# Resource Summary Report

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## ChIPseeqer

RRID:SCR_001545
Type: Tool

### Proper Citation

ChIPseeqer (RRID:SCR_001545)

### Resource Information

**URL:** http://physiology.med.cornell.edu/faculty/elemento/lab/chipseq.shtml

**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, software application, data analysis software, sequence analysis software, software resource

**Defining Citation:** DOI:10.1186/1471-2105-12-277

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

**Funding:**

**Availability:** Available for download

**Resource Name:** ChIPseeqer

**Resource ID:** SCR_001545

**Alternate IDs:** OMICS_00422

**Record Creation Time:** 20220129T080208+0000

**Record Last Update:** 20250421T053244+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

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 18 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.


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.

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.

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

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

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

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

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

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.

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

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-?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.