# Resource Summary Report

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# pybedtools

RRID:SCR_021018
Type: Tool

## Proper Citation

pybedtools (RRID:SCR_021018)

## Resource Information

**URL:** https://daler.github.io/pybedtools/#

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**Description:** Software Python wrapper for bedtools. Wraps and extends BEDTools and offers feature level manipulations from within Python. Flexible Python library for manipulating genomic datasets and annotations.

**Resource Type:** software toolkit, software resource

**Defining Citation:** PMID:21949271

**Keywords:** Exploring complex genomics datasets, manipulating genomic datasets, Python, bedtools

**Funding:** Intramural Program of the National Institute of Diabetes and Digestive and Kidney Diseases

**Availability:** Free, Available for download, Freely available

**Resource Name:** pybedtools

**Resource ID:** SCR_021018

**Alternate IDs:** biotools:pybedtools

**Alternate URLs:** https://pypi.python.org/pypi/pybedtools, https://bio.tools/pybedtools

**Record Creation Time:** 20220129T080353+0000

**Record Last Update:** 20250412T060310+0000

## Ratings and Alerts

No rating or validation information has been found for pybedtools.

No alerts have been found for pybedtools.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Buzzao D, et al. (2025) FunCoup 6: advancing functional association networks across species with directed links and improved user experience. Nucleic acids research, 53(D1), D658.

Hariprakash JM, et al. (2024) Leveraging Tissue-Specific Enhancer-Target Gene Regulatory Networks Identifies Enhancer Somatic Mutations That Functionally Impact Lung Cancer. Cancer research, 84(1), 133.

Perkiö A, et al. (2024) Locus-specific LINE-1 expression in clinical ovarian cancer specimens at the single-cell level. Scientific reports, 14(1), 4322.

Carrick BH, et al. (2024) PUF partner interactions at a conserved interface shape the RNA-binding landscape and cell fate in Caenorhabditis elegans. Developmental cell, 59(5), 661.

Bedran G, et al. (2023) The Immunopeptidome from a Genomic Perspective: Establishing the Noncanonical Landscape of MHC Class I-Associated Peptides. Cancer immunology research, 11(6), 747.

Schleussner N, et al. (2023) Transcriptional reprogramming by mutated IRF4 in lymphoma. Nature communications, 14(1), 6947.

Lee RRQ, et al. (2023) Generating minimum set of gRNA to cover multiple targets in multiple genomes with MINORg. Nucleic acids research, 51(8), e43.

Lofgren LA, et al. (2022) The pan-genome of Aspergillus fumigatus provides a high-resolution view of its population structure revealing high levels of lineage-specific diversity driven by recombination. PLoS biology, 20(11), e3001890.

Terakawa A, et al. (2022) Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes. iScience, 25(5), 104231.

Donohue LKH, et al. (2022) A cis-regulatory lexicon of DNA motif combinations mediating cell-type-specific gene regulation. Cell genomics, 2(11).

Witchley JN, et al. (2021) Recording of DNA-binding events reveals the importance of a repurposed Candida albicans regulatory network for gut commensalism. Cell host & microbe, 29(6), 1002.

Fu L, et al. (2020) Predicting transcription factor binding in single cells through deep learning. Science advances, 6(51).

Gu J, et al. (2018) GoldCLIP: Gel-omitted Ligation-dependent CLIP. Genomics, proteomics & bioinformatics, 16(2), 136.

Gruber AJ, et al. (2018) Terminal exon characterization with TECtool reveals an abundance of cell-specific isoforms. Nature methods, 15(10), 832.

Winter DJ, et al. (2015) Whole Genome Sequencing of Field Isolates Reveals Extensive Genetic Diversity in Plasmodium vivax from Colombia. PLoS neglected tropical diseases, 9(12), e0004252.