

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

BamView

RRID:SCR_004207

Type: Tool

Proper Citation

BamView (RRID:SCR_004207)

Resource Information

URL: <http://bamview.sourceforge.net/>

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Description: A free interactive display of read alignments in BAM data files that can be launched with Java Web Start or downloaded. This interactive Java application for visualizing the large amounts of data stored for sequence reads which are aligned against a reference genome sequence can be used in a number of contexts including SNP calling and structural annotation. It has been integrated into Artemis so that the reads can be viewed in the context of the nucleotide sequence and genomic features. The source code is available as part of the Artemis code which can be downloaded from GitHub.

Abbreviations: BamView

Resource Type: source code, software resource

Defining Citation: [PMID:22253280](#), [PMID:20071372](#)

Keywords: bam, next-generation sequencing, java, snp calling, structural annotation, macosx, unix, windows, visualize, analyze, sequence read, reference sequence, single nucleotide polymorphism, bio.tools

Availability: GNU General Public License

Resource Name: BamView

Resource ID: SCR_004207

Alternate IDs: biotools:bamview, OMICS_00878, nlx_22933

Alternate URLs: <https://bio.tools/bamview>

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260729T044056+0000

Ratings and Alerts

No rating or validation information has been found for BamView.

No alerts have been found for BamView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Jung YH, et al. (2023) Characterization of a strain-specific CD-1 reference genome reveals potential inter- and intra-strain functional variability. *BMC genomics*, 24(1), 437.

Gomez-Escribano JP, et al. (2021) Genome editing reveals that pSCL4 is required for chromosome linearity in *Streptomyces clavuligerus*. *Microbial genomics*, 7(11).

Roberts LW, et al. (2020) Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing *Enterobacter hormaechei*. *Nature communications*, 11(1), 466.

Peng P, et al. (2020) Genome-wide capture sequencing to detect hepatitis C virus at the end of antiviral therapy. *BMC infectious diseases*, 20(1), 632.

Fablet M, et al. (2019) Dynamic Interactions Between the Genome and an Endogenous Retrovirus: Tirant in *Drosophila simulans* Wild-Type Strains. *G3 (Bethesda, Md.)*, 9(3), 855.

Holt KE, et al. (2018) Frequent transmission of the *Mycobacterium tuberculosis* Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam. *Nature genetics*, 50(6), 849.

Hücker SM, et al. (2017) Discovery of numerous novel small genes in the intergenic regions of the *Escherichia coli* O157:H7 Sakai genome. *PloS one*, 12(9), e0184119.

Schmöckel SM, et al. (2017) Identification of Putative Transmembrane Proteins Involved in Salinity Tolerance in *Chenopodium quinoa* by Integrating Physiological Data, RNAseq, and SNP Analyses. *Frontiers in plant science*, 8, 1023.

Neuhaus K, et al. (2017) Differentiation of ncRNAs from small mRNAs in *Escherichia coli* O157:H7 EDL933 (EHEC) by combined RNAseq and RIBOseq - *ryhB* encodes the regulatory RNA *RyhB* and a peptide, *RyhP*. *BMC genomics*, 18(1), 216.

Bolhuis H, et al. (2017) Transcriptome analysis of *Haloquadratum walsbyi*: vanity is but the surface. *BMC genomics*, 18(1), 510.

Pegoraro S, et al. (2017) SC83288 is a clinical development candidate for the treatment of severe malaria. *Nature communications*, 8, 14193.

Rath EC, et al. (2017) Identification of streptococcal small RNAs that are putative targets of RNase III through bioinformatics analysis of RNA sequencing data. *BMC bioinformatics*, 18(Suppl 14), 540.

Balsingh J, et al. (2016) Draft Genome Sequence of *Bacillus pumilus* ku-bf1 Isolated from the Gut Contents of Wood Boring *Mesomorphus* sp. *Frontiers in microbiology*, 7, 1037.

Jang IA, et al. (2016) Endogenous hydrogen peroxide increases biofilm formation by inducing exopolysaccharide production in *Acinetobacter oleivorans* DR1. *Scientific reports*, 6, 21121.

Suárez-Esquivel M, et al. (2016) *Brucella abortus* Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. *Frontiers in microbiology*, 7, 1557.

Okoro CK, et al. (2015) Signatures of adaptation in human invasive *Salmonella* Typhimurium ST313 populations from sub-Saharan Africa. *PLoS neglected tropical diseases*, 9(3), e0003611.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.

Butcher J, et al. (2015) Refined analysis of the *Campylobacter jejuni* iron-dependent/independent Fur- and PerR-transcriptomes. *BMC genomics*, 16(1), 498.

Quintero A, et al. (2013) Identification of ta-siRNAs and cis-nat-siRNAs in cassava and their roles in response to cassava bacterial blight. *Genomics, proteomics & bioinformatics*, 11(3), 172.

Carver T, et al. (2013) BamView: visualizing and interpretation of next-generation sequencing read alignments. *Briefings in bioinformatics*, 14(2), 203.