

NEIL3 cleaves 5-guanidinohydantoin (Gh) from damaged telomeric DNA

Orlic-Milacic, M., Zhou, J.

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](#).

06/05/2024

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

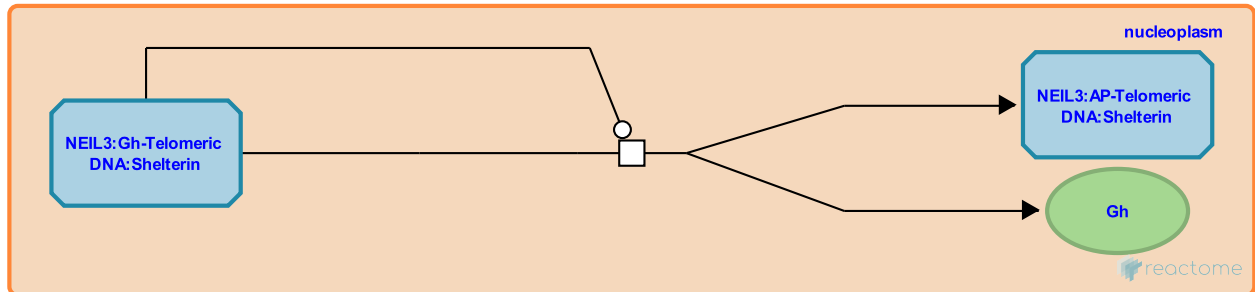
This document contains 1 reaction ([see Table of Contents](#))

NEIL3 cleaves 5-guanidinohydantoin (Gh) from damaged telomeric DNA [↗](#)

Stable identifier: R-HSA-9629216

Type: transition

Compartments: nucleoplasm



NEIL3 cleaves oxidatively damaged guanine, in the form of 5-guanidinohydantoin (Gh), from telomeric DNA, creating an abasic (AP) site. NEIL3 expression is highest in late S phase, overlapping with telomeric DNA synthesis. NEIL3 localization at telomeres increases in response to oxidative stress. NEIL3 knockdown results in telomere dysfunction, which can lead to metaphase arrest or increased DNA bridging during anaphase. NEIL3 interacts with enzymes involved in PCNA-dependent long patch base excision repair (BER) of AP sites, but the exact mechanism of NEIL3-mediated long patch BER of damaged telomeric DNA has not been elucidated (Zhou et al. 2017).

Besides telomeres, NEIL3 is also enriched in replisomes in the S phase of the cell cycle, co-localizing with RPA in replication foci (Bjoras et al. 2017).

Expression of the NEIL3 gene in the S phase may be induced by E2F transcription factors, as the NEIL3 promoter contains E2F binding elements (Neurauter et al. 2012).

Literature references

Chan, J., Opresko, PL., Lambelé, M., Yusufzai, T., Wallace, SS., Stumpff, J. et al. (2017). NEIL3 Repairs Telomere Damage during S Phase to Secure Chromosome Segregation at Mitosis. *Cell Rep*, 20, 2044-2056. [↗](#)

Editions

2019-01-05	Authored	Orlic-Milacic, M.
2019-02-11	Reviewed	Zhou, J.
2019-02-12	Edited	Orlic-Milacic, M.