

Resource Summary Report

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Albacore

RRID:SCR_015897

Type: Tool

Proper Citation

Albacore (RRID:SCR_015897)

Resource Information

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

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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

Funding:

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: 20250426T060515+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 409 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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

Hooykaas MJG, et al. (2025) Crown Gall Induced by a Natural Isolate of *Brucella* (*Ochrobactrum*) pseudogrignonense Containing a Tumor-Inducing Plasmid. *Microorganisms*, 13(1).

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.

Yao B, et al. (2024) Effective training of nanopore callers for epigenetic marks with limited labelled data. *Open biology*, 14(6), 230449.

Hao Q, et al. (2024) Monoallelically expressed noncoding RNAs form nucleolar territories on NOR-containing chromosomes and regulate rRNA expression. *eLife*, 13.

Hu J, et al. (2024) Two high quality chromosome-scale genome assemblies of female and male silver pomfret (*Pampus argenteus*). *Scientific data*, 11(1), 1100.

Cho ST, et al. (2024) Evolution of extended-spectrum β -lactamase-producing ST131 *Escherichia coli* at a single hospital over 15 years. *Scientific reports*, 14(1), 19750.

Yadav P, et al. (2024) Analysis of Culturable Bacterial Diversity of Pangong Tso Lake via a 16S rRNA Tag Sequencing Approach. *Microorganisms*, 12(2).

Ochieng TA, et al. (2024) Interactions between *Bacillus thuringiensis* and selected plant extracts for sustainable management of *Phthorimaea absoluta*. *Scientific reports*, 14(1), 9299.

Williams SK, et al. (2024) Extreme mitochondrial reduction in a novel group of free-living metamonads. *Nature communications*, 15(1), 6805.

Li L, et al. (2024) Comparative analysis of the complete mitogenomes of *Camellia sinensis* var. *sinensis* and *C. sinensis* var. *assamica* provide insights into evolution and phylogeny relationship. *Frontiers in plant science*, 15, 1396389.

Talsma DT, et al. (2024) Nosocomial transmission of *tet(x3)*, *bla* NDM-1 and *bla* OXA-97-carrying *Acinetobacter baumannii* conferring resistance to eravacycline and omadacycline, the Netherlands, March to August 2021. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 29(28).

Timofeev V, et al. (2024) Avirulence of a spontaneous *Francisella tularensis* subsp. *mediasiatica* *prmA* mutant. *PloS one*, 19(6), e0305569.

Tracy KC, et al. (2024) Reversion to sensitivity explains limited transmission of resistance in a hospital pathogen. *bioRxiv : the preprint server for biology*.

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant *Staphylococcus aureus* clone during its transmission in a regional community outbreak in Japan. *Microbial genomics*, 10(7).

Giermasińska-Buczek K, et al. (2024) Interaction of bacteriophage P1 with an epiphytic *Pantoea agglomerans* strain-the role of the interplay between various mobilome elements. *Frontiers in microbiology*, 15, 1356206.

Buyse M, et al. (2024) Detection of *Anaplasma* and *Ehrlichia* bacteria in humans, wildlife, and ticks in the Amazon rainforest. *Nature communications*, 15(1), 3988.

Aminuddin A, et al. (2024) Potential role of heteroplasmic mitochondrial DNA mutations in modulating the subtype-specific adaptation of oral squamous cell carcinoma to cisplatin therapy. *Discover oncology*, 15(1), 573.

Wang Z, et al. (2024) Chromosome-level genome assembly of the cashmere goat. *Scientific data*, 11(1), 1107.

Quan ZJ, et al. (2023) GREPore-seq: A Robust Workflow to Detect Changes After Gene Editing Through Long-range PCR and Nanopore Sequencing. *Genomics, proteomics & bioinformatics*, 21(6), 1221.