ERCC1:XPF cleaves flaps generated by SSA

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27/02/2021

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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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. ↗

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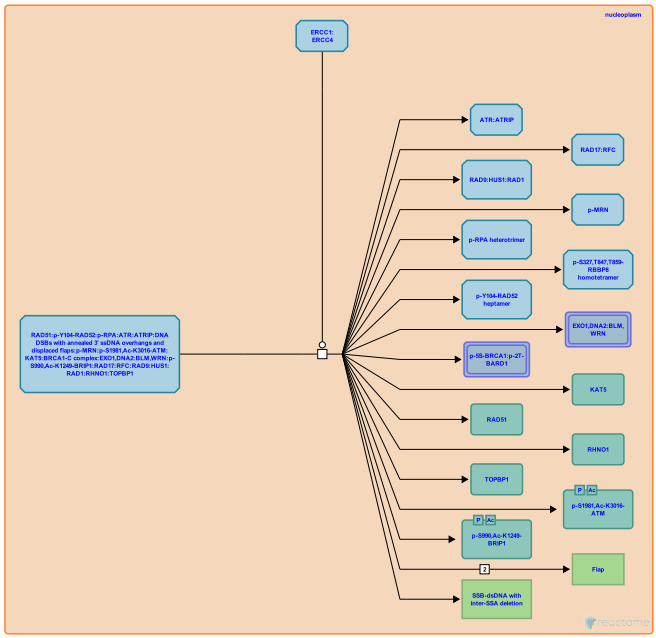
Stable identifier: R-HSA-5686657

Type: transition

Compartments: nucleoplasm



The endonuclease complex ERCC1:XPF (ERCC1:ERCC4) is recruited to single strand annealing (SSA) sites of DNA double strand break (DSB) repair through direct interaction between XPF (ERCC4) and RAD52 (Motycka et al. 2004). ERCC1:XPF cleaves the ssDNA flaps generated by displacement of non-complementary 3' parts of 3' ssDNA overhangs during RAD52-mediated annealing. The enzymatic activity of ERCC1:XPF is necessary for the completion of SSA (Motycka et al. 2004, Al-Minawi et al. 2008, Ahmad et al. 2008).

Literature references

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Editions

2015-05-12	Authored, Edited	Orlic-Milacic, M.
2015-06-12	Reviewed	Borowiec, JA.