

Resource Summary Report

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Juicer

RRID:SCR_017226

Type: Tool

Proper Citation

Juicer (RRID:SCR_017226)

Resource Information

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

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

Defining Citation: [PMID:27467249](#)

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

Funding Agency: NIH Office of the Director , NHLBI , NSF , NHGRI , 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 , PD Soros Fellowship

Availability: Free, Available for download, Freely available

Resource Name: Juicer

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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 61 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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).

Chen Y, et al. (2024) An improved chromosome-level genome assembly of perennial ryegrass (Lolium perenne L.). GigaByte (Hong Kong, China), 2024, gigabyte112.

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

Ballard JWO, et al. (2023) The Australasian dingo archetype: De novo chromosome-length genome assembly, DNA methylome, and cranial morphology. bioRxiv : the preprint server for biology.

Kim J, et al. (2023) Cohesin mediated loop extrusion from active enhancers form chromatin jets in C. elegans. bioRxiv : the preprint server for biology.

Liu Z, et al. (2023) Chromosome-level genome assembly of the deep-sea snail Phymorhynchus buccinoides provides insights into the adaptation to the cold seep habitat. BMC genomics, 24(1), 679.

Ballard JWO, et al. (2023) The Australasian dingo archetype: de novo chromosome-length genome assembly, DNA methylome, and cranial morphology. GigaScience, 12.

Winter S, et al. (2023) A chromosome-scale high-contiguity genome assembly of the cheetah (*Acinonyx jubatus*). *The Journal of heredity*.

Herliana L, et al. (2023) A chromosome-level genome assembly of *Plantago ovata*. *Scientific reports*, 13(1), 1528.

Stefanova ME, et al. (2023) Doxorubicin Changes the Spatial Organization of the Genome around Active Promoters. *Cells*, 12(15).

Russ BE, et al. (2023) Active maintenance of CD8 + T cell naïvety through regulation of global genome architecture. *bioRxiv : the preprint server for biology*.

Singh S, et al. (2023) The fate of sex chromosomes during the evolution of monoicy from dioicy in liverworts. *Current biology : CB*, 33(17), 3597.

Russ BE, et al. (2023) Active maintenance of CD8+ T cell naïvety through regulation of global genome architecture. *Cell reports*, 42(10), 113301.

Dong Z, et al. (2023) A chromosome-level genome assembly of *Ostrea denselamellosa* provides initial insights into its evolution. *Genomics*, 115(2), 110582.

Ramesh B, et al. (2023) Improvements to the Gulf pipefish *Syngnathus scovelli* genome. *GigaByte (Hong Kong, China)*, 2023, gigabyte76.

He X, et al. (2022) The whole-genome assembly of an endangered Salicaceae species: *Chosenia arbutifolia* (Pall.) A. Skv. *GigaScience*, 11.

Mu X, et al. (2022) Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. *GigaScience*, 11.

Luo F, et al. (2022) A chromosome-level genome of the human blood fluke *Schistosoma japonicum* identifies the genomic basis of host-switching. *Cell reports*, 39(1), 110638.