

SPO11 hydrolyzes DNA forming double-strand breaks

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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: 88

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

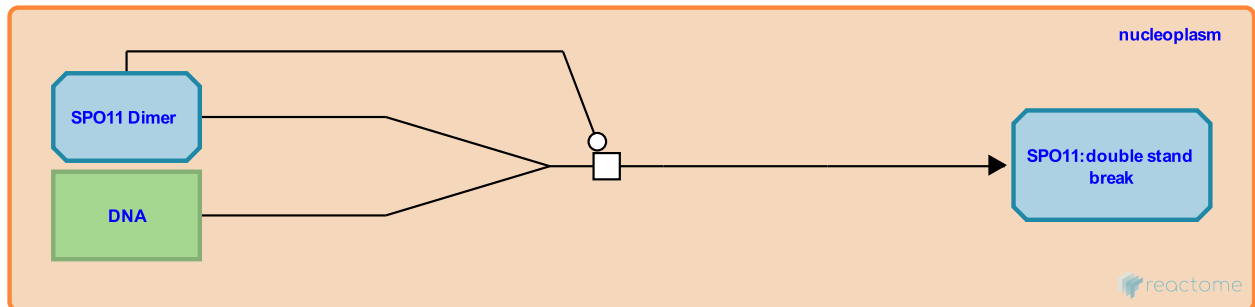
SPO11 hydrolyzes DNA forming double-strand breaks ↗

Stable identifier: R-HSA-912368

Type: transition

Compartments: nucleoplasm

Inferred from: [Formation of Double-strand Break in DNA by Spo11 \(Mus musculus\)](#)



The gene encoding SPO11 shares sequence similarity to TopoVI, a type II topoisomerase. SPO11 dimers cleave both strands of DNA. Each subunit of the dimer remains covalently attached to the 5' end of one strand of DNA via a phosphodiester linkage to a conserved tyrosine residue of SPO11. In addition to SPO11, work from budding yeast has shown a total of 7 proteins essential for double strand break formation. The mammalian ortholog of Mei4 (*S. cerevisiae*) as well as a mammalian-specific gene called Mei1 are essential to formation of meiotic double strand breaks.

Editions

2010-07-19	Authored, Edited	May, B.
2011-02-05	Reviewed	Schimenti, JC., Cohen, PE., Holloway, JK.
2011-02-25	Reviewed	Bolcun-Filas, E., Lyndaker, A., Strong, E.