Product

Oxford NANOPORE Technologies

Our goal is to enable the analysis of **anything, by anyone, anywhere.**

Nanopore DNA and direct RNA sequencing has been performed on board the International Space Station.
Image credit: NASA's Johnson Space Center.

Nanopore sequencing — how it works

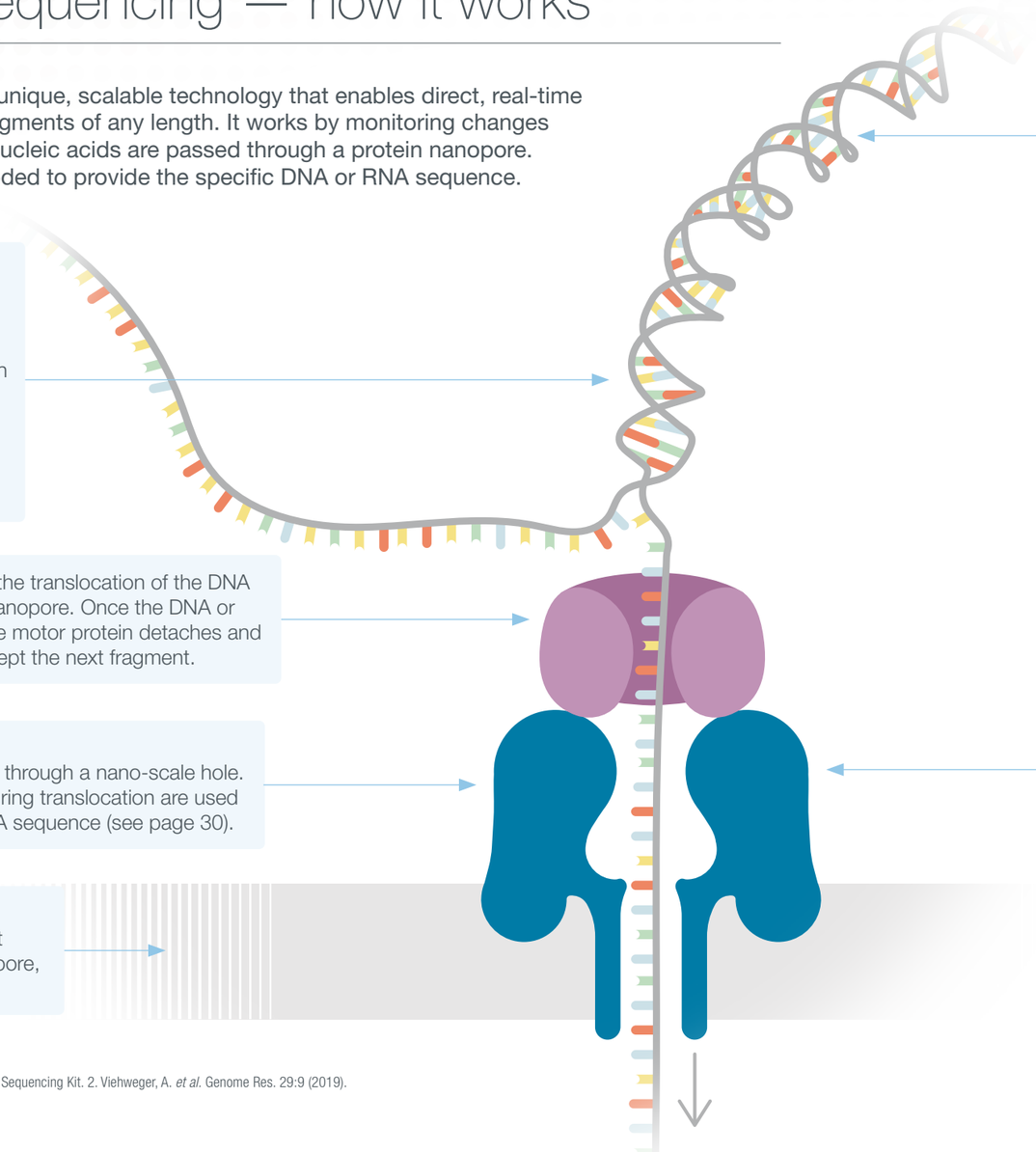
Nanopore sequencing is a unique, scalable technology that enables direct, real-time analysis of DNA or RNA fragments of any length. It works by monitoring changes to an electrical current as nucleic acids are passed through a protein nanopore. The resulting signal is decoded to provide the specific DNA or RNA sequence.

The nanopore processes the length of **DNA** or **RNA** presented to it. The user can control fragment length through the library preparation protocol utilised, allowing the generation of any desired read length — from short to ultra-long (e.g. >4 Mb DNA[1] and >20 kb RNA[2]).

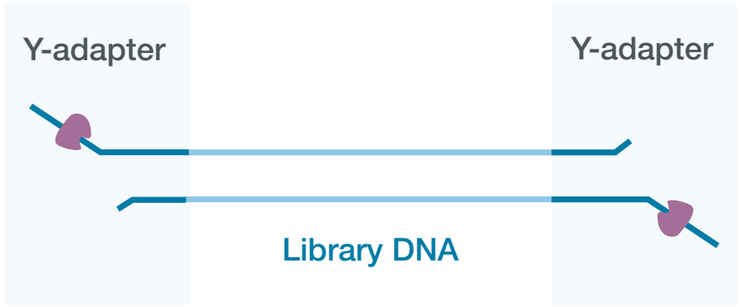
An **enzyme motor** controls the translocation of the DNA or RNA strand through the nanopore. Once the DNA or RNA has passed through, the motor protein detaches and the nanopore is ready to accept the next fragment.

Nanopore reader
DNA or RNA fragments pass through a nano-scale hole. The fluctuations in current during translocation are used to determine the DNA or RNA sequence (see page 30).

An electrically resistant **membrane** means all current must pass through the nanopore, ensuring a clean signal.



Library prep
Library preparation results in the addition of a sequencing adapter and motor protein at each end of the fragment.



Translocation
Both the template and complement strands carry the motor protein which means both strands are able to translocate the nanopore.

1. Internal data generated using the Ultra-Long DNA Sequencing Kit. 2. Viehweger, A. *et al.* Genome Res. 29:9 (2019).

Discover the benefits of nanopore technology

Unrestricted read length — short to ultra-long (longest >4 Mb[1])

- Ultimate flexibility — optimise for your application
- Easier genome assembly
- Resolve structural variants, repeats, and phasing
- Characterise and quantify full-length transcripts

Real-time analysis

- Immediate access to actionable results
- Enrich regions of interest without additional sample prep using adaptive sampling
- Early sample insights and QC
- Enough data? Stop, wash, store, or run another sample

Direct sequencing

- Sequence native DNA or RNA, not a copy
- Eliminate amplification bias
- Identify base modifications

Using the MinION in Antarctica. Image courtesy of Dr. Sarah Stewart Johnson, Georgetown University.

Scalable — portable to ultra-high throughput

- One technology across all devices — scale to your needs
- Sequence at sample source with Flongle™ and MinION™
- Compact, high-throughput benchtop sequencing with GridION™ and PromethION™

Streamlined library prep

- Rapid 10-minute (DNA) library prep
- Automated, portable prep — VolTRAX™
- High DNA and RNA yields from low input amounts
- Maximise throughput with barcoding

On-demand sequencing

- Sequence what you need when you need it
- No sample batching required
- Flexible throughput with modular GridION and PromethION

1. Internal data generated using the Ultra-Long DNA Sequencing Kit (September 2020).

Discover more nanoporetech.com

Generate new biological insights

Whole genome sequencing

- *De novo* assembly and resequencing
- Scaffolding and finishing
- Variant analysis: structural variation, SNVs, phasing, base modifications
- Chromatin conformation

Targeted sequencing

- Amplicon and PCR-free enrichment
- Real-time targeting with adaptive sampling (see page 15)
- 16S rRNA analysis
- Variant analysis: structural variation, SNVs, phasing, base modifications

RNA sequencing

- Direct RNA, direct cDNA, and cDNA
- Characterise and quantify full-length transcripts
- Sequence complete viral genomes
- Variant analysis: splice variants, gene fusions, SNVs, base modifications

Metagenomics

- Real-time, unbiased analysis of mixed samples
- Enhanced species identification using long reads

Epigenetics

- Base modifications (e.g. methylation)
- Histone modification
- Non-coding RNA activity (e.g. lncRNA)

Clinical research

Cancer research

Transcriptome analysis

Human genomics

Population genomics

Microbiology

Infectious disease

Plant research

Animal research

Environmental research

Latest information nanoporetech.com/applications

A complete and streamlined workflow — real-time answers to biological questions

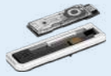
PREPARE

Library preparation kits

VolTRAX

SEQUENCE

Compatible with Flongle



MinION

MinION Mk1C

GridION

PromethION P2 / P2 Solo*

PromethION P24 / P48

ANALYSE

	Bioinformatic capability needed	
EPI2ME™	● ○ ○ ○	Use the cloud-based or local EPI2ME platform for real-time analysis workflows. **nanoporetech.com/analyse**
EPI2ME Labs	● ● ○ ○	Explore your data and develop your bioinformatics skills with interactive tutorials and best practice workflows. **nanoporetech.com/analyse**
Community-developed tools	● ● ● ○	Run open-source tools written and developed by the Nanopore Community. **community.nanoporetech.com**
Research software and custom analysis	● ● ● ●	Access the latest research algorithms from Oxford Nanopore or use your own custom analysis pipelines. **github.com/nanoporetech**

* PromethION P2 and P2 Solo devices are currently available for preorder, with Early Access devices expected to ship in 2022.

More information nanoporetech.com/products

Library preparation kits

Select the library preparation kit that matches your specific experimental needs — your choice of read length (short to ultra-long), turnaround time, input amount, sample multiplexing, modification detection, and output requirements. Find out more and view our complete library prep portfolio at **store.nanoporetech.com**.

	Native DNA			Amplified DNA		RNA		Targeted		
	Ligation	**Rapid/Field**	**Ultra-Long**	**PCR**	**Rapid PCR**	**PCR-cDNA**	**Direct RNA**	**16S**	**Cas9**	**Adaptive sampling**
Prep time	60 mins	10 mins	90 min + 1 x O/N incubation	60 mins + PCR	15 mins + PCR	160 mins + PCR	105 mins	10 mins + PCR	110 mins	–
Input	1,000 ng dsDNA	From 50 ng HMW gDNA	6M cells / 1 ml blood	100 ng dsDNA	1–5 ng gDNA	4 ng poly-A$^+$ RNA, or 200 ng total RNA	500 ng RNA	10 ng gDNA	1–10 µg dsDNA	–
Multiplexing options	Yes	Yes	–	Yes	Yes	Yes	In development	Yes	Coming soon	–
Read length	Equal to fragment length	Random distribution, dependent on input fragment length	N50 >50 kb	Equal to fragment length post-PCR	~2 kb	Enriched for full-length cDNA	Equal to RNA length	Full-length 16S gene (~1.5kb)	Equal to fragment length	Equal to fragment length
PCR required	No	No	No	Yes	Yes	Yes	No	Yes	No	–
Product range highlights	Detect modified bases for free. Automatable workflows and XL kits enable production-scale sequencing			Ideal for low input amounts		Detect modified bases for free with direct RNA kits		Read more about adaptive sampling on page 15. Generate your own or view pre-defined panels on the Nanopore Community		

View all kits store.nanoporetech.com

Cost-effective analysis of multiple samples

Barcoding

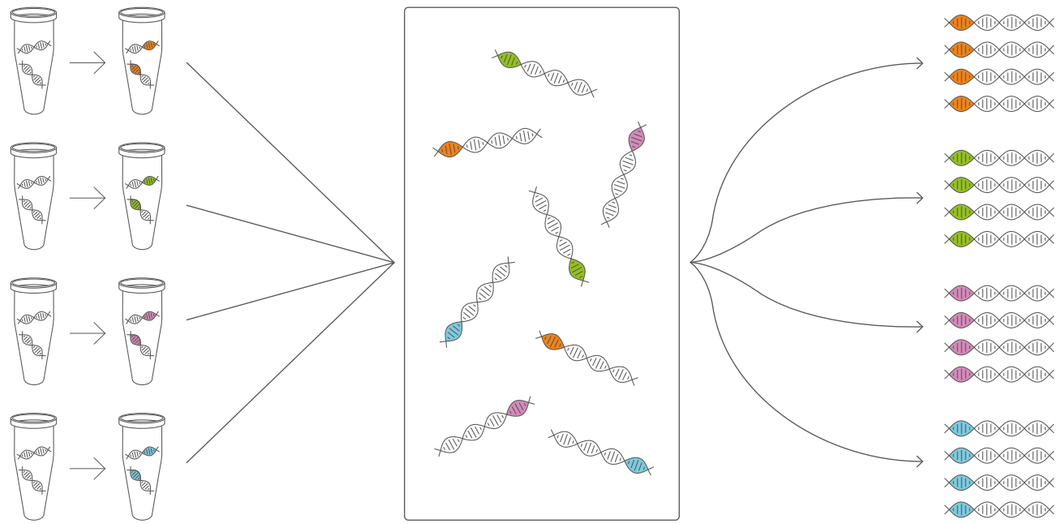
Barcoding kits allow users to multiplex samples to generate maximum data from a single flow cell, to separate the reads from sequential library loadings, and to lower the cost per sample.

- Native Barcoding Kit for a PCR-free approach (up to 96 samples)
- PCR Barcoding Kits (up to 96 samples)
- Native and PCR barcoding can be combined to increase multiplexing capabilities to thousands of samples
- Barcode libraries of gDNA, amplicon, or cDNA either with a dedicated barcoding kit or a barcoding expansion pack

Washing

The wash kit allows re-use of flow cells after short sequencing runs, meaning multiple libraries can be run sequentially.

Maximising flow cell usage



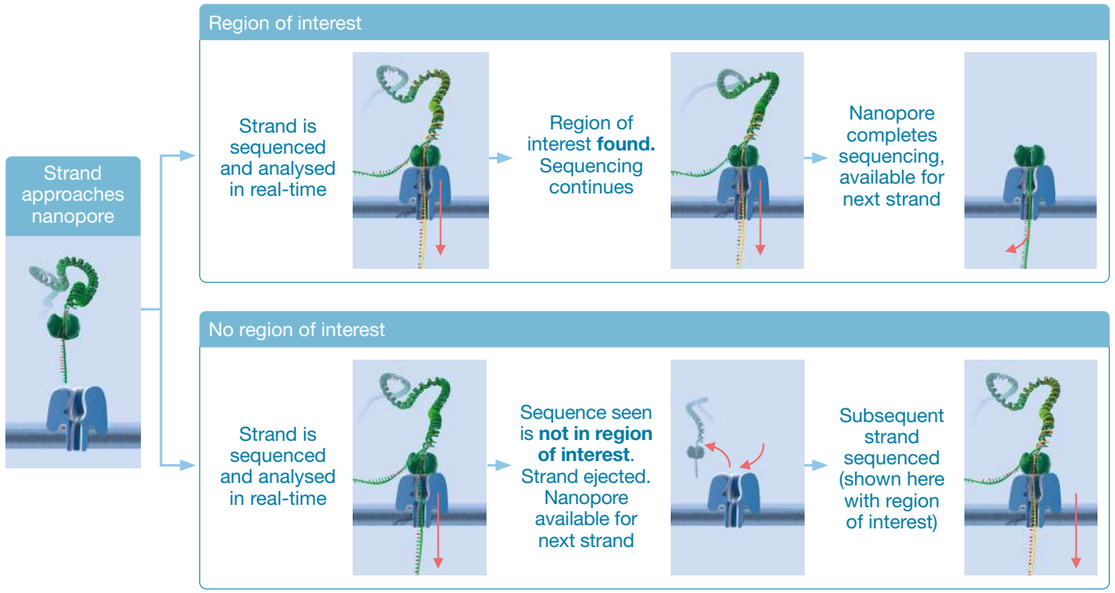
More information nanoporetech.com

A novel approach to targeted sequencing

Adaptive sampling

Adaptive sampling is a unique, on-device approach to targeted sequencing, which requires no upfront library enrichment steps. Using real-time basecalling, DNA fragments can be accepted or rejected for further sequencing based on their initial sequence composition. Furthermore, adaptive sequencing can be implemented in advance of, or even during, a run to increase coverage of specific targets.

- Target multiple regions of interest — without lengthy lab-based enrichment steps
- No limit on read length — expand targeted assays to include SNVs, SVs, and phasing
- Enrich long, native DNA molecules — retain base modifications
- Adjust enrichment in real time — enhance coverage of key regions or low-abundance species



More information nanoporetech.com

VolTRAX

Automated library preparation solution for nanopore sequencing

VolTRAX is a small USB-powered device that automates laboratory processes upstream of nanopore sequencing — from sample extraction to library preparation. Predefined or custom protocols can be utilised, enabling complete optimisation of sample preparation and the development of novel methods.

Automation of library preparation methods integrating capabilities such as PCR

Consumable cartridge preparing any biological sample ready for nanopore sequencing

Fluorescence detector, magnetic array, heater, and **Peltier** for flexible sample preparation

Only **minutes of hands-on time**, even for novel/complex experiments

USB powered and portable, liquids are moved around the cartridge in a path programmed by software, performing individual reactions in sequence

Specification

Weight	Size
301 g including cartridge	W 58 mm | H 64 mm | D 134 mm

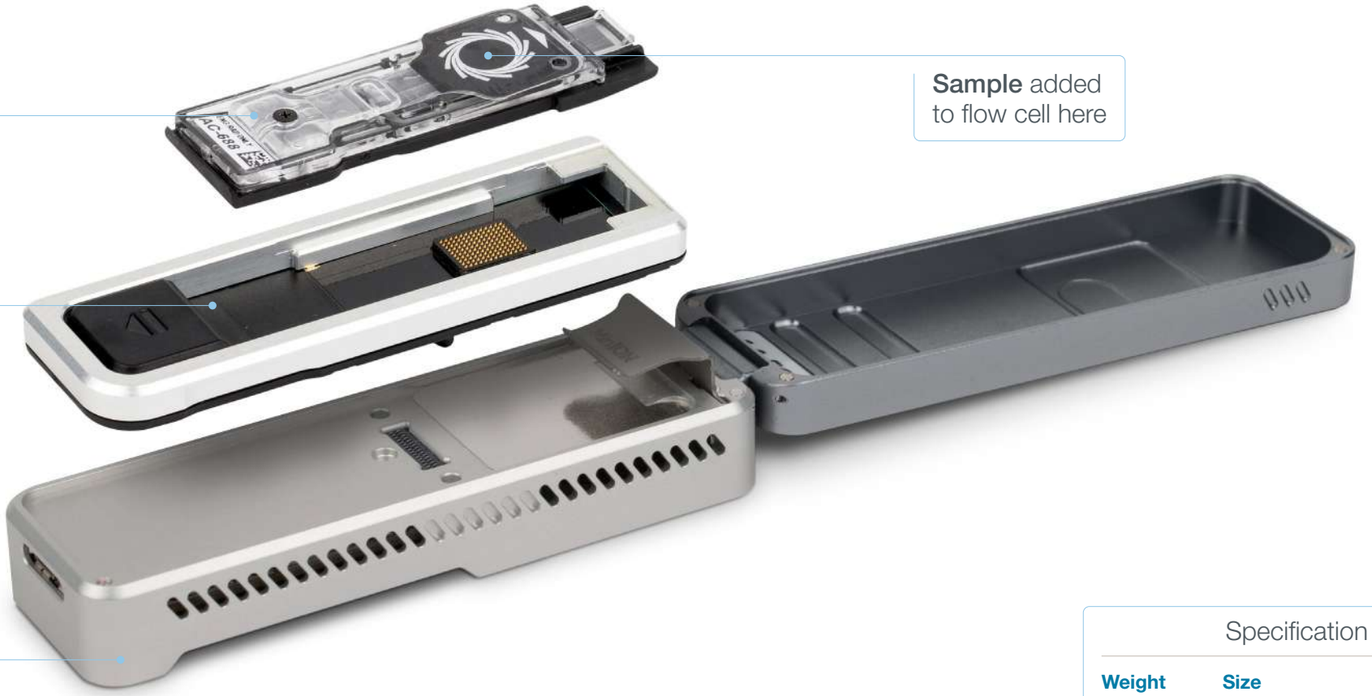
Find out more nanoporetech.com/products/voltrax

Flongle

Adapting MinION and GridION for smaller rapid tests and analyses

Flongle is an adapter for MinION or GridION that enables direct, real-time DNA or RNA sequencing on smaller, single-use flow cells. Providing immediate access to sequence data, Flongle is designed to be the most rapid, accessible, and cost-efficient sequencing system for smaller or more frequently performed tests and experiments.

COMPATIBLE WITH
GridION, MinION, and MinION Mk1C



Specification

Weight	Size
20 g	W 105 mm | H 23 mm | D 8 mm

Order now store.nanoporetech.com

MinION

Your personal, portable DNA and RNA sequencer

Get complete control and creativity over when, where, and how often you sequence. MinION provides the power of nanopore sequencing in an accessible, fully portable device. Weighing only 100 g and running off a laptop, MinION generates tens of gigabases of real-time data in the field or lab.

Sensor array with multiple nanopores for scaled-up sequencing

Sensor chip works with custom **ASIC** for control and data acquisition

Sample added to flow cell here

Flow cell with **512 active channels**

Consumable flow cell where the biology and electronics come together for nanopore sequencing

USB powered device; link to laptop or desktop computer to operate

Specification

Weight	**Size**
87 g (103 g with flow cell)	W 105 mm | H 23 mm | D 33 mm

Flongle COMPATIBLE

Order now store.nanoporetech.com

MinION Mk1C

Your all-in-one, portable DNA and RNA sequencer

MinION Mk1C provides the power of nanopore sequencing in a fully portable device with integrated real-time basecalling and data analysis, touchscreen operation, and wireless connectivity. Sequence and analyse your samples in the lab or field, and easily standardise assays across multiple sites or collaborators.

Connected: Ethernet and Wi-Fi enabled — upload and share your data, wherever you are

High-resolution touchscreen display allowing complete device control and easy visualisation of results

Integrated, real-time compute with pre-installed basecalling and analysis software

Use **Flongle** for smaller tests and analyses, or **MinION Flow Cells** for tens of gigabases of data

Data files are written to an **onboard, 1 TB SSD;** data can then be transferred to your own system

Specification

Weight	Size
420 g	W 140 mm | H 30 mm | D 114 mm

Flongle COMPATIBLE

Order now store.nanoporetech.com

GridION Mk1

Self-contained, easily deployable DNA/RNA benchtop nanopore sequencer

A flexible, self-contained, benchtop nanopore sequencer, running up to five MinION or Flongle Flow Cells (or combinations of each) that can respond to the needs of multiple users on demand, across varied applications. Integrated, high-performance data processing alleviates the need for complex IT infrastructure.

Sample added to flow cell here

Five individual MinION or Flongle Flow Cells can be operated individually or together, suitable for research labs and service providers

Consumable flow cell where the biology and electronics come together for nanopore sequencing

Onboard data analysis offering real-time basecalling and adaptive sampling

Specification

Weight	Size
11 kg	W 370 mm | H 220 mm | D 365 mm

Flongle COMPATIBLE

NANOPORE Service Certified

Service provider certification is available for the GridION

Order now store.nanoporetech.com

PromethION 2 Solo and PromethION 2

Low-cost access to high-yield PromethION sequencing

Offering the flexibility of two independent, high-output PromethION Flow Cells, the compact PromethION 2 (P2) devices deliver the benefits of high-coverage nanopore sequencing to users with lower sample processing requirements. Get fully integrated sequencing and analysis with P2 or expand your GridION/existing compute infrastructure with P2 Solo.*

PromethION 2 Solo

Two high-output flow cells can be operated individually or together for flexible, on-demand sequencing

Connect to GridION or existing compute infrastructure

PromethION 2

High-resolution touchscreen display allowing complete device control

Standalone, fully integrated device with powerful GPU for onboard data analysis

NANOPORE Service Certified

Service provider certification is available for the PromethION

* PromethION P2 and P2 Solo devices are currently available for preorder, with Early Access devices expected to ship in 2022.

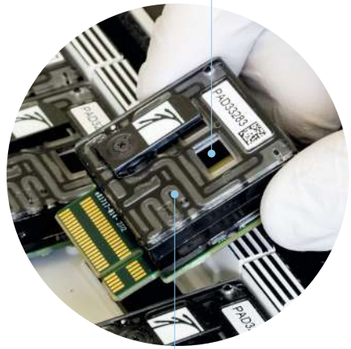
Pre-order now store.nanoporetech.com

PromethION 24 and PromethION 48

Flexible DNA/RNA high-throughput nanopore sequencers

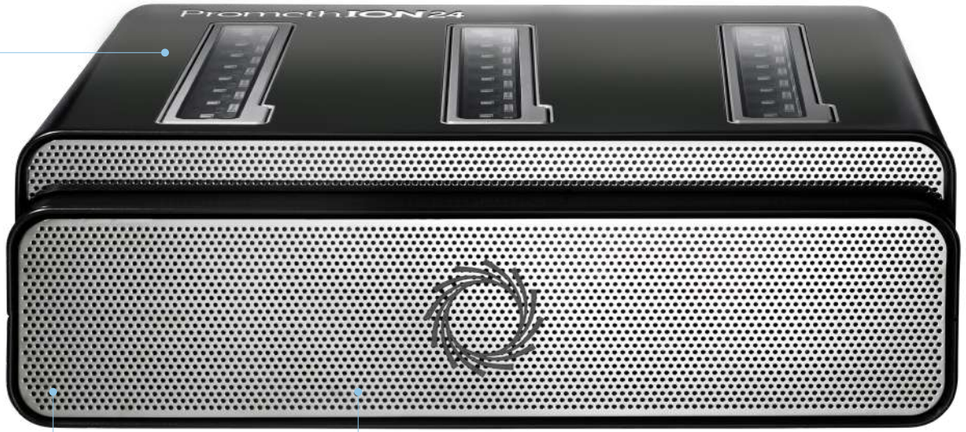
Offering the flexibility of 24 independently controllable, high-output flow cells and leveraging state-of-the-art algorithms and GPU technology, PromethION 24 provides single or multiple users with on-demand access to terabases of sequencing data. PromethION 48, our most powerful sequencing device, delivers twice the capacity and output of PromethION 24 — ideal for large- and production-scale sequencing projects.

Sample added to flow cell here



Each flow cell comprises up to 2,675 active channels

24 (P24) or 48 (P48) flow cells can be operated individually or together for flexible, on-demand sequencing



Sequencing Unit

Data Acquisition Unit

PromethION 24 can deliver **up to 7 Tb* of data** in a single run

Specification

	Weight	Size
Sequencing module:	28 kg	W 590 mm | H 190 mm | D 430 mm
Compute module:	25 kg	W 178 mm | H 440 mm | D 470 mm

NANOPORE Service Certified

Service provider certification is available for the PromethION

* Theoretical max output (TMO). Assumes system is run for 72 hours at 420 bases / second.
Actual output varies according to library type, run conditions, etc. TMO noted may not be available for all applications or all chemistries.

Order now store.nanoporetech.com

Data analysis and basecalling

Nanopore sequencing provides real-time data streaming, enabling basecalling and subsequent data analysis to be performed in parallel for immediate access to results.

Data structure

Raw data

Sequence

CCGACTCCGGTTACCCGCGTTGATTTGCTGGGGCAGGGCCG

Basecalled

As a DNA or RNA strand passes through the nanopore, the current is measured several thousand times per second. These current samples are known as raw data, which is subsequently processed using machine learning techniques into basecalled data — the sequence of DNA or RNA bases

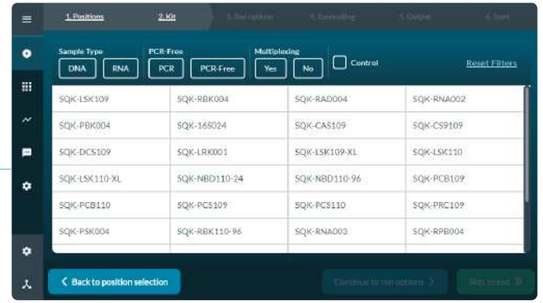
The facility of nanopore technology to sequence native DNA and RNA without the requirement for amplification or reverse transcription, allows the retention and detection of base modifications (e.g. methylation) alongside nucleotide sequence

Nanopore data is provided in standard FASTQ and FAST5 formats suitable for analysis using a range of downstream analysis tools (see page 11), including Oxford Nanopore's best practice EPI2ME pipelines.

Basecalling and device control

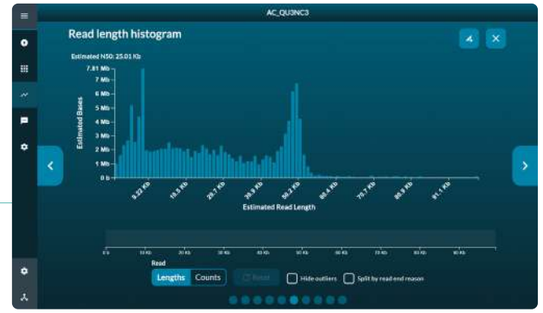
MinKNOW™, the device control and primary analysis software for all nanopore devices, provides easy experimental setup and real-time visualisation of sequencing performance.

MinKNOW enables complete control of sequencing parameters: start runs, set run parameters, and group experiments



Visualise sequencing progress and performance in real time. Quality check your run, and if there's a problem with the library, stop sequencing, wash the flow cell, and start again

Live output of basecalled reads in .fastq or .fast5 formats for immediate analysis. Basecalling can also be performed after the sample run using a range of algorithms



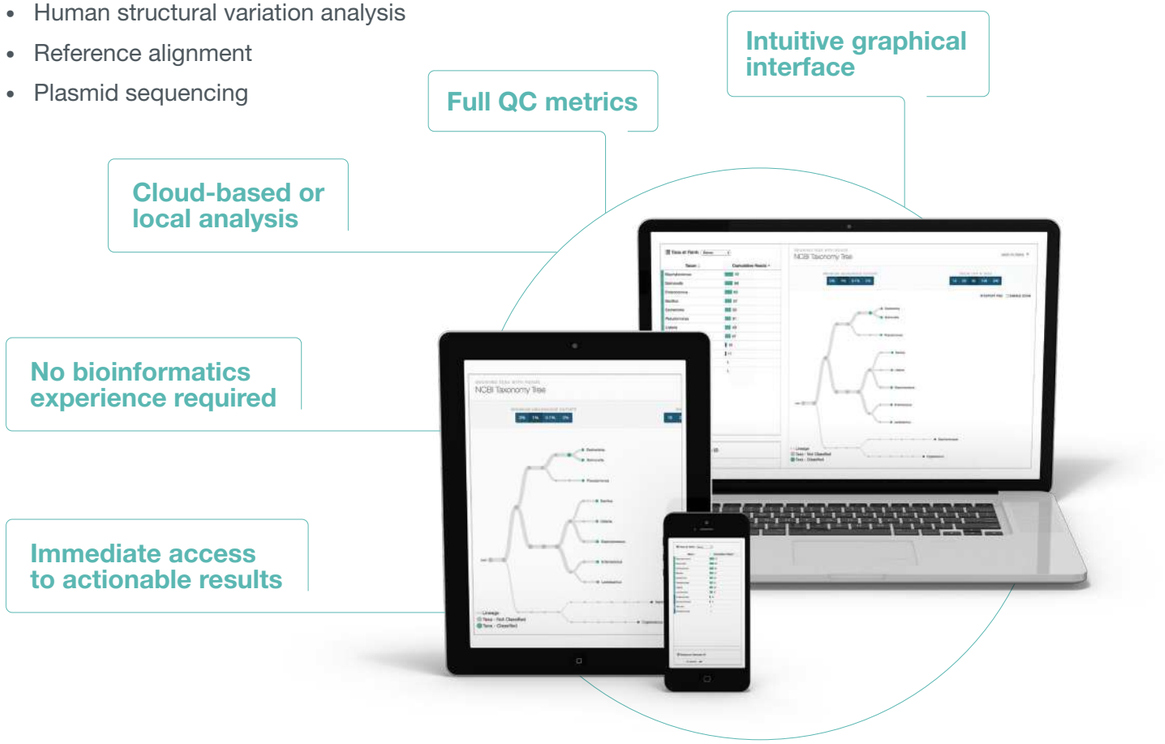
More information nanoporetech.com/analyse

Real-time insights with EPI2ME

The cloud-based or local data analysis platform EPI2ME provides easy access to a growing number of real-time data analysis workflows.

Workflows include:

- SARS-CoV-2 analysis — generate consensus sequences and identify genetic variants
- Metagenomic species identification
- Antimicrobial resistance profiling
- 16S-based bacteria and archaea identification
- Human structural variation analysis
- Reference alignment
- Plasmid sequencing



Simplified analysis with EPI2ME Labs

EPI2ME Labs offers two streamlined approaches to analysing your nanopore sequencing data.

- **Tutorials:** develop your bioinformatics skills with interactive tutorials and customisable, best practice analysis pipelines, using your own data or model datasets
- **Workflows:** utilise a growing number of simplified, standardised pipelines, from plasmid assembly to small variant calling — ideal for high-throughput, automated analyses

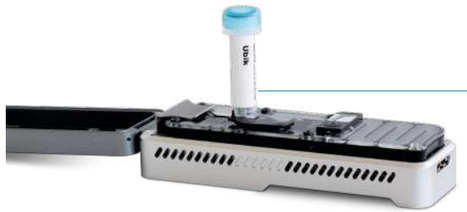
	EPI2ME	EPI2ME Labs Tutorials	EPI2ME Labs Workflows
Location	Cloud-based or local	Local	Local & distributed (cluster and/or cloud)
Aim	Simple, one-click analysis solutions	Bioinformatics best practices and training	Formalised workflows
Configurability	Pre-configured	Configurable	Configurable
Shareability	Limited	Extensive	Extensive
Focus	Simple, rapid, real-time analysis	Customisable, exploratory, post-run analysis	Standardised, high-throughput analysis

More information nanoporetech.com/analyse

In development

MinION Mk1D

An accessory keyboard with integrated sequencer for tablet devices



Ubik™

Rapid and portable, single-tube sample preparation

Plongle™

High-throughput analysis of smaller, frequently preformed tests and assays in a 96-well plate format

SmidgION™

Real-time nanopore sequencing and analysis on a smartphone

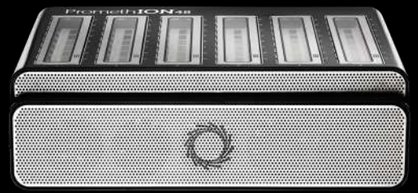
Biology for anyone, anywhere

GridION Mk1

MinION Mk1C

PromethION P2

PromethION P24 / P48



Flongle

PromethION P2 Solo

MinION

VolTRAX

Discover more nanoporetech.com

Oxford Nanopore Technologies
phone +44 (0)845 034 7900
email sales@nanoporetech.com
twitter @nanopore

www.nanoporetech.com

BR_1009(EN)_V9_01Mar2022