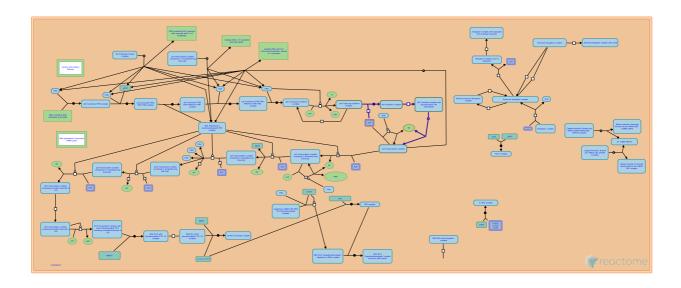


RNA Polymerase II Transcription Initi-

ation



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

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.

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Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 77

This document contains 1 pathway and 3 reactions (see Table of Contents)

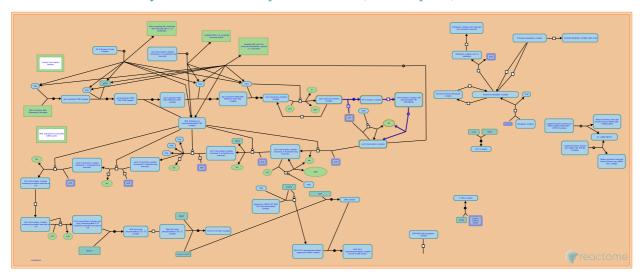
https://reactome.org Page 1

RNA Polymerase II Transcription Initiation

Stable identifier: R-DDI-75953

Compartments: nucleoplasm

Inferred from: RNA Polymerase II Transcription Initiation (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

NTP Binds Active Site of RNA Polymerase II 7

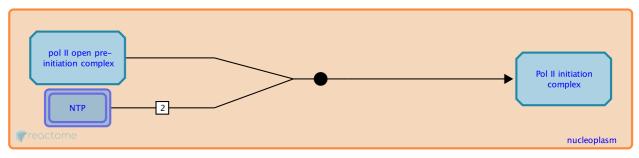
Location: RNA Polymerase II Transcription Initiation

Stable identifier: R-DDI-75861

Type: binding

Compartments: nucleoplasm

Inferred from: NTP Binds Active Site of RNA Polymerase II (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

Followed by: Nucleophillic Attack by 3'-hydroxyl Oxygen of nascent transcript on the Alpha Phosphate of NTP

https://reactome.org Page 3

Nucleophillic Attack by 3'-hydroxyl Oxygen of nascent transcript on the Alpha Phosphate of NTP ✓

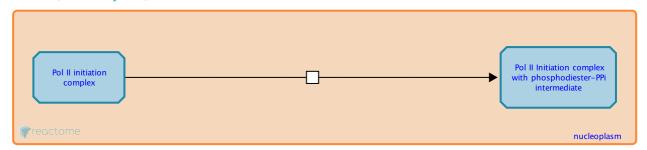
Location: RNA Polymerase II Transcription Initiation

Stable identifier: R-DDI-75866

Type: transition

Compartments: nucleoplasm

Inferred from: Nucleophillic Attack by 3'-hydroxyl Oxygen of nascent transcript on the Alpha Phosphate of NTP (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: NTP Binds Active Site of RNA Polymerase II

Followed by: Newly Formed Phosphodiester Bond Stabilized and PPi Released

Newly Formed Phosphodiester Bond Stabilized and PPi Released 7

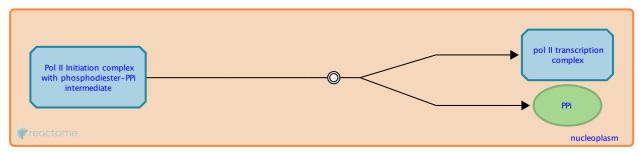
Location: RNA Polymerase II Transcription Initiation

Stable identifier: R-DDI-75864

Type: dissociation

Compartments: nucleoplasm

Inferred from: Newly Formed Phosphodiester Bond Stabilized and PPi Released (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: Nucleophillic Attack by 3'-hydroxyl Oxygen of nascent transcript on the Alpha Phosphate of NTP

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