

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

SICER

RRID:SCR_010843

Type: Tool

Proper Citation

SICER (RRID:SCR_010843)

Resource Information

URL: <http://home.gwu.edu/~wpeng/Software.htm>

Proper Citation: SICER (RRID:SCR_010843)

Description: A clustering software package for identification of enriched domains from histone modification ChIP-Seq data.

Abbreviations: SICER

Synonyms: SICER: A clustering approach for identification of enriched domains from histone modification ChIP-Seq data

Resource Type: software resource

Defining Citation: [PMID:19505939](#)

Keywords: python, bio.tools

Resource Name: SICER

Resource ID: SCR_010843

Alternate IDs: biotools:sicer, OMICS_00461

Alternate URLs: <https://bio.tools/sicer>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190703+0000

Ratings and Alerts

No rating or validation information has been found for SICER.

No alerts have been found for SICER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 409 mentions in open access literature.

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

Klenja-Skudrinja D, et al. (2025) Identification of a BACH1 lung cancer signature: A novel tool for understanding BACH1 biology and identifying new inhibitors. *Redox biology*, 85, 103789.

Colando S, et al. (2025) Selecting ChIP-seq normalization methods from the perspective of their technical conditions. *Briefings in bioinformatics*, 26(4).

Luo L, et al. (2025) PRC1-Mediated H2Aub Loop Formation and Function in Arabidopsis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(35), e04377.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. *medRxiv : the preprint server for health sciences*.

Zhang J, et al. (2025) Histone methyltransferases MLL2 and SETD1A/B play distinct roles in H3K4me3 deposition during the transition from totipotency to pluripotency. *The EMBO journal*, 44(2), 437.

Kosmara D, et al. (2025) The sex-biased chromatin modifier SMC1A promotes autoimmunity by shaping inflammatory pathways in patients with SLE. *Nature communications*, 16(1), 10350.

Otsuka N, et al. (2025) Small molecules and heat treatments reverse vernalization via epigenetic modification in Arabidopsis. *Communications biology*, 8(1), 108.

Hu SS, et al. (2025) PATTY corrects open chromatin bias for improved bulk and single-cell CUT&Tag profiling. *bioRxiv : the preprint server for biology*.

Wolf van der Meer J, et al. (2025) Hao-Fountain syndrome protein USP7 controls neuronal differentiation via BCOR-ncPRC1.1. *Genes & development*, 39(5-6), 401.

Perrella G, et al. (2025) TANDEM ZINC-FINGER/PLUS3 integrates light signaling and flowering regulatory pathways at the chromatin level. *The New phytologist*, 247(2), 706.

Brul?? B, et al. (2025) Accelerated epigenetic aging in Huntington's disease involves polycomb repressive complex 1. *Nature communications*, 16(1), 1550.

Yang Y, et al. (2025) TET2 deficiency increases the competitive advantage of hematopoietic stem and progenitor cells through upregulation of thrombopoietin receptor

signaling. *Nature communications*, 16(1), 2384.

Wan D, et al. (2025) Histone chaperone HIRA facilitates transcription elongation to regulate insulin sensitivity and obesity-associated adipose expansion. *bioRxiv : the preprint server for biology*.

Hassan O, et al. (2025) Inhibition of HDAC7 reprograms the histone H3.3 landscape to induce heterochromatin spreading and DNA replication defects in cancer cells. *The Journal of biological chemistry*, 301(10), 110732.

Fang J, et al. (2025) The context-dependent epigenetic and organogenesis programs determine 3D vs. 2D cellular fitness of MYC-driven murine liver cancer cells. *eLife*, 14.

Samo N, et al. (2025) Polycomb repressive complex 2 facilitates the transition from heterotrophy to photoautotrophy during seedling emergence. *The Plant cell*, 37(7).

Gupta NJ, et al. (2025) Chrom-Sig: de-noising 1D genomic profiles by signal processing methods. *Bioinformatics (Oxford, England)*, 41(12).

Rupasinghe M, et al. (2024) PRAMEL7 and CUL2 decrease NuRD stability to establish ground-state pluripotency. *EMBO reports*, 25(3), 1453.

Ohnezeit D, et al. (2024) Merkel cell polyomavirus small tumor antigen contributes to immune evasion by interfering with type I interferon signaling. *PLoS pathogens*, 20(8), e1012426.

Du K, et al. (2024) The chromatin remodeling factor OsINO80 promotes H3K27me3 and H3K9me2 deposition and maintains TE silencing in rice. *Nature communications*, 15(1), 10919.