BEDTools
RRID:SCR_006646
Type: Tool

Proper Citation

BEDTools (RRID:SCR_006646)

Resource Information

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

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.

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Resource Type: Resource, software resource

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

Resource ID: SCR_006646

Related resources: Hydra

References: PMID: 20110278

Availability: GNU General Public License, v2, Acknowledgement requested

Website Status: Last checked up
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 2464 mentions in open access literature.

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


Kentepozidou E, et al. (2020) Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. Genome biology, 21(1), 5.


Adrian-Kalchhauser I, et al. (2020) The round goby genome provides insights into mechanisms that may facilitate biological invasions. BMC biology, 18(1), 11.


Yao RA, et al. (2020) Quality of whole genome sequencing from blood versus saliva derived DNA in cardiac patients. BMC medical genomics, 13(1), 11.
