

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

SOAPdenovo

RRID:SCR_010752

Type: Tool

Proper Citation

SOAPdenovo (RRID:SCR_010752)

Resource Information

URL: <http://soap.genomics.org.cn/soapdenovo.html>

Proper Citation: SOAPdenovo (RRID:SCR_010752)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 24,2023. Software tool for de novo assembly of human genomes with massively parallel short read sequencing.Short-read assembly method that can build de novo draft assembly for human sized genomes.Software package for assembling short oligonucleotide into contigs and scaffolds., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: SOAPdenovo2

Resource Type: software resource

Defining Citation: [PMID:20019144](#)

Keywords: next generation sequencing, rna, dna, de novo, genome assembly, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAPdenovo

Resource ID: SCR_010752

Alternate IDs: biotools:soapdenovo, OMICS_00031, SCR_014986

Alternate URLs: <https://github.com/aquaskyline/SOAPdenovo2>,
<https://bio.tools/soapdenovo>, <https://sources.debian.org/src/soapdenovo/>,

License: GNU General Public License v3.0

License URLs: <https://github.com/aquaskyline/SOAPdenovo2/blob/master/LICENSE>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190415+0000

Ratings and Alerts

No rating or validation information has been found for SOAPdenovo.

No alerts have been found for SOAPdenovo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1299 mentions in open access literature.

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

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Liu H, et al. (2025) Multi-omics reveal the gut microbiota-mediated severe foraging environment adaption of small wild ruminants in the Three-River-Source National Park, China. *Integrative zoology*, 20(5), 916.

Li Y, et al. (2025) Investigation and pathogenetic testing of *Shewanella* spp. positive diarrhea cases in Beijing, China. *Scientific reports*, 15(1), 30334.

Ruiz-García M, et al. (2025) Effects of the Ecuadorian Andes on genetic structure of the spectacled bear with new genetic datasets. *Scientific reports*, 15(1), 32735.

Li F, et al. (2025) Ammonifying and phosphorus-solubilizing function of *Aliikangiella maris* sp. nov. isolated from *Phaeocystis globosa* bloom and algal-bacterial interactions. *Frontiers in microbiology*, 16, 1516993.

Chen S, et al. (2025) *Magnaporthe oryzae* infection triggers rice resistance to brown planthopper through the influence of jasmonic acid on the flavonoid biosynthesis pathway. *Insect science*, 32(1), 243.

Yong Q, et al. (2025) Complete chloroplast genomes of 13 species of the *Impatiens* genus for genomic features and phylogenetic relationships studies. *Scientific reports*, 15(1), 4258.

Ma J, et al. (2025) Detection and characterization of bovine hepatitis virus in cattle and sheep from Hulunbuir, northeastern China. *Frontiers in cellular and infection microbiology*, 15, 1540849.

Zheng Z, et al. (2025) Comparative and phylogenetic study on the chloroplast genomes of CMS with the cytoplasm of *Aegilops ovata* and its maintainer line in wheat. *BMC genomics*, 26(1), 1155.

Cui J, et al. (2025) High-alcohol-producing *Klebsiella pneumoniae* aggravates lung injury by affecting neutrophils and the airway epithelium. *Cell reports. Medicine*, 6(1), 101886.

Vignale FA, et al. (2025) Yerba mate (*Ilex paraguariensis*) genome provides new insights into convergent evolution of caffeine biosynthesis. *eLife*, 14.

Shen Y, et al. (2025) Comparative microbiomic analysis of fecal microbiota associated with abdominal fat in ducks. *Poultry science*, 104(8), 105282.

Y?lmaz S, et al. (2025) Genome mining of *Bacillus thuringiensis* strain SY49.1 reveals novel candidate pesticidal and bioactive compounds. *Pest management science*, 81(1), 298.

Xiao X, et al. (2025) Comparative Analysis of Complete Chloroplast Genomes and Phylogenetic Relationships of 21 Sect. *Camellia* (*Camellia* L.) Plants. *Genes*, 16(1).

Li Z, et al. (2025) Characterization of OXA232-Producing Carbapenem-Resistant *Klebsiella pneumoniae*: Genomic Analysis and Virulence Assessment. *Polish journal of microbiology*, 74(1), 82.

Chen H, et al. (2025) Structural characteristics of intestinal microbiota of domestic ducks with different body sizes. *Poultry science*, 104(4), 104930.

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.

Xue Z, et al. (2025) *Helicobacter pylori* antimicrobial resistance and gene variants in Shandong Province. *Scientific reports*, 15(1), 34244.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. *GigaScience*, 13.

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, *Berghia stephanieae*. *The Journal of comparative neurology*, 532(6), e25628.