

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

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: 20260813T055150+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 [dkNET](#) .

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.

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.

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

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

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

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.

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.

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.