**BEDTools**

**RRID:** SCR_006646  
**Type:** Tool

**Proper Citation**

BEDTools (RRID:SCR_006646)

**Resource Information**

- **URL:** [https://github.com/arq5x/bedtools2](https://github.com/arq5x/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


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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 7512 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Abuggestaisa I, et al. (2024) OVCH1 Antisense RNA 1 is differentially expressed between non-frail and frail old adults. GeroScience, 46(2), 2063.


Xie WZ, et al. (2024) Two haplotype-resolved genome assemblies for AAB allotriploid bananas provide insights into banana subgenome asymmetric evolution and Fusarium wilt control. Plant communications, 5(2), 100766.


Zhu X, et al. (2024) MAE-seq refines regulatory elements across the genome. Nucleic acids research, 52(2), e9.

Xi M, et al. (2024) Short-chain fatty acids in breast milk and their relationship with the infant gut microbiota. Frontiers in microbiology, 15, 1356462.

Rubio S, et al. (2024) Nuclear VANGL2 Inhibits Lactogenic Differentiation. Cells, 13(3).

Zhao H, et al. (2024) Transcriptomics and metabolomics of blood, urine and ovarian follicular fluid of yak at induced estrus stage. BMC genomics, 25(1), 201.


Slaman E, et al. (2024) Comparison of Cas12a and Cas9-mediated mutagenesis in tomato cells. Scientific reports, 14(1), 4508.


Kvapilova K, et al. (2024) Validated WGS and WES protocols proved saliva-derived gDNA as an equivalent to blood-derived gDNA for clinical and population genomic analyses. BMC genomics, 25(1), 187.