BRCA1 forms a heterodimer with BARD1

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03/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

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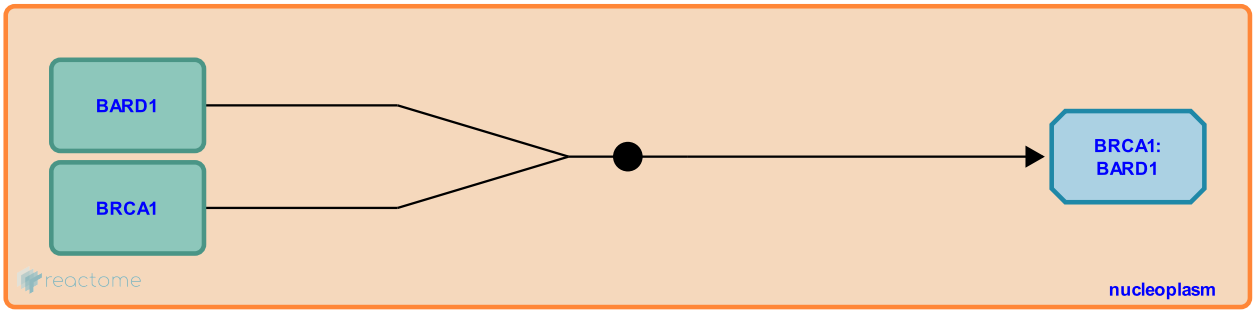
Stable identifier: R-HSA-5659781

Type: binding

Compartments: nucleoplasm



BRCA1 and BARD1 form a stable heterodimer through an interaction between sequences encompassing their N-terminal RING domains (Wu et al. 1996, Brzovic et al. 2001). In addition to the RING domains, BRCA1 and BARD1 both have 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), BRCA1-mediated tumor suppression (Shakya et al. 2008) and normal development (McCarthy et al. 2003). Tumorigenic BRCA1 mutations that abolish the formation of BRCA1:BARD1 heterodimers have been reported (Wu et al. 1996, Brzovic et al. 2001).

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Editions

2015-05-12	Authored, Edited	Orlic-Milacic, M.
2015-06-12	Reviewed	Borowiec, JA.
2020-11-04	Reviewed	Baer, RJ.