Formation of the Spliceosomal B* 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


Reactome database release: 83

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DHX16 (homolog of yeast Prp2) hydrolyzes ATP in the Spliceosomal B* complex to form the Spliceosomal B* complex (Gencheva et al. 2010), possibly by pulling the intron to dissociate the RES complex and the SF3A and SF3B subcomplexes of the U2 snRNP from the spliceosome (Bessonov et al. 2010, Agafonov et al. 2011, Schmidt et al. 2014, Kastner et al. 2019). The intron branch point now docks near the 5’ splice site (Zhan et al. 2018), displacing RNF113A (homolog of yeast Cwc24) (Schmidt et al. 2014, Zhan et al. 2018). YJU2 and ISY1 bind and distort the helix of the branch point to fit the active site (Zhan et al. 2018). Prior to the transesterification reaction between the adenosine residue of the intron branch point and the 5’ splice site, the complex is called the Spliceosomal B* complex.

Components of the core exon junction complex (EJC) comprising EIF4A3, CASC3, MAGOH, and RBM8A are recruited to the spliceosome around this time (Kataoka and Dreyfuss 2004) by an interaction between CWC22 and EIF4A3 (Reichert et al. 2002, Alexandrov et al. 2012, Barbosa et al. 2012, Steckelberg et al. 2012, Busetto et al. 2020), though they may not yet bind RNA. CWC27 must be displaced in order for RBM8A (Y14) to bind (Busetto et al. 2020). Due to the position of CWC22 in the spliceosome, the EJC will be deposited on the 5’ exon about 20-24 nucleotides upstream of the 5’ splice site. The components and formation of the spliceosomal B* complex are partly inferred from the composition of the spliceosomal C complex (Jurica et al. 2002, Makarov et al. 2002, Rappsilber et al. 2002, Reichert et al. 2002, Bessonov et al. 2010, Agafonov et al. 2011, Schmidt et al. 2014, Zhan et al. 2018, Kastner et al. 2019).

**Literature references**


**Editions**

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