Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

dPeak

RRID:SCR_010855
Type: Tool

Proper Citation

dPeak (RRID:SCR_010855)

Resource Information

URL: http://www.stat.wisc.edu/~chungdon/dpeak/

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Description: A high resolution transcription factor binding site (TFBS) identification (deconvolution) algorithm. dPeak implements a probabilistic model that accurately describes ChIP-exo and ChIP-Seq data generation process for both the SET and PET assays.

Abbreviations: dPeak

Synonyms: dPeak: High Resolution TFBS Identification using ChIP-exo PET and SET ChIP-Seq Data

Resource Type: software resource

Defining Citation: PMID:24146601

Keywords: chip-seq

Resource Name: dPeak

Resource ID: SCR_010855

Alternate IDs: OMICS_00437

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260912T195724+0000

Ratings and Alerts

No rating or validation information has been found for dPeak.

No alerts have been found for dPeak.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Kolade JO, et al. (2025) The impact of a superfood chocolate beverage on indices of peripheral vascular function. Physiological reports, 13(13), e70448.

Bu L, et al. (2024) CHD6 eviction of promoter nucleosomes maintains housekeeping transcriptional program in prostate cancer. Molecular therapy. Nucleic acids, 35(4), 102397.

Zandi B, et al. (2021) Deep learning-based pupil model predicts time and spectral dependent light responses. Scientific reports, 11(1), 841.

Myers KS, et al. (2015) Defining bacterial regulons using ChIP-seq. Methods (San Diego, Calif.), 86, 80.