

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 [dkNET](#) .

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).