

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

BAMStats

RRID:SCR_006973

Type: Tool

Proper Citation

BAMStats (RRID:SCR_006973)

Resource Information

URL: <http://sourceforge.net/projects/bamstats/>

Proper Citation: BAMStats (RRID:SCR_006973)

Description: A GUI desktop tool for calculating and displaying metrics to assess the success of Next Generation Sequencing mapping tools. BAMstats is written in Java and based around the Picard API.

Abbreviations: BAMStats

Resource Type: software resource

Keywords: matlab, next generation sequencing, java

Availability: GNU General Public License

Resource Name: BAMStats

Resource ID: SCR_006973

Alternate IDs: OMICS_01034

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260725T190631+0000

Ratings and Alerts

No rating or validation information has been found for BAMStats.

No alerts have been found for BAMStats.

Data and Source Information

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Cassens J, et al. (2025) The Genome of the American Dog Tick (*Dermacentor variabilis*). bioRxiv : the preprint server for biology.

Cassens J, et al. (2025) The genome of the American dog tick (*Dermacentor variabilis*). G3 (Bethesda, Md.), 15(8).

Sim EM, et al. (2023) Persistent *Salmonella enterica* serovar Typhi sub-populations within host interrogated by whole genome sequencing and metagenomics. PLoS one, 18(8), e0289070.

Campos PE, et al. (2021) First historical genome of a crop bacterial pathogen from herbarium specimen: Insights into citrus canker emergence. PLoS pathogens, 17(7), e1009714.

Wein T, et al. (2021) Essential gene acquisition destabilizes plasmid inheritance. PLoS genetics, 17(7), e1009656.

Eisenhofer R, et al. (2020) Investigating the demographic history of Japan using ancient oral microbiota. Philosophical transactions of the Royal Society of London. Series B, Biological sciences, 375(1812), 20190578.

Ilhan J, et al. (2019) Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. Molecular biology and evolution, 36(3), 472.

Wein T, et al. (2019) Emergence of plasmid stability under non-selective conditions maintains antibiotic resistance. Nature communications, 10(1), 2595.

Namouchi A, et al. (2018) Integrative approach using *Yersinia pestis* genomes to revisit the historical landscape of plague during the Medieval Period. Proceedings of the National Academy of Sciences of the United States of America, 115(50), E11790.

Ilic A, et al. (2017) Ubiquitin C-terminal hydrolase isozyme L1 is associated with shelterin complex at interstitial telomeric sites. Epigenetics & chromatin, 10(1), 54.