**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)

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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.

**Resource Type:** Resource, software resource

**References:** PMID:20110278

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

**Related resources:** Hydra, pybedtools

**Availability:** GNU General Public License, v2, Acknowledgement requested

**Website Status:** Last checked up

**Abbreviations:** BEDTools

**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

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 3386 mentions in open access literature.

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


Sanford EM, et al. (2020) Gene regulation gravitates toward either addition or multiplication when combining the effects of two signals. eLife, 9.


Zhang Y, et al. (2020) Estrogen induces dynamic ERα and RING1B recruitment to control gene and enhancer activities in luminal breast cancer. Science advances, 6(23), eaaz7249.


Duncan EJ, et al. (2020) Genome architecture facilitates phenotypic plasticity in the honeybee (Apis mellifera). Molecular biology and evolution.