

GridION

One sequencer for many

GridIONTM is the benchtop nanopore sequencer that flexes with you, offering up to five independent MinIONTM Flow Cells to use as and when you need.

Made with multiple projects and teams in mind, it gives you the freedom to start, stop, and scale experiments without impacting others. Meanwhile, onboard compute keeps your real-time data optimised.



Small genome
sequencing



Targeted
sequencing



Microbial
identification



Antimicrobial
resistance
profiling



Gene expression
studies



GridION

Flexible, multi-user, multi-project sequencing with five independent flow cells

On-demand sequencing

— no more batching, just run

Any read length

sequencing with built-in, best-in-class modification detection



Intuitive analysis

using best-practice EPI2ME™ workflows

Powerful onboard

compute for real-time insights without complex IT infrastructure

GridION specifications: Flow cells: 1–5 MinION Flow Cells. Typical output: 15–35 Gb/flow cell; 75–175 Gb/device. Read length: From 20 bp to over 4 Mb. Sequencing run time: <1–72 hours. Weight | Size (W x H x D): 14.4 kg | 365 x 220 x 370 mm.

End-to-end workflows

Our best-practice, sample-to-answer workflows guide you step-by-step from sample extraction to informative results. We're continually developing new workflows to help you simplify your processes and accelerate access to meaningful results. View a selection of examples below.

Example end-to-end workflows	Whole-plasmid sequencing	Microbial isolate sequencing	Pathogen metagenomics	Microbial amplicon sequencing
Benefits	Same-day full-length plasmid sequencing — no primers required	Reference-quality genome assemblies, species identification, plasmid analysis, and resistance profiling	Streamlined pathogen identification from mixed microbial samples	Rapid, high-resolution identification of bacteria, archaea, and fungi
Rich data	Full-length plasmids, including SNVs, SVs, indels, and methylation	SNVs, SVs, indels, and methylation	Unbiased bacterial, fungal, and/or viral pathogen profiling	Full-length 16S gene and internal transcribed spacer (ITS) region for enhanced taxonomic resolution
Rapid results	Same day	From 1 day	From 1 day	Same day
Scalable throughput (samples/run/device)	Up to 480 samples	Up to 120 samples	Up to 110 (separate) / 55 (combined) samples	Up to 120 samples
Streamlined analysis	Intuitive local or cloud-based EPI2ME data analysis			

Reveal more biology. In one go

With the ability to sequence native DNA and RNA of any length, Oxford Nanopore sequencing helps you capture more types of genetic variation for deeper, more comprehensive insights. Built-in methylation detection means no bisulfite or enzymatic conversion is required.

‘Nanopore sequencing, with its ability to generate ultra-long reads (N50 > 100 kb) and perform real-time sequencing, enables rapid analysis of bacterial genomes and metagenomes’

Peng, K. *et al.* NPJ Antimicrob. Resist. (2025)



Discover more

Explore GridION, compare our devices, and see how Oxford Nanopore sequencing helps you reveal deeper biological insights at [vwr.com](https://www.vwr.com)



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