

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Celera assembler

RRID:SCR_010750

Type: Tool

Proper Citation

Celera assembler (RRID:SCR_010750)

Resource Information

URL: http://sourceforge.net/apps/mediawiki/wgs-assembler/index.php?title=Main_Page

Proper Citation: Celera assembler (RRID:SCR_010750)

Description: A de novo whole-genome shotgun (WGS) DNA sequence assembler.

Abbreviations: Celera assembler

Resource Type: software resource

Availability: GNU General Public License, v2

Resource Name: Celera assembler

Resource ID: SCR_010750

Alternate IDs: OMICS_00009

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T132645+0000

Ratings and Alerts

No rating or validation information has been found for Celera assembler.

No alerts have been found for Celera assembler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Bi D, et al. (2026) Integrating ANI and phylogenies for re-evaluation of *Fusobacterium* taxonomy and disease associations. *Nature communications*, 17(1).

Long W, et al. (2026) Comprehensive Analysis of Wild Rice Mitochondrial Genomes Reveals Structural Variation, Repeat Dynamics, and the Evolution of orf182. *Plants* (Basel, Switzerland), 15(7).

Kosushkin SA, et al. (2026) Genome sequencing uncovers the history of the Russian desman's gradual population decline and contributes to the evolutionary history of *Talpidae*. *BMC ecology and evolution*, 26(1), 12.

Burtnick MN, et al. (2024) Identification of *Burkholderia cepacia* strains that express a *Burkholderia pseudomallei*-like capsular polysaccharide. *Microbiology spectrum*, 12(3), e0332123.

Shallom SJ, et al. (2023) Evolution of *Mycobacterium abscessus* in the human lung: Cumulative mutations and genomic rearrangement of porin genes in patient isolates. *Virulence*, 14(1), 2215602.

Leng H, et al. (2023) Identification of a deep-branching thermophilic clade sheds light on early bacterial evolution. *Nature communications*, 14(1), 4354.

Huene AL, et al. (2022) A family of unusual immunoglobulin superfamily genes in an invertebrate histocompatibility complex. *Proceedings of the National Academy of Sciences of the United States of America*, 119(40), e2207374119.

Wang H, et al. (2022) Next-Generation Sequencing of Four Mitochondrial Genomes of *Dolichovespula* (Hymenoptera: Vespidae) with a Phylogenetic Analysis and Divergence Time Estimation of Vespidae. *Animals : an open access journal from MDPI*, 12(21).

Xu Y, et al. (2021) Biogeographic and Evolutionary Patterns of Trace Element Utilization in Marine Microbial World. *Genomics, proteomics & bioinformatics*, 19(6), 958.

Cheng X, et al. (2021) Cadmium stress triggers significant metabolic reprogramming in *Enterococcus faecium* CX 2-6. *Computational and structural biotechnology journal*, 19, 5678.

Lin M, et al. (2021) Comparative Analysis of Genome of *Ehrlichia* sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. *BMC genomics*, 22(1), 11.

Liu P, et al. (2020) Physiological and genomic features of *Paraoceanicella profunda* gen. nov., sp. nov., a novel piezophile isolated from deep seawater of the Mariana Trench. *MicrobiologyOpen*, 9(2), e966.

Warr A, et al. (2020) An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, 9(6).

Barth JMI, et al. (2020) Stable species boundaries despite ten million years of hybridization in tropical eels. *Nature communications*, 11(1), 1433.

Mohanty I, et al. (2020) Multi-Omic Profiling of *Melophlus* Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. *Marine drugs*, 18(2).

Mu DS, et al. (2020) *Bradymonabacteria*, a novel bacterial predator group with versatile survival strategies in saline environments. *Microbiome*, 8(1), 126.

Deng C, et al. (2019) Metabolic engineering of *Corynebacterium glutamicum* S9114 based on whole-genome sequencing for efficient N-acetylglucosamine synthesis. *Synthetic and systems biotechnology*, 4(3), 120.

Wang S, et al. (2019) A Multidrug Resistance Plasmid pIMP26, Carrying blaIMP-26, fosA5, blaDHA-1, and qnrB4 in *Enterobacter cloacae*. *Scientific reports*, 9(1), 10212.

Takahashi Y, et al. (2019) Domesticating *Vigna stipulacea*: A Potential Legume Crop With Broad Resistance to Biotic Stresses. *Frontiers in plant science*, 10, 1607.

Ma Y, et al. (2019) The first two mitochondrial genomes of wood wasps (Hymenoptera: Symphyta): Novel gene rearrangements and higher-level phylogeny of the basal hymenopterans. *International journal of biological macromolecules*, 123, 1189.