

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 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: algorithm resource, software 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: 20260815T182940+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 29 mentions in open access literature.

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

Hoxie HR, et al. (2026) Multiple modes of transcriptional regulation by the nuclear hormone receptor RAR γ in human squamous cell carcinoma. The Journal of biological chemistry, 302(1), 110965.

Davis E, et al. (2026) Ezh2 Control of Bivalent Genes Fine-Tunes Developmental Competence During Retinogenesis. Investigative ophthalmology & visual science, 67(6), 18.

Qin M, et al. (2026) SLC13A2-transported citrate remodels transcriptional regulation through protein acetylation to suppress tumor growth. Science advances, 12(15), eaec4368.

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

Riley DM, et al. (2026) Functional genomics analysis of developing zebrafish and human endoderm reveals highly conserved cis-regulatory modules acting during vertebrate organogenesis. Genome research, 36(4), 695.

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.

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.

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

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.

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.

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