

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

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>

Proper Citation: BayesPeak (RRID:SCR_013011)

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

Resource Name: BayesPeak

Resource ID: SCR_013011

Alternate IDs: OMICS_00432

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T195757+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 [Kravitz](#) .

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.

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

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

Eyboulet F, et al. (2015) Mediator independently orchestrates multiple steps of preinitiation complex assembly in vivo. *Nucleic acids research*, 43(19), 9214.

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.

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