

Resource Summary Report

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SAMtools/BCFtools

RRID:SCR_005227

Type: Tool

Proper Citation

SAMtools/BCFtools (RRID:SCR_005227)

Resource Information

URL: <http://samtools.sourceforge.net/mpileup.shtml>

Proper Citation: SAMtools/BCFtools (RRID:SCR_005227)

Description: Provide various utilities for manipulating alignments in the SAM format, including sorting, merging, indexing and generating alignments in a per-position format.

Abbreviations: BCFtools

Resource Type: software resource

Defining Citation: [DOI:10.1101/090811](https://doi.org/10.1101/090811)

Keywords: snp, indel, bio.tools

Resource Name: SAMtools/BCFtools

Resource ID: SCR_005227

Alternate IDs: biotools:bcftools, OMICS_13458

Alternate URLs: <https://bio.tools/bcftools>, <https://sources.debian.org/src/bcftools/>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260801T190248+0000

Ratings and Alerts

No rating or validation information has been found for SAMtools/BCFtools.

No alerts have been found for SAMtools/BCFtools.

Data and Source Information

Usage and Citation Metrics

We found 904 mentions in open access literature.

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

Taylor RS, et al. (2026) Accurate Runs of Homozygosity Estimation From Low Coverage Genome Sequences in Non-Model Species. *Molecular ecology resources*, 26(1), e70083.

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. *Journal of virology*, 100(1), e0148725.

Keogh SM, et al. (2025) Secondary contact erodes Pleistocene diversification in a wide-ranging freshwater mussel (*Quadrula*). *Molecular ecology*, 34(1), e17572.

Wang MY, et al. (2025) Chromosome-level genome assembly, annotation, and population genomic resource of argali (*Ovis ammon*). *Scientific data*, 12(1), 57.

Cassens J, et al. (2025) Whole Genome Sequencing Reveals Clade-Specific Genetic Variation in Blacklegged Ticks. *Ecology and evolution*, 15(2), e70987.

Park K, et al. (2025) Epidemiological surveillance and phylogenetic diversity of Orthohantavirus hantanense using high-fidelity nanopore sequencing, Republic of Korea. *PLoS neglected tropical diseases*, 19(2), e0012859.

Horaud M, et al. (2025) Allochrony in Atlantic Lumpfish: Genomic and Otolith Shape Divergence Between Spring and Autumn Spawners. *Ecology and evolution*, 15(2), e70946.

Krause-Kyora B, et al. (2025) Neolithic introgression of IL23R-related protection against chronic inflammatory bowel diseases in modern Europeans. *EBioMedicine*, 113, 105591.

Yuan Z, et al. (2025) High-quality phenotypic and genotypic dataset of barley genebank core collection to unlock untapped genetic diversity. *GigaScience*, 14.

Wall BPG, et al. (2025) Beyond Blacklists: A Critical Assessment of Exclusion Set Generation Strategies and Alternative Approaches. *bioRxiv* : the preprint server for biology.

Borges VM, et al. (2025) Genomic Exploration of Essential Hypertension in African-Brazilian Quilombo Populations: A Comprehensive Approach With Pedigree Analysis and Family-Based Association Studies. *Journal of the American Heart Association*, 14(7), e036193.

Bai ??? F, et al. (2025) LCORL and STC2 Variants Increase Body Size and Growth Rate in Cattle and Other Animals. *Genomics, proteomics & bioinformatics*, 23(3).

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. *GigaScience*, 14.

Colenutt C, et al. (2025) Detection and genomic characterisation of foot-and-mouth disease virus serotypes circulating in Cameroon using environmental sampling. *Scientific reports*, 15(1), 2834.

Kyrgiafini MA, et al. (2025) Integrative Analysis of Whole-Genome and Transcriptomic Data Reveals Novel Variants in Differentially Expressed Long Noncoding RNAs Associated with Asthenozoospermia. *Non-coding RNA*, 11(1).

Hayakawa T, et al. (2025) Genome-scale evolution in local populations of wild chimpanzees. *Scientific reports*, 15(1), 548.

Trubanová N, et al. (2025) Genome-specific association study (GSAS) for exploration of variability in hemp (*Cannabis sativa*). *Scientific reports*, 15(1), 8371.

Chovanec P, et al. (2025) Generalization of the sci-L3 method to achieve high-throughput linear amplification for replication template strand sequencing, genome conformation capture, and the joint profiling of RNA and chromatin accessibility. *Nucleic acids research*, 53(4).