Resource Summary Report

Generated by dkNET on Apr 30, 2025

MaSuRCA

RRID:SCR_010691

Type: Tool

Proper Citation

MaSuRCA (RRID:SCR_010691)

Resource Information

URL: http://www.genome.umd.edu/masurca.html

Proper Citation: MaSuRCA (RRID:SCR_010691)

Description: A whole genome assembly software that combines the efficiency of the de

Bruijn graph and Overlap-Layout-Consensus (OLC) approaches.

Abbreviations: MaSuRCA

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: MaSuRCA

Resource ID: SCR 010691

Alternate IDs: OMICS_00020, biotools:masurca

Alternate URLs: https://bio.tools/masurca

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014506+0000

Ratings and Alerts

No rating or validation information has been found for MaSuRCA.

No alerts have been found for MaSuRCA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 422 mentions in open access literature.

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

Alejo-Jacuinde G, et al. (2025) Gene family rearrangements and transcriptional priming drive the evolution of vegetative desiccation tolerance in Selaginella. The Plant journal: for cell and molecular biology, 121(1), e17169.

Willemsen A, et al. (2025) Novel High-Quality Amoeba Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. Genome biology and evolution, 17(1).

Akdeniz Z, et al. (2025) The expanded genome of Hexamita inflata, a free-living diplomonad. Scientific data, 12(1), 192.

Patel J, et al. (2025) Whole genome sequencing, assembly and annotation of the Southern Ground Hornbill - Bucorvus leadbeateri. Scientific data, 12(1), 58.

Liu X, et al. (2025) Rumen DNA virome and its relationship with feed efficiency in dairy cows. Microbiome, 13(1), 14.

Nagy NA, et al. (2024) The updated genome of the Hungarian population of Aedes koreicus. Scientific reports, 14(1), 7545.

Poikela N, et al. (2024) Chromosomal Inversions and the Demography of Speciation in Drosophila montana and Drosophila flavomontana. Genome biology and evolution, 16(3).

Ermann Lundberg L, et al. (2024) Bifidobacterium longum subsp. longum BG-L47 boosts growth and activity of Limosilactobacillus reuteri DSM 17938 and its extracellular membrane vesicles. Applied and environmental microbiology, 90(7), e0024724.

Iqbal Z, et al. (2024) A New Species of Scymnus (Coleoptera, Coccinellidae) from Pakistan with Mitochondrial Genome and Its Phylogenetic Implications. Insects, 15(5).

Rey Redondo E, et al. (2024) Genomic characterisation and ecological distribution of Mantoniella tinhauana: a novel Mamiellophycean green alga from the Western Pacific. Frontiers in microbiology, 15, 1358574.

Fields PD, et al. (2024) Genome Evolution and Introgression in the New Zealand mud Snails Potamopyrgus estuarinus and Potamopyrgus kaitunuparaoa. Genome biology and evolution, 16(5).

Luan T, et al. (2024) Benchmarking short and long read polishing tools for nanopore assemblies: achieving near-perfect genomes for outbreak isolates. BMC genomics, 25(1), 679.

Granados-Casas AO, et al. (2024) Genomic Sequencing and Functional Analysis of the Ex-Type Strain of Malbranchea zuffiana. Journal of fungi (Basel, Switzerland), 10(9).

Murugesan SN, et al. (2024) Genome Assembly and Annotation of the Dark-Branded Bushbrown Butterfly Mycalesis mineus (Nymphalidae: Satyrinae). Genome biology and evolution, 16(3).

Zimmermann J, et al. (2024) Gut-associated functions are favored during microbiome assembly across a major part of C. elegans life. mBio, 15(5), e0001224.

Singh K, et al. (2024) Genome and transcriptome based comparative analysis of Tilletia indica to decipher the causal genes for pathogenicity of Karnal bunt in wheat. BMC plant biology, 24(1), 676.

Estrada R, et al. (2024) Draft genome sequence data of Fusarium verticillioides strain REC01, a phytopathogen isolated from a Peruvian maize. Data in brief, 57, 110951.

van Dam L, et al. (2024) GastronOmics: Edibility and safety of mycelium of the oyster mushroom Pleurotus ostreatus. Current research in food science, 9, 100866.

Sigova EA, et al. (2024) Nanopore Data-Driven T2T Genome Assemblies of Colletotrichum lini Strains. Journal of fungi (Basel, Switzerland), 10(12).

Zuza A, et al. (2024) An exploration of unusual antimicrobial resistance phenotypes in Salmonella Typhi from Blantyre, Malawi reveals the ongoing role of IncHI1 plasmids. Gates open research, 8, 143.