Resource Summary Report

Generated by nidm-terms on Aug 9, 2026

bam readcount

RRID:SCR_023653
Type: Tool

Proper Citation

bam readcount (RRID:SCR_023653)

Resource Information

URL: https://github.com/genome/bam-readcount

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Description: Software tool that runs on BAM or CRAM file and generates low level information about sequencing data at specific nucleotide positions. Its outputs include observed bases, readcounts, summarized mapping and base qualities, strandedness information, mismatch counts, and position within the reads.

Synonyms: bam-readcount

Resource Type: software resource, software application

Defining Citation: PMID:34341766

Keywords: BAM file, CRAM file, sequencing data, nucleotide positions,

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Availability: Free, Available for download, Freely available

Resource Name: bam readcount

Resource ID: SCR_023653

License: MIT license

Record Creation Time: 20230606T050221+0000

Record Last Update: 20260808T190539+0000

Ratings and Alerts

No rating or validation information has been found for bam readcount.

No alerts have been found for bam readcount.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Terekhanova NV, et al. (2026) Reactivation of a TAL1 progenitor cell enhancer region by non-coding somatic variants in T-lineage acute lymphoblastic leukemia. bioRxiv : the preprint server for biology.

Wang C, et al. (2026) A Deep Learning-Driven Framework Integrating Organoid-Based Functional Validation Identifies Universal Neoantigens from Recurrent Glioma Mutations. Cancer research, 86(12), 3074.

Barthe M, et al. (2025) Exon Capture Museomics Deciphers the Nine-Banded Armadillo Species Complex and Identifies a New Species Endemic to the Guiana Shield. Systematic biology, 74(2), 177.

Fiore D, et al. (2025) A patient-derived T cell lymphoma biorepository uncovers pathogenetic mechanisms and host-related therapeutic vulnerabilities. Cell reports. Medicine, 6(4), 102029.

Shinohara S, et al. (2025) The difference in tumor immune microenvironment and IFN-? response between solid and non-solid adenocarcinoma. Translational lung cancer research, 14(9), 3753.

Muller A, et al. (2025) High-efficiency base editing in the retina in primates and human tissues. Nature medicine, 31(2), 490.

Gonzalez Martinez A, et al. (2025) C to U RNA editing of MFN1 is regulated by ADARB1 and associates with favourable prognosis in chronic lymphocytic leukemia. Scientific reports, 15(1), 29856.

Chen H, et al. (2025) Fifteenth century CE Bolivian maize reveals genetic affinities with ancient Peruvian maize. eLife, 14.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Frommeyer YN, et al. (2025) tRNA hydroxylation is an epitranscriptomic modulator of metabolic states affecting Pseudomonas aeruginosa pathogenicity. Nucleic acids research, 53(14).

Sethna Z, et al. (2025) RNA neoantigen vaccines prime long-lived CD8+ T cells in pancreatic cancer. Nature, 639(8056), 1042.

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. Cell reports, 44(10), 116449.

Garsmeur O, et al. (2025) The genomic footprints of wild Saccharum species trace domestication, diversification, and modern breeding of sugarcane. Cell, 188(25), 7252.

Iglesia MD, et al. (2024) Differential chromatin accessibility and transcriptional dynamics define breast cancer subtypes and their lineages. Nature cancer, 5(11), 1713.

Karimnezhad A, et al. (2024) Empirical Bayes single nucleotide variant-calling for next-generation sequencing data. Scientific reports, 14(1), 1550.

D'Ambrosi S, et al. (2024) Global and single-nucleotide resolution detection of 7-methylguanosine in RNA. RNA biology, 21(1), 1.

Porreca I, et al. (2024) An aptamer-mediated base editing platform for simultaneous knockin and multiple gene knockout for allogeneic CAR-T cells generation. Molecular therapy : the journal of the American Society of Gene Therapy, 32(8), 2692.

Lin Y, et al. (2024) HiFi long-read amplicon sequencing for full-spectrum variants of human mtDNA. BMC genomics, 25(1), 538.

Schwitzgebel VM, et al. (2024) Enhancing fetal outcomes in GCK-MODY pregnancies: a precision medicine approach via non-invasive prenatal GCK mutation detection. Frontiers in medicine, 11, 1347290.

Hynds RE, et al. (2024) Representation of genomic intratumor heterogeneity in multi-region non-small cell lung cancer patient-derived xenograft models. Nature communications, 15(1), 4653.