

Resource Summary Report

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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: 20260821T193920+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 [ASWG](#) .

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).

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.

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

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.

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

- 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.
- 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.
- 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).
- Yang X, et al. (2026) Ancient genomes uncover dynamic cultural and genetic interplay in the eastern Tianshan. *Molecular biology and evolution*, 43(3).
- 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.
- 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.
- 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.
- 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.
- Bergström A, et al. (2026) Genomic history of early dogs in Europe. *Nature*, 651(8107), 986.
- 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).
- 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.
- Dou Y, et al. (2026) Genomic landscape and fine-scale population structure of *Helicobacter pylori* across China. *Biomarker research*, 14(1).
- Kim G, et al. (2026) Comprehensive molecular profiling of the African swine fever virus in Korean wild boars between 2019 and 2024. *Veterinary research*, 57(1).