

NEIL3 D132V does not cleave 5-guanidino-hydantoin (Gh)

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses).

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](#))

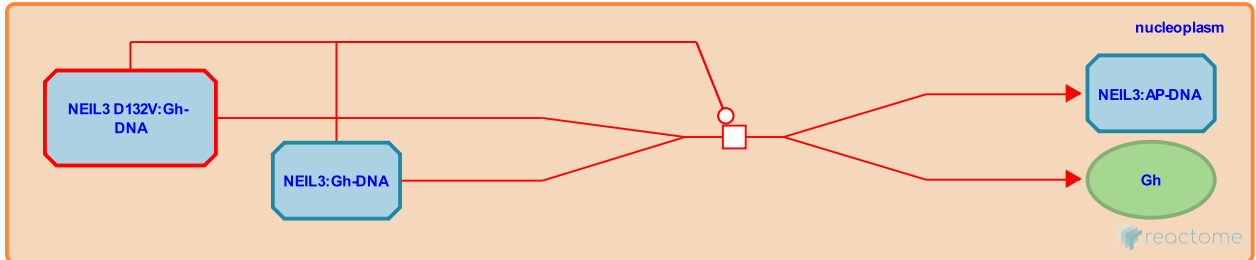
NEIL3 D132V does not cleave 5-guanidinohydantoin (Gh) ↗

Stable identifier: R-HSA-9629245

Type: transition

Compartments: nucleoplasm

Diseases: autoimmune hypersensitivity disease



NEIL3 D132V is a NEIL3 disease variant caused by a missense mutation that results in the substitution of aspartic acid residue (D) at position 132 to valine (V). NEIL3 D132V is unable to cleave 5-guanidinohydantoin (Gh) from oxidatively damaged DNA. Individuals harbouring a homozygous NEIL3 D132V mutation are predisposed to development of autoimmune diseases (Massaad et al. 2016). Primary fibroblasts from a patient with a NEIL3 D132V homozygous mutation show an increase in telomere loss compared to control wild type fibroblasts derived from the patient's healthy sibling (Zhou et al. 2017).

Literature references

Chou, J., Megarbane, A., Ohsumi, TK., Jabara, H., Geha, RS., Al-Herz, W. et al. (2016). Deficiency of base excision repair enzyme NEIL3 drives increased predisposition to autoimmunity. *J. Clin. Invest.*, 126, 4219-4236. ↗

Editions

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