

Resource Summary Report

Generated by [NIF](#) on Aug 2, 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: software resource, software toolkit, source code

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: 20260801T191432+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 2 mentions in open access literature.

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

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.

Hanninen 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.