

Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 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: 20260801T190135+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 363 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Tang J, et al. (2026) Social Stratification Without Genetic Differentiation at the Xisima Site in the Late Shang Dynasty. *Molecular biology and evolution*, 43(1).

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

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Gilardet A, et al. (2025) A High-Throughput Ancient DNA Extraction Method for Large-Scale Sample Screening. *Molecular ecology resources*, 25(4), e14077.

Heinrich F, et al. (2025) Genomic analysis of three medieval parchments from German monasteries. *Scientific reports*, 15(1), 3156.

Kim J, et al. (2025) Dokdo sea lion *Zalophus japonicus* genome reveals its evolutionary trajectory before extinction. *BMC biology*, 23(1), 234.

Llamas B, et al. (2025) Coexistence, Extinction and Survival-The Evolutionary History of Bison Species in Western Eurasia. *Global change biology*, 31(8), e70354.

Garcia-Erill G, et al. (2025) Genomes of critically endangered saola are shaped by population structure and purging. *Cell*, 188(12), 3102.

Campbell MA, et al. (2025) Using sedimentary ancient DNA in coastal and marine contexts to explore past human-environmental interactions in Australia. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1930), 20240032.

Gwee CY, et al. (2025) Reconciling Gene Tree Discordance and Biogeography in European Crows. *Molecular ecology*, 34(10), e17764.

Bretos Ezcurra M, et al. (2025) Genomic insights from a final Bronze Age community buried in a collective tumulus in an Urnfield settlement in Northeastern Iberia.

Communications biology, 8(1), 1299.

Bandyopadhyay E, et al. (2025) Dynamic human admixture histories over the past ~1300 years at the northern Himalayan frontier. *Science advances*, 11(44), eadu9625.

Tommasi A, et al. (2025) Fifteen millennia of human mitogenome evolution in Sicily. *Science advances*, 11(46), eady1674.

O'Hare C, et al. (2025) Palaeogenomics suggest domesticated camelid herding and wild camelid hunting in early pastoralist societies in the Atacama Desert. *Nature communications*, 16(1), 11007.

Gelabert P, et al. (2025) A sedimentary ancient DNA perspective on human and carnivore persistence through the Late Pleistocene in El Mirón Cave, Spain. *Nature communications*, 16(1), 107.

Wu X, et al. (2025) Ancient genomes reveal the genetic structure and population interaction in the Central Plains of China during the Eastern Zhou Period. *Frontiers in microbiology*, 16, 1602625.

Koptekin D, et al. (2025) Pre-processing of paleogenomes: mitigating reference bias and postmortem damage in ancient genome data. *Genome biology*, 26(1), 6.

Ewers C, et al. (2025) Museomics of an extinct European flat oyster population. *Scientific reports*, 15(1), 13906.

Wang J, et al. (2025) Ancient DNA reveals a two-clanned matrilineal community in Neolithic China. *Nature*, 643(8074), 1304.

Grasso G, et al. (2025) Ancient Microbiomes as Mirrored by DNA Extracted From Century-Old Herbarium Plants and Associated Soil. *Molecular ecology resources*, 25(7), e14122.