

Resource Summary Report

Generated by [NIF](#) on Aug 19, 2026

[bamUtil](#)

RRID:SCR_027781

Type: Tool

Proper Citation

bamUtil (RRID:SCR_027781)

Resource Information

URL: <https://github.com/statgen/bamUtil>

Proper Citation: bamUtil (RRID:SCR_027781)

Description: Software set of programs and utilities for working on SAM/BAM files.

Resource Type: source code, software toolkit, software resource

Keywords: working on SAM/BAM files,

Availability: Free, Available for download, Freely available

Resource Name: bamUtil

Resource ID: SCR_027781

Record Creation Time: 20251213T054634+0000

Record Last Update: 20260818T043833+0000

Ratings and Alerts

No rating or validation information has been found for bamUtil.

No alerts have been found for bamUtil.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Yang X, et al. (2026) Ancient genomes uncover dynamic cultural and genetic interplay in the eastern Tianshan. *Molecular biology and evolution*, 43(3).

Satokangas I, et al. (2026) Introgression and Divergence in a Young Species Group. *Molecular ecology*, 35(12), e70448.

Llamazares-Prada M, et al. (2026) Epigenetic dysregulation of IRF9 drives excessive interferon signaling in COPD. *EMBO molecular medicine*, 18(4), 1202.

Jayaram A, et al. (2026) Combined ctDNA and serum PSA for dynamic monitoring of metastatic prostate cancer starting first-line treatment: a prospective national cohort study. *Nature cancer*, 7(6), 915.

Heidbreder P, et al. (2026) Genomic incompatibilities are persistent barriers when speciation happens with gene flow in *Formica* ants. *Molecular biology and evolution*, 43(5).

Lv X, et al. (2026) Population history and subsistence of farming communities in an agro-pastoral transition zone of northern China: ancient DNA and isotopic evidence from the Erdaojingzi site. *Scientific reports*, 16(1).

Davidson R, et al. (2025) Optimized in-solution enrichment of over a million ancient human SNPs. *Genome biology*, 26(1), 190.

Liu B, et al. (2025) Multi-omics analysis identifies different molecular subtypes with unique outcomes in early-stage poorly differentiated lung adenocarcinoma. *Molecular cancer*, 24(1), 129.

Roca-Rada X, et al. (2025) Genetic transitions in the Neolithic and Bronze Age at Mas d'en Boixos (Catalonia, Spain). *iScience*, 28(7), 112871.

Cox OH, et al. (2024) Implementation of the Methyl-Seq platform to identify tissue- and sex-specific DNA methylation differences in the rat epigenome. *Epigenetics*, 19(1), 2393945.

Solmundson K, et al. (2023) Genomic population structure and inbreeding history of Lake Superior caribou. *Ecology and evolution*, 13(7), e10278.

Zhang Y, et al. (2022) Dynamic enhancer transcription associates with reprogramming of immune genes during pattern triggered immunity in *Arabidopsis*. *BMC biology*, 20(1), 165.

Hänninen UA, et al. (2019) Exome and immune cell score analyses reveal great variation within synchronous primary colorectal cancers. *British journal of cancer*, 120(9), 922.