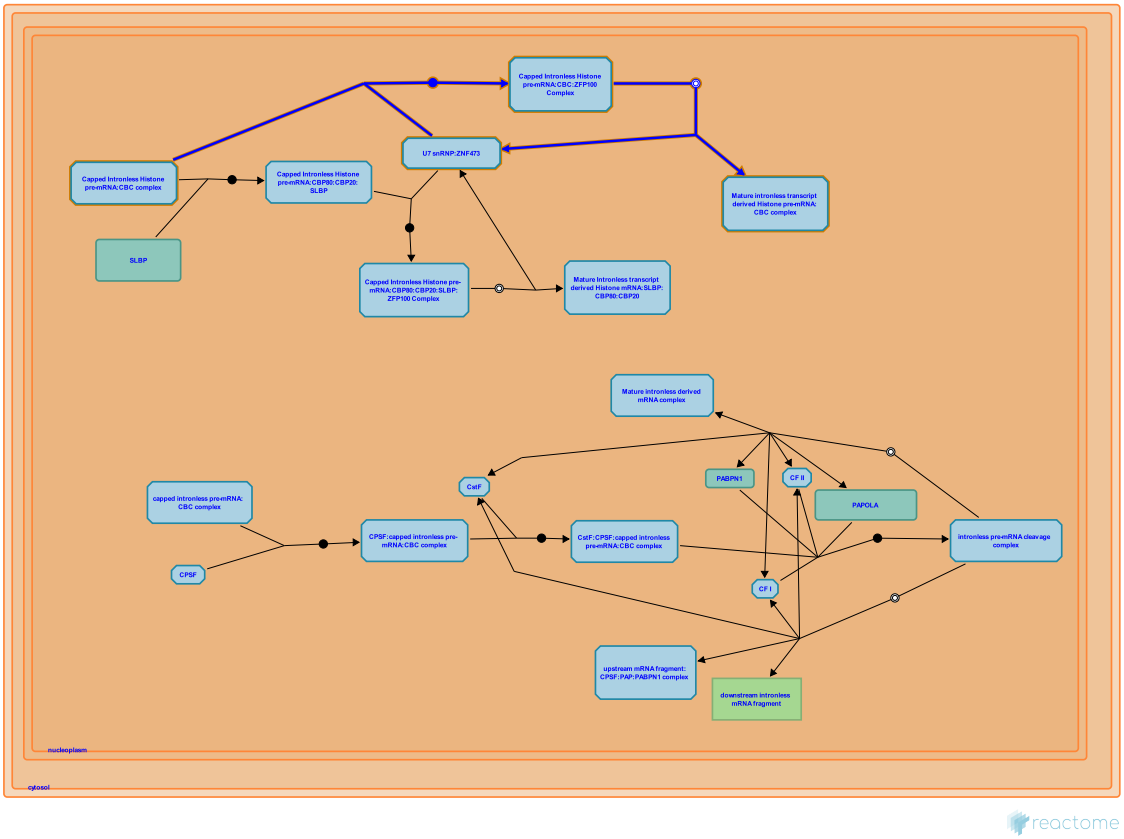
SLBP independent Processing of Histone Pre-mRNAs



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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.
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. ↗

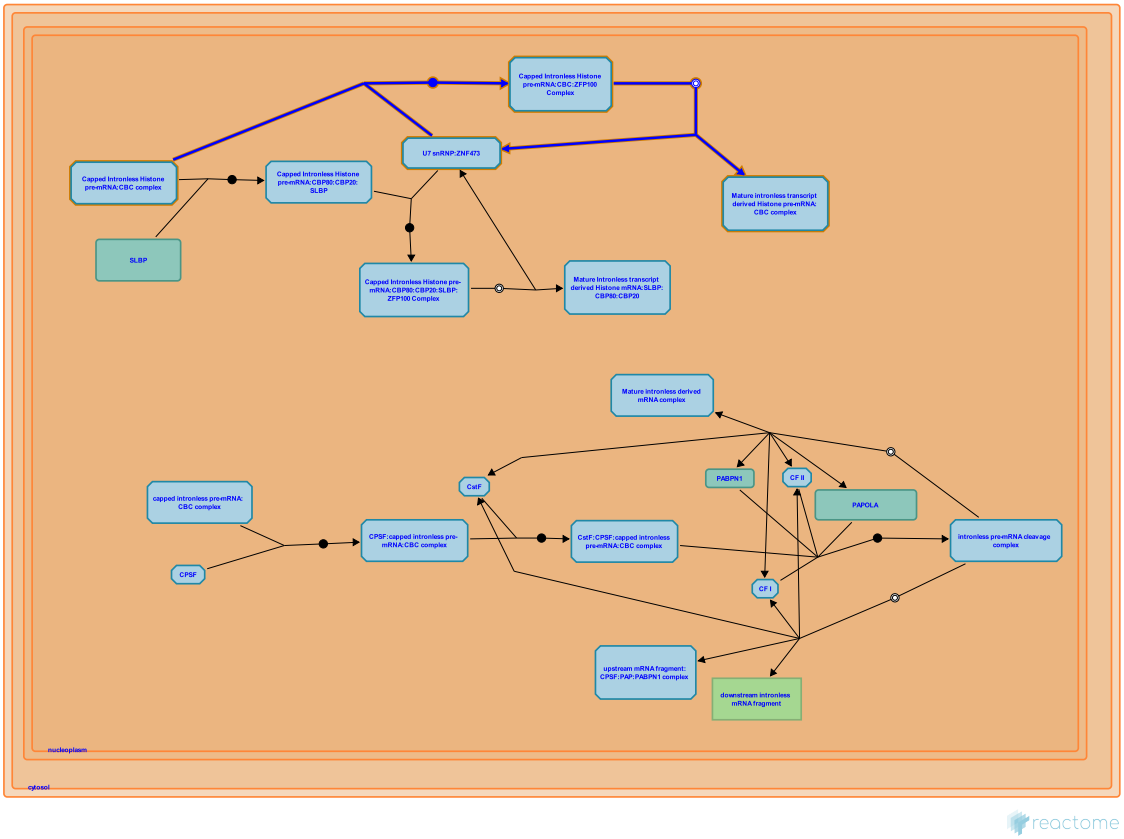
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

SLBP independent Processing of Histone Pre-mRNAs ↗

Stable identifier: R-HSA-111367

Compartments: nucleoplasm



reactome

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.

Editions

2003-08-22	Authored	Marzluff, WF.
2024-03-06	Edited	Gillespie, ME.

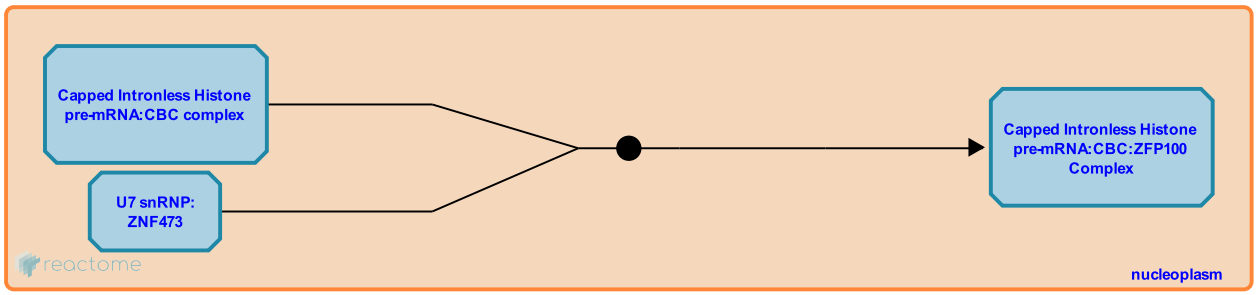
Recruitment of U7 snRNP:ZFP100 complex to the Histone Pre-mRNA ↗

Location: SLBP independent Processing of Histone Pre-mRNAs

Stable identifier: R-HSA-111438

Type: binding

Compartments: nucleoplasm



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.

Followed by: Cleavage of the 3'-end of the Histone Pre-mRNA

Editions

2003-08-22	Authored	Marzluff, WF.
2024-03-06	Edited	Gillespie, ME.

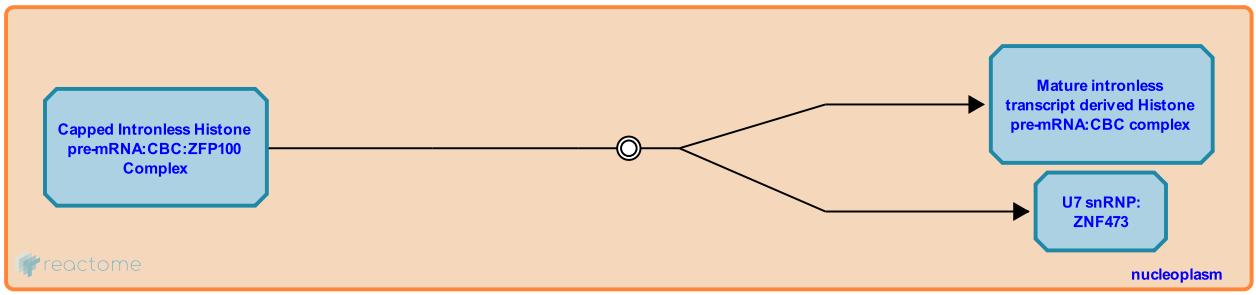
Cleavage of the 3'-end of the Histone Pre-mRNA ↗

Location: SLBP independent Processing of Histone Pre-mRNAs

Stable identifier: R-HSA-111437

Type: dissociation

Compartments: nucleoplasm



Processing is initiated once the U7 snRNP is loaded onto the pre-mRNA. The pre-mRNA HDE makes base-pairing contacts with the 5”² end of U7 snRNA. Binding of the U7 snRNP to the pre-mRNA is stabilized by interactions between a U7 snRNP protein, hZFP100 and other trans-acting factors, including the factor that catalyzes the cleavage reaction, which have yet to be defined. The cleavage occurs in the presence of EDTA as does the cleavage reaction in polyadenylation, it is likely that this reaction is catalyzed by a protein. There may well be additional proteins associated with the U7 snRNP, since the in vitro processing occurs in the absence of SLBP, it is possible that all the other factors required for processing are associated with the active form of the U7 snRNP.

Preceded by: Recruitment of U7 snRNP:ZFP100 complex to the Histone Pre-mRNA

Editions

2003-08-22	Authored	Marzluff, WF.
2024-03-06	Edited	Gillespie, ME.

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