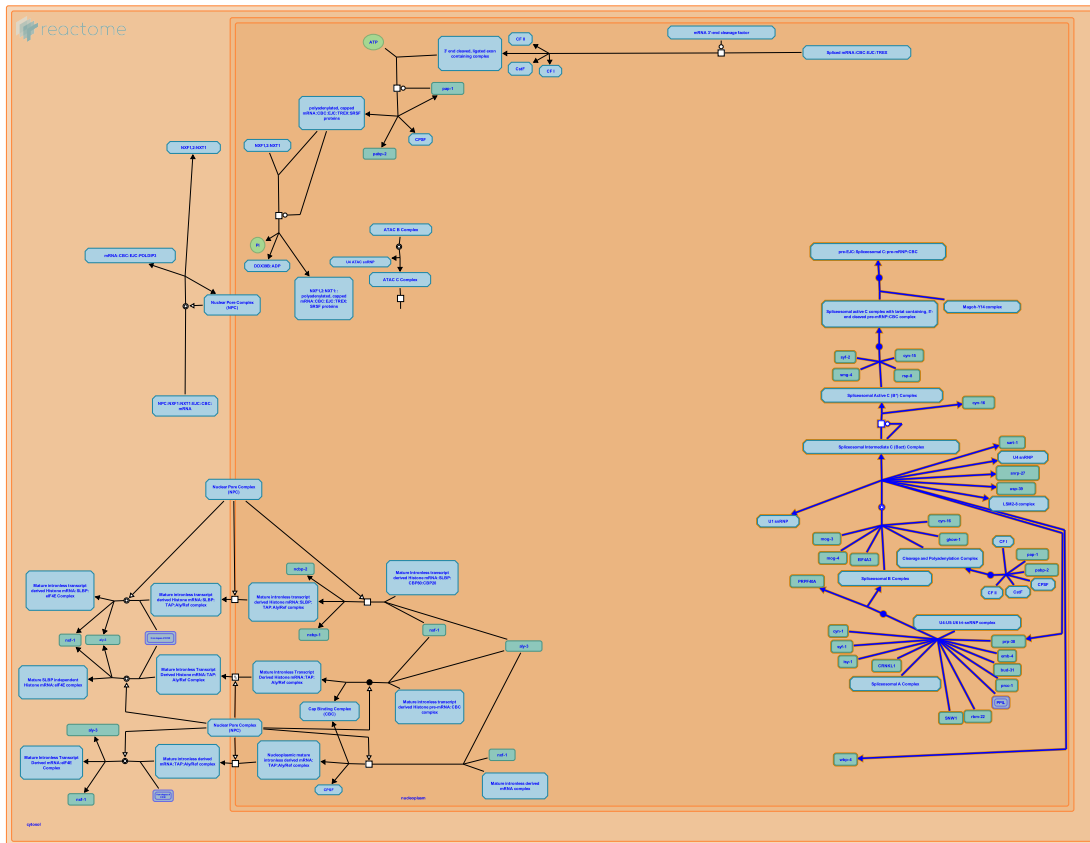


mRNA Splicing - Major Pathway



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

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Reactome database release: 75

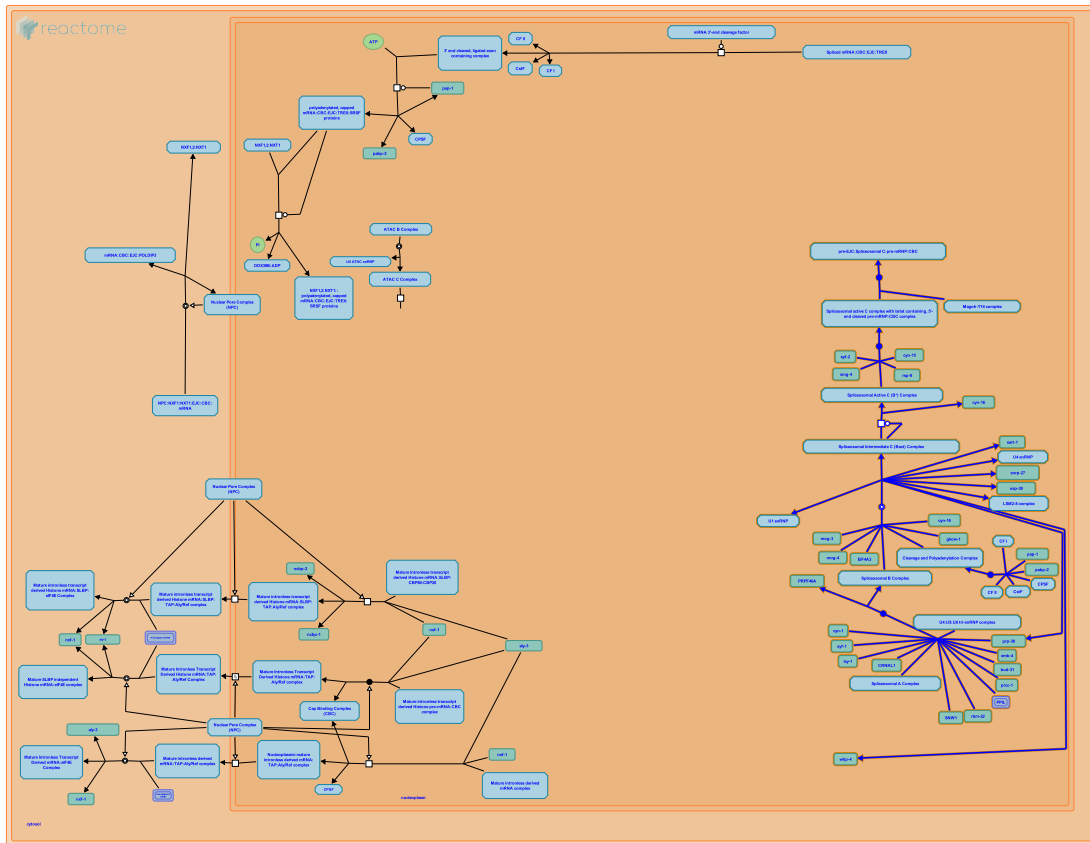
This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

mRNA Splicing - Major Pathway ↗

Stable identifier: R-CEL-72163

Compartments: nucleoplasm

Inferred from: mRNA Splicing - Major Pathway (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>

Formation of the Spliceosomal B Complex ↗

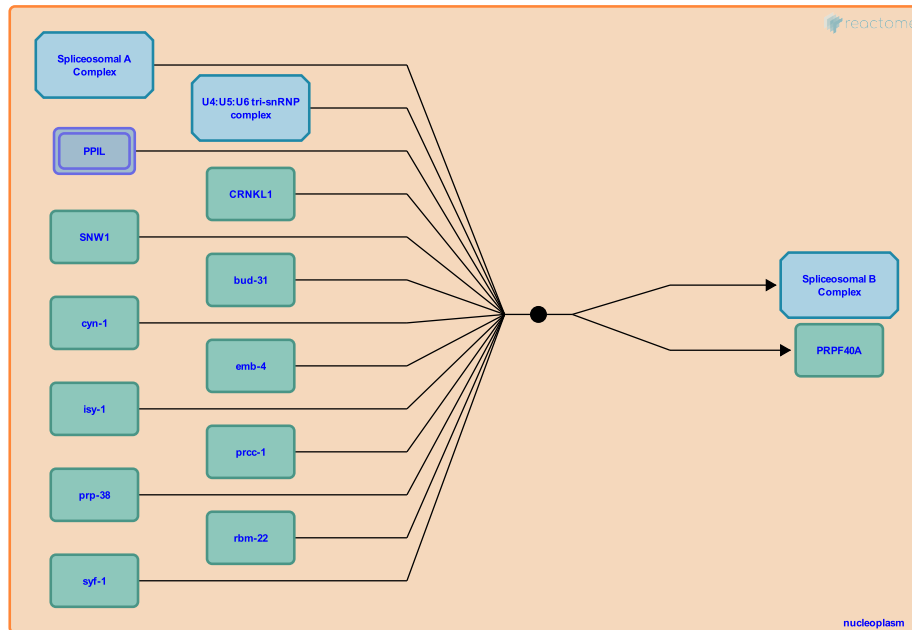
Location: mRNA Splicing - Major Pathway

Stable identifier: R-CEL-72127

Type: binding

Compartments: nucleoplasm

Inferred from: Formation of the Spliceosomal B 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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Followed by: Formation of an intermediate Spliceosomal C (Bact) complex

Formation of the Cleavage and Polyadenylation Complex ↗

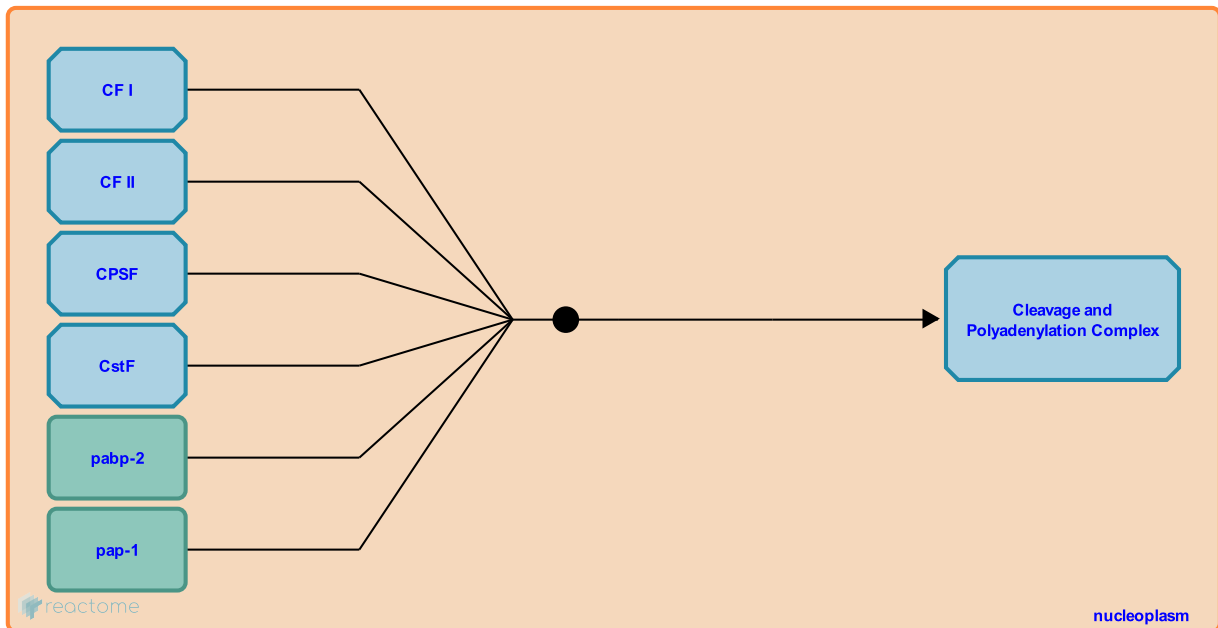
Location: [mRNA Splicing - Major Pathway](#)

Stable identifier: R-CEL-72231

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of the Cleavage and Polyadenylation 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>

Followed by: [Formation of an intermediate Spliceosomal C \(Bact\) complex](#)

Formation of an intermediate Spliceosomal C (Bact) complex ↗

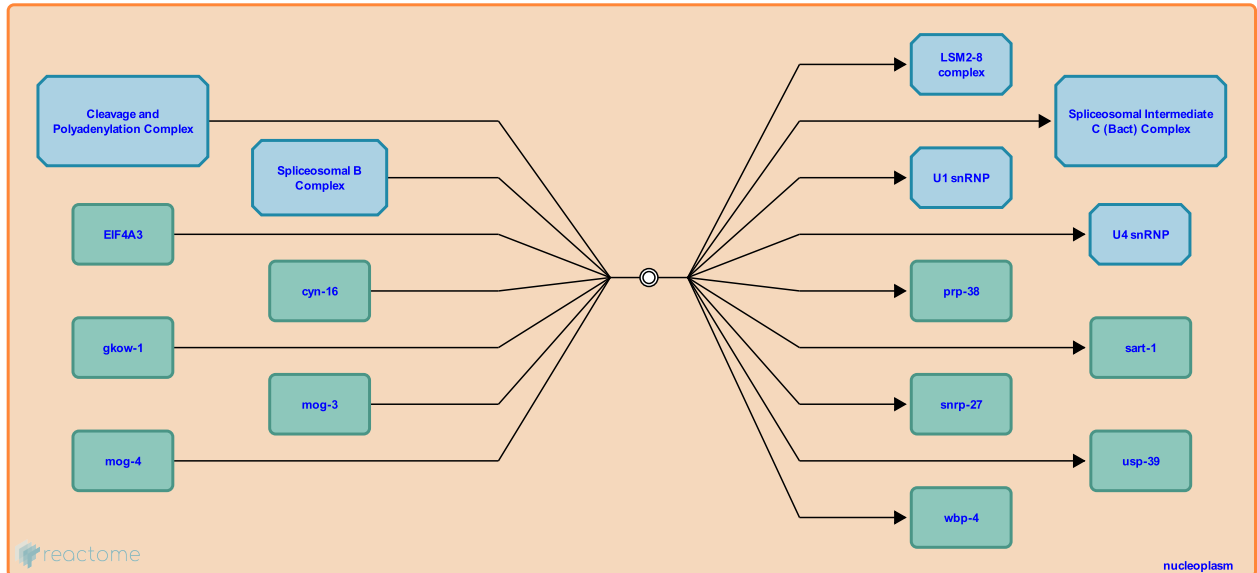
Location: mRNA Splicing - Major Pathway

Stable identifier: R-CEL-72130

Type: dissociation

Compartments: nucleoplasm

Inferred from: Formation of an intermediate Spliceosomal C (Bact) 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: [Formation of the Spliceosomal B Complex](#), [Formation of the Cleavage and Polyadenylation Complex](#)

Followed by: [Formation of the active Spliceosomal C \(B*\) complex](#)

Formation of the active Spliceosomal C (B*) complex ↗

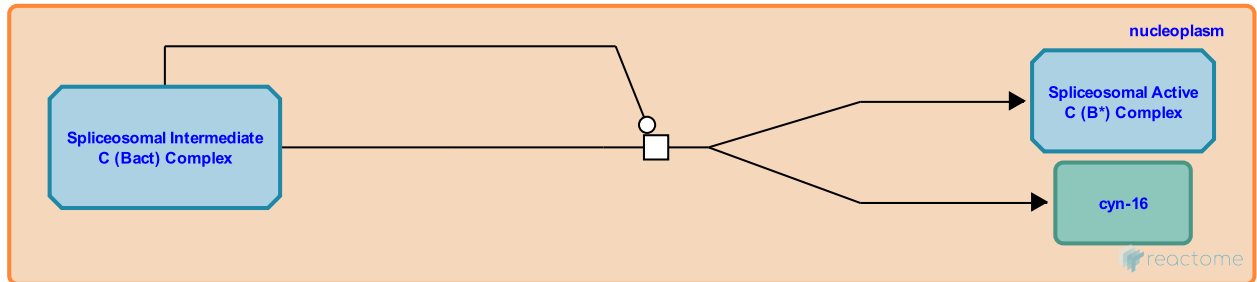
Location: [mRNA Splicing - Major Pathway](#)

Stable identifier: R-CEL-72139

Type: transition

Compartments: nucleoplasm

Inferred from: [Formation of the active Spliceosomal C \(B*\) 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: [Formation of an intermediate Spliceosomal C \(Bact\) complex](#)

Followed by: [Lariat Formation and 5'-Splice Site Cleavage](#)

Lariat Formation and 5'-Splice Site Cleavage ↗

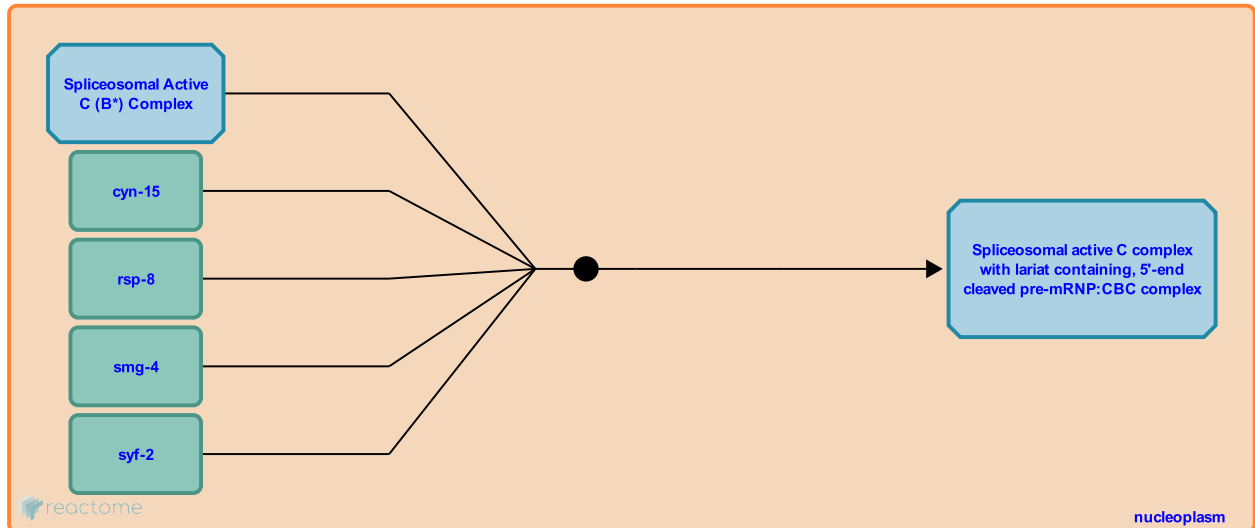
Location: mRNA Splicing - Major Pathway

Stable identifier: R-CEL-72143

Type: binding

Compartments: nucleoplasm

Inferred from: Lariat Formation and 5'-Splice Site Cleavage (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: [Formation of the active Spliceosomal C \(B*\) complex](#)

Followed by: [Formation of Exon Junction Complex](#)

Formation of Exon Junction Complex ↗

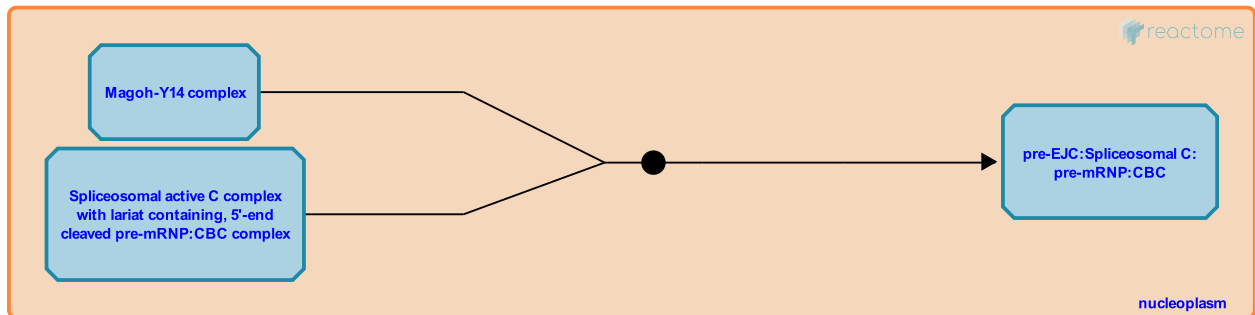
Location: [mRNA Splicing - Major Pathway](#)

Stable identifier: R-CEL-156661

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of Exon Junction 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: [Lariat Formation and 5'-Splice Site Cleavage](#)

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