BRCA1 forms a heterodimer with BARD1

Borowiec, JA., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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: 73

This document contains 1 reaction (see Table of Contents)
BRCA1 forms a heterodimer with BARD1

**Stable identifier:** R-HSA-5659781

**Type:** binding

**Compartments:** nucleoplasm

BRCA1 and BARD1 form a stable heterodimer through interaction of their RING domain-containing N-termini (Wu et al. 1996, Brzovic et al. 2001). Both BRCA1 and BARD1 have a RING domain in their N-terminal regions and tandem BRCT motifs at their C termini. The central region of BARD1 contains ankyrin repeats (Wu et al. 1996). Formation of BRCA1:BARD1 heterodimers is necessary for the repair of double strand DNA breaks by homologous recombination (Westermark et al. 2003, Laufer et al. 2007) and for the function of BRCA1 in tumor suppression (Shakya et al. 2008) and normal development (McCarthy et al. 2003). Tumorigenic BRCA1 and BARD1 mutations that abolish formation of BRCA1:BARD1 heterodimers have been reported (Wu et al. 1996, Brzovic et al. 2001, Morris et al. 2002, Caleca et al. 2014).

**Literature references**


**Editions**

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