

Resource Summary Report

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Oxford: Nanopore Technologies MinION

RRID:SCR_017985

Type: Tool

Proper Citation

Oxford: Nanopore Technologies MinION (RRID:SCR_017985)

Resource Information

URL: <https://nanoporetech.com/products/minion>

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Description: Portable, real time device for DNA and RNA sequencing, putting you in control of your sequence data. Portable DNA/RNA sequencing by Oxford Nanopore Technologies.

Resource Type: instrument resource

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Availability: Restricted

Resource Name: Oxford: Nanopore Technologies MinION

Resource ID: SCR_017985

Alternate URLs: <https://nanoporetech.com/sites/default/files/s3/literature/MinION-Mk1C-brochure.pdf>

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Ratings and Alerts

No rating or validation information has been found for Oxford: Nanopore Technologies MinION.

No alerts have been found for Oxford: Nanopore Technologies MinION.

Data and Source Information

Usage and Citation Metrics

We found 107 mentions in open access literature.

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

Brügger M, et al. (2025) Aging shapes infection profiles of influenza A virus and SARS-CoV-2 in human precision-cut lung slices. *Respiratory research*, 26(1), 112.

Ngomtcho SCH, et al. (2025) Continued T12 transmission and shared antibiotic resistance during 2018-2023 *Vibrio cholerae* outbreaks in Cameroon. *PLOS global public health*, 5(2), e0003763.

Laëtitia LD, et al. (2025) On the Difficulty to Detect Carbapenem Resistance in the Environment: Characterisation of *Escherichia coli* With Reduced Carbapenem Susceptibility Isolated in a French River. *Environmental microbiology reports*, 17(4), e70162.

Rahman MM, et al. (2025) Development of a culture-independent whole-genome sequencing of Nipah virus using the MinION Oxford Nanopore platform. *Microbiology spectrum*, 13(6), e0249224.

Sánchez-Vendizú P, et al. (2025) Decoding the Peruvian Amazon with in situ DNA barcoding of vertebrate and plant taxa. *Scientific data*, 12(1), 1545.

Yasuoka K, et al. (2025) Genome Analysis of Japanese *Yersinia pseudotuberculosis* Strains Isolated From Kawasaki Disease Patients and Other Sources and Their Phylogenetic Positions in the Global *Y. pseudotuberculosis* Population. *Microbiology and immunology*, 69(3), 182.

Chen LT, et al. (2025) Nanopore-based consensus sequencing enables accurate multimodal tumor cell-free DNA profiling. *Genome research*, 35(4), 886.

Arini GS, et al. (2025) A multi-omics reciprocal analysis for characterization of bacterial metabolism. *Frontiers in molecular biosciences*, 12, 1515276.

Luo Y, et al. (2025) Diagnostic value of nanopore-based metagenomic third-generation sequencing in the diagnosis of *Pneumocystis jirovecii* infection in patients with lung cancer. *Journal of medical microbiology*, 74(7).

Signore AV, et al. (2025) Spatiotemporal reconstruction of the North American A(H5N1) outbreak reveals successive lineage replacements by descendant reassortants. *Science advances*, 11(28), eadu4909.

McDowell CD, et al. (2025) Targeted Whole Genome Sequencing of African Swine Fever Virus and Classical Swine Fever Virus on the MinION Portable Sequencing Platform. *bioRxiv* : the preprint server for biology.

Coelho MA, et al. (2025) Tracing the evolution and genomic dynamics of mating-type loci in *Cryptococcus* pathogens and closely related species. *bioRxiv : the preprint server for biology*.

Batool SM, et al. (2025) Deregulating m6A regulators leads to altered RNA biology in glioma cell lines. *bioRxiv : the preprint server for biology*.

Wang TY, et al. (2025) Chromosome-Level Genome Assembly of the Loach Goby *Rhyacichthys aspro* Offers Insights Into Gobioidae Evolution. *Molecular ecology resources*, 25(7), e14110.

Devonshire AS, et al. (2025) Interlaboratory evaluation of high molecular weight DNA extraction methods for long-read sequencing and structural variant analysis. *BMC genomics*, 26(1), 698.

Ng NKL, et al. (2025) Mechanism of Initial Favorable Response to Decitabine in TP53-Mutated MDS/AML and Potential Mechanisms of Subsequent Relapse. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(14), 3048.

Xiao S, et al. (2024) New *Vibrio cholerae* sequences from Eastern and Southern Africa alter our understanding of regional cholera transmission. *medRxiv : the preprint server for health sciences*.

Nakamura K, et al. (2024) Diversity of Shiga toxin transducing phages in *Escherichia coli* O145:H28 and the different Shiga toxin 2 production levels associated with short- or long-tailed phages. *Frontiers in microbiology*, 15, 1453887.

Kasianova AM, et al. (2024) Trans2express - de novo transcriptome assembly pipeline optimized for gene expression analysis. *Plant methods*, 20(1), 128.

Holmes MJ, et al. (2024) HaplotagLR: An efficient and configurable utility for haplotagging long reads. *PloS one*, 19(3), e0298688.