Resource Summary Report

Generated by NIF on Apr 17, 2025

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

Funding:

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: 20250410T070018+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 56 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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).

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.

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

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.

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.

Lindblad KA, et al. (2019) Capture of complete ciliate chromosomes in single sequencing reads reveals widespread chromosome isoforms. BMC genomics, 20(1), 1037.

Bai CM, et al. (2019) RNA-seq of HaHV-1-infected abalones reveals a common transcriptional signature of Malacoherpesviruses. Scientific reports, 9(1), 938.

Bai CM, et al. (2019) Long-range PCR and high-throughput sequencing of Ostreid herpesvirus 1 indicate high genetic diversity and complex evolution process. Virology, 526, 81.