

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

BEDTools

RRID:SCR_006646

Type: Tool

Proper Citation

BEDTools (RRID:SCR_006646)

Resource Information

URL: <https://github.com/arg5x/bedtools2>

Proper Citation: BEDTools (RRID:SCR_006646)

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/>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260912T195643+0000

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 11365 mentions in open access literature.

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

Adami A, et al. (2026) Protocol for efficient CRISPRi-mediated silencing of retrotransposons in human pluripotent stem cells. STAR protocols, 7(1), 104398.

Adams NM, et al. (2026) Chromatin-mediated anticipatory control of type I interferon production in plasmacytoid dendritic cells. Immunity, 59(2), 270.

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. Cell stem cell, 33(4), 642.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple-negative breast cancer. Genome medicine, 18(1).

Lyu P, et al. (2026) Genetic variation reveals a homeotic long noncoding RNA that modulates human hematopoietic stem cells. Cell, 189(13), 4022.

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in Schistosoma japonicum. iScience, 29(6), 116118.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. Cancer research, 86(13), 3160.

Smolen C, et al. (2026) Protocol for identifying genetic modifiers of phenotypes in individuals with disease-associated variants. STAR protocols, 7(2), 104546.

- Gautier M, et al. (2026) A regulatory circuitry driving a noradrenergic to mesenchymal transition highlights YAP/TAZ as critical players in neuroblastoma plasticity. *Cell reports*, 45(5), 117351.
- Vuong TT, et al. (2026) DNA Methyltransferase Inhibition Prevents Platinum-Induced Ovarian Cancer Stem Cell Enrichment. *Cancer research communications*, 6(7), 1721.
- Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. *Stem cell reports*, 21(7), 102968.
- Zhang J, et al. (2026) RNA exonuclease REXO4 resolves m6A-marked R-loops and suppresses anti-tumor immunity. *Molecular cell*.
- Takhaveev V, et al. (2026) Click-code-seq reveals strand biases of DNA oxidation and depurination in human genome. *Nature chemical biology*, 22(5), 716.
- Zheng C, et al. (2026) GlycoRNAdb: a database of glycoRNA sequences, structures, abundance, and glycan information across tissues and cell lines. *Nucleic acids research*, 54(D1), D158.
- 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.
- Liang W, et al. (2026) Evolutionary Analysis of Transcriptional Regulation Mediated by Cdx2 in Rodents. *Cell proliferation*, 59(3), e70103.
- Lin J, et al. (2026) Mapping the Genomic Limits of De-Extinction in the Face of Ancient DNA Degradation. *Genome biology and evolution*, 18(1).
- Cevher MA, et al. (2026) Biochemical and epigenomic dissection of TFIIE function reveals gene-selective requirement in human transcription. *Scientific reports*, 16(1), 5797.
- Rodriguez S, et al. (2026) Genomic plasticity and mobilome architecture of *Vibrio europaeus* reveal key mechanisms of evolutionary adaptation. *Microbial genomics*, 12(1).