

Resource Summary Report

Generated by [dkNET](#) on Sep 21, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MaSuRCA

Resource Type: software resource

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260919T195158+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 468 mentions in open access literature.

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

Zheng C, et al. (2026) Biological characteristics and genetics differentiation of smut fungi in Coix L. *Frontiers in microbiology*, 17, 1746178.

Dong W, et al. (2026) PHR-Mediated Pi Starvation Response Mobile Messenger RNAs Represent Noncoding Transcripts in Recipient Tissues. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e02911.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Whelan R, et al. (2025) Genetic and phenotypic analysis of the virulence plasmid of a non-Shigatoxigenic enteroaggregative *Escherichia coli* O104:H4 outbreak strain. *Microbiology* (Reading, England), 171(3).

Zhang J, et al. (2025) Chromosome-level genome and annotation of the tetraploid *Rhodiola kirilowii*. *Scientific data*, 12(1), 620.

Oda AH, et al. (2025) Advantages of Mutant Generation by Genome Rearrangements of Non-Conventional Yeast via Direct Nuclease Transfection. *Genes to cells : devoted to molecular & cellular mechanisms*, 30(2), e70010.

Secker B, et al. (2025) Genomic and phenotypic characterisation of *Pseudomonas aeruginosa* isolates from canine otitis externa reveals high-risk sequence types identical to those found in human nosocomial infections. *Frontiers in microbiology*, 16, 1526843.

Feng H, et al. (2025) Genome and Tissue-Specific Transcriptome of the Tropical Milkweed (*Asclepias curassavica*). *Plant direct*, 9(3), e70031.

Dombey R, et al. (2025) Atypical epigenetic and small RNA control of degenerated transposons and their fragments in clonally reproducing *Spirodela polyrhiza*. *Genome research*, 35(3), 522.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Chen P, et al. (2025) Chromosome-scale assembly of *Artemia tibetiana* genome, first aquatic invertebrate genome from Tibet Plateau. *Scientific data*, 12(1), 777.

Catalán A, et al. (2025) Sex-biased Migration and Demographic History of the Big European Firefly *Lampyris noctiluca*. *Molecular biology and evolution*, 42(6).

Van Laere Y, et al. (2025) Assessing the authenticity and purity of a commercial *Bacillus thuringiensis* bioinsecticide through whole genome sequencing and metagenomics approaches. *Frontiers in microbiology*, 16, 1532788.

Lerminiaux N, et al. (2025) Plasmid genomic epidemiology of bla NDM carbapenemase-producing *Enterobacterales* in Canada from 2010 to 2023. *Microbial genomics*, 11(8).

Muñoz-Barrera A, et al. (2025) Benchmarking of bioinformatics tools for the hybrid de novo assembly of human and non-human whole-genome sequencing data. *Computational and structural biotechnology journal*, 27, 3099.

Chen CC, et al. (2025) High-quality chromosome-level genome of three *Meretrix* species using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 1141.

Willemssen 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).

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.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Schmidt TL, et al. (2025) Populations of the Australian Saltmarsh Mosquito *Aedes vigilax* Vary Between Panmixia and Temporally Stable Local Genetic Structure. *Evolutionary applications*, 18(6), e70119.