Resource Summary Report

Generated by NIF on Apr 18, 2025

BroadPeak

RRID:SCR_001857
Type: Tool

Proper Citation

BroadPeak (RRID:SCR_001857)

Resource Information

URL: http://jordan.biology.gatech.edu/page/software/broadpeak/

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

Funding:

Availability: Open source, Available for download

Resource Name: BroadPeak

Resource ID: SCR_001857

Alternate IDs: OMICS_00433

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250418T054948+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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? 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.

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 Reprograming. 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.

Avila Cobos F, et al. (2017) Zipper plot: visualizing transcriptional activity of genomic regions. BMC bioinformatics, 18(1), 231.

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

Labrie V, et al. (2016) Lactase nonpersistence is directed by DNA-variation-dependent epigenetic aging. Nature structural & molecular biology, 23(6), 566.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Silva TC, et al. (2016) TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 5, 1542.