

MRN complex binds DNA 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: 74

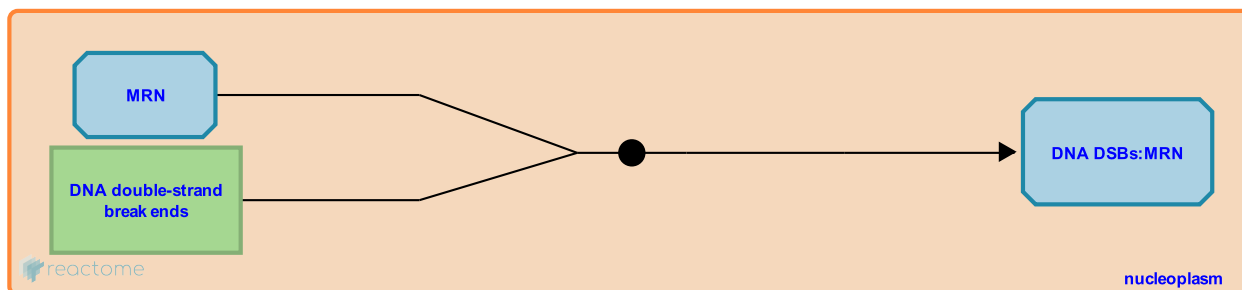
This document contains 1 reaction ([see Table of Contents](#))

MRN complex binds DNA double strand breaks [↗](#)

Stable identifier: R-HSA-3785768

Type: binding

Compartments: nucleoplasm



The MRN complex (MRE11A:RAD50:NBN) binds to DNA ends found at double strand breaks (DNA DSBs) (Lee and Paull 2005). In budding yeast, the Mre11:Rad50:Xrs2 complex, homologous to human MRN, rapidly localizes to DNA breaks (Shroff et al. 2004, Lisby et al. 2004).

Literature references

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Shroff, R., Arbel-Eden, A., Pilch, D., Ira, G., Bonner, WM., Petrini, JH. et al. (2004). Distribution and dynamics of chromatin modification induced by a defined DNA double-strand break. *Curr. Biol.*, 14, 1703-11. [↗](#)

Editions

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