Resource Summary Report

Generated by NIF on Sep 15, 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: 20260912T195521+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 NIF .

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 darwinii. 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).