

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 resource, software library, 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: 20260801T042919+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 159 mentions in open access literature.

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

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

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

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

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

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

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 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.

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

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.

van den Brand T, et al. (2025) A 3D genome compendium of breast cancer progression. *iScience*, 28(9), 113268.

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.

Falk S, et al. (2025) The genome sequence of the Coppice Mining Bee, *Andrena helvola* (Linnaeus, 1758). *Wellcome open research*, 10, 102.

Willink B, et al. (2025) The genome sequence of the Tropical Bluetail Damselfly, *Ischnura senegalensis* (Rambur, 1842). *Wellcome open research*, 10, 104.

Hutchinson F, et al. (2025) The genome sequence of the Maple Pug moth, *Eupithecia inturbata* (Hübner, 1817). *Wellcome open research*, 10, 141.

González-Almela E, et al. (2025) Herpes simplex virus type 1 reshapes host chromatin architecture via transcription machinery hijacking. *Nature communications*, 16(1), 5313.

Mitchell R, et al. (2025) The genome sequence of a soldier beetle, *Malthinus seriepunctatus* Kiesenwetter, 1851. *Wellcome open research*, 10, 80.

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

Boyes D, et al. (2025) The genome sequence of the Large Birch Bell moth, Large Birch Roller, *Epinotia brunnichana* (Linnaeus, 1767). *Wellcome open research*, 10, 101.

Barclay MVL, et al. (2025) The genome sequence of a longhorn beetle, *Rhagium mordax* (Degeer, 1775). *Wellcome open research*, 10, 51.