

Resource Summary Report

Generated by SPARC SAWG on Jul 28, 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: software application, software resource, data processing software

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: 20260727T040627+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 427 mentions in open access literature.

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

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.

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).

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).

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

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

Flinkstrom Z, et al. (2025) Identifying microbial functional guilds performing cryptic organotrophic and lithotrophic redox cycles in anaerobic granular biofilms. *PloS one*, 20(8), e0330380.

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

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

Vishwanatha A, et al. (2025) *Plasmodium falciparum* DNA repair dynamics reveal unique roles for TLS polymerases and PfRad51 in genome diversification. *Nucleic acids research*, 53(21).

Hooykaas MJG, et al. (2025) Crown Gall Induced by a Natural Isolate of *Brucella* (*Ochrobactrum*) *pseudogrignonense* Containing a Tumor-Inducing Plasmid.

Microorganisms, 13(1).

Wu K, et al. (2025) The detection, function, and therapeutic potential of RNA 2'-O-methylation. *The innovation life*, 3(1).

Hebbar P, et al. (2025) Characterization of microbiome diversity unveils substantial microbial variation in mangrove soil sediments from coastal regions of Malaysia. *Access microbiology*, 7(6).

Samson R, et al. (2025) Deciphering the comprehensive microbiome of glacier-fed Ganges and functional aspects: implications for one health. *Microbiology spectrum*, 13(8), e0172024.

Sundermann AJ, et al. (2025) Enhanced discrimination of *Clostridioides difficile* transmission using whole-genome sequencing and in silico multi-locus variable number tandem repeat analysis. *Microbiology spectrum*, 13(12), e0328724.

K??ppen K, et al. (2025) Complete genome and plasmid sequence, and chemotaxonomic analysis of *Francisella* sp. strain W12-1067, now designated as *Allofrancisella heilbronni*. *BMC microbiology*, 25(1), 793.

Yue X, et al. (2025) Loss of Pathogenicity and Evidence of Horizontal Gene Transfer in *Colletotrichum gloeosporioides* From a Medicinal Plant. *Molecular plant pathology*, 26(6), e70098.

Gagnon MC, et al. (2024) An integrated strategy involving high-throughput sequencing to characterize an unknown GM wheat event in Canada. *Plant biotechnology journal*, 22(4), 904.