

# 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:** data processing software, sequence analysis software, data analysis software, software resource, software application

**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:** 20260731T042617+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 [kravitz2](#) .

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.

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

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

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.

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

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.

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

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

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

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.