

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: 20260810T040752+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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Delamonica B, et al. (2026) Exon Targeted Retrieval and Classification Toolbox (ExTRaCT): a gene search pipeline to find APOBEC3 Z-domains in novel bat genomes. bioRxiv : the preprint server for biology.

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. Cancer research, 86(7), 1769.

Vuong TT, et al. (2026) DNA Methyltransferase Inhibition Prevents Platinum-Induced Ovarian Cancer Stem Cell Enrichment. Cancer research communications, 6(7), 1721.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. Stem cell reports, 21(7), 102968.

Xie B, et al. (2025) Noncoding function of super enhancer derived CpoX pre-mRNA in modulating neighbouring gene expression and chromatin interactions. RNA biology, 22(1), 1.

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.

Piovani L, et al. (2025) The genomic origin of the unique chaetognath body plan. Nature, 645(8082), 964.

Lopez-Pajares V, et al. (2025) Glucose modulates IRF6 transcription factor dimerization to enable epidermal differentiation. Cell stem cell, 32(5), 795.

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.

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.

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.

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.

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.

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).

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