Oxford Nanopore Technologies

PromethION 24

Sequencing to the power of 24

Multiply your insights with PromethION™ 24, the production-scale nanopore sequencer that puts you in control of up to 24 high-output PromethION Flow Cells.

With superpowered GPUs giving you access to terabases of data in real time, it shines in high-throughput large-genome applications. With no batching required, sequence what you need, when you need it.

Human and large genome sequencing

Cancer research

Metagenomics

Isoform-level transcriptomics

Single-cell sequencing

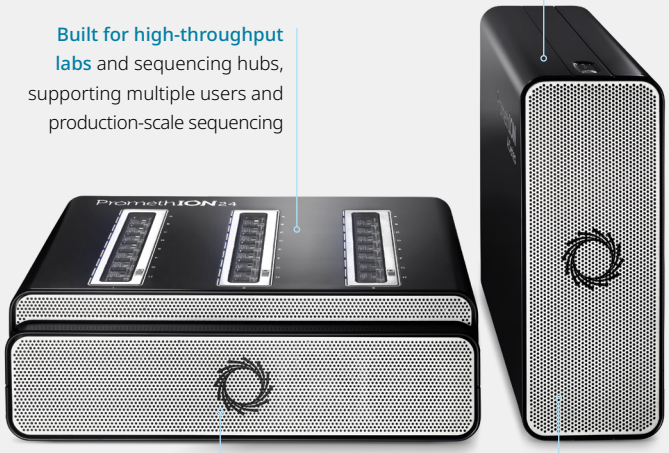
Find your application at **nanoporetech.com/applications**

PromethION 24

Flexible, high-output, high-throughput sequencing with up to 24 independent PromethION Flow Cells

Powerful, state-of-the-art compute delivering terabases of real-time data

Built for high-throughput labs and sequencing hubs, supporting multiple users and production-scale sequencing



Any read length sequencing with built-in, best-in-class modification detection

Intuitive and scalable analysis using best-practice EPI2ME™ workflows

PromethION 24 specifications: Flow cells: 1–24 PromethION Flow Cells. **Typical output:** 100–200 Gb/flow cell; 2.4–4.8 Tb/device. **Read length:** From 20 bp to over 4 Mb. **Sequencing run time:** <1–72 hours. **Weight | Size (W x H x D):** Sequencing Unit 23 kg | 590 x 190 x 430 mm; Data Acquisition Unit 26 kg | 178 x 440 x 470 mm.

End-to-end workflows

Our best-practice, sample-to-answer workflows guide you step-by-step from sample extraction to informative results. Explore the latest workflows at **nanoporetech.com/application-workflows**.

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.

Example end-to-end workflows	Human variation	24-hour human genome	Hereditary cancer	Single-cell transcriptomics
Benefits	Comprehensive whole-genome variant identification	Ultrarapid, comprehensive whole-genome variant identification	Rich multiomic data from 258 key genes	Streamlined isoform-level analysis of 10x Genomics cDNA
Rich data	SNVs, SVs, STRs, CNVs, phasing, and methylation	SNVs, SVs, STRs, CNVs, phasing, and methylation	SNVs, SVs, CNVs, pseudogenes, repeats, and methylation	~80 M full-length, cell-assigned reads per sample
Rapid results	3 days	1 day	5 days	4 days
Scalable throughput (samples/run/device)	Up to 24 samples	Up to 8 samples	Up to 72 samples	Up to 24 samples
Streamlined analysis	Flexible EPI2ME software with multiple deployment options and partner integrations			

'Currently there is no single genotyping platform that can match the overall performance of our Oxford Nanopore-based pipeline in the detection of a wide array of genomic alterations'

Sen, S. and Handler, H.P. *et al.* Front. Genet. (2025)

Discover more

Explore PromethION 24, compare our devices, and see how Oxford Nanopore sequencing helps you reveal deeper biological insights at **nanoporetech.com/promethion**.

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