

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

Funding:

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: 20250420T014246+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 680 mentions in open access literature.

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

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).

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

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

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

Lee MK, et al. (2025) Genome scan reveals several loci associated with torus palatinus. *Orthodontics & craniofacial research*, 28(1), 159.

Li R, et al. (2025) Photosymbiosis shaped animal genome architecture and gene evolution as revealed in giant clams. *Communications biology*, 8(1), 7.

Worm AJ, et al. (2025) Repeated Successful Nest Sharing and Cooperation Between Western Kingbirds (*Tyrannus verticalis*) and a Female Western Kingbird?×?Scissor-Tailed Flycatcher (*T. forficatus*) Hybrid. *Ecology and evolution*, 15(1), e70818.

Zou X, et al. (2025) Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers. *Nature communications*, 16(1), 682.

Zeng J, et al. (2025) Protocol for genetic analysis of population-scale ultra-low-depth sequencing data. *STAR protocols*, 6(1), 103579.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae: Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Jung M, et al. (2025) Evaluation of genomic and phenomic prediction for application in apple breeding. *BMC plant biology*, 25(1), 103.

Zaccaron AZ, et al. (2024) Analysis of five near-complete genome assemblies of the tomato pathogen *Cladosporium fulvum* uncovers additional accessory chromosomes and structural variations induced by transposable elements effecting the loss of avirulence genes. *BMC biology*, 22(1), 25.

Dalapicolla J, et al. (2024) Whole genomes show contrasting trends of population size changes and genomic diversity for an Amazonian endemic passerine over the late quaternary. *Ecology and evolution*, 14(4), e11250.

Leon-Apodaca AV, et al. (2024) Genomic Consequences of Isolation and Inbreeding in an Island Dingo Population. *Genome biology and evolution*, 16(7).

Wang M, et al. (2024) Multiple Human Population Movements and Cultural Dispersal Events Shaped the Landscape of Chinese Paternal Heritage. *Molecular biology and evolution*, 41(7).

Backenstose NJC, et al. (2024) Origin of the Laurentian Great Lakes fish fauna through upward adaptive radiation cascade prior to the Last Glacial Maximum. *Communications biology*, 7(1), 978.

Beiki H, et al. (2024) Enhanced bovine genome annotation through integration of transcriptomics and epi-transcriptomics datasets facilitates genomic biology. *GigaScience*, 13.

Wurst C, et al. (2024) Genetic Predisposition of Atherosclerotic Cardiovascular Disease in Ancient Human Remains. *Annals of global health*, 90(1), 6.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish *Entelurus aequoreus* (Syngnathiformes: Syngnathidae). *GigaByte* (Hong Kong, China), 2024, gigabyte105.

Talimi H, et al. (2024) A comparative genomics approach reveals a local genetic signature of *Leishmania tropica* in Morocco. *Microbial genomics*, 10(4).