

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Oxford Nanopore Technologies

RRID:SCR_003756

Type: Tool

Proper Citation

Oxford Nanopore Technologies (RRID:SCR_003756)

Resource Information

URL: <https://www.nanoporetech.com/>

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Description: Commercial organization developing a disruptive, proprietary technology platform for the direct, electronic analysis of single molecules. The instruments GridION and MinION are adaptable for the analysis of DNA, RNA, proteins, small molecules and other types of molecule. Consequently, the platform has a broad range of potential applications, including scientific research, personalized medicine, crop science and security / defence.

Abbreviations: Oxford Nanopore

Synonyms: Oxford Nanopore Technologies Ltd

Resource Type: commercial organization

Keywords: nanopore technology, dna, rna, protein, small molecule, molecule, analysis, nanopore, nanopore sensing

Resource Name: Oxford Nanopore Technologies

Resource ID: SCR_003756

Alternate IDs: nlx_158233

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260905T132507+0000

Ratings and Alerts

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

No alerts have been found for Oxford Nanopore Technologies.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 448 mentions in open access literature.

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

Cunningham-Oakes E, et al. (2026) Implementing portable, real-time 16S rRNA sequencing in the healthcare sector enhances antimicrobial stewardship. *EBioMedicine*, 129, 106317.

Jian Y, et al. (2026) BacPhase: Long-insert paired-end sequencing for bin marker construction and genome phasing. *aBIOTECH*, 7(1), 100012.

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

Chuquimia Valdez JA, et al. (2026) Detection of and Early Genomic Insights into Chikungunya Virus, Bolivia, 2025. *Emerging infectious diseases*, 32(7), 1198.

Kneubehl AR, et al. (2026) Geographically Distinct Circulation of Genotype II and III St. Louis Encephalitis Virus, Texas, USA, 2009-2024. *Emerging infectious diseases*, 32(4), 521.

Dennu L, et al. (2026) Biological and genomic resources for the cosmopolitan phytoplankton *Bathycoccus*: insights into genetic diversity and function of outlier chromosomes. *The Plant journal : for cell and molecular biology*, 126(5), e70982.

Evans D, et al. (2026) *Neisseria gonorrhoeae* Sequence Type 16676 in Disseminated Infections, Minnesota, USA, 2025. *Emerging infectious diseases*, 32(6), 1022.

Pang C, et al. (2026) Translating transcriptomics analysis into diagnostic workflows: clinical variant identification and interpretation in hypothesis-driven and hypothesis-free approaches. *EBioMedicine*, 128, 106313.

Perez MM, et al. (2026) Chikungunya Outbreak, Cuba, July 2025. *Emerging infectious diseases*, 32(7), 1222.

Vander Donck L, et al. (2025) Host-independent synergism between *Lactobacillus crispatus* and other vaginal lactobacilli. *Cell reports*, 44(9), 116171.

Shi X, et al. (2025) Transcript isoform diversity defines molecular subtypes and prognosis in acute myeloid leukemia through long-read sequencing. *Cell reports*, 44(9), 116216.

Mears HV, et al. (2025) Emergence of SARS-CoV-2 subgenomic RNAs that enhance viral fitness and immune evasion. *PLoS biology*, 23(1), e3002982.

Priyono DS, et al. (2025) The first complete mitochondrial genome of Sumatran striped rabbit *Nesolagus netscheri* (Schlegel, 1880), and its phylogenetic relationship with other Leporidae. *Scientific reports*, 15(1), 2002.

Baeza JA, et al. (2025) Assembly of Mitochondrial Genomes Using Nanopore Long-Read Technology in Three Sea Chubs (Teleostei: Kyphosidae). *Molecular ecology resources*, 25(1), e14034.

Bailey S, et al. (2025) Assembly of female and male hihi genomes (stitchbird; *Notiomystis cincta*) enables characterization of the W chromosome and resources for conservation genomics. *Molecular ecology resources*, 25(5), e13823.

Neira V, et al. (2025) Genetic Characterization of Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b, Antarctica, 2024. *Emerging infectious diseases*, 31(8), 1618.

Lowe CF, et al. (2025) Diphtheria Toxin-Producing *Corynebacterium ramonii* in Inner-City Population, Vancouver, British Columbia, Canada, 2019-2023. *Emerging infectious diseases*, 31(2), 323.

David SS, et al. (2025) Multidimensional third-generation sequencing of modified DNA bases allows interrogation of complex biological systems. *Nature communications*, 16(1), 5676.

Ge C, et al. (2025) Development and characterization of a fully humanized ACE2 mouse model. *BMC biology*, 23(1), 194.

Piispa M, et al. (2025) Detecting plasmid-mediated dissemination of bla KPC-3 and bla OXA-48-like genes in Enterobacterales across Finnish healthcare organizations using hybrid genome assembly. *Frontiers in microbiology*, 16, 1567913.