

# ERCC1:XPF cleaves flaps generated by SSA

Borowiec, JA., Orlic-Milacic, M.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

19/05/2024

## 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

- 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: 88

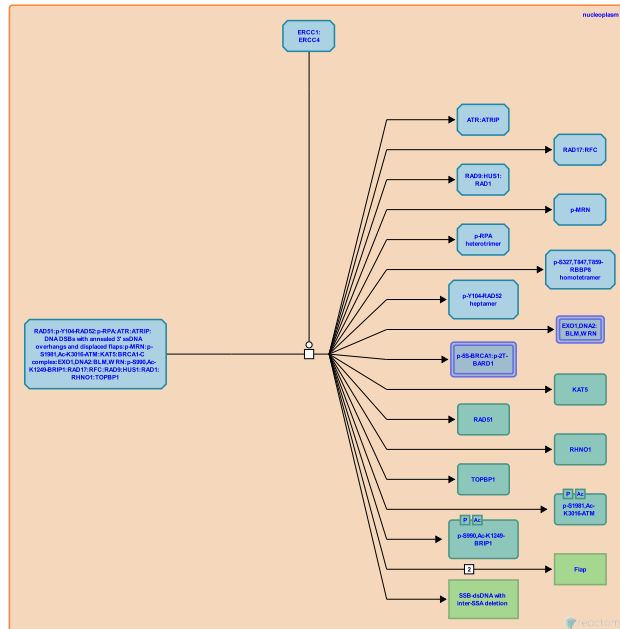
This document contains 1 reaction ([see Table of Contents](#))

## ERCC1:XPf cleaves flaps generated by SSA [↗](#)

**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

van Drunen, E., Ahmad, A., Beverloo, HB., Niedernhofer, LJ., Robinson, AR., Weisberg, DB. et al. (2008). ERCC1-XPf endonuclease facilitates DNA double-strand break repair. *Mol. Cell. Biol.*, 28, 5082-92. [↗](#)

Saleh-Gohari, N., Helleday, T., Al-Minawi, AZ. (2008). The ERCC1/XPf endonuclease is required for efficient single-strand annealing and gene conversion in mammalian cells. *Nucleic Acids Res.*, 36, 1-9. [↗](#)

Bessho, T., Post, SM., Motycka, TA., Sung, P., Tomkinson, AE. (2004). Physical and functional interaction between the XPf/ERCC1 endonuclease and hRad52. *J. Biol. Chem.*, 279, 13634-9. [↗](#)

### Editions

2015-05-12

Authored, Edited

Orlic-Milacic, M.

2015-06-12

Reviewed

Borowiec, JA.