

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: 20260806T054652+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 [PRECISE-TBI](#) .

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

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

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

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

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

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

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

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

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).

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.

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.