

Resource Summary Report

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BEDTools

RRID:SCR_006646

Type: Tool

Proper Citation

BEDTools (RRID:SCR_006646)

Resource Information

URL: <https://github.com/arq5x/bedtools2>

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Description: A powerful toolset for genome arithmetic allowing one to address common genomics tasks such as finding feature overlaps and computing coverage. Bedtools allows one to intersect, merge, count, complement, and shuffle genomic intervals from multiple files in widely-used genomic file formats such as BAM, BED, GFF/GTF, VCF. While each individual tool is designed to do a relatively simple task (e.g., intersect two interval files), quite sophisticated analyses can be conducted by combining multiple bedtools operations on the UNIX command line.

Abbreviations: BEDTools

Synonyms: bedtools - a swiss army knife for genome arithmetic, bedtools: a flexible suite of utilities for comparing genomic features

Resource Type: software resource

Defining Citation: [PMID:20110278](#), [DOI:10.1093/bioinformatics/btq033](#)

Keywords: genomics, bed, sam, bam, overlap, sequencing, intersect, coverage, gff, vcf, bedgraph, interval, genome arithmetic, bio.tools

Availability: GNU General Public License, v2, Acknowledgement requested

Resource Name: BEDTools

Resource ID: SCR_006646

Alternate IDs: OMICS_01159, biotools:bedtools

Alternate URLs: <https://code.google.com/p/bedtools/>, <https://bio.tools/bedtools>, <https://sources.debian.org/src/bedtools/>

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Ratings and Alerts

No rating or validation information has been found for BEDTools.

No alerts have been found for BEDTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10394 mentions in open access literature.

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

Tu Y, et al. (2026) Identification of molecular markers associated with comb traits through genome-wide association study on a specialized strain of yellow feathered broilers. Poultry science, 105(1), 106125.

Garc??a JF, et al. (2026) Intraspecies sequence-graph analysis of the Phytophthora theobromicola genome reveals a dynamic structure and variable effector repertoires. G3 (Bethesda, Md.), 16(1).

Venkatasubramani AV, et al. (2026) Chameau (HBO1) regulates starvation resistance in Drosophila melanogaster in a temperature-dependent manner. Life science alliance, 9(1).

Crnovrsanin N, et al. (2026) Combining cell-free DNA fragmentomes and total tumour volume improves prognostication and tumour response evaluation in patients with colorectal cancer liver metastases. EBioMedicine, 123, 106081.

de Oliveira LF, et al. (2026) Genome-Wide Detection of Copy Number Variation and Association Studies With Physiological and Anatomical Indicators of Heat Stress Response in Lactating Sows. Journal of animal breeding and genetics = Zeitschrift fur Tierzucht und Zuchtungsbiologie, 143(1), 183.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. Molecular biology and evolution, 43(1).

Jeon JY, et al. (2026) Short-Read Pangenomes and Their Potential Utility in Population and Conservation Genomics. Molecular ecology resources, 26(1), e70060.

Huang X, et al. (2026) PMEL governs autosomal dominant inheritance of white-tail independent of yellow body plumage in chickens (Gallus gallus domesticus). Poultry science, 105(1), 106127.

Yoo D, et al. (2026) Epigenetic and evolutionary features of ape subterminal heterochromatin. *Genome research*, 36(1), 38.

James DQ, et al. (2026) Optimized ChIP-exo for mammalian cells and patterned sequencing flow cells. *G3 (Bethesda, Md.)*, 16(1).

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Zhang G, et al. (2026) Spatial Reorganization of Chromatin Architecture Shapes the Expression Phenotype of Therapy-Induced Senescent Cells. *Aging cell*, 25(1), e70366.

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. *Science advances*, 12(1), eady2539.

Silva-Llanes I, et al. (2026) GASDERMIN D-mediated pyroptosis as a therapeutic target in TAU-dependent frontotemporal dementia mouse model. *Journal of biomedical science*, 33(1), 6.

Leichter SM, et al. (2026) Polycomb misregulation in enterocytes drives tissue decline in the aging *Drosophila* intestine. *Genome research*, 36(1), 102.

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. *Nature*, 649(8095), 216.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Johnson NR, et al. (2026) Antagonistic regulation of nitrogen and drought signaling mediated by NIN-like protein 7 transcription factor in *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2509904122.

Visser M, et al. (2026) *Neisseria gonorrhoeae* Sequence Types During an Increase of Gonorrhea Among Young Women in 2022 and 2023 in the Netherlands. *Open forum infectious diseases*, 13(1), ofaf767.