

Resource Summary Report

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PeaKDEck

RRID:SCR_004268

Type: Tool

Proper Citation

PeaKDEck (RRID:SCR_004268)

Resource Information

URL: <http://www.ccmp.ox.ac.uk/peakdeck>

Proper Citation: PeaKDEck (RRID:SCR_004268)

Description: A peak-calling software program for DNaseI-seq data.

Abbreviations: PeaKDEck

Resource Type: software resource

Defining Citation: [PMID:24407222](#)

Keywords: perl, command line, gui

Resource Name: PeaKDEck

Resource ID: SCR_004268

Alternate IDs: OMICS_02207

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260725T190551+0000

Ratings and Alerts

No rating or validation information has been found for PeaKDEck.

No alerts have been found for PeaKDEck.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Saotome M, et al. (2024) Genomic transcription factor binding site selection is edited by the chromatin remodeling factor CHD4. *Nucleic acids research*, 52(7), 3607.

Wang Y, et al. (2024) Disruption of Super-Enhancers in Activated Pancreatic Stellate Cells Facilitates Chemotherapy and Immunotherapy in Pancreatic Cancer. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(16), e2308637.

Gabitto MI, et al. (2020) Characterizing chromatin landscape from aggregate and single-cell genomic assays using flexible duration modeling. *Nature communications*, 11(1), 747.

Johnson JS, et al. (2020) A Comprehensive Map of the Monocyte-Derived Dendritic Cell Transcriptional Network Engaged upon Innate Sensing of HIV. *Cell reports*, 30(3), 914.

Lhoumaud P, et al. (2019) EpiMethylTag: simultaneous detection of ATAC-seq or ChIP-seq signals with DNA methylation. *Genome biology*, 20(1), 248.

Miraldi ER, et al. (2019) Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. *Genome research*, 29(3), 449.

Gundra UM, et al. (2017) Vitamin A mediates conversion of monocyte-derived macrophages into tissue-resident macrophages during alternative activation. *Nature immunology*, 18(6), 642.

Ponnaluri VKC, et al. (2017) NicE-seq: high resolution open chromatin profiling. *Genome biology*, 18(1), 122.

Mullenders J, et al. (2015) Cohesin loss alters adult hematopoietic stem cell homeostasis, leading to myeloproliferative neoplasms. *The Journal of experimental medicine*, 212(11), 1833.

Reschen ME, et al. (2015) Lipid-induced epigenomic changes in human macrophages identify a coronary artery disease-associated variant that regulates PPAP2B Expression through Altered C/EBP-beta binding. *PLoS genetics*, 11(4), e1005061.