



Oxford
Nanopore
Technologies

Oxford Nanopore sequencing solutions

for microbiology and
infectious disease research

No microbe left behind

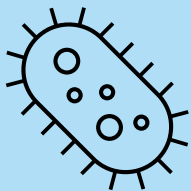
Your all-in-one genomics platform to uncover the microbial world

Fast, accurate microbe detection and characterisation is vital in identifying pathogens and antimicrobial resistance (AMR), guiding public health surveillance, and implementing quality control measures throughout manufacturing processes. Microbial genome sequencing is key to this, from targeted identification techniques to high-quality whole-genome assembly and metagenomic approaches.

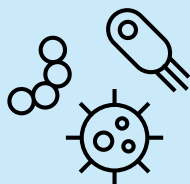
With Oxford Nanopore technology, reveal rich, multidimensional data and get fast results. Nanopore sequencing produces reads of any length, from short to ultra-long, for complete microbial whole-genome assembly and high-resolution microbial identification. The reads span genomic regions that are inaccessible to legacy short-read technologies, such as repetitive sequences and structural variants (SVs). While legacy instruments are confined to centralised laboratories, our flexible, portable devices enable sequencing at the point of sampling. With simple, end-to-end workflows available across a wide range of microbial research applications, access the insights you need from a single platform.

Oxford Nanopore sequencing delivers:

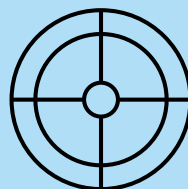
- Accurate, rich data — for comprehensive insights
- Unrestricted read lengths — for complete microbial genome assembly
- PCR-free data — no amplification bias and built-in methylation detection
- Sequencing that keeps up with you — real-time analysis for immediate access to actionable insights
- Accessible sequencing technology — portable devices for sequencing at source
- Scalable workflows — batching at the scale you need
- End-to-end analysis solutions — no bioinformatics experience required



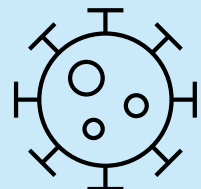
Microbial isolate
WGS



Metagenomics



Full-length 16S/ITS

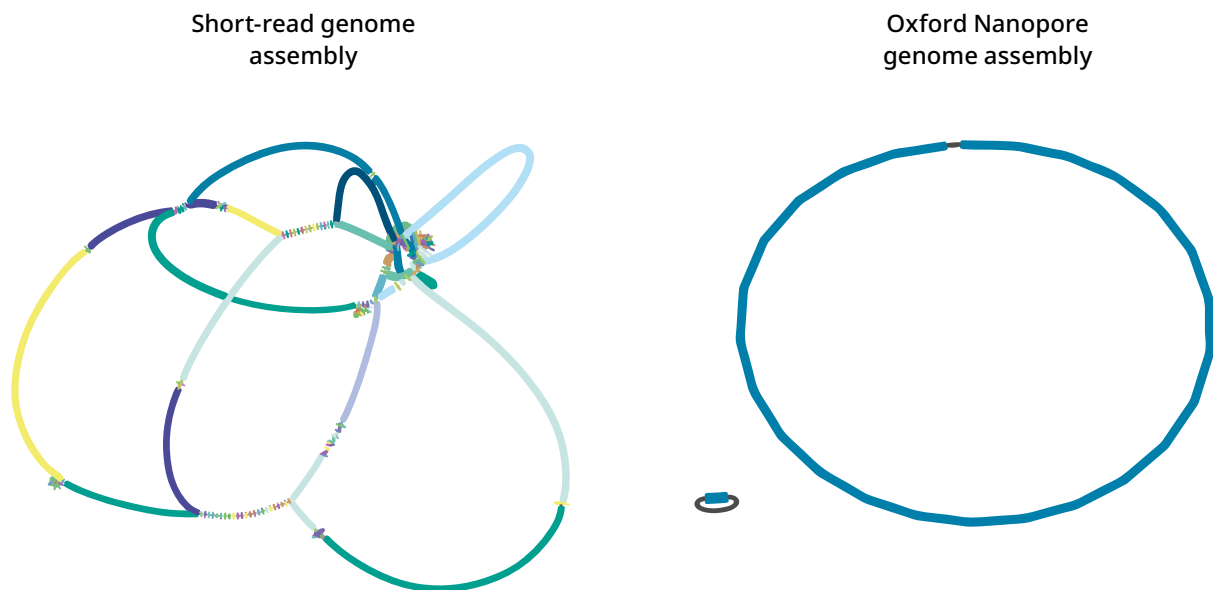


Viral amplicon

Microbial isolate whole-genome sequencing (WGS)

Complete microbial genome analysis via isolate WGS is critical in detecting and characterising transmission clusters in outbreaks, and identifying AMR genes, virulence factors, serotypes, plasmids, and other mobile genetic elements.

Our nanopore-only microbial isolate sequencing solution (NO-MISS) is a rapid, end-to-end workflow that delivers complete, reference-quality microbial genome assemblies¹. NO-MISS uses unrestricted nanopore read lengths, which span repetitive elements that are challenging to resolve correctly with legacy short-read technology, to produce highly complete genome sequences for thorough isolate characterisation.



'We believe that access to nanopore sequencing devices and streamlined open-source pipelines ... will facilitate implementation of nanopore-only clonality and outbreak analysis in the context of public health and clinical microbiology, contributing critically to hospital infection control.'

Vereecke, N. *et al.*²

Why Oxford Nanopore?

- Perform outbreak surveillance at or near the sample source in healthcare settings to help guide rapid public health responses
- Resolve repeat-rich sequences and SVs for highly complete microbial assembly
- Rapidly identify serotypes, locate AMR and virulence genes, and easily resolve gene copy numbers
- Distinguish between chromosomal and plasmid AMR transmission in outbreak scenarios
- Conduct in-house quality control monitoring and identify transient and resident strains at manufacturing plants
- Characterise engineered microorganisms in biomanufacturing

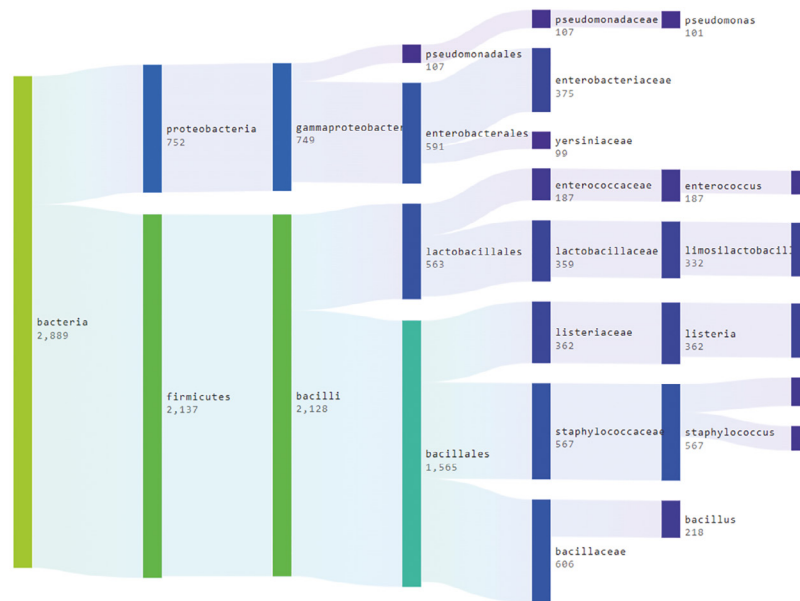
Metagenomic sequencing

Metagenomic sequencing is a powerful tool for microbial community analysis. The technique characterises known and unknown viruses, bacteria, archaea, and fungi, including unculturable microbes, allowing target-agnostic, whole-microbiome analysis.

Any-length nanopore reads distinguish between even closely related microbes in mixed microbial samples that may appear identical to legacy short-read technologies. This produces high-quality metagenome-assembled genomes (MAGs), in contrast to the fragmented assemblies produced by short-read methods, giving you unprecedented insights into microbial communities.

Our end-to-end pathogen metagenomics workflow delivers rapid bacterial, fungal, and viral pathogen identification from a single respiratory research sample, spanning from extraction to intuitive data analysis with the EPI2ME™ platform³.

Metagenomic Sankey plot of lineages

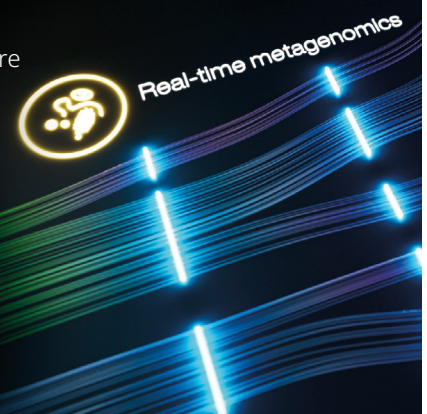


'we're using nanopore [sequencing] for clinical metagenomics mainly because we're interested in doing this very quickly'

Snell, L.B.⁴

Why Oxford Nanopore?

- Detect known and unknown microorganisms in a 'hypothesis-free' manner
- Generate complete, high-quality MAGs from mixed microbial samples and capture mobile genetic elements such as plasmids
- Predict or detect novel variants of known pathogens that escape routine detection methods
- Extract virulence and AMR gene information in a single assay
- Deliver rapid surveillance results to help inform potentially urgent public health responses
- Rapidly identify respiratory pathogens with our end-to-end research-use metagenomic workflow³



Targeted sequencing

Full-length 16S and ITS sequencing

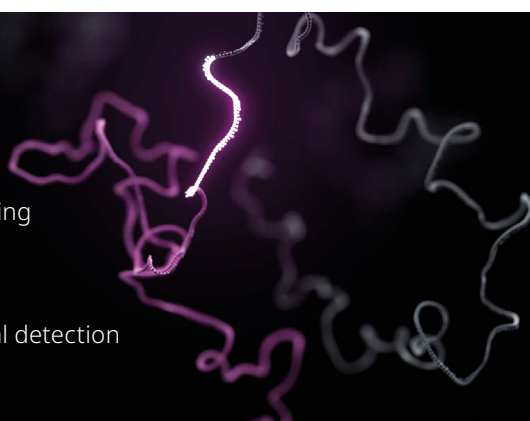
Targeted 16S ribosomal RNA (rRNA) and internal transcribed spacer (ITS) region sequencing are cost-efficient methods for bacterial/archaeal and fungal identification, respectively. This approach enables microbe identification from mixed microbial communities, with applications spanning from pathogen detection to environmental microbiome characterisation.

Our end-to-end microbial amplicon barcoding workflow offers streamlined 16S or ITS sequencing and analysis for accurate polymicrobial community profiling in a research setting⁵.

Long nanopore reads span both the complete 16S gene and full ITS region. This often achieves greater bacterial taxonomic resolution than what is possible with short-read sequencing methods, which capture only part of the gene, and effective fungal microbe detection.

Why Oxford Nanopore?

- Detect bacteria, archaea, and fungi with a streamlined targeted workflow
- Get high taxonomic resolution with full-length 16S/ITS sequencing
- Accurately resolve microbial communities using targeted amplicon sequencing
- Rapidly identify pathogenic microbes and perform polymicrobial detection



Viral amplicon sequencing

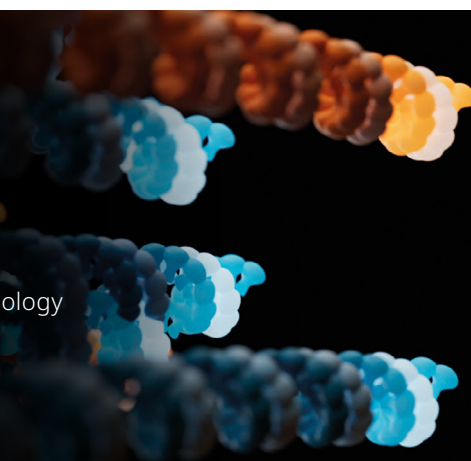
With the threat of infectious disease outbreaks from known and novel pathogens ever increasing, rapid access to viral pathogen data is of critical importance for fast and appropriate public health guidance.

Viral amplicon sequencing is an effective method of characterising these pathogens. Our fast library preparation options, combined with real-time data streaming, achieve whole viral pathogen genome coverage to promptly deliver actionable insights into disease outbreaks and inform vaccine programmes.

The nanopore sequencing device range offers portable sequencing at the sample source and flexible sample batch sizes, avoiding the delays associated with legacy techniques.

Why Oxford Nanopore?

- Rapidly classify known and novel or recombinant variants across viral pathogen genomes
- Deliver fast, actionable insights to help guide public health measures
- Perform rapid, accurate, and cost-effective pathogen surveillance
- Identify and characterise emerging pathogens to understand epidemiology and transmission patterns
- Import community developed workflows into our EPI2ME platform to analyse your viral genomes of interest



About Oxford Nanopore Technologies

Founded in 2005, Oxford Nanopore has developed a new generation of DNA/RNA sequencing technology. It is the only sequencing technology that offers real-time analysis, in fully scalable formats from pocket to population scale, that can analyse full-length native DNA or RNA. The technology is used in over 125 countries worldwide to deliver rapid, comprehensive genomic insights to users across academic, healthcare, environmental, and industrial settings. The company is headquartered in Oxford, UK, with satellite offices around the world.



Your single-platform solution for microbial sequencing

- Accessible devices and simple workflows empower labs to deploy in-house genomic sequencing
- Real-time data streaming allows rapid sample-to-answer turnaround times and fast access to results
- Accurate, any-length reads generate complete microbial genome assemblies, resolve plasmids and mobile elements, and characterise complex microbiomes



Find out more about microbial sequencing at
nanoporetech.com/infectious-disease

References

1. Oxford Nanopore Technologies. Nanopore-only microbial isolate sequencing solution (NO-MISS) from cell cultures using SQK-RBK114 (.24 or .96). <https://nanoporetech.com/document/no-miss-isolate-sequencing-rapid-barcoding-v14> [Accessed 20 August 2026]
2. Vereecke, N. et al. An open-source nanopore-only sequencing workflow for analysis of clonal outbreaks delivers short-read level accuracy. *J. Clin. Microbiol.* 63(8):e0066425 (2025). DOI: <https://doi.org/10.1128/jcm.00664-25>
3. Oxford Nanopore Technologies. Rapid metagenomic sequencing for surveillance of bacterial, fungal and viral pathogens using SQK-RPB114.24. <https://nanoporetech.com/document/rapid-sequencing-metagenomics-sqk-rpb114-24> [Accessed 20 August 2026]
4. Snell, L.B. and Alcolea-Medina, A. Embedding clinical metagenomics into NHS diagnostic pathways. Presentation. Available at: <https://nanoporetech.com/resources/document-repository/resource-centre/embedding-clinical-metagenomics-into-nhs-diagnostic-pathways-lc26> (2026) [Accessed 13 August 2026]
5. Oxford Nanopore Technologies. Microbial Amplicon Barcoding Sequencing for 16S and ITS (SQK-MAB114.24). <https://nanoporetech.com/document/microbial-amplicon-barcoding-sequencing-for-16s-and-its-sqk-mab114-24> [Accessed 20 August 2026]



**Oxford Nanopore
Technologies**

www.nanoporetech.com

phone +44 (0)845 034 7900

email support@nanoporetech.com



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