

Resource Summary Report

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SMARTdenovo

RRID:SCR_017622

Type: Tool

Proper Citation

SMARTdenovo (RRID:SCR_017622)

Resource Information

URL: <https://github.com/ruanjue/smartdenovo>

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Description: Software tool as de novo assembler for PacBio and Oxford Nanopore data. It produces assembly from all-vs-all raw read alignments without error correction stage. Allows to read overlapping, rescue missing overlaps, identify low-quality regions and chimaera and produce better consensus.

Resource Type: alignment software, data processing software, image analysis software, software application, software resource

Keywords: De novo, assembler, PacBio, Oxford Nanopore, data, sequence, raw, read, alignment, error, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SMARTdenovo

Resource ID: SCR_017622

Alternate IDs: BioTools:SMARTdenovo, biotools:SMARTdenovo

Alternate URLs: <https://bio.tools/SMARTdenovo>, <https://bio.tools/SMARTdenovo>, <https://bio.tools/SMARTdenovo>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260905T133009+0000

Ratings and Alerts

No rating or validation information has been found for SMARTdenovo.

No alerts have been found for SMARTdenovo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 191 mentions in open access literature.

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

Chen D, et al. (2026) Analysis of mobile genetic elements carrying mcr genes in clinical *Leclercia* spp. isolates. *BMC microbiology*, 26(1).

Luan Y, et al. (2026) Mechanisms of Aristolochic Acid Resistance in Specialist Butterflies and Evolutionary Insights for Potential Protective Pathways. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), e18072.

Yulfo-Soto GE, et al. (2026) First genome and transcription factor profile for *Asimina triloba*, a native North American fruit tree. *The plant genome*, 19(1), e70181.

Tian Y, et al. (2026) Genome and transcriptomics provide insights on stipular spine morphogenesis in *Robinia pseudoacacia*. *Forestry research*, 6, e003.

Pecrix Y, et al. (2026) Phylogenomics of *Plasmopara halstedii* Reveals Genomic Regions Associated With the Breakdown of Sunflower Downy Mildew Resistance Genes. *Molecular ecology*, 35(4), e70270.

Wang J, et al. (2026) Mitochondrial genome assembly, comparative analysis of two caprifoliaceae species, and insights into adaptive evolution. *BMC plant biology*, 26(1).

Jiang XL, et al. (2026) Population genomics of *Quercus gilva* provides insights into the conservation of fengshui forests. *Communications biology*, 9(1).

Yao W, et al. (2026) Chromosome-level genome assemblies of two maize inbred lines with contrasting plant architectures. *Scientific data*, 13(1), 276.

Santos LBD, et al. (2026) Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation. *BMC genomics*, 27(1), 177.

Kirzinger MW, et al. (2026) Haploid Mutation Mapping Identifies a Homoeologous Non-Reciprocal Translocation Linked to Reduced Fibre and Enhanced Protein in *Brassica napus*. *Plant biotechnology journal*, 24(5), 3219.

Huang T, et al. (2025) Chromosome-level genome assembly of the aphid *Megoura crassicauda*. *Scientific data*, 12(1), 994.

Zhang H, et al. (2025) Assembly and comparative analysis of the complete mitochondrial genome of red raspberry (*Rubus idaeus* L.) revealing repeat-mediated recombination and

gene transfer. BMC plant biology, 25(1), 85.

Ni Y, et al. (2025) Advance in the assembly of the plant mitochondrial genomes using high-throughput DNA sequencing data of total cellular DNAs. Plant biotechnology journal, 23(11), 4944.

Bojdová T, et al. (2025) Sorghum embryos undergoing B chromosome elimination express B-variants of mitotic-related genes. Genome biology, 27(1), 8.

Dotto-Maurel A, et al. (2025) Evaluation of long-read sequencing for Ostreid herpesvirus type 1 genome characterization from Magallana gigas infected tissues. Microbiology spectrum, 13(3), e0208224.

Lu X, et al. (2025) Plasmids of two novel incompatibility groups IncFIIpPROV114-NR and IncpCHS4.1-3 from Providencia. Virulence, 16(1), 2512034.

Liu S, et al. (2025) Origin and de novo domestication of sweet orange. Nature genetics, 57(3), 754.

Lu X, et al. (2025) Iterative SCRaMbLE for engineering synthetic genome modules and chromosomes. Nature communications, 16(1), 7278.

Lu K, et al. (2025) Chromosome-Level Genome and Variation Map of Eri Silkworm *Samia cynthia ricini*. Biology, 14(6).

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. Frontiers in zoology, 22(1), 7.