Oxford Nanopore Technologies

PromethION 2 Integrated

Small box, big picture

PromethION™ 2 Integrated is as powerful as it is streamlined. Designed to give more labs access to high-output sequencing, it's able to run up to two independent PromethION Flow Cells, supported by high-performance onboard compute for real-time insights.

When you need a multiomic view to see the bigger picture, this is the fully integrated, on-demand sequencer you can count on for greater insights into human health and disease.

Human and large genome sequencing

Cancer research

Metagenomics

Isoform-level transcriptomics

Single-cell sequencing

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

PromethION 2 Integrated

Flexible, on-demand high-output sequencing with two independent PromethION Flow Cells

Compact, fully integrated device with powerful onboard compute for real-time insights

High-resolution touchscreen for complete device control

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

Intuitive analysis using best-practice EPI2ME™ workflows

PromethION 2i specifications: Flow cells: 1–2 PromethION Flow Cells. **Typical output:** 100–200 Gb/flow cell; 200–400 Gb/device. **Read length:** From 20 bp to over 4 Mb. **Sequencing run time:** <1–72 hours. **Weight | Size (W x H x D):** 10.6 kg | 225 x 180 x 430 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	Pharmacogenomics (PGx)	Hereditary cancer	Single-cell transcriptomics
Benefits	Comprehensive whole-genome variant identification	375 PGx targets, including *CYP2D6*	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, star alleles, plus enhanced *CYP2D6* analysis	SNVs, SVs, CNVs, pseudogenes, repeats, and methylation	~80 M full-length, cell-assigned reads per sample
Rapid results	3 days	3.5 days	5 days	4 days
Scalable throughput (samples/run/device)	Up to 2 samples	Up to 8 samples	Up to 6 samples	Up to 2 samples
Streamlined analysis	Flexible EPI2ME software with multiple deployment options and partner integrations			

‘Oxford Nanopore’s long-read sequencing capability creates a window into parts of the genome that have been out of reach’

Kári Stefánsson, CEO, deCODE Genetics

Discover more

Explore PromethION 2 Integrated, compare our devices, and see how Oxford Nanopore sequencing helps you reveal deeper biological insights at **nanoporetech.com/promethion**.

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