Resource Summary Report

Generated by RRID on Apr 8, 2025

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

Funding:

Resource Name: Oxford Nanopore Technologies

Resource ID: SCR_003756

Alternate IDs: nlx_158233

Record Creation Time: 20220129T080220+0000

Record Last Update: 20250214T183000+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 349 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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

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.

Hemara LM, et al. (2025) Identification and Characterization of Innate Immunity in Actinidia melanandra in Response to Pseudomonas syringae pv. actinidiae. Plant, cell & environment, 48(2), 1037.

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

Xu D, et al. (2025) Comparative analysis of mitochondrial genomes of Stemona tuberosa lour. reveals heterogeneity in structure, synteny, intercellular gene transfer, and RNA editing. BMC plant biology, 25(1), 23.

Perslow NG, et al. (2025) The virulence regulator bvgS is required for nutrient-induced filamentation in Bordetella avium. bioRxiv : the preprint server for biology.

Ripoll L, et al. (2025) Insect-specific RNA viruses detection in Field-Caught Aedes aegypti mosquitoes from Argentina using NGS technology. PLoS neglected tropical diseases, 19(1), e0012792.

Miller D, et al. (2025) Pooled PPIseq: Screening the SARS-CoV-2 and human interface with a scalable multiplexed protein-protein interaction assay platform. PloS one, 20(1), e0299440.

Monecke S, et al. (2025) Characterisation of Staphylococcus aureus Strains and Their Prophages That Carry Horse-Specific Leukocidin Genes lukP/Q. Toxins, 17(1).

Wang CW, et al. (2024) A Revised Molecular Model of Ovarian Cancer Biomarker CA125 (MUC16) Enabled by Long-read Sequencing. Cancer research communications, 4(1), 253.

Sun J, et al. (2024) Correcting PCR amplification errors in unique molecular identifiers to generate accurate numbers of sequencing molecules. Nature methods, 21(3), 401.

Klein JA, et al. (2024) Pathogenic diversification of the gut commensal Providencia alcalifaciens via acquisition of a second type III secretion system. Infection and immunity, 92(10), e0031424.

Yan Y, et al. (2024) Chromosome-level genome assembly and annotation of Clanis bilineata tsingtauica Mell (Lepidoptera: Sphingidae). Scientific data, 11(1), 1062.

Dierickx G, et al. (2024) What Quality Suffices for Nanopore Metabarcoding? Reconsidering Methodology and Ectomycorrhizae in Decaying Fagus sylvatica Bark as Case Study. Journal of fungi (Basel, Switzerland), 10(10).

Gardner C, et al. (2024) Chromosome-level Subgenome-aware de novo Assembly of Saccharomyces bayanus Provides Insight into Genome Divergence after Hybridization. bioRxiv : the preprint server for biology.

Ogger PP, et al. (2024) SARS-CoV-2 strains bearing Omicron BA.1 spike replicate in C57BL/6 mice. Frontiers in immunology, 15, 1383612.

Rahman N, et al. (2024) Mobilisation and analyses of publicly available SARS-CoV-2 data for pandemic responses. Microbial genomics, 10(2).

Duker EO, et al. (2024) First Molecular Detection of SARS-CoV-2 in Sewage and Wastewater in Ghana. BioMed research international, 2024, 9975781.

Feng X, et al. (2024) Genomes of multicellular algal sisters to land plants illuminate signaling network evolution. Nature genetics, 56(5), 1018.