Resource Summary Report

Generated by Kravitz on Sep 10, 2026

bwtool

RRID:SCR_003035
Type: Tool

Proper Citation

bwtool (RRID:SCR_003035)

Resource Information

URL: https://github.com/CRG-Barcelona/bwtool/wiki

Proper Citation: bwtool (RRID:SCR_003035)

Description: A command-line utility for bigWig files designed to read bigWig files rapidly and efficiently, providing functionality for extracting data and summarizing it in several ways, globally or at specific regions. Its functionality is subdivided into subprograms that roughly fall into three categories: data extraction, analysis, and data modification, although e.g. in the case of the matrix program or the sax program, the boundary between data extraction and analysis isn't very strong. The data modification programs all have the behavior that a bigWig is inputted and a new bigWig is outputted.

Resource Type: software resource

Defining Citation: PMID:2448936

Keywords: standalone software, unix/linux, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: bwtool

Resource ID: SCR_003035

Alternate IDs: biotools:bwtool, OMICS_05125

Alternate URLs: https://bio.tools/bwtool

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260905T132457+0000

Ratings and Alerts

No rating or validation information has been found for bwtool.

No alerts have been found for bwtool.

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 Kravitz .

Kuli??ski TM, et al. (2026) DIS3 mutations enhance AID-driven translocations during B-cell activation, promoting transformation to multiple myeloma. Nature communications, 17(1).

So CL, et al. (2025) TFE3 fusion oncoprotein condensates drive transcriptional reprogramming and cancer progression in translocation renal cell carcinoma. Cell reports, 44(4), 115539.

Li J, et al. (2025) Single-nucleus transcriptional and chromatin accessible profiles reveal critical cell types and molecular architecture underlying chicken sex determination. Journal of advanced research, 70, 29.

Mondal S, et al. (2025) The Super Enhancer-Driven Long Noncoding RNA PRKCQ-AS1 Promotes Neuroblastoma Tumorigenesis by Interacting With MSI2 Protein and Is Targetable by Small Molecule Compounds. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2412520.

Morikawa M, et al. (2025) SMAD1/5-mediated recruitment of the histone demethylase KDM1A controls cell fate programs in embryonic stem cells. The Journal of biological chemistry, 301(9), 110591.

Masoudi-Sobhanzadeh Y, et al. (2024) Interpretable deep residual network uncovers nucleosome positioning and associated features. Nucleic acids research, 52(15), 8734.

Zhang Q, et al. (2024) Variation of C-terminal domain governs RNA polymerase II genomic locations and alternative splicing in eukaryotic transcription. Nature communications, 15(1), 7985.

Abassah-Oppong S, et al. (2024) A gene desert required for regulatory control of pleiotropic Shox2 expression and embryonic survival. Nature communications, 15(1), 8793.

Chambers C, et al. (2023) SWI/SNF Blockade Disrupts PU.1-Directed Enhancer Programs in Normal Hematopoietic Cells and Acute Myeloid Leukemia. Cancer research, 83(7), 983.

Tammer L, et al. (2022) Gene architecture directs splicing outcome in separate nuclear spatial regions. Molecular cell, 82(5), 1021.

Dahlet T, et al. (2021) E2F6 initiates stable epigenetic silencing of germline genes during embryonic development. Nature communications, 12(1), 3582.

Aleman JR, et al. (2021) Correct dosage of X chromosome transcription is controlled by a nuclear pore component. Cell reports, 35(11), 109236.

Harris RA, et al. (2020) Unusual sequence characteristics of human chromosome 19 are conserved across 11 nonhuman primates. BMC evolutionary biology, 20(1), 33.

Nativio R, et al. (2020) An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. Nature genetics, 52(10), 1024.

Wells D, et al. (2020) ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. eLife, 9.

Samee MAH, et al. (2019) A De Novo Shape Motif Discovery Algorithm Reveals Preferences of Transcription Factors for DNA Shape Beyond Sequence Motifs. Cell systems, 8(1), 27.

Scharer CD, et al. (2019) Epigenetic programming underpins B cell dysfunction in human SLE. Nature immunology, 20(8), 1071.

Gan W, et al. (2019) A computational method to predict topologically associating domain boundaries combining histone Marks and sequence information. BMC genomics, 20(Suppl 13), 980.

Org T, et al. (2019) Genome-wide histone modification profiling of inner cell mass and trophectoderm of bovine blastocysts by RAT-ChIP. PloS one, 14(11), e0225801.

Hsieh YC, et al. (2019) Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA Splicing and Neurodegeneration in Alzheimer's Disease. Cell reports, 29(2), 301.