Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 24, 2025

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

Funding:

Resource Name: dPeak

Resource ID: SCR_010855

Alternate IDs: OMICS_00437

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250519T203628+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 3 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.