

Resource Summary Report

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ChIPseeqer

RRID:SCR_001545

Type: Tool

Proper Citation

ChIPseeqer (RRID:SCR_001545)

Resource Information

URL: <https://github.com/ElementoLab/ChIPseeqer>

Proper Citation: ChIPseeqer (RRID:SCR_001545)

Description: Software that provides a comprehensive framework for the analysis of ChIP-seq data.

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software

Defining Citation: [DOI:10.1186/1471-2105-12-277](https://doi.org/10.1186/1471-2105-12-277)

Keywords: sequence analysis, framework, ChIP, chip-seq, chip-seq data, sequencing, data, algorithm

Availability: Free, Available for download, Freely available

Resource Name: ChIPseeqer

Resource ID: SCR_001545

Alternate IDs: OMICS_00422

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260729T044013+0000

Ratings and Alerts

No rating or validation information has been found for ChIPseeqer.

No alerts have been found for ChIPseeqer.

Data and Source Information

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Meyer SN, et al. (2019) Unique and Shared Epigenetic Programs of the CREBBP and EP300 Acetyltransferases in Germinal Center B Cells Reveal Targetable Dependencies in Lymphoma. *Immunity*, 51(3), 535.

Verma N, et al. (2018) TET proteins safeguard bivalent promoters from de novo methylation in human embryonic stem cells. *Nature genetics*, 50(1), 83.

Brescia P, et al. (2018) MEF2B Instructs Germinal Center Development and Acts as an Oncogene in B Cell Lymphomagenesis. *Cancer cell*, 34(3), 453.

Teater M, et al. (2018) AICDA drives epigenetic heterogeneity and accelerates germinal center-derived lymphomagenesis. *Nature communications*, 9(1), 222.

Namous H, et al. (2018) Integrative analysis of methylomic and transcriptomic data in fetal sheep muscle tissues in response to maternal diet during pregnancy. *BMC genomics*, 19(1), 123.

Frattini S, et al. (2017) Genome-wide analysis of DNA methylation in hypothalamus and ovary of *Capra hircus*. *BMC genomics*, 18(1), 476.

Fish L, et al. (2016) Muscleblind-like 1 suppresses breast cancer metastatic colonization and stabilizes metastasis suppressor transcripts. *Genes & development*, 30(4), 386.

Deignan L, et al. (2016) Regulation of the BMP Signaling-Responsive Transcriptional Network in the *Drosophila* Embryo. *PLoS genetics*, 12(7), e1006164.

Pan H, et al. (2015) Epigenomic evolution in diffuse large B-cell lymphomas. *Nature communications*, 6, 6921.

Ceballos-Chávez M, et al. (2015) The chromatin Remodeler CHD8 is required for activation of progesterone receptor-dependent enhancers. *PLoS genetics*, 11(4), e1005174.

Kacmarczyk TJ, et al. (2015) Multiplexing of ChIP-Seq Samples in an Optimized Experimental Condition Has Minimal Impact on Peak Detection. *PloS one*, 10(6), e0129350.

Zhang J, et al. (2015) Disruption of KMT2D perturbs germinal center B cell development and promotes lymphomagenesis. *Nature medicine*, 21(10), 1190.

Hatzi K, et al. (2015) BCL6 orchestrates Tfh cell differentiation via multiple distinct mechanisms. *The Journal of experimental medicine*, 212(4), 539.

Walker SR, et al. (2015) The transcriptional modulator BCL6 as a molecular target for breast cancer therapy. *Oncogene*, 34(9), 1073.

Zhang X, et al. (2015) RNA-Seq and ChIP-Seq reveal SQSTM1/p62 as a key mediator of JunB suppression of NF- κ B-dependent inflammation. *The Journal of investigative dermatology*, 135(4), 1016.

Giannopoulou EG, et al. (2013) Inferring chromatin-bound protein complexes from genome-wide binding assays. *Genome research*, 23(8), 1295.

Giannopoulou EG, et al. (2011) An integrated ChIP-seq analysis platform with customizable workflows. *BMC bioinformatics*, 12, 277.

Qin ZS, et al. (2010) HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. *BMC bioinformatics*, 11, 369.