

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, software application, software resource, sequence analysis software, data processing software

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 ;
US Department of Homeland Security (DHS) HSHQDC-07-C-00020;
National Science Foundation NSF IOS-1237993

Availability: Free, Available for download

Resource Name: Canu

Resource ID: SCR_015880

Alternate IDs: biotools:canu, OMICS_14592

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: 20260801T190523+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 2255 mentions in open access literature.

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

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.

Hernandez-Bird J, et al. (2026) Resistance, heteroresistance, and fitness costs drive colistin treatment failure during *Acinetobacter baumannii* pneumonia. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2515303123.

Jeon JY, et al. (2026) Short-Read Pangenomes and Their Potential Utility in Population and Conservation Genomics. *Molecular ecology resources*, 26(1), e70060.

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. *G3 (Bethesda, Md.)*, 16(1).

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Starcevic A, et al. (2025) Long-read metagenomic sequencing negates inferred loss of cytosine methylation in *Myxosporea* (Cnidaria: Myxozoa). *GigaScience*, 14.

Dowell NL, et al. (2025) Loss of a major venom toxin gene in a Western Diamondback rattlesnake population. *PloS one*, 20(7), e0319316.

Hospodářská M, et al. (2025) Multiple Origins of Sex Chromosomes in *Nothobranchius* Killifishes. *Molecular ecology*, 34(16), e70029.

Hernandez-Bird J, et al. (2025) Resistance and heteroresistance as a consequence of colistin therapy during *Acinetobacter baumannii* murine pneumonia. *bioRxiv : the preprint server for biology*.

Chen J, et al. (2025) Whole genome sequencing of a novel carrageenan-degrading bacterium *Photobacterium rosenbergii* and oligosaccharide preparation. *Frontiers in microbiology*, 16, 1519074.

Wang T, et al. (2025) Molecular phylogeny and comparative chloroplast genome analysis of the type species *Crucigenia quadrata*. *BMC plant biology*, 25(1), 64.

Coulon PML, et al. (2025) Quorum sensing and DNA methylation play active roles in clinical *Burkholderia* phase variation. *Journal of bacteriology*, 207(3), e0053124.

Pan T, et al. (2025) Genomic insights and the conservation potential of captive breeding: The case of Chinese alligator. *Science advances*, 11(14), eadm7980.

Huang C, et al. (2025) A comparative genomic analysis at the chromosomal-level reveals evolutionary patterns of aphid chromosomes. *Communications biology*, 8(1), 427.

Major SR, et al. (2025) Novel and diverse features identified in the genomes of bacteria isolated from a hydrothermal vent plume. *Applied and environmental microbiology*, 91(4), e0259324.

Sampaio AM, et al. (2025) Diversification, loss, and virulence gains of the major effector *AvrStb6* during continental spread of the wheat pathogen *Zymoseptoria tritici*. *PLoS pathogens*, 21(3), e1012983.

Su Y, et al. (2025) Probiotic characteristics and whole genome sequencing of *Pediococcus pentosaceus* SNF15 and its protective effect on mice diarrhea induced by *Escherichia coli* K99. *Frontiers in veterinary science*, 12, 1524658.

Bruno M, et al. (2025) Young KRAB-zinc finger gene clusters are highly dynamic incubators of ERV-driven genetic heterogeneity in mice. *bioRxiv : the preprint server for biology*.

Saxena AS, et al. (2025) High rate of mutation and efficient removal by selection of structural variants from natural populations of *Caenorhabditis elegans*. *bioRxiv : the preprint server for biology*.