

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

BroadPeak

RRID:SCR_001857

Type: Tool

Proper Citation

BroadPeak (RRID:SCR_001857)

Resource Information

URL: <https://jordan.biosci.gatech.edu/software/broadpeak/index.html>

Proper Citation: BroadPeak (RRID:SCR_001857)

Description: Algorithm for identifying broad peaks in diffuse ChIP-seq datasets.

Resource Type: software resource, algorithm resource

Defining Citation: [PMID:23300134](#)

Keywords: source code, algorithm, chip seq, rna, dna, sequencing, peak calling

Availability: Free, Available for download, Freely available

Resource Name: BroadPeak

Resource ID: SCR_001857

Alternate IDs: OMICS_00433

Old URLs: <http://jordan.biology.gatech.edu/page/software/broadpeak/>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260805T044029+0000

Ratings and Alerts

No rating or validation information has been found for BroadPeak.

No alerts have been found for BroadPeak.

Data and Source Information

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *Nature*, 649(8095), 152.

Sankar V, et al. (2025) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *bioRxiv : the preprint server for biology*.

Cunniff PJ, et al. (2025) KLF5 enables dichotomous lineage programs in pancreatic cancer via the AAA+ ATPase coactivators RUVBL1 and RUVBL2. *Nature communications*, 16(1), 9996.

Huang H, et al. (2025) Deciphering the role of histone modifications in memory and exhausted CD8 T cells. *Scientific reports*, 15(1), 17359.

Weichenhan D, et al. (2024) Altered enhancer-promoter interaction leads to MNX1 expression in pediatric acute myeloid leukemia with t(7;12)(q36;p13). *Blood advances*, 8(19), 5100.

Xiong S, et al. (2024) Super enhancer acquisition drives expression of oncogenic PPP1R15B that regulates protein homeostasis in multiple myeloma. *Nature communications*, 15(1), 6810.

Kim SJ, et al. (2023) EZH2 inhibition stimulates repetitive element expression and viral mimicry in resting splenic B cells. *The EMBO journal*, 42(24), e114462.

Maia-Silva D, et al. (2023) Marker-based CRISPR screening reveals a MED12-p63 interaction that activates basal identity in pancreatic ductal adenocarcinoma. *bioRxiv : the preprint server for biology*.

Baxter M, et al. (2022) Circadian clock function does not require the histone methyltransferase MLL3. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 36(7), e22356.

Delacher M, et al. (2021) Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory T cells. *Immunity*, 54(4), 702.

Smallegan MJ, et al. (2021) Genome-wide binding analysis of 195 DNA binding proteins reveals "reservoir" promoters and human specific SVA-repeat family regulation. *PloS one*, 16(6), e0237055.

Richter F, et al. (2020) Genomic analyses implicate noncoding de novo variants in congenital heart disease. *Nature genetics*, 52(8), 769.

Oda Y, et al. (2020) Deletion of Mediator 1 suppresses TGF β signaling leading to changes in epidermal lineages and regeneration. PLoS one, 15(8), e0238076.

Chèneby J, et al. (2020) ReMap 2020: a database of regulatory regions from an integrative analysis of Human and Arabidopsis DNA-binding sequencing experiments. Nucleic acids research, 48(D1), D180.

Bae S, et al. (2020) H3K4me1 Distribution Predicts Transcription State and Poising at Promoters. Frontiers in cell and developmental biology, 8, 289.

Navarro C, et al. (2020) An embryonic stem cell-specific heterochromatin state promotes core histone exchange in the absence of DNA accessibility. Nature communications, 11(1), 5095.

Boshans LL, et al. (2019) The Chromatin Environment Around Interneuron Genes in Oligodendrocyte Precursor Cells and Their Potential for Interneuron Reprogramming. Frontiers in neuroscience, 13, 829.

Hao X, et al. (2018) Identifying and exploiting trait-relevant tissues with multiple functional annotations in genome-wide association studies. PLoS genetics, 14(1), e1007186.

Melé M, et al. (2017) Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs. Genome research, 27(1), 27.

Kanduri C, et al. (2017) Genome build information is an essential part of genomic track files. Genome biology, 18(1), 175.