

Resource Summary Report

Generated by dkNET on May 20, 2025

Juicer

RRID:SCR_017226

Type: Tool

Proper Citation

Juicer (RRID:SCR_017226)

Resource Information

URL: <https://github.com/aidenlab/juicer.git>

Proper Citation: Juicer (RRID:SCR_017226)

Description: Software platform for analyzing kilobase resolution Hi-C data. Open source tool for analyzing terabase scale Hi-C datasets. Allows to transform raw sequence data into normalized contact maps.

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: [PMID:27467249](#)

Keywords: analysis, kilobase, resolution, Hi-C, data, terabase, dataset, transform, raw, sequence, normalized, contact, map

Funding: NIH Office of the Director DP2 OD008540; NHLBI U01 HL130010; NSF PHY-1427654; NHGRI HG006193; Welch Foundation ; Cancer Prevention Research Institute of Texas ; NVIDIA Research Center Award ; IBM University Challenge Award ; Google Research Award ; McNair Medical Institute Scholar Award ; President Early Career Award in Science and Engineering ; NHGRI HG003067; PD Soros Fellowship

Availability: Free, Available for download, Freely available

Resource Name: Juicer

Resource ID: SCR_017226

License: MIT License

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250519T203952+0000

Ratings and Alerts

No rating or validation information has been found for Juicer.

No alerts have been found for Juicer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 79 mentions in open access literature.

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

Jo S, et al. (2025) Unlocking saponin biosynthesis in soapwort. Nature chemical biology, 21(2), 215.

Xu Y, et al. (2024) Chromosome-level genome of the poultry shaft louse Menopon gallinae

provides insight into the host-switching and adaptive evolution of parasitic lice. *GigaScience*, 13(1).

Jiang Z, et al. (2024) Gene flow and an anomaly zone complicate phylogenomic inference in a rapidly radiated avian family (Prunellidae). *BMC biology*, 22(1), 49.

, et al. (2024) Genome assembly of the rare and endangered Grantham's camellia, *Camellia granthamiana*. *GigaByte* (Hong Kong, China), 2024, gigabyte124.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of *Peucedanum praeruptorum* Dunn provides insights into the genome evolution and coumarin biosynthesis. *GigaScience*, 13.

Souza-Borges CH, et al. (2024) De novo assembly and characterization of a highly degenerated ZW sex chromosome in the fish *Megaleporinus macrocephalus*. *GigaScience*, 13.

Huang Y, et al. (2024) A reference genome of Commelinaceae provides insights into the commelinids evolution and global spread of water hyacinth (*Pontederia crassipes*). *GigaScience*, 13.

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber *Chiridota heheva* and its hydrothermal adaptation. *GigaScience*, 13.

Yin D, et al. (2024) Telomere-to-telomere gap-free genome assembly of the endangered Yangtze finless porpoise and East Asian finless porpoise. *GigaScience*, 13.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. *GigaScience*, 13.

Cheng S, et al. (2024) Haplotype-resolved chromosome-level genome assembly of *Ehretia macrophylla*. *Scientific data*, 11(1), 589.

Ferguson S, et al. (2024) Exploring the role of polymorphic interspecies structural variants in reproductive isolation and adaptive divergence in *Eucalyptus*. *GigaScience*, 13.

Ma X, et al. (2024) Chromosome-level genome assembly of the freshwater mussel *Sinosolenaia oleivora* (Heude, 1877). *Scientific data*, 11(1), 606.

Švara A, et al. (2024) Advancing apple genetics research: *Malus coronaria* and *Malus ioensis* genomes and a gene family-based pangenome of native North American apples. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(5).

Shen X, et al. (2024) Exploring the cobia (*Rachycentron canadum*) genome: unveiling putative male heterogametic regions and identification of sex-specific markers. *GigaScience*, 13.

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. *GigaScience*, 13.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. *GigaScience*, 13.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. *GigaScience*, 13.

Emonet A, et al. (2024) Polyploid genome assembly of *Cardamine chenopodiifolia*. *GigaByte* (Hong Kong, China), 2024, gigabyte145.

, et al. (2024) Chromosome-level genome assembly of the common chiton, *Liolophura japonica* (Lischke, 1873). *GigaByte* (Hong Kong, China), 2024, gigabyte123.