Resource Summary Report

Generated by RRID on May 14, 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. Allowes to transform raw sequence data into normalized contact maps.

Resource Type: software resource, data analysis software, software application, 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;
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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: 20250514T061805+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 RRID.

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 Commelinales 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).

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

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

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

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

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

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