

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

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: 20260731T043012+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 159 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

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.

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.

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

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.

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

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).

Li X, et al. (2025) Unraveling the genomic epidemiology and plasmid-mediated carbapenem resistance of *Klebsiella pasteurii*. *Frontiers in microbiology*, 16, 1561624.

Puthumana MA, et al. (2025) Genome assembly and insights into globally invasive Red-vented Bulbul (*Pycnonotus cafer*). *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Liu J, et al. (2025) Ecological Niche Adaptations Influence Transposable Element Dynamics in Pollinating and Non-Pollinating Fig Wasps. *Ecology and evolution*, 15(6), e71553.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

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.

Yang Y, et al. (2025) Genomic insights and SSR marker development for trait improvement in *Pleurotus giganteus* for tropical cultivation. *BMC plant biology*, 25(1), 1679.

Xu S, et al. (2024) Two chromosome-level genome assemblies of galling aphids *Slavum lentiscoides* and *Chaetogeoica ovagalla*. *Scientific data*, 11(1), 803.

Chen J, et al. (2024) Datasets of fungal diversity and pseudo-chromosomal genomes of mangrove rhizosphere soil in China. *Scientific data*, 11(1), 901.

Wang P, et al. (2024) De novo assembling a high-quality genome sequence of Amur grape (*Vitis amurensis* Rupr.) gives insight into *Vitis* divergence and sex determination. *Horticulture research*, 11(6), uhae117.

Fang Y, et al. (2024) Pan-genome and phylogenomic analyses highlight *Hevea* species delineation and rubber trait evolution. *Nature communications*, 15(1), 7232.

Li Y, et al. (2024) Dissection of a rapidly evolving wheat resistance gene cluster by long-read genome sequencing accelerated the cloning of Pm69. *Plant communications*, 5(1), 100646.

Zhang Y, et al. (2024) Structural variation reshapes population gene expression and trait variation in 2,105 *Brassica napus* accessions. *Nature genetics*, 56(11), 2538.