

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 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: OMICS_00031, biotools:soapdenovo, 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: 20260821T193925+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 1342 mentions in open access literature.

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

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing Cobitis. GigaScience, 15.

Zheng W, et al. (2026) Mutation elevation and functional alterations in Escherichia coli are pertinent to the onset of gestational diabetes mellitus. Cell reports, 45(4), 117143.

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. GigaScience, 15.

Hattori-Muroi K, et al. (2026) Dietary soy shapes the microbiome to induce commensal-specific T follicular helper cells and IgA production. Immunity, 59(6), 1616.

Quintela M, et al. (2026) Genetics in the Ocean's Twilight Zone: Population Structure of the Silvery Lightfish Across Its Distribution Range. Evolutionary applications, 19(3), e70188.

Tao X, et al. (2026) Co-occurrence of mcr-9 and bla NDM-1 in carbapenem-resistant Enterobacter hormaechei from burn patients. Frontiers in cellular and infection microbiology, 16, 1742596.

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.

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

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.

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.

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.

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.

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.

Ding X, et al. (2025) Whole-Genome Analysis of a Novel Multidrug-Resistant *Escherichia coli* Strain from Dairy Calves in Northeast China: Mechanisms of Antibiotic Resistance and Biofilm Formation. *Biology*, 14(9).

Lin Z, et al. (2025) Gut microbiota-derived metabolite isovalerylcarnitine modulates salt sensitivity of blood pressure and incident hypertension: a multicenter dietary salt intervention trial. *Nature communications*, 17(1), 808.

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.