

Formation of the Spliceosomal E complex

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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

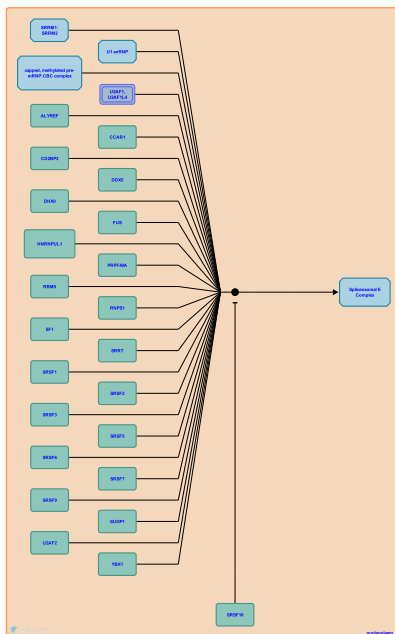
This document contains 1 reaction ([see Table of Contents](#))

Formation of the Spliceosomal E complex ↗

Stable identifier: R-HSA-72107

Type: binding

Compartments: nucleoplasm



Pre-mRNA transcripts become rapidly associated with many RNA-binding proteins, including hnRNP proteins, cap-binding proteins, SR proteins, etc; in the test tube this binding does not require splice sites or ATP. The E complex, or early complex, is the first detectable functional intermediate in spliceosome assembly *in vitro*. It is an ATP-independent complex. When a functional 5' splice site is present, it is bound by the U1 snRNP. The splicing factor U2AF (65 and 35 kDa subunits) binds to the polypyrimidine tract (Y)_n and the AG dinucleotide at the 3' splice site, respectively. SF1/mBBP binds to the branch site. Binding of many of these factors is cooperative; e.g., SR proteins and U2AF apparently interact with each other, facilitating their binding to the pre-mRNA. In the presence of ATP, the E complex is converted to the first ATP-dependent spliceosomal complex, namely the A complex.

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