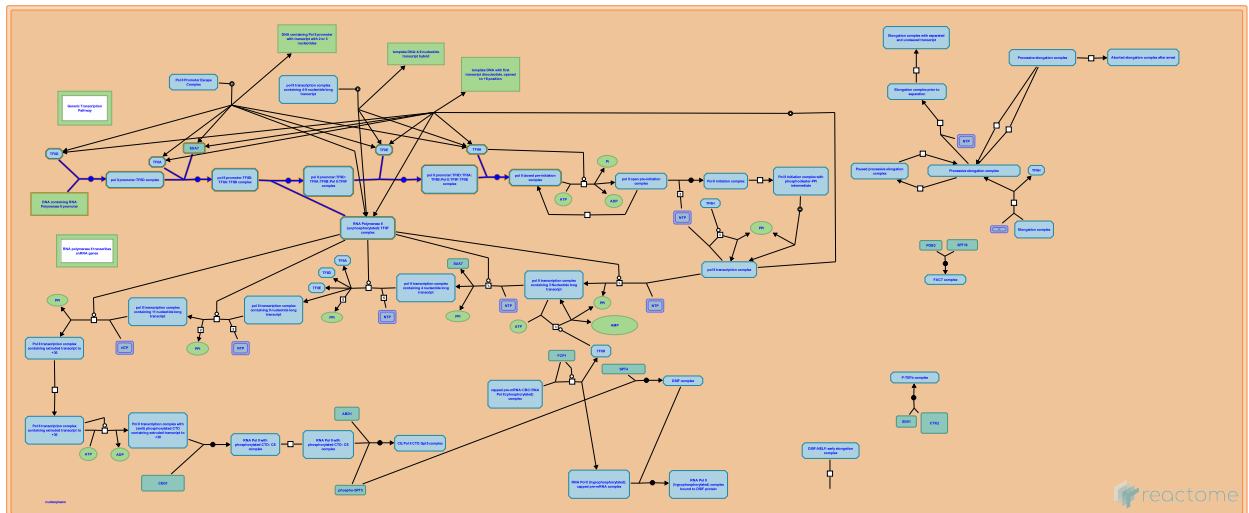


RNA Polymerase II Transcription Pre-Initiation And Promoter Opening



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: 76

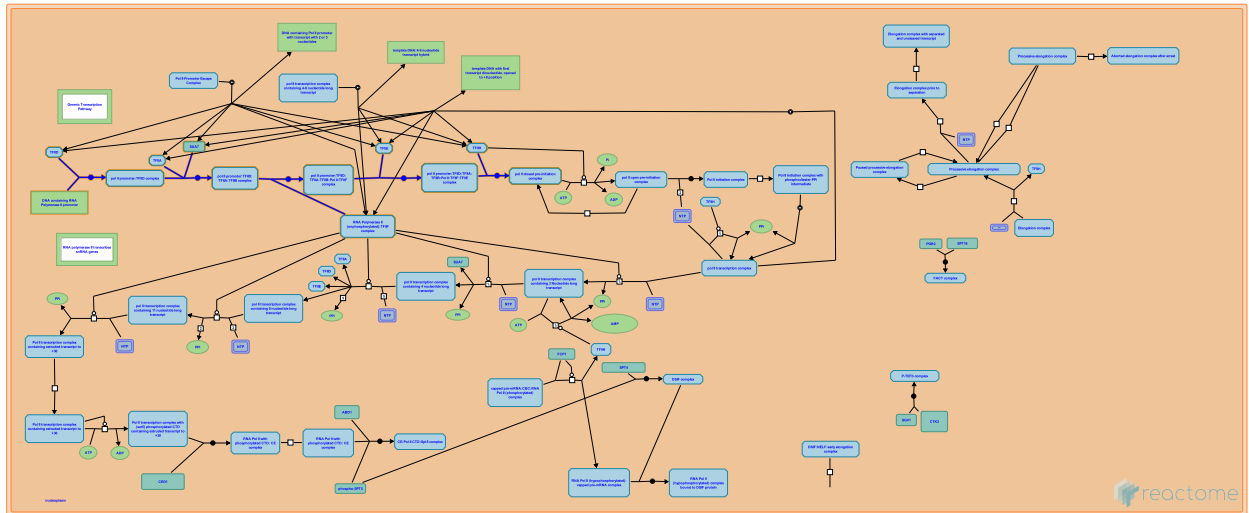
This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

RNA Polymerase II Transcription Pre-Initiation And Promoter Opening ↗

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

Recognition and Binding of Core Promoter Elements by TFIID ↗

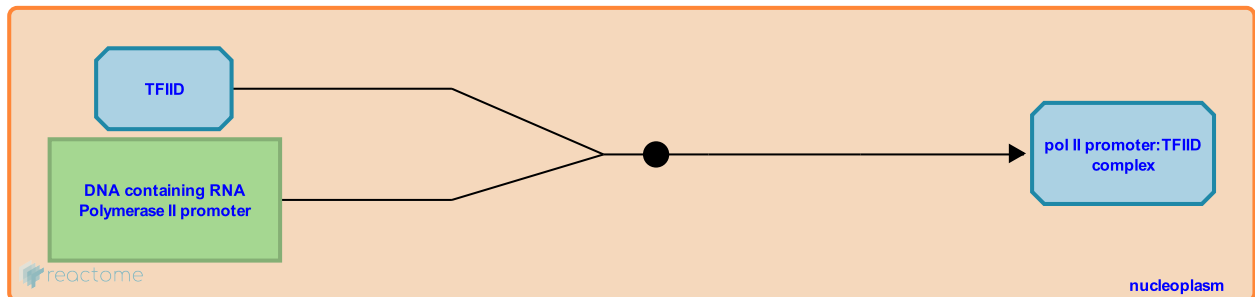
Location: RNA Polymerase II Transcription Pre-Initiation And Promoter Opening

Stable identifier: R-SCE-109636

Type: binding

Compartments: nucleoplasm

Inferred from: Recognition and Binding of Core Promoter Elements by TFIID (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: [Binding of TFIIA and TFIIB to the pol II promoter:TFIID complex](#)

Binding of TFIIA and TFIIB to the pol II promoter:TFIID complex ↗

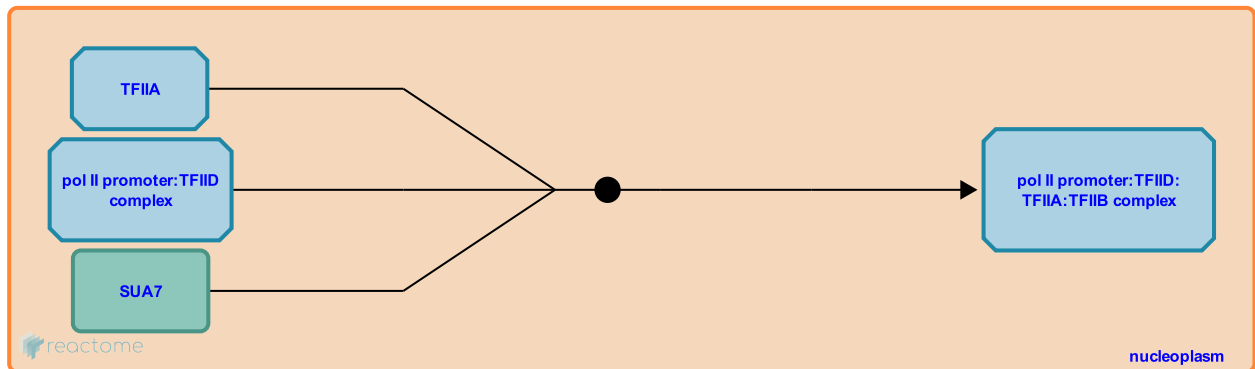
Location: [RNA Polymerase II Transcription Pre-Initiation And Promoter Opening](#)

Stable identifier: R-SCE-109637

Type: binding

Compartments: nucleoplasm

Inferred from: [Binding of TFIIA and TFIIB to the pol II promoter:TFIID 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Recognition and Binding of Core Promoter Elements by TFIID](#)

Followed by: [Recruitment of RNA Polymerase II Holoenzyme by TFIIF to the pol II promoter:TFIID:TFIIA:TFIIB complex](#)

Recruitment of RNA Polymerase II Holoenzyme by TFIIF to the pol II promoter:TFIID:TFIIA:TFIIB complex ↗

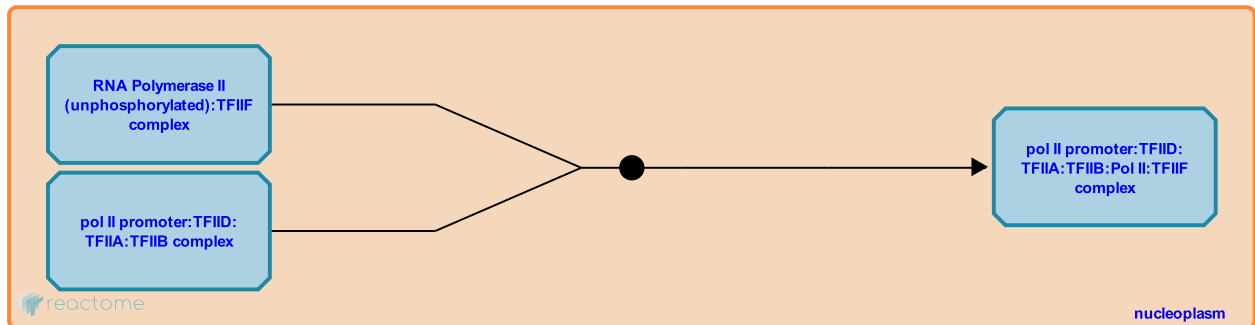
Location: RNA Polymerase II Transcription Pre-Initiation And Promoter Opening

Stable identifier: R-SCE-109638

Type: binding

Compartments: nucleoplasm

Inferred from: Recruitment of RNA Polymerase II Holoenzyme by TFIIF to the pol II promoter:TFIID:TFIIA:TFIIB 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: Binding of TFIIA and TFIIB to the pol II promoter:TFIID complex

Followed by: Binding of TFIIE to the growing preinitiation complex

Binding of TFIIE to the growing preinitiation complex ↗

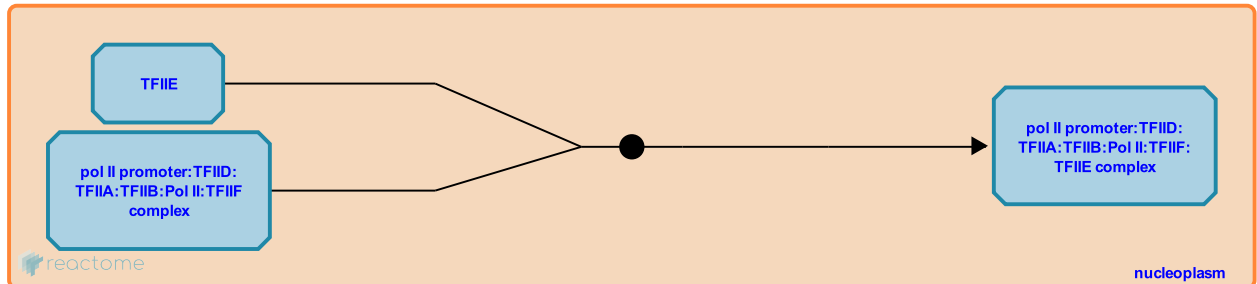
Location: RNA Polymerase II Transcription Pre-Initiation And Promoter Opening

Stable identifier: R-SCE-75095

Type: binding

Compartments: nucleoplasm

Inferred from: Binding of TFIIE to the growing preinitiation 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Recruitment of RNA Polymerase II Holoenzyme by TFIIF to the pol II promoter:TFIID:TFIIA:TFIIB complex](#)

Followed by: [Formation of the closed pre-initiation complex](#)

Formation of the closed pre-initiation complex ↗

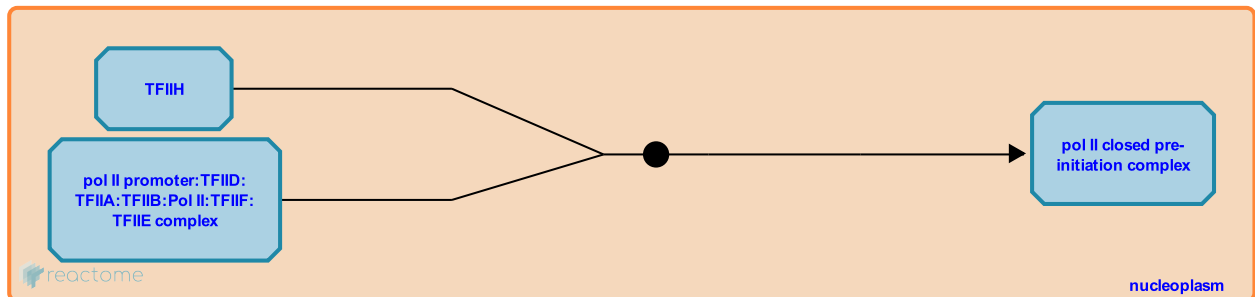
Location: [RNA Polymerase II Transcription Pre-Initiation And Promoter Opening](#)

Stable identifier: R-SCE-109639

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of the 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Binding of TFIIE to the growing preinitiation complex](#)

Table of Contents

Introduction	1
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	2
↳ Recognition and Binding of Core Promoter Elements by TFIID	3
↳ Binding of TFIIA and TFIIB to the pol II promoter:TFIID complex	4
↳ Recruitment of RNA Polymerase II Holoenzyme by TFIIF to the pol II promoter:TFIID:TFIIA:TFIIB complex	5
↳ Binding of TFIIIE to the growing preinitiation complex	6
↳ Formation of the closed pre-initiation complex	7
Table of Contents	8