

# Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

## Sim3C

RRID:SCR\_015772

Type: Tool

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### Proper Citation

Sim3C (RRID:SCR\_015772)

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### Resource Information

**URL:** <https://github.com/cerebis/sim3C/tree/0.1>

**Proper Citation:** Sim3C (RRID:SCR\_015772)

**Description:** Software for read-pair simulation of 3C-based sequencing methodologies (HiC, Meta3C, DNase-HiC). Sim3C's potential applications include addressing questions directed at the spatial organization of DNA in samples of eukaryotic tissue, single cells, and microbial communities.

**Resource Type:** simulation software, software application, software resource

**Keywords:** hic, simulation, dna sequencing, python, 3c, read-pair simulation, chromosome conformation capture

**Funding:** Australian Research Council LP150100912;  
Education Investment Fund (EIF) ;  
National Collaborative Research Infrastructure Strategy (NCRIS)

**Availability:** Free, Available for download

**Resource Name:** Sim3C

**Resource ID:** SCR\_015772

**Alternate URLs:** <https://zenodo.org/badge/latestdoi/85548752>

**License:** GNU General Public License v3.0

**Record Creation Time:** 20220129T080327+0000

**Record Last Update:** 20260912T195830+0000

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### Ratings and Alerts

No rating or validation information has been found for Sim3C.

No alerts have been found for Sim3C.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Wang S, et al. (2023) SpecHLA enables full-resolution HLA typing from sequencing data. Cell reports methods, 3(9), 100589.

Taylor D, et al. (2022) Locus-specific chromatin profiling of evolutionarily young transposable elements. Nucleic acids research, 50(6), e33.

Magnitov MD, et al. (2020) Benchmark of software tools for prokaryotic chromosomal interaction domain identification. Bioinformatics (Oxford, England), 36(17), 4560.

DeMaere MZ, et al. (2019) bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. Genome biology, 20(1), 46.

DeMaere MZ, et al. (2018) Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. GigaScience, 7(2), 1.