**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 3383 mentions in open access literature.

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


