

Resource Summary Report

Generated by SPARC SAWG on Aug 30, 2026

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>

Proper Citation: Oxford: Nanopore Technologies MinION (RRID:SCR_017985)

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>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260829T182550+0000

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 115 mentions in open access literature.

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

Mancini A, et al. (2026) Genomic and functional analysis of stress-responsive prophages in *Lactobacillus helveticus*. *Frontiers in microbiology*, 17, 1819103.

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Emura S, et al. (2026) Background-Free Nanopore Decoding of microRNA Expression Patterns Using Circular Diagnostic DNA. *Analytical chemistry*, 98(3), 2080.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Lacy-Roberts N, et al. (2026) Bridging the bioinformatics gap: tool selection for decentralized AMR genomic surveillance in Africa. *Frontiers in public health*, 14, 1756324.

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.

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.

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.

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.

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.

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.

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*.

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*.

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.

Coelho MA, et al. (2025) The complex evolution and genomic dynamics of mating-type loci in *Cryptococcus* and *Kwoniella*. *PLoS biology*, 23(10), e3003417.