

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[scPrinter](#)

RRID:SCR_026644

Type: Tool

Proper Citation

scPrinter (RRID:SCR_026644)

Resource Information

URL: <https://github.com/buenrostrolab/scPrinter>

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Description: Software framework for multi-scale footprinting analysis of single-cell ATAC-seq data. Designed to identify and visualize regulatory elements that drive cell-type-specific gene expression programs through footprinting. Uses deep learning model to predict activity of transcription factors from single-cell ATAC-seq data. Provides suite of visualization tools to explore calculated multi-scale footprints.

Resource Type: data processing software, software application, data analysis software, source code, software resource

Defining Citation: [PMID:39843737](#)

Keywords: multi-scale footprinting analysis, single-cell ATAC-seq data, identify and visualize regulatory elements, predict activity of transcription factors,

Availability: Free, Available for download, Freely available

Resource Name: scPrinter

Resource ID: SCR_026644

License: MIT license

Record Creation Time: 20250326T060329+0000

Record Last Update: 20260815T042920+0000

Ratings and Alerts

No rating or validation information has been found for scPrinter.

No alerts have been found for scPrinter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Dickmann H, et al. (2026) Evaluating single-cell ATAC-seq atlasing technologies using sequence-to-function modeling. Nature communications, 17(1).

Dudek MF, et al. (2025) Protocol for discovering genetic variants associated with ATAC-seq footprint-inferred transcription factor binding. STAR protocols, 6(4), 104148.

Buenrostro J, et al. (2025) Clonal memory of colitis accumulates and promotes tumor growth. Research square.