## **Resource Summary Report**

Generated by RRID on May 21, 2025

# <u>dPeak</u>

RRID:SCR\_010855

Type: Tool

## **Proper Citation**

dPeak (RRID:SCR\_010855)

#### **Resource Information**

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

**Proper Citation:** dPeak (RRID:SCR\_010855)

**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 RRID.

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.