

Resource Summary Report

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leeHom

RRID:SCR_002710

Type: Tool

Proper Citation

leeHom (RRID:SCR_002710)

Resource Information

URL: <https://github.com/grenaud/leeHom>

Proper Citation: leeHom (RRID:SCR_002710)

Description: Software program for the Bayesian reconstruction of ancient DNA fragments. The algorithm removes the adaptors and reconstructs the original DNA sequences using a Bayesian maximum a posteriori probability approach.

Resource Type: software resource

Defining Citation: [PMID:25100869](#)

Keywords: standalone software, illumina, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: leeHom

Resource ID: SCR_002710

Alternate IDs: biotools:leehom, OMICS_05254

Alternate URLs: <https://bio.tools/leehom>

License: GNU General Public License, v3

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260801T190214+0000

Ratings and Alerts

No rating or validation information has been found for leeHom.

No alerts have been found for leeHom.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Liu J, et al. (2025) East Asian Gene flow bridged by northern coastal populations over past 6000 years. *Nature communications*, 16(1), 1322.

Pigott EM, et al. (2025) A new late Neanderthal from Crimea reveals long-distance connections across Eurasia. *Proceedings of the National Academy of Sciences of the United States of America*, 122(45), e2518974122.

Guo Y, et al. (2025) A haplotype-based evolutionary history of barley domestication. *Nature*, 647(8090), 680.

Kutanan W, et al. (2025) Maternal genetic origin of Chao Lay coastal maritime populations from Thailand. *BMC biology*, 23(1), 146.

Liu S, et al. (2025) Mitogenomes of museum specimens provide new insight into species classification and recently reduced diversity of highly endangered *Nomascus gibbons*. *Integrative zoology*, 20(3), 674.

S??mer AP, et al. (2025) Earliest modern human genomes constrain timing of Neanderthal admixture. *Nature*, 638(8051), 711.

Fu Q, et al. (2025) Denisovan mitochondrial DNA from dental calculus of the >146,000-year-old Harbin cranium. *Cell*, 188(15), 3919.

Ran J, et al. (2025) Ancient genomes reveal basal Asian ancestries and dynamic population interactions over time on the southern Tibetan Plateau. *iScience*, 28(11), 113676.

Zhang M, et al. (2024) Ancient Mitogenomes Reveal the Maternal Genetic History of East Asian Dogs. *Molecular biology and evolution*, 41(4).

Michel M, et al. (2024) Ancient *Plasmodium* genomes shed light on the history of human malaria. *Nature*, 631(8019), 125.

Liu Y, et al. (2024) Bronze Age cheese reveals human-*Lactobacillus* interactions over evolutionary history. *Cell*, 187(21), 5891.

Bai F, et al. (2024) Ancient genomes revealed the complex human interactions of the ancient western Tibetans. *Current biology : CB*, 34(12), 2594.

Wang H, et al. (2023) Human genetic history on the Tibetan Plateau in the past 5100 years. *Science advances*, 9(11), eadd5582.

Essel E, et al. (2023) Ancient human DNA recovered from a Palaeolithic pendant. *Nature*, 618(7964), 328.

Lien A, et al. (2023) Benchmarking software tools for trimming adapters and merging next-generation sequencing data for ancient DNA. *Frontiers in bioinformatics*, 3, 1260486.

Woravatin W, et al. (2023) South Asian maternal and paternal lineages in southern Thailand and the role of sex-biased admixture. *PloS one*, 18(9), e0291547.

Diaz Quiroz JF, et al. (2023) Development of a selection assay for small guide RNAs that drive efficient site-directed RNA editing. *Nucleic acids research*, 51(7), e41.

Yilmaz F, et al. (2023) Ancient AMY1 gene duplications primed the amylase locus for adaptive evolution upon the onset of agriculture. *bioRxiv : the preprint server for biology*.

Irie N, et al. (2023) DMRT1 regulates human germline commitment. *Nature cell biology*, 25(10), 1439.

Cohen P, et al. (2023) Ancient DNA from a lost Negev Highlands desert grape reveals a Late Antiquity wine lineage. *Proceedings of the National Academy of Sciences of the United States of America*, 120(17), e2213563120.