

Formation of meiotic single-stranded DNA invasion 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](#))

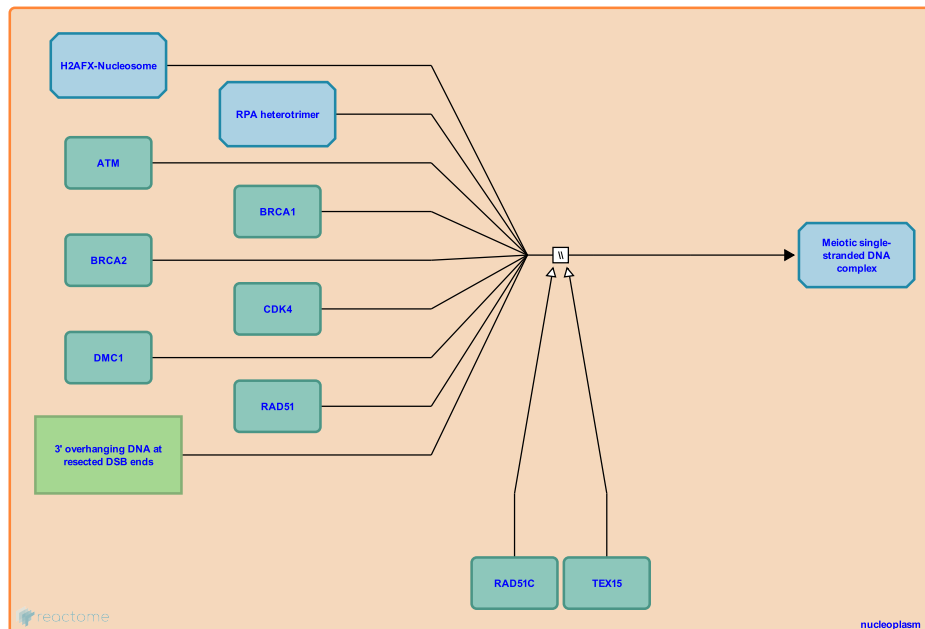
Formation of meiotic single-stranded DNA invasion complex ↗

Stable identifier: R-HSA-912503

Type: omitted

Compartments: nucleoplasm

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Two RecA homologs, RAD51 and the meiosis-specific DMC1, coat single-stranded 3' ends of DNA produced by resection of double-strand breaks (Barlow et al. 1997, Masson et al. 1999, Sehorn et al. 2004, Sheridan et al. 2008, Okorokov et al. 2010). RAD51 and DMC1 interact and colocalize to the same early recombination nodules (Masson et al. 1999). Knockouts of DMC1 abolish recombination and synapsis therefore RAD51 is not sufficient for recombination.

Immunocytology shows the RPA heterotrimer arrives at recombination nodules with or after RAD51 and DMC1 (Golub et al. 1999, Oliver-Bonet et al. 2005, Oliver-Bonet et al. 2007). (In mitotic recombination RPA precedes RAD51.)

BRCA1 and BRCA2 are found extensively distributed on synaptonemal complexes. Results from human cells and knockout mice indicate that BRCA2, RAD51C, and TEX15 participate in loading RAD51 and DMC1 onto single-stranded DNA (Thorslund et al. 2007). BRCA1 participates in loading RAD51 but not DMC1 (Scully et al. 1997).

The kinase ATM is also localized to double-strand breaks where it phosphorylates histone H2AX.

In human spermatocytes about 350 early recombination nodules form but only about 10% will continue on to make crossovers. The remaining 90% are believed to be resolved by synthesis-dependent strand annealing, which transfers short segments of DNA (about 0.2-2.0 kilobases) between homologs.

Literature references

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Editions

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