

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 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 [SPARC SAWG](#) .

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.

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*.

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

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.