Processing of Capped Intronless Pre-mRNA

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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.

Literature references

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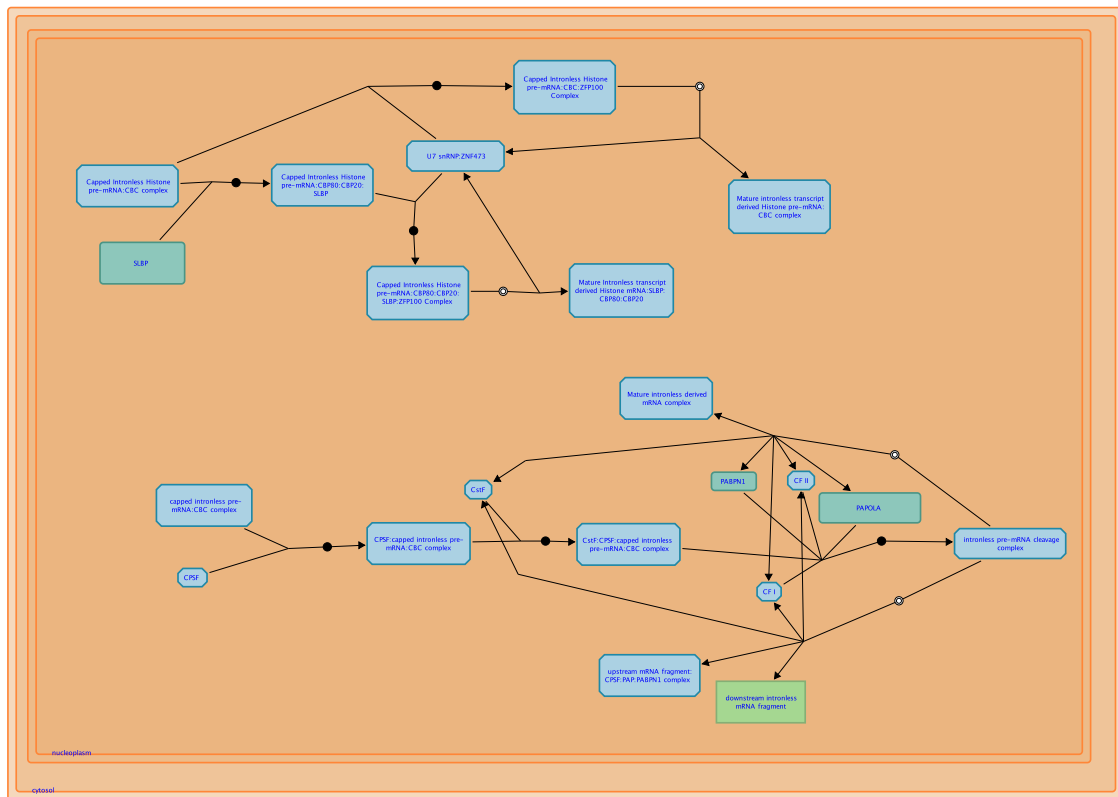
Reactome database release: 77

This document contains 4 pathways (see Table of Contents)

Processing of Capped Intronless Pre-mRNA ↗

Stable identifier: R-HSA-75067

Compartments: nucleoplasm

Co-transcriptional pre-mRNA splicing is not obligatory. Pre-mRNA splicing begins co-transcriptionally and often continues post-transcriptionally. Human genes contain an average of nine introns per gene, which cannot serve as splicing substrates until both 5' and 3' ends of each intron are synthesized. Thus the time that it takes for pol II to synthesize each intron defines a minimal time and distance along the gene in which splicing factors can be recruited. The time that it takes for pol II to reach the end of the gene defines the maximal time in which splicing could occur co-transcriptionally. Thus, the kinetics of transcription can affect the kinetics of splicing.

There are two classes of intronless pre-mRNAs (mRNAs expressed from genes that lack introns). The first class encodes the replication dependent histone mRNAs. These mRNAs have unique 3' ends that do not have a polyA tail. The replication dependent histone mRNAs in all metazoans, as well as Chlamydomonas and Volvox fall into this class.

The second class of mRNAs end in polyA tails, which are formed by a mechanism similar to that which poly-adenylate pre-mRNAs containing introns. In the intronless genes there is a different method of replacing the 3' splice site that activates polyadenylation.

Literature references

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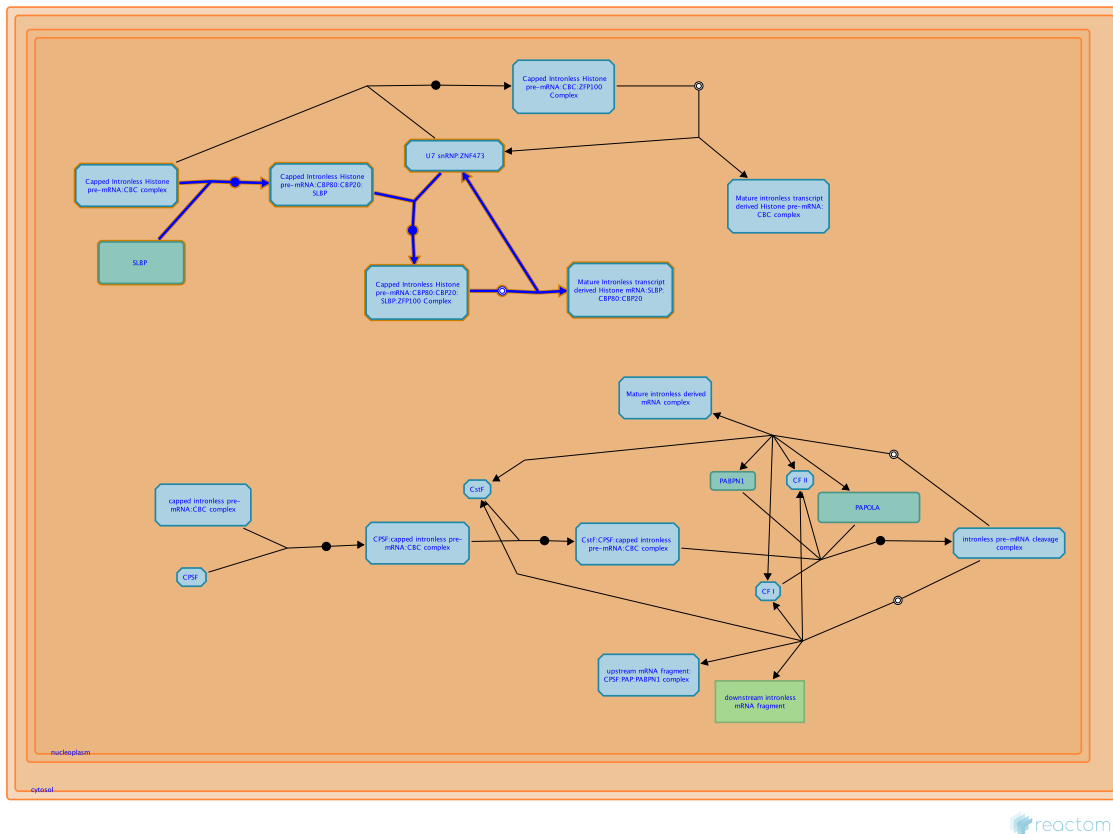
Editions

2003-08-22	Authored	Marzluff, WF.
2021-05-18	Edited	Joshi-Tope, G.

SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs ↗

Location: Processing of Capped Intronless Pre-mRNA

Stable identifier: R-HSA-77588

Compartments: nucleoplasm

There are two well-documented trans-acting factors required for histone pre-mRNA processing. These are:

1 Stem-loop binding protein (SLBP), also termed hairpin binding protein (HBP). This 32 kDa protein is likely the first protein that binds to the histone pre-mRNA as it is being transcribed.

The U7 snRNP. This particle contains the U7 snRNA, the smallest of the snRNAs which varies from 57-70 nts long depending on the species. The 5' end of U7 snRNA binds to a sequence 3' of the stemloop, termed the histone downstream element (HDE). There are a number of proteins found in the U7 snRNP. There are 7 Sm proteins, as are present in the spliceosomal snRNP. Five of these proteins are the same as ones found in the spliceosomal snRNPs and there are 2, Lsm10 and Lsm11 that are unique to U7 snRNP.

A third protein joins the U7 snRNP, ZFP100, a large zinc finger protein. ZFP100 interacts with SLBP bound to the histone pre-mRNA and with Lsm11 and likely plays a critical role in recruiting U7 snRNP to the histone pre-mRNA.

It should be noted that there must be other trans-acting factors, including the factor that catalyzes the cleavage reaction. The cleavage occurs in the presence of EDTA as does the cleavage reaction in poly-adenylation, it is likely that this reaction is catalyzed by a protein. There may well be additional proteins associated with U7 snRNP, and since under some conditions in vitro processing occurs in the absence of SLBP, it is possible that all of the other factors required for processing are associated with the active form of U7 snRNP.

Literature references

Harris, ME., Bohni, R., Schneiderman, MH., Ramamurthy, L., Schumperli, D., Marzluff, WF. (1991). Regulation of histone mRNA in the unperturbed cell cycle: evidence suggesting control at two posttranscriptional steps. *Mol Cell Biol, 11*, 2416-24. ↗

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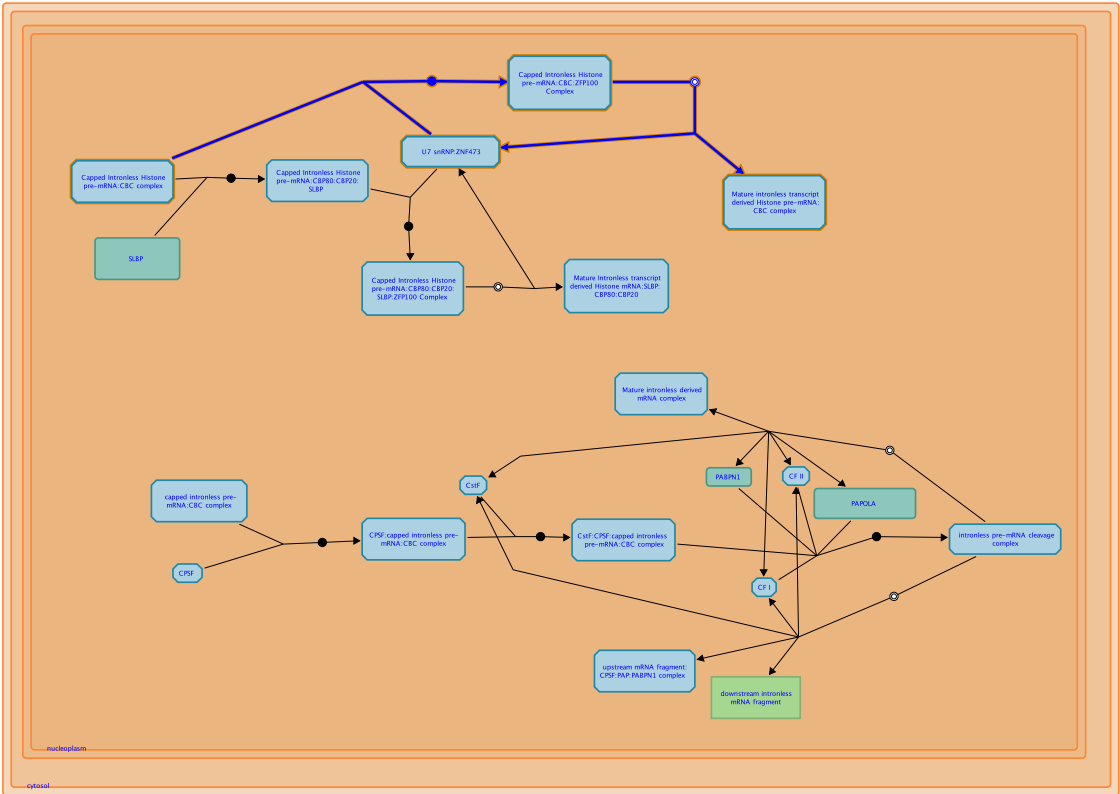
Editions

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SLBP independent Processing of Histone Pre-mRNAs ↗

Location: Processing of Capped Intronless Pre-mRNA

Stable identifier: R-HSA-111367

Compartments: nucleoplasm

This class of mRNAs is expressed from genes that lack introns yet the transcripts end in polyA tails. These tails are formed by a mechanism similar to that for pre-mRNAs containing introns. It is believed that there is a cis-element that replaces the 3' splice site that normally serves to activate polyadenylation of intron containing pre-mRNAs.
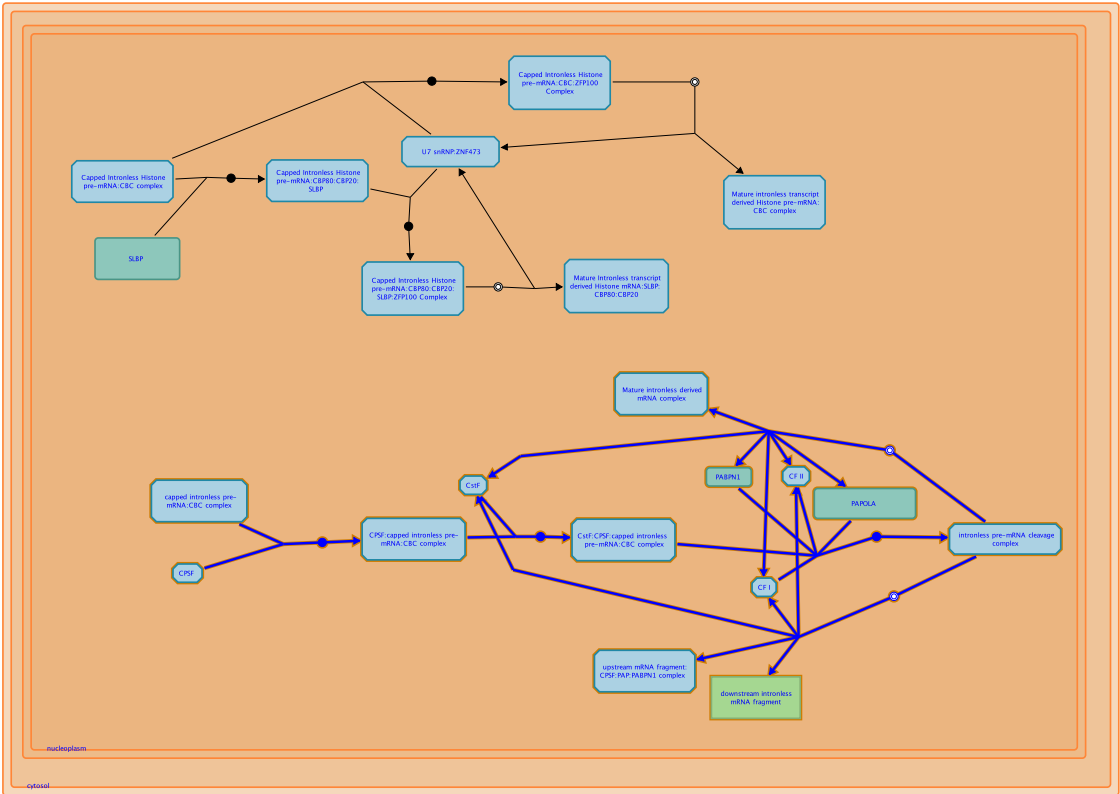
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Processing of Intronless Pre-mRNAs ↗

Location: Processing of Capped Intronless Pre-mRNA

Stable identifier: R-HSA-77595

Compartments: nucleoplasm

The 3' ends of eukaryotic mRNAs are generated by posttranscriptional processing of an extended primary transcript. For almost all RNAs, 3' processing consists of two steps: The mRNA is first cleaved at a particular phosphodiester bond downstream of the coding sequence. The upstream fragment then receives a poly(A) tail of approximately 250 adenylate residues whereas the downstream fragment is degraded. The two partial reactions are coupled so that reaction intermediates are usually undetectable. While 3' processing can be studied as an isolated event in vitro, it appears to be connected to transcription, splicing and transcription termination in vivo.

Literature references

Proudfoot, NJ., Furger, A., Dye, MJ. (2002). Integrating mRNA processing with transcription. *Cell, 108*, 501-12. ↗

Editions

2003-06-05	Authored	Wahle, E.
2021-05-18	Edited	Gillespie, ME.

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