

Resource Summary Report

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cooltools

RRID:SCR_026118

Type: Tool

Proper Citation

cooltools (RRID:SCR_026118)

Resource Information

URL: <https://github.com/open2c/cooltools>

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Description: Software suite of computational tools that enables flexible, scalable, and reproducible analysis of high-resolution contact frequency data. Provides suite of computational tools with paired python API and command line access, which facilitates workflows either on high-performance computing clusters or via custom analysis notebooks. As part of the Open2C ecosystem, cooltools also provides detailed introductions to key concepts in Hi-C-data analysis with interactive notebook documentation.

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:38709825](#)

Keywords: enables reproducible analysis, high-resolution contact frequency data, paired python API,

Funding: NIGMS R35 GM143116;
NHGRI UM1 HG011536;
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Availability: Free, Available for download, Freely available

Resource Name: cooltools

Resource ID: SCR_026118

License: MIT license

Record Creation Time: 20241203T053255+0000

Record Last Update: 20260815T183234+0000

Ratings and Alerts

No rating or validation information has been found for cooltools.

No alerts have been found for cooltools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Li Y, et al. (2026) Hi-C calibration by chemically induced chromosomal interactions. EMBO reports, 27(10), 2549.

Fu Y, et al. (2026) Topologically associating domains define the 3D genome architecture of mouse totipotent-like stem cells. The Journal of biological chemistry, 302(3), 111236.

Wang X, et al. (2026) Boosting the detection of enhancer-promoter loops via normalization methods for chromatin interaction data. Nature communications, 17(1).

Zhou Z, et al. (2026) Pan-3D Genome Analysis Reveals the Roles of Structural Variation in Chicken Chromatin Architectures, Domestication and Production Traits. Advanced science (Weinheim, Baden-Wuerttemberg, Germany), 13(24), e20068.

Playter C, et al. (2026) Reversibility of Nuclear and 3D Genomic Changes in Non-Cancerous Fibroblasts After Constricted Migration. bioRxiv : the preprint server for biology.

Obaji D, et al. (2026) TFIIIC regulates SMC complex binding and 3D DNA contacts between tRNA genes. bioRxiv : the preprint server for biology.

Jiang WJ, et al. (2026) Harmonizing single-cell 3D genome data with STARK and scNucleome. Genome biology, 27(1).

Chen Z, et al. (2026) Highly efficient chromatin conformation capture with post-enrichment in single cells by HiChew. Genome biology, 27(1).

Wu J, et al. (2026) Hi-C for genome-wide detection of enhancer-hijacking rearrangements in routine lymphoid cancer biopsies. Cell genomics, 6(5), 101166.

Smith RG, et al. (2025) Histone Acetylation Differentially Modulates CTCF-CTCF Loops and Intra-TAD Interactions. bioRxiv : the preprint server for biology.

Gong Y, et al. (2025) Multi-dimensional epigenomic dynamics converge on H3K4-mediated regulation of low-CO₂ adaptation in *Nannochloropsis oceanica*. Plant communications, 6(12), 101534.

Aharonoff A, et al. (2025) Parallel Evolution of X Chromosome-Specific Structural Maintenance of Chromosomes Complexes in Two Nematode Lineages. *Molecular biology and evolution*, 42(11).

Lucero K, et al. (2025) CTCF-RNA interactions orchestrate cell-specific chromatin loop organization. *Science advances*, 11(48), eady5507.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. *Molecular cell*, 85(1), 24.

Smaruj PN, et al. (2025) Interpreting the CTCF-mediated sequence grammar of genome folding with AkitaV2. *PLoS computational biology*, 21(2), e1012824.

Kim J, et al. (2025) Cohesin organizes 3D DNA contacts surrounding active enhancers in *C. elegans*. *Genome research*, 35(5), 1108.

Almassalha LM, et al. (2025) Chromatin conformation, gene transcription, and nucleosome remodeling as an emergent system. *Science advances*, 11(2), eadq6652.

Kim IV, et al. (2025) Chromatin loops are an ancestral hallmark of the animal regulatory genome. *Nature*, 642(8069), 1097.

Bai J, et al. (2025) Architectural transcription factors collectively shape nuclear radial positioning of chromatin contacts. *Science advances*, 11(35), eadw8040.

Wu H, et al. (2025) Single-cell Micro-C profiles 3D genome structures at high resolution and characterizes multi-enhancer hubs. *Nature genetics*, 57(7), 1777.