

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## SAMtools/BCFtools

RRID:SCR\_005227

Type: Tool

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### Proper Citation

SAMtools/BCFtools (RRID:SCR\_005227)

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### 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:** 20260905T132531+0000

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### Ratings and Alerts

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

No alerts have been found for SAMtools/BCFtools.

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### Data and Source Information

## Usage and Citation Metrics

We found 1066 mentions in open access literature.

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

Luo L, et al. (2026) Paternal genomic history and Y-chromosome phylogeny from the Chengdu Plain reveal multiple Indigenous East Asian farmer contributions to ancient Shu and their descendants. *BMC biology*, 24(1).

Tensen L, et al. (2026) Genomic divergence of leopards in the Cape Floristic Region of South Africa: potential drivers for local adaptation. *Heredity*, 135(2), 86.

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Jalal D, et al. (2026) Dual Transmission Dynamics of Carbapenem Resistance in Pediatric Oncology: Plasmid-Mediated and Clonal Spread of blaNDM-5 Enterobacterales. *Infectious diseases and therapy*, 15(1), 245.

Kalinich CC, et al. (2026) A tiled amplicon protocol for culture-free whole-genome sequencing of *M. tuberculosis* from clinical specimens. *Journal of clinical microbiology*, 64(3), e0182325.

Liu W, et al. (2026) Photosynthesis-related genetic and transcriptomic variations contribute to adaptive trait diversity in global *Arabidopsis thaliana* populations. *BMC plant biology*, 26(1).

Liu H, et al. (2026) Genomics of rafting crustaceans reveals adaptation to climate change in tropical oceans. *Nature communications*, 17(1).

Han Y, et al. (2026) The late arrival of domestic cats in China via the Silk Road after 3,500 years of human-leopard cat commensalism. *Cell genomics*, 6(1), 101099.

Nguyen HA, et al. (2026) AMR-GNN: a multi-representation graph neural network framework to enable genomic antimicrobial resistance prediction. *Nature communications*, 17(1).

Hossain M, et al. (2026) EffectorFisher: association of disease phenotype with pangenomic protein-isoform profiles for improved prediction of fungal pathogenicity effectors. *Scientific reports*, 16(1).

Zhang S, et al. (2026) Genomic Insights into Adaptation of *Lagerstroemia supracreticulata* to Limestone Karst Habitats. *Plants (Basel, Switzerland)*, 15(4).

Pal D, et al. (2026) Integrative transcriptome and genome resequencing reveals conserved flowering regulators and allelic variants in early- and late-flowering linseed (*Linum usitatissimum* L.) accessions. *Scientific reports*, 16(1).

Han Y, et al. (2026) Development and application of a genotyping by target sequencing single-nucleotide polymorphism array panel in *Salix suchowensis*. *BMC genomics*, 27(1).

Wall BPG, et al. (2026) Beyond blacklists: a critical assessment of exclusion set generation strategies and alternative approaches. *Bioinformatics (Oxford, England)*, 42(3).

Meyerson NR, et al. (2026) CXCR4-tropic HIV-1 infection in an immunocompetent monkey model. *Nature communications*, 17(1).

Tomomatsu K, et al. (2026) Double flower is associated with defects in a *Phantastica*-like gene in *Catharanthus roseus*. *Scientific reports*, 16(1).

Hernández-Roco D, et al. (2026) Chromosome-level genome assembly of the common tenrec, *Tenrec ecaudatus* (Schreber, 1778), a new model for early placental mammal evolution. *BMC genomics*, 27(1).

Nickel J, et al. (2026) Complex Patterns of Hitchhiking Mutation Load Among Stickleback Populations. *Genome biology and evolution*, 18(4).

Verspagen N, et al. (2026) Mild Warming Induces Divergent Plastic Responses in Gene Expression Among Populations of a Temperate Butterfly. *Molecular ecology*, 35(7), e70309.

Waller MM, et al. (2026) Kinship Analysis Confirms Tolerant Galapagos Mockingbirds Are a Source of Nest Flies That Threaten Darwin's Finches. *Molecular ecology*, 35(7), e70334.