

Resource Summary Report

Generated by T1D on Sep 20, 2026

mapDamage

RRID:SCR_001240

Type: Tool

Proper Citation

mapDamage (RRID:SCR_001240)

Resource Information

URL: <http://ginolhac.github.io/mapDamage/>

Proper Citation: mapDamage (RRID:SCR_001240)

Description: Software for tracking and quantifying DNA damage patterns among ancient DNA sequencing reads generated by Next-Generation Sequencing platforms.

Abbreviations: mapDamage

Synonyms: mapDamage 2.0, mapDamage: tracking and quantifying damage patterns in ancient DNA sequences, mapDamage2.0

Resource Type: software resource

Defining Citation: [PMID:23613487](#), [PMID:21659319](#), [DOI:10.1093/bioinformatics/btt193](#)

Keywords: python, r, illumina, windows, perl, dna damage, dna sequencing, next-generation sequencing, dna, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: mapDamage

Resource ID: SCR_001240

Alternate IDs: OMICS_02099, biotools:mapdamage

Alternate URLs: <https://bio.tools/mapdamage>,
<https://sources.debian.org/src/mapdamage/>

License: MIT License

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260919T194937+0000

Ratings and Alerts

No rating or validation information has been found for mapDamage.

No alerts have been found for mapDamage.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 395 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Miranda I, et al. (2026) Balanced polymorphism underlies long-standing adaptation for seasonal camouflage in the least weasel. *Communications biology*, 9(1).

Bujalska B, et al. (2026) Biogeographic history of the Late Pleistocene and Holocene European small hamsters (subfamily Cricetinae). *Scientific reports*, 16(1), 4145.

Zicos MH, et al. (2026) Megaherbivore coprolite DNA: yields and comparison of three ancient DNA extraction protocols on coprolites of giant ground sloth *Mylodon darwini*. *PeerJ*, 14, e21009.

Köseler A, et al. (2026) Integrating Osteology and Ancient DNA: Cranial Variation, Hemoglobin S, and Paternal Lineage in a Roman-Period Individual from Anatolia. *Life (Basel, Switzerland)*, 16(6).

Zhao X, et al. (2026) Tracing bronze to iron age population dynamics in Northwest Xinjiang using ancient time-series genomic data. *Genome biology*, 27(1), 33.

Liang XY, et al. (2026) Ancient mitogenomes reveal the genetic relationship among extinct and extant water buffaloes. *iScience*, 29(7), 116354.

Kovács B, et al. (2026) Genetic identification of Árpád Dynasty members from the ossuary of the Royal Basilica at Székesfehérvár. *iScience*, 29(7), 116365.

McFarland LN, et al. (2026) The dilution effect of stocking and the loss of wildness among North American mallards. *Current biology : CB*.

Zhou Y, et al. (2026) Ancient genomes from the Qing Dynasty reveal unbroken genetic continuity in China's Central Plains. *Molecular biology and evolution*, 43(1).

Xu J, et al. (2026) sedimix: a workflow for the analysis of hominin nuclear DNA sequences from sediments. *Bioinformatics (Oxford, England)*, 42(2).

Wang X, et al. (2026) Population structure and domestication history of the Javan banteng. *Current biology : CB*, 36(2), 458.

Dwivedi N, et al. (2026) Combining Population Genomics With Ancient DNA to Understand Island Colonisation History of the Madagascar Turtle Dove. *Molecular ecology*, 35(6), e70299.

Ochoa A, et al. (2026) Ancient DNA analyses of remains of the Medici family (16th century) provide insights into the genetic variation of *Plasmodium falciparum*. *iScience*, 29(7), 116371.

Bongers JL, et al. (2026) Ancient DNA reveals a family ossuary and long-distance migration on the Pacific coast before the Inca Empire. *Nature communications*, 17(1).

Rocha-Méndez A, et al. (2026) Eemian palaeogenetics demonstrates loss of diversity in modern fallow deer (*Dama dama*). *iScience*, 29(6), 116204.

Guellil M, et al. (2026) Tracing 2500 years of human betaherpesvirus 6A and 6B diversity through ancient DNA. *Science advances*, 12(1), eadx5460.

Han Y, et al. (2026) The late arrival of domestic cats in China via the Silk Road after 3,500 years of human-leopard cat commensalism. *Cell genomics*, 6(1), 101099.

Moon H, et al. (2026) Ancient genomes reveal an extensive kinship network and endogamy in a Three-Kingdoms period society in Korea. *Science advances*, 12(15), eady8614.

Yazigi JB, et al. (2026) Oncogenic HPV types identified in Paleolithic and Chalcolithic human genome sequencing data from Ust'-Ishim and Ötzi. *Scientific reports*, 16(1).

Lin J, et al. (2026) Mapping the Genomic Limits of De-Extinction in the Face of Ancient DNA Degradation. *Genome biology and evolution*, 18(1).