

Resource Summary Report

Generated by [dkNET](#) on Aug 5, 2026

CCS

RRID:SCR_024379

Type: Tool

Proper Citation

CCS (RRID:SCR_024379)

Resource Information

URL: <https://github.com/PacificBiosciences/unanimity>

Proper Citation: CCS (RRID:SCR_024379)

Description: Software to generate highly accurate single molecule consensus reads.

Synonyms: ccs ; unanimity

Resource Type: software resource, source code

Keywords: HiFi Reads, generate highly accurate single molecule consensus reads, generate consensus reads,

Availability: Free, Available for download, Freely available,

Resource Name: CCS

Resource ID: SCR_024379

Alternate IDs: OMICS_26281

Alternate URLs: <https://sources.debian.org/src/unanimity/>

License: BSD 3-Clause Clear License

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260804T043816+0000

Ratings and Alerts

No rating or validation information has been found for CCS.

No alerts have been found for CCS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Liu R, et al. (2025) Chromosome-level reference genome and annotation of the Arctic fish *Anisarchus medius*. *Scientific data*, 12(1), 68.

Zhang D, et al. (2025) Chromosome level genome assembly of 'Wanfeng' almond (*Prunus dulcis*). *Scientific data*, 12(1), 179.

Zheng H, et al. (2025) Chromosome-level genome assembly of the *Phoxinus lagowskii*. *Scientific data*, 12(1), 1400.

Wang K, et al. (2025) Whole-genome variant detection in long-read sequencing data from ultra-low input patient samples. *medRxiv : the preprint server for health sciences*.

Han C, et al. (2025) The telomere-to-telomere chromosome-scale genome assembly of *Acremonium chrysogenum*. *Scientific data*, 12(1), 1378.

Zhang M, et al. (2025) Telomere-to-telomere genome assembly uncovers Wolbachia-driven recurrent male bottleneck effect and selection in a sawfly. *Communications biology*, 8(1), 1211.

Cui J, et al. (2025) Telomere-to-telomere *Phragmites australis* reference genome assembly with a B chromosome provides insights into its evolution and polysaccharide biosynthesis. *Communications biology*, 8(1), 73.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

She J, et al. (2024) Chromosome-level assembly of *Triplophysa yarkandensis* genome based on the single molecule real-time sequencing. *Scientific data*, 11(1), 39.

Gu Y, et al. (2024) Genomic insights into bamboo witches' broom disease: pathogenicity and phytohormone biosynthesis in *Aciculosporium take*. *Frontiers in microbiology*, 15, 1432979.

Wang Q, et al. (2024) A consensus genome of sika deer (*Cervus nippon*) and transcriptome analysis provided novel insights on the regulation mechanism of transcript factor in antler development. *BMC genomics*, 25(1), 617.

Li X, et al. (2024) The grasshopper genome reveals long-term gene content conservation of the X Chromosome and temporal variation in X Chromosome evolution. *Genome research*, 34(7), 997.

Wang ZH, et al. (2024) Genomic, transcriptomic, and metabolomic analyses provide insights into the evolution and development of a medicinal plant *Saposhnikovia divaricata* (Apiaceae). *Horticulture research*, 11(6), uhae105.

Xia W, et al. (2024) Haplotypes analysis reveals the genetic basis of type I CD36 deficiency. *Scientific reports*, 14(1), 23977.

Li H, et al. (2024) The structure and assembly mechanisms of T4-like cyanophages community in the South China Sea. *Microbiology spectrum*, 12(2), e0200223.

Cheng Y, et al. (2024) *Gossypium purpurascens* genome provides insight into the origin and domestication of upland cotton. *Journal of advanced research*, 56, 15.

Wang C, et al. (2024) Chromosome-level genome assembly of *Triplophysa bombifrons* using PacBio HiFi sequencing and Hi-C technologies. *Scientific data*, 11(1), 1451.

Li M, et al. (2024) Chromosome-level genome assembly of *Aquilaria yunnanensis*. *Scientific data*, 11(1), 790.

Li Y, et al. (2023) Multi-omics data provide insight into the adaptation of the glasshouse plant *Rheum nobile* to the alpine subnival zone. *Communications biology*, 6(1), 906.