

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 resource, software toolkit, source code

Defining Citation: [PMID:38709825](#)

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

Funding: NIGMS R35 GM143116;
NHGRI UM1 HG011536;
NHGRI R01 HG003143

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: 20260801T191331+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 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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).

Hildebrand EM, et al. (2025) TOP2B is required for compartment strength changes upon retinoic acid treatment in SH-SY5Y cells. *Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology*, 33(1), 5.

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.

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.

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

Ege T, et al. (2025) Mapping of chromatin architecture and enhancer-promoter interactions in the cochlea. *Frontiers in molecular biosciences*, 12, 1683964.

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. *Cell genomics*, 4(2), 100484.

Liu P, et al. (2024) 3D chromatin maps of a brown alga reveal U/V sex chromosome spatial organization. *Nature communications*, 15(1), 9590.

Liu X, et al. (2024) Footprint-C reveals transcription factor modes in local clusters and long-range chromatin interactions. *Nature communications*, 15(1), 10922.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. *eLife*, 12.

Doronin SA, et al. (2024) Nucleoporin Elys attaches peripheral chromatin to the nuclear pores in interphase nuclei. *Communications biology*, 7(1), 783.

Cheng G, et al. (2024) High resolution maps of chromatin reorganization through mouse meiosis reveal novel features of the 3D meiotic structure. *bioRxiv : the preprint server for biology*.

Aharonoff A, et al. (2024) SMC-mediated dosage compensation in *C. elegans* evolved in the presence of an ancestral nematode mechanism. *bioRxiv : the preprint server for biology*.

Xie Y, et al. (2024) Spatial chromatin accessibility sequencing resolves high-order spatial interactions of epigenomic markers. *eLife*, 12.