

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, software application, 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

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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: 20260808T190105+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 119 mentions in open access literature.

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

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3* (Bethesda, Md.), 16(2).

Dong H, et al. (2026) The genome of *Phlebotomus chinensis*, the primary vector of visceral leishmaniasis in China: insights from chromosome-level assembly and comparative analysis. *Infectious diseases of poverty*, 15(1), 20.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Obaji D, et al. (2026) TFIIIC regulates SMC complex binding and 3D DNA contacts between tRNA genes. *bioRxiv : the preprint server for biology*.

Reed KSM, et al. (2026) Genome reorganization and its functional impact during breast cancer progression. *eLife*, 14.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop,

Carthamus tinctorius L. GigaScience, 15.

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. The Journal of heredity, 117(2), 272.

Wu J, et al. (2026) Hi-C for genome-wide detection of enhancer-hijacking rearrangements in routine lymphoid cancer biopsies. Cell genomics, 6(5), 101166.

Choubey P, et al. (2026) Cohesin complex cooperates with PU.1 at super-enhancers to regulate the differentiation and identity of conventional dendritic cells. Cell reports, 45(5), 117331.

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.

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.

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.

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.