

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 13, 2026

Btrim

RRID:SCR_011836

Type: Tool

Proper Citation

Btrim (RRID:SCR_011836)

Resource Information

URL: <http://graphics.med.yale.edu/trim/>

Proper Citation: Btrim (RRID:SCR_011836)

Description: A fast and lightweight software to trim adapters and low quality regions in reads from ultra high-throughput next-generation sequencing machines.

Abbreviations: Btrim

Resource Type: software resource

Defining Citation: [PMID:21651976](#)

Keywords: bio.tools

Resource Name: Btrim

Resource ID: SCR_011836

Alternate IDs: biotools:btrim, OMICS_01083

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

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260808T185936+0000

Ratings and Alerts

No rating or validation information has been found for Btrim.

No alerts have been found for Btrim.

Data and Source Information

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Ma C, et al. (2026) Ultrarapid MC1R protein and associated plumage color evolution in the domestic chicken. Proceedings of the National Academy of Sciences of the United States of America, 123(24), e2605288123.

Kwon J, et al. (2025) Prospective comparison of the digestive tract resistome and microbiota in cattle raised in grass-fed versus grain-fed production systems. mSphere, 10(3), e0073824.

Qi X, et al. (2025) The diversity of prokaryotes and fungi hosted in crude oils. Microbiology spectrum, 13(7), e0168924.

Bai S, et al. (2025) Iron is an important influence of volcanic ash input on the evolution of deep-sea ecosystems. Microbiology spectrum, 13(9), e0071525.

Kwon J, et al. (2025) Microbiome signatures of Clostridioides difficile toxin production and toxin gene presence: a shotgun metagenomic approach. mSphere, 10(10), e0043525.

Crucianelli S, et al. (2024) Effects of sulphur thermal water inhalations in long-COVID syndrome: Spa-centred, double-blinded, randomised case-control pilot study. Clinical medicine (London, England), 24(6), 100251.

Ahmed AA, et al. (2024) Mutation detection in saliva from oral cancer patients. Oral oncology, 151, 106717.

Wang J, et al. (2024) Transcriptome and Weighted Gene Co-Expression Network Analysis for Feather Follicle Density in a Chinese Indigenous Breed. Animals : an open access journal from MDPI, 14(1).

Wang J, et al. (2024) Identification of key modules and hub genes involved in regulating the feather follicle development of Wannan chickens using WGCNA. Poultry science, 103(8), 103903.

Xiong Z, et al. (2024) The influence of temperature and river runoff on phytoplankton community diversity in Beibu Gulf: insight from 18S rDNA metabarcoding analysis. BMC ecology and evolution, 24(1), 129.

Paduano S, et al. (2024) Characterization by 16S Amplicon Sequencing of Bacterial Communities Overall and During the Maturation Process of Peloids in Two Spas of an Italian Thermal Complex. Microbial ecology, 87(1), 152.

Schuster M, et al. (2024) Extracellular vesicles secreted by 3D tumor organoids are enriched for immune regulatory signaling biomolecules compared to conventional 2D glioblastoma cell systems. Frontiers in immunology, 15, 1388769.

Byarugaba DK, et al. (2023) Genome Analysis of *Klebsiella pneumoniae* Reveals International High-Risk Pandemic MDR Clones Emerging in Tertiary Healthcare Settings in Uganda. *Pathogens* (Basel, Switzerland), 12(11).

Byarugaba DK, et al. (2023) Resistome and virulome of high-risk pandemic clones of multidrug-resistant extra-intestinal pathogenic *Escherichia coli* (ExPEC) isolated from tertiary healthcare settings in Uganda. *PloS one*, 18(11), e0294424.

Cheng Z, et al. (2023) *Cortinarius* and *Tomentella* Fungi Become Dominant Taxa in Taiga Soil after Fire Disturbance. *Journal of fungi* (Basel, Switzerland), 9(11).

Qin Y, et al. (2023) Effects of error, chimera, bias, and GC content on the accuracy of amplicon sequencing. *mSystems*, 8(6), e0102523.

Li F, et al. (2023) Effects of Mineral on Taxonomic and Functional Structures of Microbial Community in Tengchong Hot Springs via in-situ cultivation. *Environmental microbiome*, 18(1), 22.

Bai S, et al. (2023) Changes of In Situ Prokaryotic and Eukaryotic Communities in the Upper Sanya River to the Sea over a Nine-Hour Period. *Microorganisms*, 11(2).

Guo X, et al. (2022) Genome-wide scan for selection signatures and genes related to heat tolerance in domestic chickens in the tropical and temperate regions in Asia. *Poultry science*, 101(7), 101821.

Wang L, et al. (2022) Fungi and cercozoa regulate methane-associated prokaryotes in wetland methane emissions. *Frontiers in microbiology*, 13, 1076610.