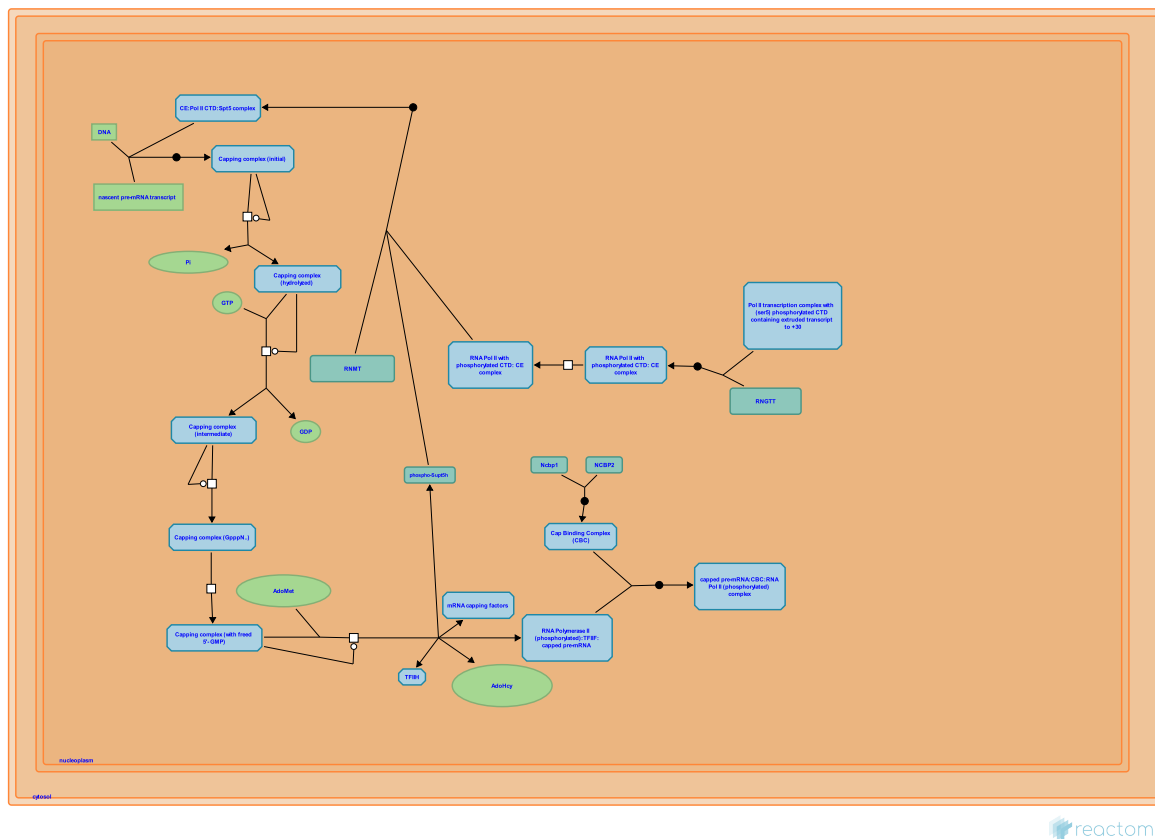


mRNA Capping



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](#).

17/05/2024

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

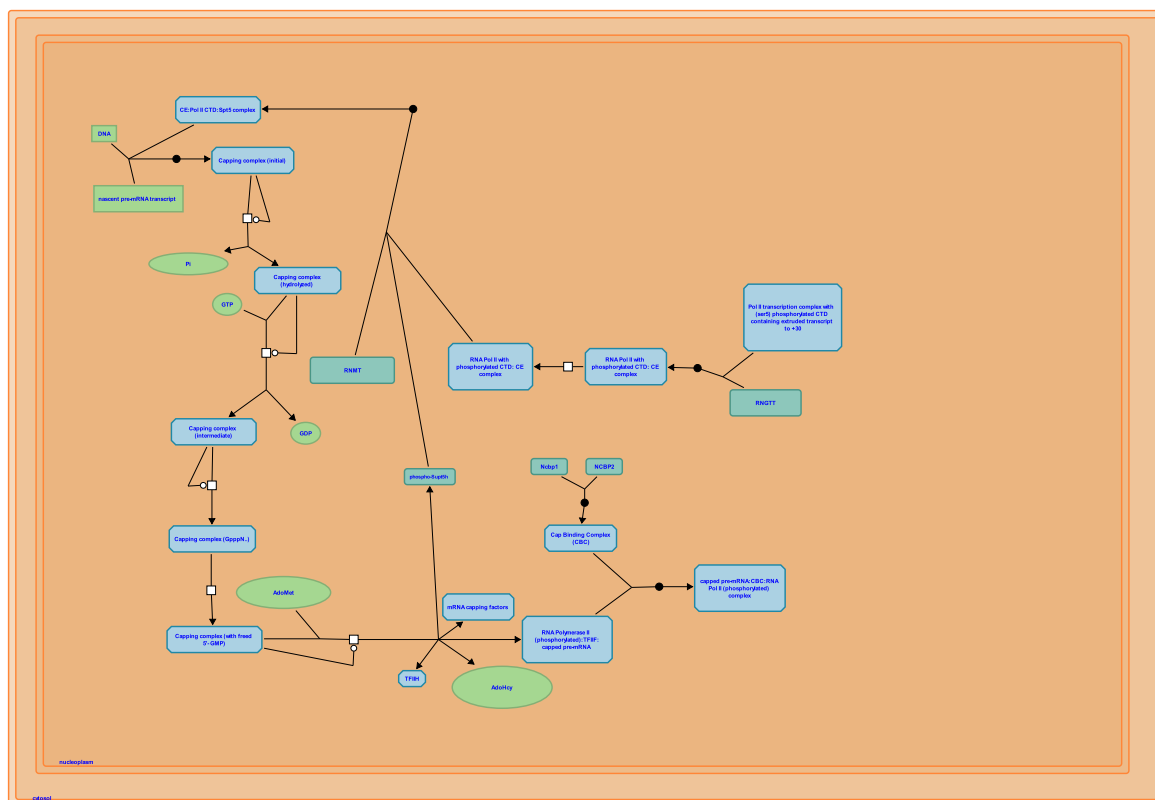
This document contains 1 pathway and 11 reactions ([see Table of Contents](#))

mRNA Capping ↗

Stable identifier: R-MMU-72086

Compartments: nucleoplasm

Inferred from: mRNA Capping (Homo sapiens)



reactome

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>

Capping complex formation ↗

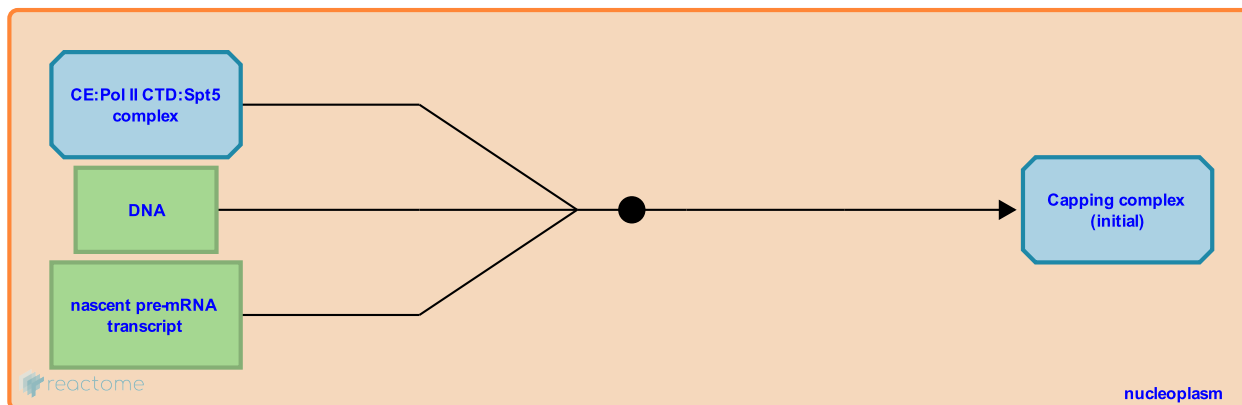
Location: mRNA Capping

Stable identifier: R-MMU-77077

Type: binding

Compartments: nucleoplasm

Inferred from: Capping complex formation (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: SPT5 subunit of Pol II binds the RNA triphosphatase (RTP)

Followed by: Hydrolysis of the 5'-end of the nascent transcript by the capping enzyme

Hydrolysis of the 5'-end of the nascent transcript by the capping enzyme ↗

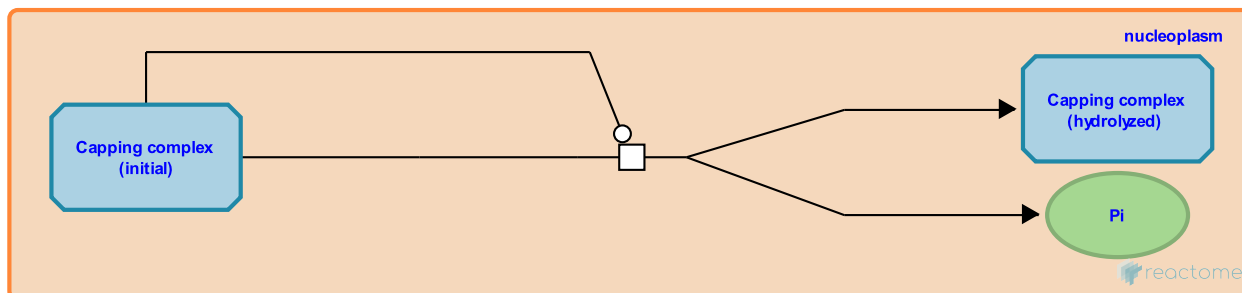
Location: mRNA Capping

Stable identifier: R-MMU-77078

Type: transition

Compartments: nucleoplasm

Inferred from: Hydrolysis of the 5'-end of the nascent transcript by the capping enzyme (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: Capping complex formation

Followed by: Formation of the CE:GMP intermediate complex

Formation of the CE:GMP intermediate complex ↗

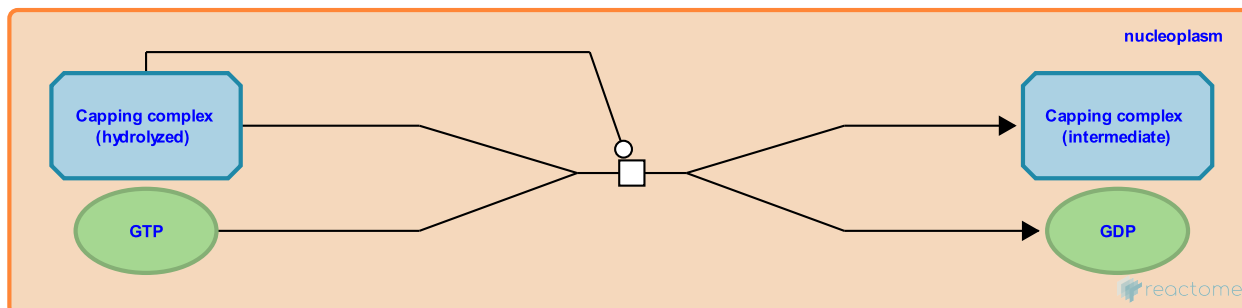
Location: mRNA Capping

Stable identifier: R-MMU-77081

Type: transition

Compartments: nucleoplasm

Inferred from: Formation of the CE:GMP intermediate 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>

Preceded by: Hydrolysis of the 5'-end of the nascent transcript by the capping enzyme

Followed by: Transfer of GMP from the capping enzyme GT site to 5'-end of mRNA

Transfer of GMP from the capping enzyme GT site to 5'-end of mRNA ↗

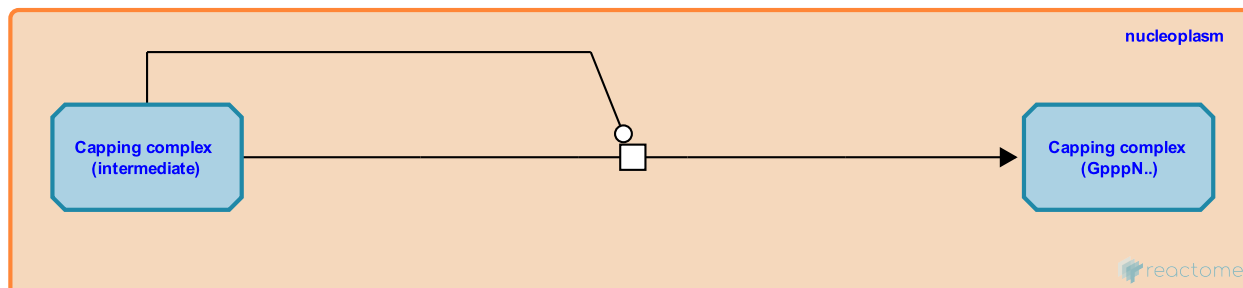
Location: mRNA Capping

Stable identifier: R-MMU-77083

Type: transition

Compartments: nucleoplasm

Inferred from: Transfer of GMP from the capping enzyme GT site to 5'-end of mRNA (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: Formation of the CE:GMP intermediate complex

Followed by: Dissociation of transcript with 5'-GMP from GT

Dissociation of transcript with 5'-GMP from GT ↗

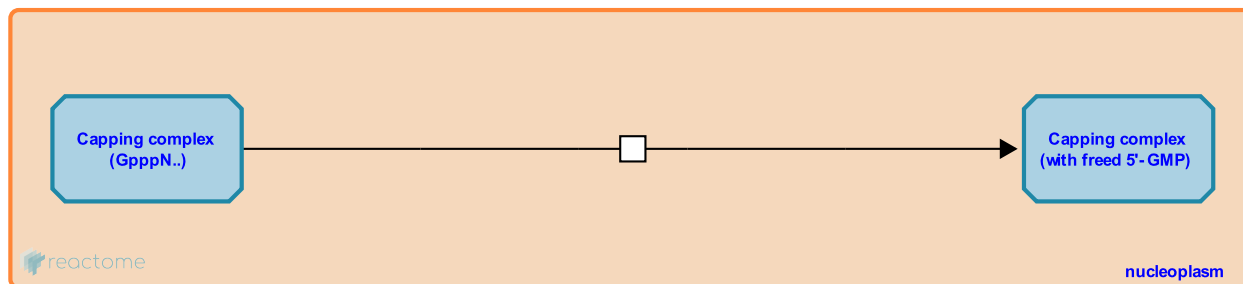
Location: mRNA Capping

Stable identifier: R-MMU-77085

Type: transition

Compartments: nucleoplasm

Inferred from: Dissociation of transcript with 5'-GMP from GT (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: Transfer of GMP from the capping enzyme GT site to 5'-end of mRNA

Followed by: Methylation of GMP-cap by RNA Methyltransferase

Methylation of GMP-cap by RNA Methyltransferase ↗

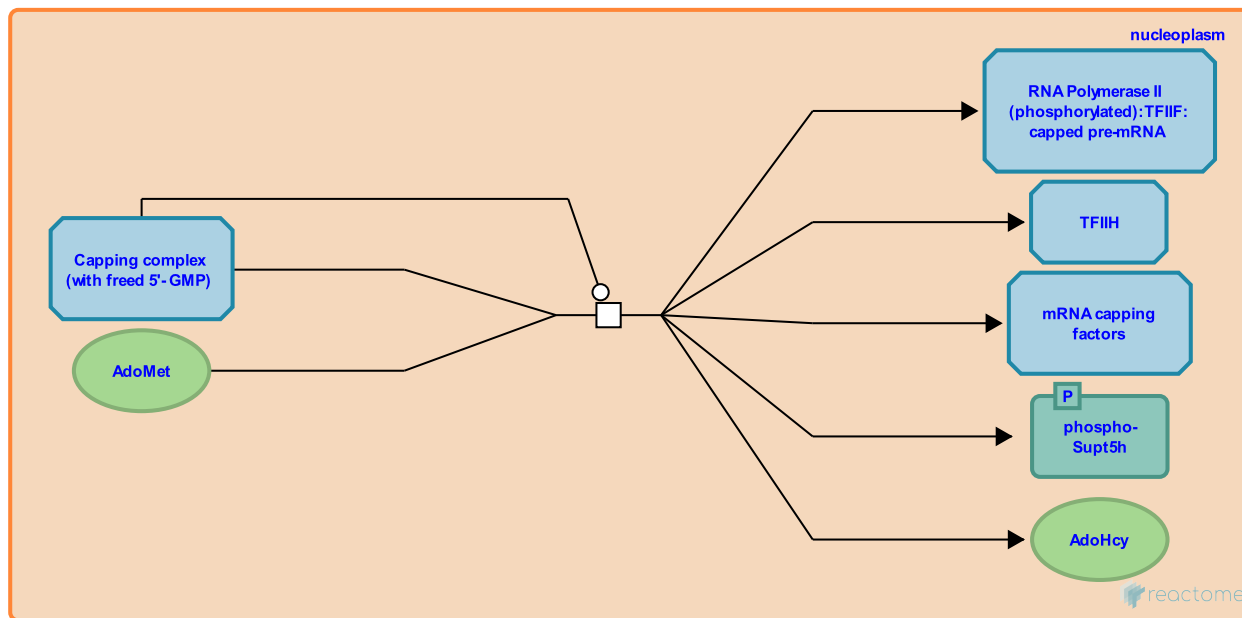
Location: mRNA Capping

Stable identifier: R-MMU-77090

Type: transition

Compartments: nucleoplasm

Inferred from: Methylation of GMP-cap by RNA Methyltransferase (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: Dissociation of transcript with 5'-GMP from GT

Followed by: Recognition and binding of the mRNA cap by the cap-binding complex

Recognition and binding of the mRNA cap by the cap-binding complex ↗

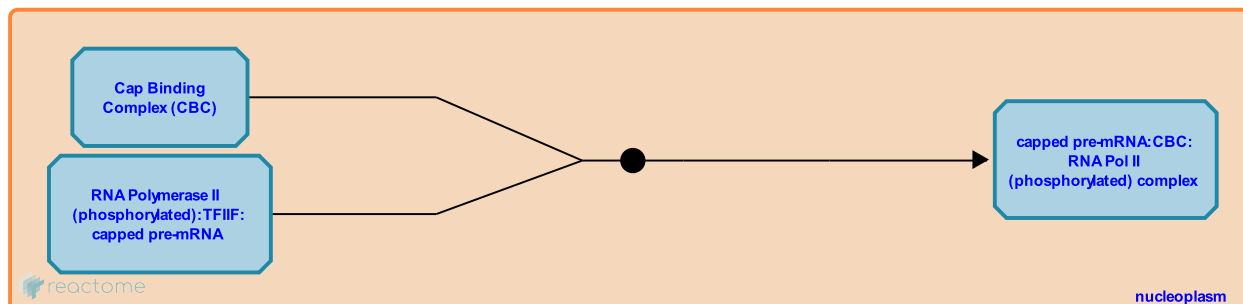
Location: [mRNA Capping](#)

Stable identifier: R-MMU-77095

Type: binding

Compartments: nucleoplasm

Inferred from: [Recognition and binding of the mRNA cap by the cap-binding 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>

Preceded by: [Methylation of GMP-cap by RNA Methyltransferase](#), [Formation of cap binding complex \(CBC\)](#)

Formation of cap binding complex (CBC) ↗

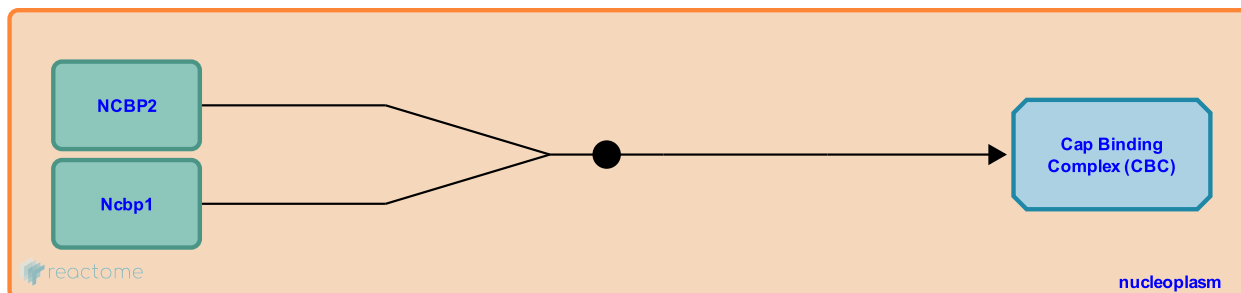
Location: [mRNA Capping](#)

Stable identifier: R-MMU-77094

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of cap binding complex \(CBC\) \(Homo sapiens\)](#)



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: [Recognition and binding of the mRNA cap by the cap-binding complex](#)

SPT5 subunit of Pol II binds the RNA triphosphatase (RTP) ↗

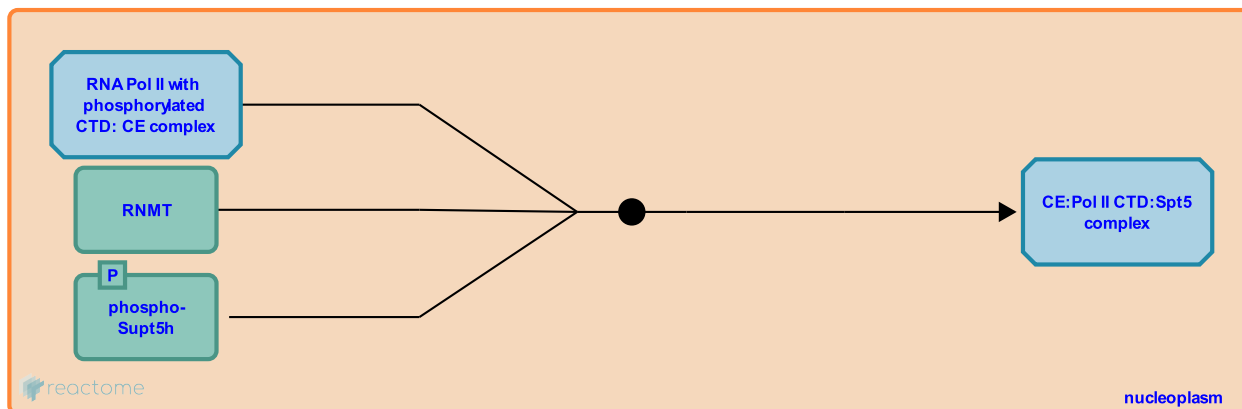
Location: [mRNA Capping](#)

Stable identifier: R-MMU-77073

Type: binding

Compartments: nucleoplasm

Inferred from: [SPT5 subunit of Pol II binds the RNA triphosphatase \(RTP\) \(Homo sapiens\)](#)



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: [Activation of GT](#)

Followed by: [Capping complex formation](#)

Activation of GT ↗

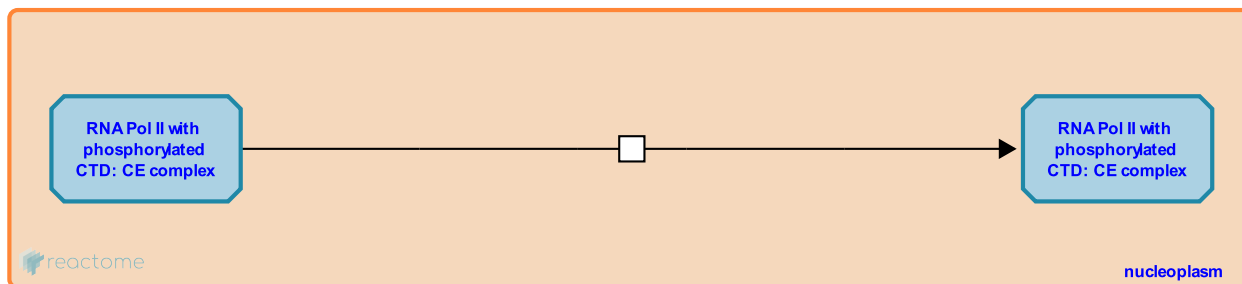
Location: mRNA Capping

Stable identifier: R-MMU-77068

Type: transition

Compartments: nucleoplasm

Inferred from: Activation of GT (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: RNA Polymerase II CTD (phosphorylated) binds to CE

Followed by: SPT5 subunit of Pol II binds the RNA triphosphatase (RTP)

RNA Polymerase II CTD (phosphorylated) binds to CE ↗

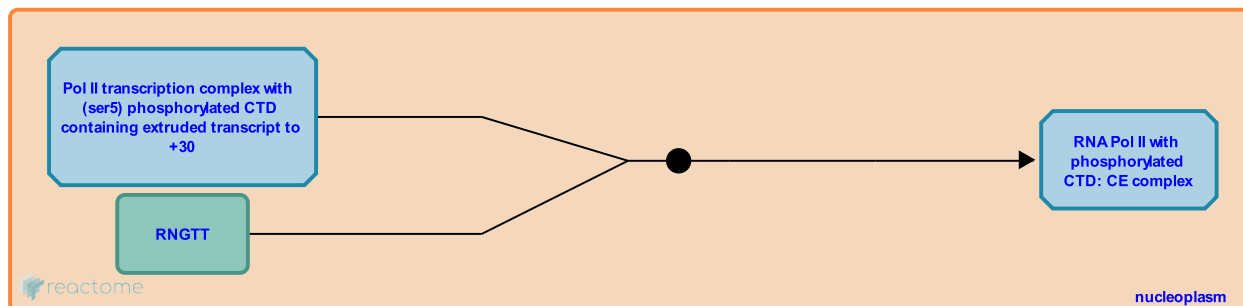
Location: [mRNA Capping](#)

Stable identifier: R-MMU-77069

Type: binding

Compartments: nucleoplasm

Inferred from: [RNA Polymerase II CTD \(phosphorylated\) binds to CE \(Homo sapiens\)](#)



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/parologue (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: [Activation of GT](#)

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