Processing of Capped Intronless Pre-mRNA

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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.

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https://reactome.org
**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**


Reactome database release: 83

This document contains 4 pathways (see Table of Contents)

https://reactome.org
Processing of Capped Intronless Pre-mRNA

Stable identifier: R-CEL-75067

Compartments: nucleoplasm

Inferred from: Processing of Capped Intronless Pre-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs

Location: Processing of Capped Intronless Pre-mRNA

Stable identifier: R-CEL-77588

Compartments: nucleoplasm

Inferred from: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs (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
SLBP independent Processing of Histone Pre-mRNAs

**Location:** Processing of Capped Intronless Pre-mRNA

**Stable identifier:** R-CEL-111367

**Compartments:** nucleoplasm

**Inferred from:** SLBP independent Processing of Histone Pre-mRNAs (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](http://www.pantherdb.org/about.jsp)
Processing of Intronless Pre-mRNAs

Location: Processing of Capped Intronless Pre-mRNA

Stable identifier: R-CEL-77595

Compartments: nucleoplasm

Inferred from: Processing of Intronless Pre-mRNAs (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
**Table of Contents**

1. Introduction
2. Processing of Capped Intronless Pre-mRNA
3. SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
4. SLBP independent Processing of Histone Pre-mRNAs
5. Processing of Intronless Pre-mRNAs

Table of Contents