

Resource Summary Report

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Cooler

RRID:SCR_024194

Type: Tool

Proper Citation

Cooler (RRID:SCR_024194)

Resource Information

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

Proper Citation: Cooler (RRID:SCR_024194)

Description: Software library for sparse, compressed, binary persistent storage format used to store genomic interaction data, such as Hi-C contact matrices. Scalable storage for Hi-C data and other genomically labeled arrays.

Synonyms: python-cooler

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:31290943](#)

Keywords: store genomic interaction data, scalable storage for Hi-C data, genomically labeled arrays storage,

Availability: Free, Available for download, Freely available,

Resource Name: Cooler

Resource ID: SCR_024194

Old URLs: <https://sources.debian.org/src/python3-cooler/>

License: BSD-3-Clause license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260821T194256+0000

Ratings and Alerts

No rating or validation information has been found for Cooler.

No alerts have been found for Cooler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 169 mentions in open access literature.

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

Lee J, et al. (2026) Structural variants in human congenital heart disease disrupt distal genomic regulatory contacts of developmental genes. *bioRxiv : the preprint server for biology*.

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*.

Zhang Y, et al. (2026) A conserved hormonal signalling-H2A.Z axis rapidly reorganizes 3D chromatin interactions in adipocyte thermogenesis. *Nature metabolism*, 8(5), 1086.

Piveteau V, et al. (2026) Condensin loop extrusion properties, roadblocks, and role in homology search during recombination in *S. cerevisiae*. *The EMBO journal*, 45(9), 3124.

Yeung CCS, et al. (2026) Evaluation of acute myeloid leukemia using genomic proximity mapping-based next generation cytogenomics. *Haematologica*, 111(7), 2330.

Tortora MMC, et al. (2026) The physical chemistry of interphase loop extrusion. *Cell genomics*, 6(3), 101098.

Hasegawa K, et al. (2026) Age-related decline in nuclear envelope LINC complex drives neuronal aging via axon initial segment dysfunction. *EMBO reports*, 27(13), 3788.

Adams NM, et al. (2026) Chromatin-mediated anticipatory control of type I interferon production in plasmacytoid dendritic cells. *Immunity*, 59(2), 270.

Boyce D, et al. (2025) The genome sequence of the Warty Knot-Horn moth, *Acrobasis repandana* Fabricius, 1798. *Wellcome open research*, 10, 50.

Geiser MF, et al. (2025) The genome sequence of a flea beetle, *Neocrepidodera transversa* (Marsham, 1802). *Wellcome open research*, 10, 62.

Crowley LM, et al. (2025) The genome sequence of a snail-killing fly, *Dichetophora obliterata* (Fabricius, 1805). *Wellcome open research*, 10, 176.

Sivell D, et al. (2025) The genome sequence of a carabid beetle, *Carabus problematicus* Herbst, 1786. Wellcome open research, 10, 59.

Wangwiwatsin A, et al. (2025) The genome sequence of the liver fluke *Opisthorchis viverrini* (Poirier, 1886) Stiles & Hassall, 1896. Wellcome open research, 10, 1.

Sivell O, et al. (2025) The genome sequence of the Small Red Damselfly, *Ceragrion tenellum* (de Villers, 1789). Wellcome open research, 10, 79.

Zilov D, et al. (2025) Genome structure and molecular phylogeny of the only Eurasian *Boechera* species, *Boechera falcata* (Brassicaceae). G3 (Bethesda, Md.), 15(7).

Sivell D, et al. (2025) The genome sequence of the click beetle, *Ampedus sanguinolentus sanguinolentus* (Schrank, 1776). Wellcome open research, 10, 96.

Shi G, et al. (2025) Static three-dimensional structures determine fast dynamics between distal loci pairs in interphase chromosomes. Science advances, 11(31), eadx1763.

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.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: *Phoxinus phoxinus*) provide evidence of haplotype diversity. GigaScience, 14.

Fletcher C, et al. (2025) The genome sequence of the European smelt, *Osmerus eperlanus* (Linnaeus, 1758). Wellcome open research, 10, 118.