

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

AdapterRemoval

RRID:SCR_011834

Type: Tool

Proper Citation

AdapterRemoval (RRID:SCR_011834)

Resource Information

URL: <https://github.com/MikkelSchubert/adapterremoval>

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Description: Software program to remove residual adapter sequences from next generation sequencing reads. Used for cleaning of next-generation sequencing reads. AdapterRemoval v2 introduces improvements in throughput, through use of single instruction, multiple data (SIMD; SSE1 and SSE2) instructions and multi-threading support; handles datasets containing reads or read-pairs with different adapters or adapter pairs; provides simultaneous demultiplexing and adapter trimming; has ability to reconstruct adapter sequences from paired-end reads for poorly documented data sets; provides native gzip and bzip2 support.

Synonyms: AdapterRemoval v2

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:22748135](#), [PMID:26868221](#), [DOI:10.1186/s13104-016-1900-2](#)

Keywords: cleaning of next-generation sequencing reads, remove residual adapter sequences, adapter, sequence, residual, next generation sequencing reads,

Funding: Danish Council for Independent Research ;
Danish National Research Foundation ;
Lundbeck Foundation Grant ;
Marie Curie International Outgoing Fellowship within the 7th European Community Framework Programme

Availability: Free, Available for download, Freely available

Resource Name: AdapterRemoval

Resource ID: SCR_011834

Alternate IDs: OMICS_01081

Alternate URLs: <https://sources.debian.org/src/adapterremoval/>

Old URLs: <http://code.google.com/p/adapterremoval/>,
<https://github.com/slindgreen/AdapterRemoval>,
<https://sources.debian.org/src/adapterremoval/>

License: Apache License

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T195740+0000

Ratings and Alerts

No rating or validation information has been found for AdapterRemoval.

No alerts have been found for AdapterRemoval.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 773 mentions in open access literature.

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

Jakobsson M, et al. (2026) Homo??sapiens-specific evolution unveiled by ancient southern African genomes. Nature, 650(8100), 156.

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).

Liu MD, et al. (2026) Revisiting the phylogeny of Conioselinum (Apiaceae) by integrating nrDNA, plastomes and morphology evidence. BMC plant biology, 26(1).

Zhang P, et al. (2026) A distinct 2,2'-diphenic acid-mediated pyrene degradation pathway in a novel PAH degrader, Glutamicibacter soli ENR6. Applied and environmental microbiology, 92(4), e0206425.

Yang CJ, et al. (2026) Natural selection and recombination interact to structure genome-wide variation in pines. The Plant journal : for cell and molecular biology, 126(1), e70866.

Chen X, et al. (2026) Mechanisms of Bacillus amyloliquefaciens on alleviating lipopolysaccharide-induced oxidative stress in broilers. Animal nutrition (Zhongguo xu mu shou yi xue hui), 24, 316.

- Baca M, et al. (2026) The evolutionary history of the field vole species complex revealed by modern and ancient genomes. *Genome biology*, 27(1).
- Zampirolo G, et al. (2026) Ancient DNA reconstruction of late holocene ecosystems within the Carpathian basin from paleo-meanders and archaeological deposits. *Scientific reports*, 16(1), 4301.
- Wang X, et al. (2026) Population structure and domestication history of the Javan banteng. *Current biology : CB*, 36(2), 458.
- Savini F, et al. (2026) Outside in: assessment of microbial composition of the crust of dry-aged beef and its relevance in relation to food business operator practices. *Italian journal of food safety*, 15(2).
- 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.
- Bergstr m A, et al. (2026) Genomic history of early dogs in Europe. *Nature*, 651(8107), 986.
- Yang X, et al. (2026) Ancient genomes uncover dynamic cultural and genetic interplay in the eastern Tianshan. *Molecular biology and evolution*, 43(3).
- Ding L, et al. (2026) Integrated genomic and phenotypic characterization of representative *Salmonella Pullorum* and *Salmonella Enteritidis* isolated from a poultry farm. *Frontiers in microbiology*, 17, 1845729.
- Li L, et al. (2026) Complete Mitochondrial Genome of *Melophagus ovinus* from Qinghai-Tibet Plateau Provides Evidence for D-Loop Length Polymorphism. *Genes*, 17(6).
- Backman T, et al. (2026) Persistent trade-offs balance competition and colonization across centuries. *Proceedings of the National Academy of Sciences of the United States of America*, 123(23), e2534310123.
- 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.
- Campos PE, et al. (2026) Instance of a Heteroplasmic Mitogenome in Alvinocaridid Shrimp *Mirocaris fortunata* (Martin & Christiansen 1995) Found at the Moytirra Deep-Sea High-Temperature Hydrothermal Vent Field. *Ecology and evolution*, 16(7), e73956.
- Groot-Crego C, et al. (2026) Divergent Transcriptional Architectures Beyond Core CAM Genes in Facultative and Constitutive CAM Species in *Tillandsia L.* *Molecular ecology*, 35(6), e70313.
- 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.