

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

Defining Citation: [PMID:27467249](#)

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

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NHLBI U01 HL130010;
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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: 20260804T043701+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 108 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.

Ren L, et al. (2025) Chromosome-level genome assembly of the synanthropic fly *Chrysomya megacephala*: insights into oviposition location. BMC genomics, 26(1), 442.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. GigaScience, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Gardner JC, et al. (2025) Inter-chromosomal insertions at Xq27.1 associated with retinal dystrophy induce dysregulation of LINC00632 and CDR1as/ciRS-7. American journal of human genetics, 112(3), 523.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. GigaScience, 14.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. GigaByte (Hong Kong, China), 2025, gigabyte155.

Kim J, et al. (2025) Cohesin organizes 3D DNA contacts surrounding active enhancers in *C. elegans*. Genome research, 35(5), 1108.

Wang Y, et al. (2025) A chromosome-level genome assembly of *Electrophorus voltai*, a species of electric eel. Scientific data, 12(1), 1367.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Lee H, et al. (2025) Hi-GDT: A Hi-C-based 3D gene domain analysis tool for analyzing local chromatin contacts in plants. *GigaScience*, 14.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Dalgarno A, et al. (2025) Senescence-Associated Chromatin Rewiring Promotes Inflammation and Transposable Element Activation. *bioRxiv : the preprint server for biology*.

Lau NS, et al. (2025) Comparative genomics and multiomics analyses reveal the evolution and physiological basis of rubber biosynthesis in *Hevea* species. *GigaScience*, 14.

Gill R, et al. (2025) Dissecting regulatory non-coding GWAS loci reveals fibroblast causal genes with pathophysiological relevance to heart failure. *Nature communications*, 16(1), 9020.