

Resource Summary Report

Generated by T1D on Aug 9, 2026

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

Funding: NIH Office of the Director DP2 OD008540;
NHLBI U01 HL130010;
NSF PHY-1427654;
NHGRI HG006193;
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 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 [T1D](#) .

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).

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).

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.

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.

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.

- Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *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.
- 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.
- Jo S, et al. (2025) Unlocking saponin biosynthesis in soapwort. *Nature chemical biology*, 21(2), 215.
- 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.
- 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.
- Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.
- Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.