

Resource Summary Report

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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: 20260725T190543+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 399 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

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

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.

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.

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.

Athanasopoulou K, et al. (2025) Exploring the m5C epitranscriptome of mRNAs in breast cancer cells through genome engineering and long-read sequencing approaches. *Functional & integrative genomics*, 25(1), 136.

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.

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

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.

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.

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

Langsiri N, et al. (2025) Optimizing fungal DNA extraction and purification for Oxford Nanopore untargeted shotgun metagenomic sequencing from simulated hemoculture specimens. *mSystems*, 10(6), e0116624.

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.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Munir A, et al. (2025) Emergence of plasmid-mediated fosfomycin resistance among *Escherichia coli* harboring *fosA4*, *tet(X4)*, and *mcr-1* genes in wild birds. *mSystems*, 10(4), e0167324.

Jaggi KE, et al. (2025) A pangenome reveals LTR repeat dynamics as a major driver of genome evolution in *Chenopodium*. *The plant genome*, 18(1), e70010.

Di Martino B, et al. (2025) Detection and Genomic Characterization of Novel Mammarenavirus in European Hedgehogs, Italy. *Emerging infectious diseases*, 31(1), 155.

Davidov K, et al. (2025) Unveiling microbial succession dynamics on different plastic surfaces using WGCNA. *PloS one*, 20(2), e0318843.

López-Caamal A, et al. (2025) Substantial structural variation and repetitive DNA content contribute to intraspecific plastid genome evolution. *BMC genomics*, 26(1), 340.

Grieshop MP, et al. (2025) Replicative selfish genetic elements are driving rapid pathogenic adaptation of *Enterococcus faecium*. *bioRxiv : the preprint server for biology*.