

Resource Summary Report

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Canu

RRID:SCR_015880

Type: Tool

Proper Citation

Canu (RRID:SCR_015880)

Resource Information

URL: <https://github.com/marbl/canu>

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Description: Software for scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Canu is a fork of the Celera Assembler and is designed for high-noise single-molecule sequencing (such as the PacBio RS II/Sequel or Oxford Nanopore MinION).

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:28298431](#), [DOI:10.1101/071282](#)

Keywords: long-read, assembly, k-mer, weighting, repeat separation, adaptive, pacbio, single-molecule, sequencing, bio.tools

Funding: National Human Genome Research Institute ;
National Science Foundation NSF IOS-1237993;
US Department of Homeland Security (DHS) HSHQDC-07-C-00020

Availability: Free, Available for download

Resource Name: Canu

Resource ID: SCR_015880

Alternate IDs: OMICS_14592, biotools:canu

Alternate URLs: <http://canu.readthedocs.io/en/latest/>, <https://bio.tools/canu>,
<https://sources.debian.org/src/canu/>

License: GNU GENERAL PUBLIC LICENSE v2

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260905T132800+0000

Ratings and Alerts

No rating or validation information has been found for Canu.

No alerts have been found for Canu.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2451 mentions in open access literature.

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

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).

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in Mycobacterium tuberculosis constitutively generates subpopulations with distinct clinical phenotypes. iScience, 29(5), 115045.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. Current biology : CB, 36(7), 1659.

Gao C, et al. (2026) High-Quality Genome Assembly of Diplocarpon coronariae Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. Molecular ecology resources, 26(1), e70070.

Tan K, et al. (2026) Near-complete genome assembly of a transformation-efficient elite inbred line LH244 and its comparison with B73. Journal of integrative plant biology, 68(2), 366.

Dell M, et al. (2026) Chemical richness and diversity of uncultivated 'Entotheonella' symbionts in marine sponges. Nature chemical biology, 22(2), 217.

Ran Z, et al. (2026) Organellar genome evolution in Camellia tianeensis (Theaceae): comparative insights into RNA editing, codon usage, and DNA transfer between chloroplast and mitochondrion. BMC genomics, 27(1).

Liu W, et al. (2026) Photosynthesis-related genetic and transcriptomic variations contribute to adaptive trait diversity in global Arabidopsis thaliana populations. BMC plant biology, 26(1).

- Haase MAB, et al. (2026) Ancient co-option of LTR retrotransposons as yeast centromeres. *Nature*, 651(8107), 1004.
- Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.
- Breman FC, et al. (2026) Comparison of whole genome sequencing approaches for Capripox viruses. *BMC genomics*, 27(1), 174.
- Schaveling AS, et al. (2026) The potato cyst nematode *Globodera pallida* overcomes major potato resistance through selection on standing variation at a single locus. *The New phytologist*, 249(6), 3039.
- Scholtmeijer K, et al. (2026) Enabling breeding with the highly specific lignin-degrading white-rot fungus *Gelatoporia subvermispora*. *BMC microbiology*, 26(1), 85.
- Liu J, et al. (2026) Molecular basis of the short- and long-term osmoregulation capability in the euryhaline unicellular eukaryote *Paramecium calkinsi*. *mBio*, 17(4), e0303225.
- Tanoue T, et al. (2026) Microbiota-mediated induction of beige adipocytes in response to dietary cues. *Nature*, 653(8114), 499.
- Wu Z, et al. (2026) A gradient green-beard gene in fission yeast. *EMBO reports*, 27(8), 1904.
- Voges K, et al. (2026) *Anopheles (Kerteszia) cruzii*, the main malaria vector in the Brazilian Atlantic Forest, is a complex of at least five cryptic species. *Communications biology*, 9(1).
- Wang D, et al. (2026) Seroprevalence, isolation, comprehensive characterization, and pathogenicity of *Clostridium perfringens* strain from yak in Xizang, China. *Scientific reports*, 16(1).
- Dettman JR, et al. (2026) Evolution of genomic architecture of the plant-pathogenic fungus *Alternaria* revealed by comparative analyses of 12 chromosome-level assemblies. *Microbial genomics*, 12(4).
- Sur A, et al. (2026) Benchmarking Hi-C scaffolders using reference genomes and de novo assemblies. *Genome biology*, 27(1).