# **Resource Summary Report**

Generated by <u>dkNET</u> on May 17, 2025

# **BayesPeak**

RRID:SCR\_013011 Type: Tool

**Proper Citation** 

BayesPeak (RRID:SCR\_013011)

### **Resource Information**

URL: http://www.bioconductor.org/packages/2.12/bioc/html/BayesPeak.html

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**Description:** Software package that is an implementation of the BayesPeak algorithm for peak-calling in ChIP-seq data.

Abbreviations: BayesPeak

Synonyms: BayesPeak - Bayesian Analysis of ChIP-seq Data

Resource Type: software resource

Funding:

Resource Name: BayesPeak

Resource ID: SCR\_013011

Alternate IDs: OMICS\_00432

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250420T014629+0000

#### **Ratings and Alerts**

No rating or validation information has been found for BayesPeak.

No alerts have been found for BayesPeak.

## Data and Source Information

Source: SciCrunch Registry

#### **Usage and Citation Metrics**

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Calderon RH, et al. (2022) Shade triggers posttranscriptional PHYTOCHROME-INTERACTING FACTOR-dependent increases in H3K4 trimethylation. Plant physiology, 190(3), 1915.

Macioszek A, et al. (2021) HERON: A Novel Tool Enables Identification of Long, Weakly Enriched Genomic Domains in ChIP-seq Data. International journal of molecular sciences, 22(15).

Hristova RH, et al. (2020) Deregulated levels of RUVBL1 induce transcription-dependent replication stress. The international journal of biochemistry & cell biology, 128, 105839.

Karányi Z, et al. (2018) Nuclear dynamics of the Set1C subunit Spp1 prepares meiotic recombination sites for break formation. The Journal of cell biology, 217(10), 3398.

Kuang Z, et al. (2018) Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. Nucleic acids research, 46(1), e2.

Vergara Z, et al. (2017) Retrotransposons are specified as DNA replication origins in the gene-poor regions of Arabidopsis heterochromatin. Nucleic acids research, 45(14), 8358.

Giner-Lamia J, et al. (2017) Identification of the direct regulon of NtcA during early acclimation to nitrogen starvation in the cyanobacterium Synechocystis sp. PCC 6803. Nucleic acids research, 45(20), 11800.

Cuscó P, et al. (2016) Zerone: a ChIP-seq discretizer for multiple replicates with built-in quality control. Bioinformatics (Oxford, England), 32(19), 2896.

Jayaram N, et al. (2016) Evaluating tools for transcription factor binding site prediction. BMC bioinformatics, 17(1), 547.

Ladurner R, et al. (2016) Sororin actively maintains sister chromatid cohesion. The EMBO journal, 35(6), 635.

Zafar A, et al. (2015) The role of protein kinase-C theta in control of epithelial to mesenchymal transition and cancer stem cell formation. Genomics data, 3, 28.

Eyboulet F, et al. (2015) Mediator independently orchestrates multiple steps of preinitiation

complex assembly in vivo. Nucleic acids research, 43(19), 9214.

Okamura T, et al. (2015) TGF-?3-expressing CD4+CD25(-)LAG3+ regulatory T cells control humoral immune responses. Nature communications, 6, 6329.