

Resource Summary Report

Generated by T1D on Aug 1, 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](https://pubmed.ncbi.nlm.nih.gov/24146601/)

Keywords: chip-seq

Resource Name: dPeak

Resource ID: SCR_010855

Alternate IDs: OMICS_00437

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190417+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 [T1D](#).

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.