Resource Summary Report

Generated by NIF on Apr 27, 2025

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.

Synonyms: SOAPdenovo2

Resource Type: software resource

Defining Citation: PMID:20019144

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

Funding:

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: 20250420T014508+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 1284 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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).

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.

Yang YX, et al. (2024) The chromosome-level genome assembly of an endangered herb Bergenia scopulosa provides insights into local adaptation and genomic vulnerability under climate change. GigaScience, 13.

Chen Y, et al. (2024) Chloroplast genome data of five Amygdalus species: Clarifying genome structure and phylogenetic relationships. Data in brief, 53, 110077.

Zhao W, et al. (2024) Genomic Sequencing of Clinical Cupriavidus gilardii Isolates Revealed Their Diverse Antimicrobial Resistance Mechanisms. Infection and drug resistance, 17, 655.

Lyu D, et al. (2024) Symbiosis of a lytic bacteriophage and Yersinia pestis and characteristics of plague in Marmota himalayana. Applied and environmental microbiology, 90(8), e0099524.

Gandham P, et al. (2024) Genome assembly, comparative genomics, and identification of genes/pathways underlying plant growth-promoting traits of an actinobacterial strain, Amycolatopsis sp. (BCA-696). Scientific reports, 14(1), 15934.

Du K, et al. (2024) Phylogenomic analyses of all species of swordtail fishes (genus Xiphophorus) show that hybridization preceded speciation. Nature communications, 15(1), 6609.

Pan X, et al. (2024) Differential Strategies of Ectomycorrhizal Development between Suillus luteus and Pinus massoniana in Response to Nutrient Changes. Journal of fungi (Basel, Switzerland), 10(8).

Ning Z, et al. (2024) Mitigation of Salt Stress in Rice by the Halotolerant Plant Growth-Promoting Bacterium Enterobacter asburiae D2. Journal of xenobiotics, 14(1), 333.

Ran Z, et al. (2024) Camellia neriifolia and Camellia ilicifolia (Theaceae) as separate species: evidence from morphology, anatomy, palynology, molecular systematics. Botanical studies, 65(1), 23.

Jiang C, et al. (2024) Population genomic analysis reveals a polygenic sex determination system in Apostichopus japonicus. iScience, 27(10), 110852.

Ling LZ, et al. (2024) Genome sequencing and CAZymes repertoire analysis of Diaporthe eres P3-1W causing postharvest fruit rot of 'Hongyang' kiwifruit in China. PeerJ, 12, e17715.

Tao Z, et al. (2024) ACL1-ROC4/5 complex reveals a common mechanism in rice response to brown planthopper infestation and drought. Nature communications, 15(1), 8107.

Li LF, et al. (2024) Chloroplast genome of four Amorphophallus species: genomic features,comparative analysis, and phylogenetic relationships among Amorphophallus species. BMC genomics, 25(1), 1122.

Wang K, et al. (2024) Contamination Characteristics of Antibiotic Resistance Genes in Multi-Vector Environment in Typical Regional Fattening House. Toxics, 12(12).

Zhang D, et al. (2024) Phylogenetic placement and comparative analysis of the mitochondrial genomes of Idiostoloidea (Hemiptera: Heteroptera). Ecology and evolution, 14(5), e11328.