

# BRCA1 is recruited to unsynapsed regions

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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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 70

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

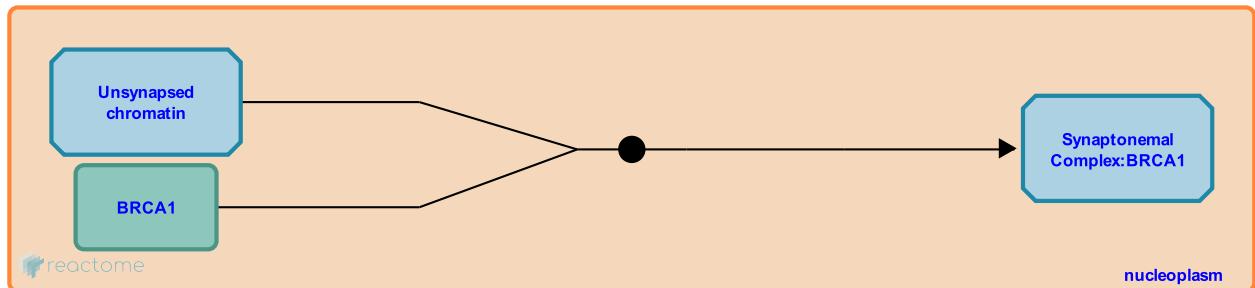
## BRCA1 is recruited to unsynapsed regions ↗

**Stable identifier:** R-HSA-912467

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [Recruitment of Brca1 to Unsynapsed Regions \(Mus musculus\)](#)



Unsynapsed regions of chromosomes are silenced during pachytene phase by a process called Meiotic Silencing of Unsynapsed Chromatin (MSUC) and, in the case of the X and Y chromosomes, Meiotic Sex Chromosome Inactivation (MSCI). Unsynapsed meiotic chromatin recruits BRCA1 (Scully et al. 1997, Garcia-Cruz et al. 2009). In mouse, the recruitment requires SYCP3 of axial elements of the synaptonemal complex, which may remain exposed in unsynapsed regions.

### Literature references

Scully, R., Chen, J., Plug, A., Xiao, Y., Weaver, D., Feunteun, J. et al. (1997). Association of BRCA1 with Rad51 in mitotic and meiotic cells. *Cell*, 88, 265-75. ↗

Garcia-Cruz, R., Roig, I., Robles, P., Scherthan, H., Garcia Caldés, M. (2009). ATR, BRCA1 and gammaH2AX localize to unsynapsed chromosomes at the pachytene stage in human oocytes. *Reprod Biomed Online*, 18, 37-44. ↗

### Editions

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