

Resource Summary Report

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scHiCluster

RRID:SCR_027854

Type: Tool

Proper Citation

scHiCluster (RRID:SCR_027854)

Resource Information

URL: <https://github.com/zhoujt1994/scHiCluster>

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Description: Software Python package for single-cell chromosome contact data analysis. It includes the identification of cell types (clusters), loop calling in cell types, and domain and compartment calling in single cells. Facilitates visualization and comparison of single-cell 3D genomes.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:31235599](#)

Keywords: single-cell chromosome contact data analysis, single-cell, chromosome, contact, data analysis,

Funding: NHGRI R21 HG009274

Availability: Free, Available for download, Freely Available

Resource Name: scHiCluster

Resource ID: SCR_027854

License: MIT license

Record Creation Time: 20260108T070050+0000

Record Last Update: 20260815T183302+0000

Ratings and Alerts

No rating or validation information has been found for scHiCluster.

No alerts have been found for scHiCluster.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Ding W, et al. (2026) A Multimodal Single-Cell Epigenomic and 3D Genome Atlas of the Human Basal Ganglia. bioRxiv : the preprint server for biology.

Zheng Y, et al. (2022) Normalization and de-noising of single-cell Hi-C data with BandNorm and scVI-3D. Genome biology, 23(1), 222.