Canu

RRID:SCR_015880
Type: Tool

Proper Citation
Canu (RRID:SCR_015880)

Resource Information

**URL:** [https://github.com/marbl/canu](https://github.com/marbl/canu)

**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 Name:** Canu

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

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

**Resource ID:** SCR_015880

**Funding Agency:** National Human Genome Research Institute, National Science Foundation, US Department of Homeland Security (DHS)

**Related resources:** Celera assembler

**References:** [PMID:28298431](https://www.ncbi.nlm.nih.gov/pubmed/28298431)

**Availability:** Free, Available for download

**Website Status:** Last checked up
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 216 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](http://canu.readthedocs.io/en/latest/).


Loiseau V, et al. (2020) Wide spectrum and high frequency of genomic structural variation, including transposable elements, in large double-stranded DNA viruses. Virus evolution, 6(1), vez060.

Moser KA, et al. (2020) Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. Genome medicine,

Pfeiffer F, et al. (2020) Whole-genome comparison between the type strain of Halobacterium salinarum (DSM 3754) and the laboratory strains R1 and NRC-1. MicrobiologyOpen, 9(2), e974.


Deb S, et al. (2020) Draft Genome Sequence of Strain MB-10, Isolated from a Rice Field in India. Microbiology resource announcements, 9(6).
