

Resource Summary Report

Generated by RRID on Aug 13, 2026

Albacore

RRID:SCR_015897

Type: Tool

Proper Citation

Albacore (RRID:SCR_015897)

Resource Information

URL: <https://github.com/dvera/albacore>

Proper Citation: Albacore (RRID:SCR_015897)

Description: Data processing basecaller for the Oxford Nanopore sequencer that identifies DNA sequences directly from raw data. It enhances accuracy of the single-read sequence data, contributing to high consensus accuracy for nanopore sequence data.

Resource Type: data processing software, software resource, software application

Keywords: sequence, dna, raw data, event detection, single-read, nanopore, basecaller, basecaller software, dockerfile

Availability: Free, Available for download

Resource Name: Albacore

Resource ID: SCR_015897

License: GNU General Public License v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260813T055123+0000

Ratings and Alerts

No rating or validation information has been found for Albacore.

No alerts have been found for Albacore.

Data and Source Information

Usage and Citation Metrics

We found 437 mentions in open access literature.

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

Williams SE, et al. (2026) OSMAC guided bioprospecting of Atlantic sponges reveals novel bacterial species and evidence for the antimicrobial thiazole alkaloid agrochelin II. *Applied and environmental microbiology*, 92(3), e0187725.

Almeida MF, et al. (2026) Promoter Engineering of the Surfactin Operon Enhances Surfactin Production in the Environmental Strain *Bacillus subtilis* RI4914. *Current microbiology*, 83(8).

Ran Z, et al. (2026) Organellar genome evolution in *Camellia tianeensis* (Theaceae): comparative insights into RNA editing, codon usage, and DNA transfer between chloroplast and mitochondrion. *BMC genomics*, 27(1).

Degnes KF, et al. (2026) Discovery of MBL-AB01: a novel antibacterial xanthone antibiotic with high activity against methicillin-resistant *Staphylococcus aureus*. *Applied and environmental microbiology*, 92(1), e0134625.

Nakajima Y, et al. (2026) Phylogenomic reclassification of *Cellulophaga* species to *Paracellulophaga* gen. nov. and description of *Allocellulophaga tsushimaensis* gen. nov., sp. nov., a novel bacterium from coastal seawater of Tsushima Island, Japan. *Antonie van Leeuwenhoek*, 119(4).

van Gorp E, et al. (2026) Ambler class C-type β -lactamases and porin alterations in *Enterobacter cloacae* complex and *Klebsiella aerogenes* in the Netherlands, 2012-2023. *BMC microbiology*, 26(1).

Mills EG, et al. (2026) High-depth whole genome sequencing of blood culture plates reveals evolutionary dynamics in cases of persistent bacteremia due to methicillin-resistant *Staphylococcus aureus*. *bioRxiv* : the preprint server for biology.

Desvillechabrol D, et al. (2026) LORA: a polymorphic multi-sample long read assembly pipeline. *NAR genomics and bioinformatics*, 8(2), lqag062.

Liu G, et al. (2026) Extraordinary diversity of antiviral immune-related gene families across 38 bat species. *BMC biology*, 24(1).

Ramirez P, et al. (2025) Diverse toxin repertoire but limited metabolic capacities inferred from the draft genome assemblies of three *Spiroplasma* (Citri clade) strains associated with *Drosophila*. *Microbial genomics*, 11(6).

Zheng S, et al. (2025) The origin, evolution, and translocation of sex chromosomes in *Silurus catfish* mediated by transposons. *BMC biology*, 23(1), 54.

Chang JJ, et al. (2025) Using synthetic RNA to benchmark poly(A) length inference from direct RNA sequencing. *GigaScience*, 14.

Whitehead M, et al. (2025) Genomic insights into clonal diversity in UK populations of the potato aphid, *Macrosiphum euphorbiae*. *BMC genomics*, 26(1), 1025.

Priyadarshini A, et al. (2025) Whole genome sequencing of a hypermucoviscous, multidrug-resistant *Klebsiella pneumoniae* subsp. *pneumoniae* K219 isolated from human sputum. *Scientific reports*, 16(1), 1237.

Yang K, et al. (2025) Characterization and Genome Analysis of *Mycocentrospora acerina*, the Causal Agent of *Panax notoginseng* Round Spot Disease in China. *Journal of fungi* (Basel, Switzerland), 11(11).

Kim JH, et al. (2025) Higher Microbial Abundance and Diversity in Bronchus-Associated Lymphoid Tissue Lymphomas Than in Non-cancerous Lung Tissues. *Cancer research and treatment*, 57(2), 580.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi* (Basel, Switzerland), 11(3).

Huang D, et al. (2025) Adaptive modification of antiviral defense systems in microbial community under Cr-induced stress. *Microbiome*, 13(1), 34.

Colp MJ, et al. (2025) The fate of artificial transgenes in *Acanthamoeba castellanii*. *BMC genomics*, 26(1), 368.

Ding D, et al. (2025) Genomic analysis of *Inonotus hispidus* provides insights into its medicinal properties and evolutionary dynamics. *Scientific reports*, 15(1), 23031.