

# NEIL1 cleaves FapyG from damaged DNA

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09/05/2024

## 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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- 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. [↗](#)
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Reactome database release: 88

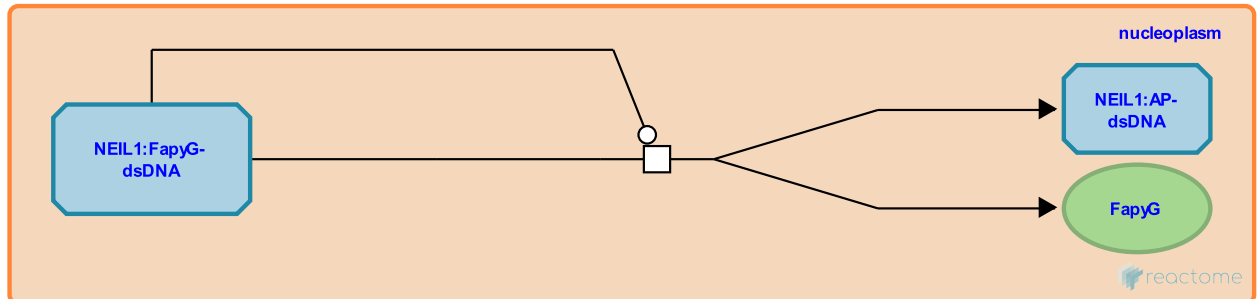
This document contains 1 reaction ([see Table of Contents](#))

## NEIL1 cleaves FapyG from damaged DNA ↗

**Stable identifier:** R-HSA-5649664

**Type:** transition

**Compartments:** nucleoplasm



NEIL1 acts as a DNA glycosylase to remove FapyG from damaged DNA, producing an AP (apurinic/apyrimidinic) site (Hazra et al. 2002).

### Literature references

Dizdaroglu, M., Imhoff, B., Kow, YW., Mitra, S., Izumi, T., Jaruga, P. et al. (2002). Identification and characterization of a human DNA glycosylase for repair of modified bases in oxidatively damaged DNA. *Proc. Natl. Acad. Sci. U.S.A.*, 99, 3523-8. ↗

### Editions

2014-12-04	Authored, Edited	Orlic-Milacic, M.
2014-12-22	Reviewed	Borowiec, JA.
2019-01-03	Reviewed	Sampath, H.
2019-01-05	Edited	Orlic-Milacic, M.