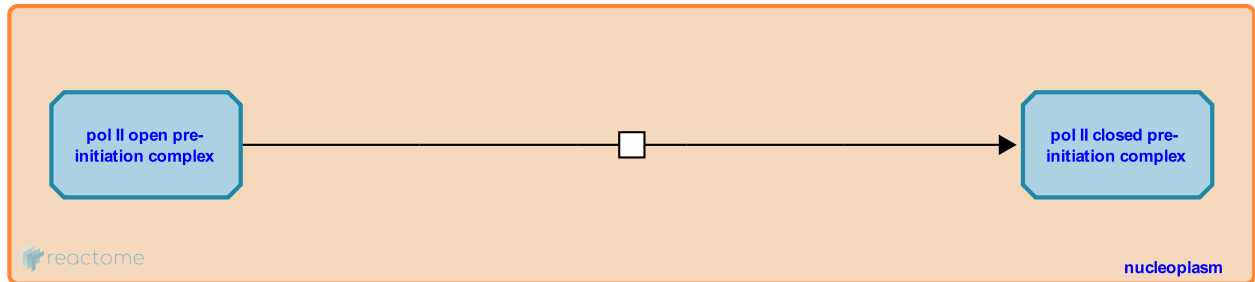
**Location:** RNA Polymerase II Pre-transcription Events

**Stable identifier:** R-GGA-75862

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** Fall Back to Closed Pre-initiation 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>

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