

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

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

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: 20260803T040603+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 675 mentions in open access literature.

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

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).

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.

Lankes HFN, et al. (2026) Moss-Accumulated eDNA Is a Promising Source for Terrestrial Biodiversity Surveys Across the Tree of Life and Biomes. *Molecular ecology resources*, 26(1), e70088.

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

Zou Y, et al. (2025) Ancient genomes from the Yellow River Bend reveal long-distance population interactions between the Central Plains, Steppe, and southern China. *Cell reports*, 44(8), 116034.

Schwartz L, et al. (2025) Obesity promotes urinary tract infection by disrupting bladder focal adhesion kinase signaling. *iScience*, 28(11), 113862.

Wold JR, et al. (2025) The promise and challenges of characterizing genome-wide structural variants: A case study in a critically endangered parrot. *Molecular ecology resources*, 25(5), e13783.

Günther T, et al. (2025) The genomic legacy of aurochs hybridisation in ancient and modern Iberian cattle. *eLife*, 13.

Ashkin EL, et al. (2025) A STAG2-PAXIP1/PAGR1 axis suppresses lung tumorigenesis. *The Journal of experimental medicine*, 222(1).

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.

Sinha E, et al. (2025) Whole-genome sequence of *Salmonella* Typhimurium E-5591 and its methionine sulfoxide reductase (*msr*) gene deletion mutant strains. *Microbiology resource announcements*, 14(7), e0014325.

Lin T, et al. (2025) Developing safe and efficient CGBE editor based on Cas-embedding strategy. *Synthetic and systems biotechnology*, 10(2), 504.

Jensen EL, et al. (2025) Synteny Enabled Upgrade of the Galapagos Giant Tortoise Genome Improves Inferences of Runs of Homozygosity. *Ecology and evolution*, 15(4), e71358.

Li B, et al. (2025) Protocol for measuring the auxin-induced changes of m6A modification. *STAR protocols*, 6(1), 103629.

de Jong MJ, et al. (2025) Red Deer Resequencing Reveals the Importance of Sex Chromosomes for Reconstructing Late Quaternary Events. *Molecular biology and evolution*, 42(2).

Macphee A, et al. (2025) Comparison of whole genome sequencing performance from fish swabs and fin clips. *BMC research notes*, 18(1), 15.

Ramirez DA, et al. (2025) 4,000-year-old *Mycobacterium lepromatosis* genomes from Chile reveal long establishment of Hansen's disease in the Americas. *Nature ecology & evolution*, 9(9), 1685.

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

Günther T, et al. (2025) Estimating allele frequencies, ancestry proportions and genotype likelihoods in the presence of mapping bias. *G3 (Bethesda, Md.)*, 15(10).

Varg JE, et al. (2025) Interplay between antipredator behavior, parasitism, and gut microbiome in wild stickleback populations. *NPJ biofilms and microbiomes*, 11(1), 138.