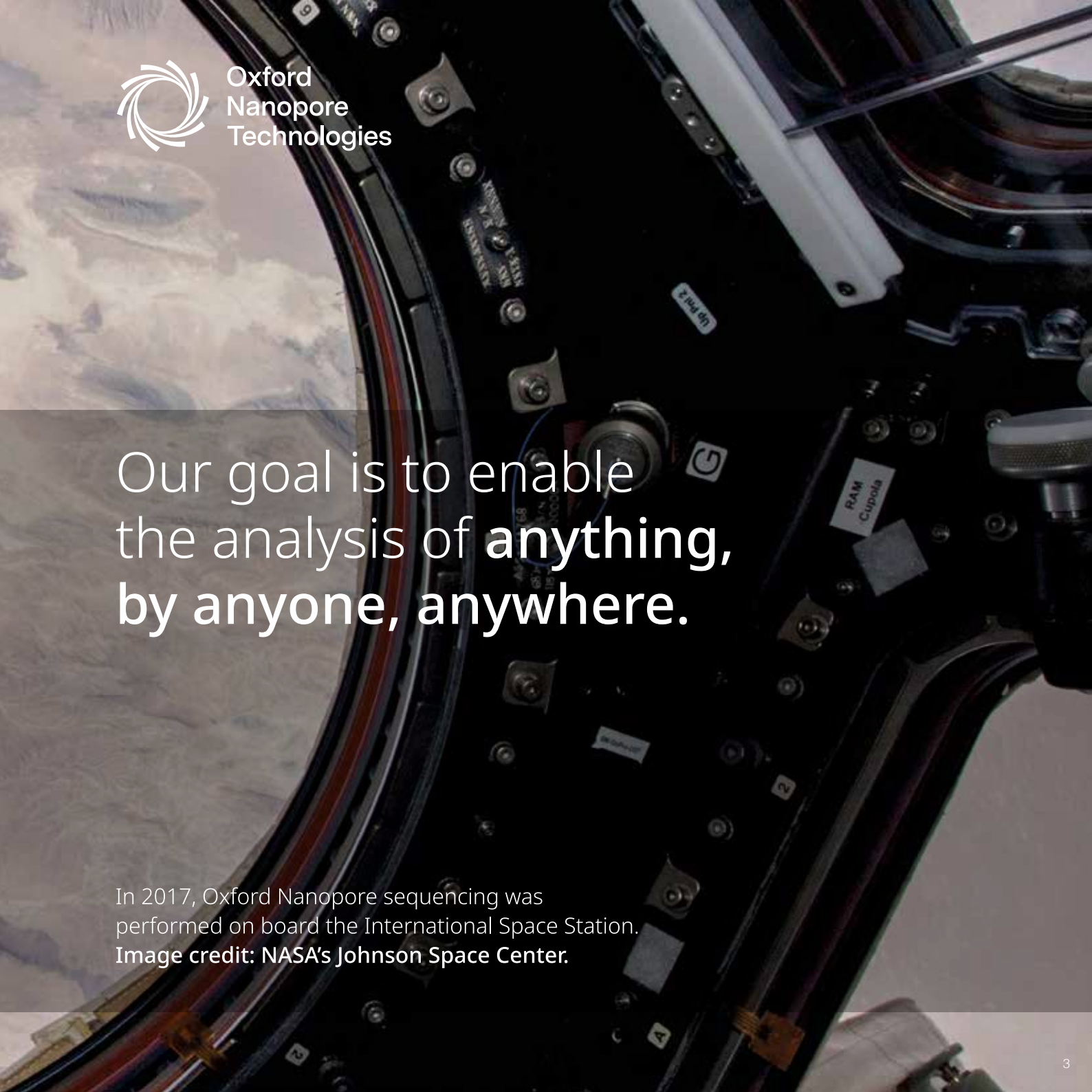
Oxford Nanopore Technologies

Products


Biomolecule Sequencer
P/N BS-BS
S/N 02
00237503J



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

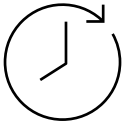
In 2017, Oxford Nanopore sequencing was performed on board the International Space Station.
Image credit: NASA's Johnson Space Center.

Why Oxford Nanopore technology?

Richer insights

Highly accurate genomic data that captures more types of genetic variation

- Any read length — short to ultra long: 20 bp to >4 Mb*
- Phasing, structural variants, and isoform detection inaccessible to legacy technologies
- SNV accuracy comparable to short-read sequencing
- Built-in modification and best-in-class methylation detection



Faster results

Near-sample, real-time workflows that don't require batching

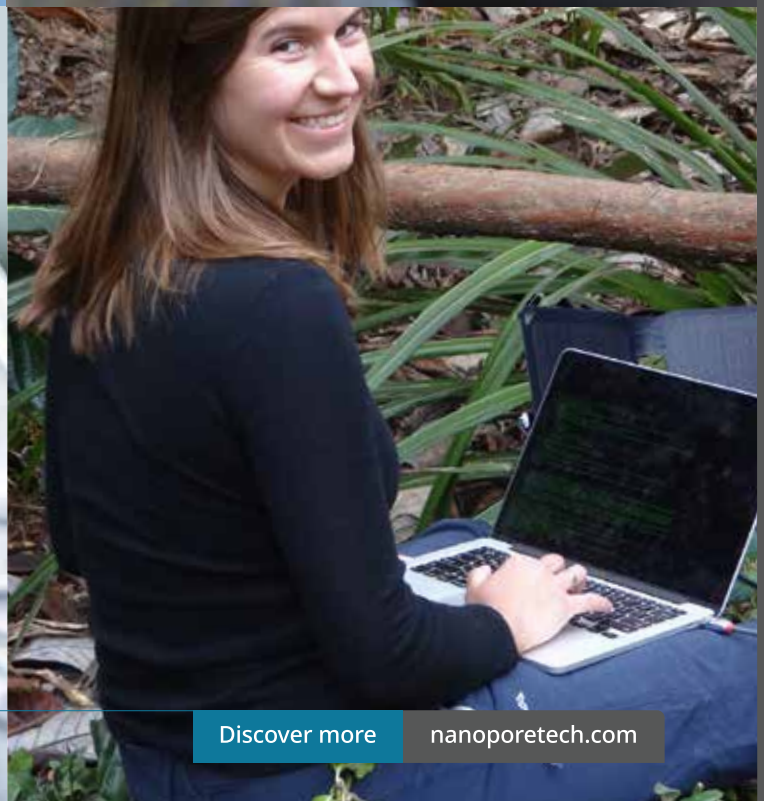
- Real-time sequencing for immediate access to actionable results
- On-device targeted sequencing via adaptive sampling software
- Independently controlled flow cells — run multiple applications on one device
- Rapid 10-minute (DNA) library prep and automatable kit formats

Accessible and affordable

Scalability that enables every application

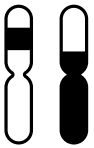
- Sequence anywhere — at the point of need, in the field or lab
- Choice of personal, project-scale, and production-scale sequencers
- From amplicons to thousands of human genomes
- End-to-end workflows and intuitive analysis software

* Internal data generated using the Ultra-Long DNA Sequencing Kit.



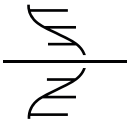
Discover more nanoporetech.com

One technology for all your biology



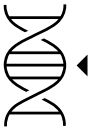
Structural variants

Accurately call SVs (e.g. 23,000 SVs detected per human genome, up to 5x greater than legacy technologies)[1]



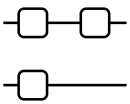
Methylation

Identify DNA and RNA base modifications alongside nucleotide sequence — no additional sample prep required



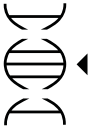
SNVs & phasing

Detect SNVs in regions inaccessible to legacy technologies and generate chromosome-scale phaseblocks



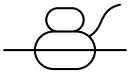
Splice variation

Fully characterise alternative splicing using full-length cDNA or direct RNA sequencing reads



Indels

Detect the same variants as existing technology while exploring new biology

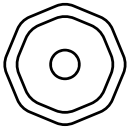


Gene expression

Accurately characterise and quantify full-length transcripts at the isoform level using long sequencing reads

Assembly

Generate highly contiguous, chromosome-scale genome assemblies



Single cell

Analyse full-length transcripts at single-cell resolution

View the latest accuracy data for all variant types at **nanoporetech.com/accuracy**.

1. Beyter, D. et al. *Nat. Genet.* 53(6), 779–786 (2021).

Latest information nanoporetech.com/applications

Nanopore sequencing — how it works

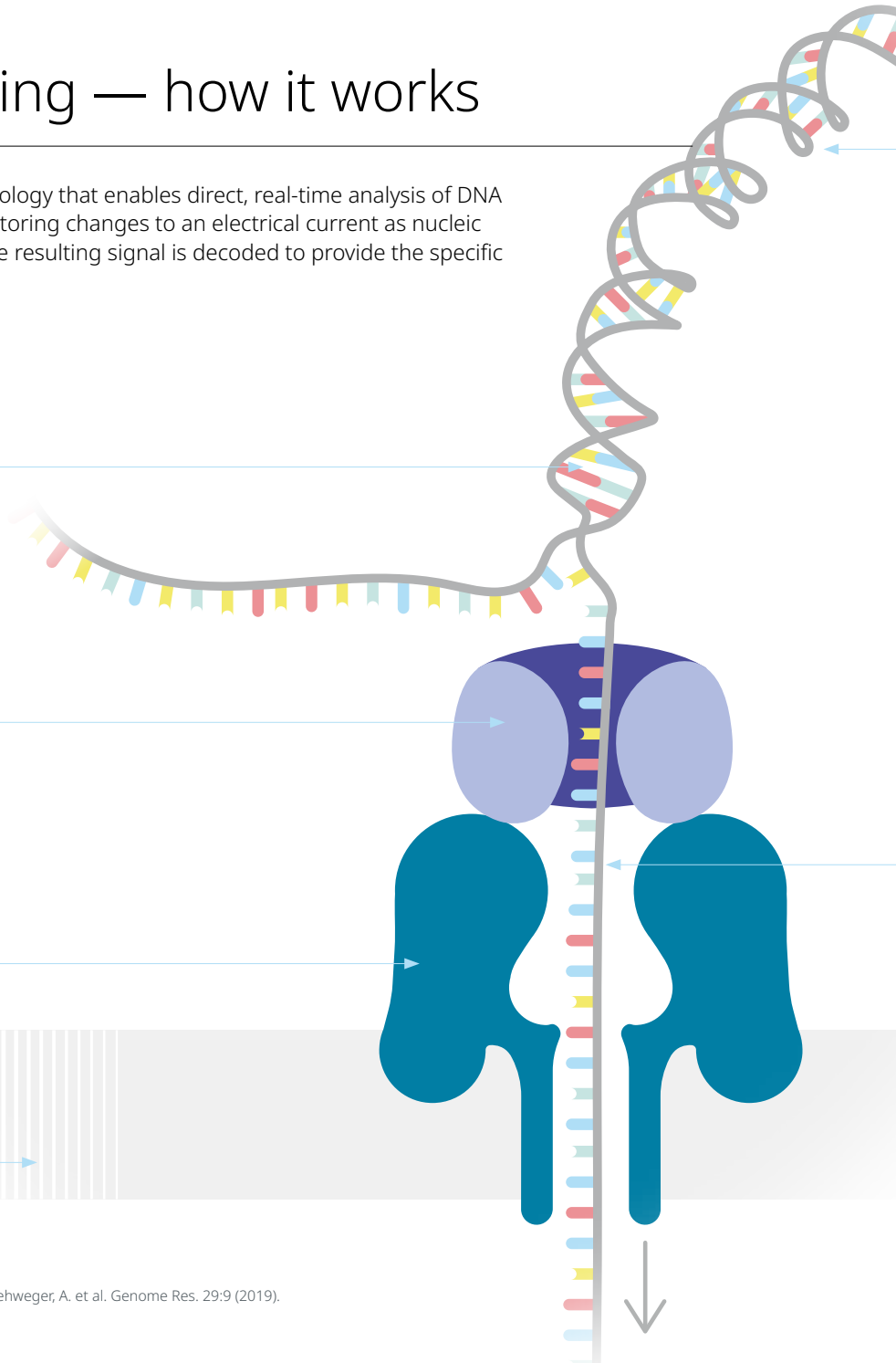
Nanopore sequencing is a unique, scalable technology that enables direct, real-time analysis of DNA or RNA fragments of any length. It works by monitoring changes to an electrical current as nucleic acids are passed through a protein nanopore. The resulting signal is decoded to provide the specific DNA 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 26).

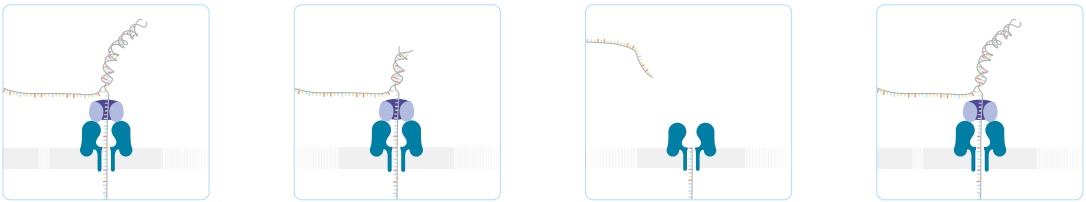
An electrically resistant **membrane** means all current must pass through the nanopore, ensuring a clean signal.



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

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

Translocation
Both DNA strands carry the motor protein allowing them both to translocate the nanopore.



First strand...

First strand...

(Exit)

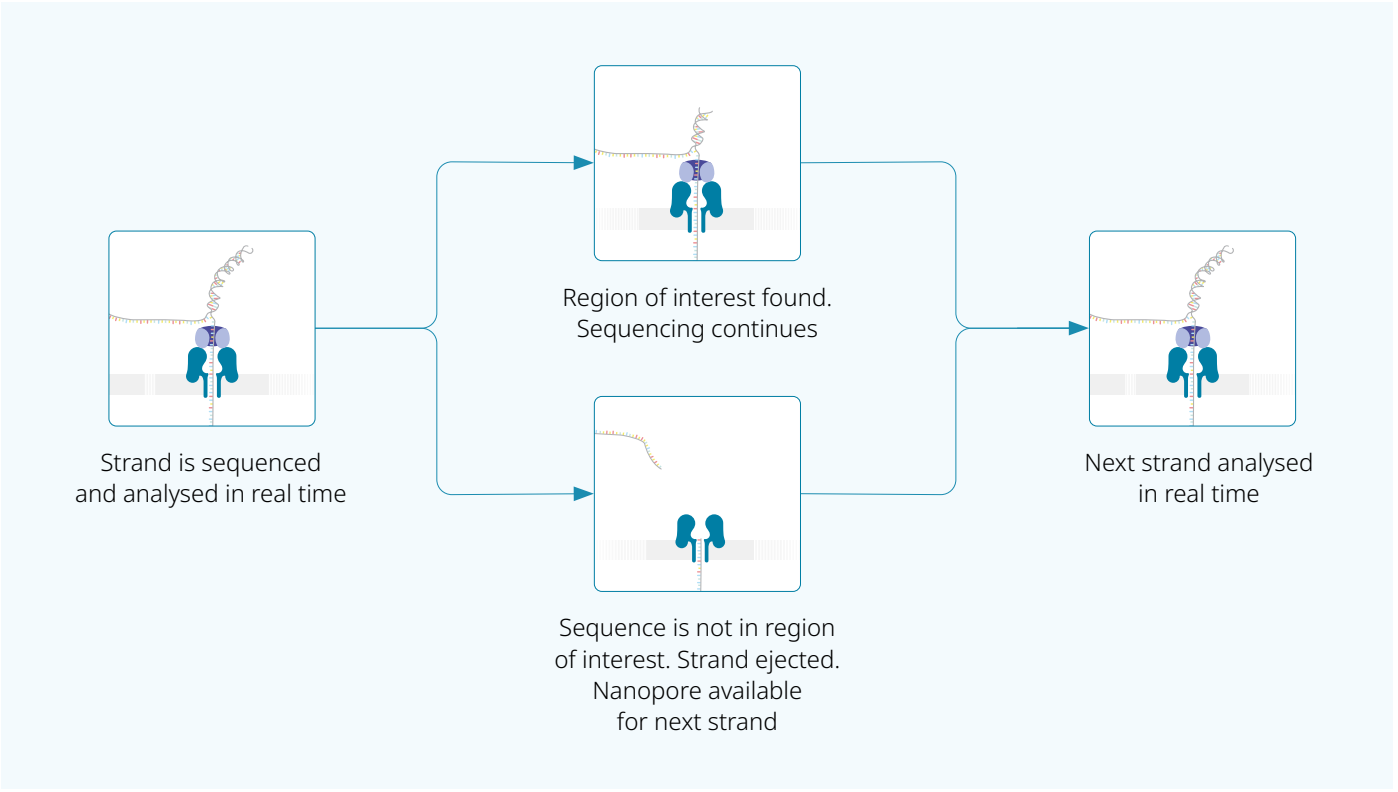
Next molecule (or second strand)...

Targeted sequencing reinvented

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 sampling 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



Streamline your workflows

End-to-end application workflows

Discover our growing range of best-practice, end-to-end workflows — designed to guide you step-by-step all the way from sample extraction to informative results. Current workflows include whole-plasmid sequencing, microbial isolate sequencing, and human whole-genome sequencing. View all workflows at nanoporetech.com/application-workflows.

Prepare	Prepare your sequencing library from DNA or RNA extracted from your sample
Sequence	Sequence your library on a flow cell and device that suits your needs
Analyse	Analyse your data from as soon as you start sequencing

Complete workflow automation

The benchtop ElysION™ device delivers a seamless, fully automated nanopore sequencing and analysis solution — taking you from sample to answer with minimal hands-on time. Discover more on page 24 or visit nanoporetech.com/elysion.

A complete and streamlined workflow — real-time ans

Prepare

Manual library prep

Automated library prep

nanoporetech.com/prepare

Sequence

MinION™ Mk1D

GridION™

PromethION™ 2 Solo/ Integrated

PromethION 24

nanoporetech.com/sequence

Nucleic acid extraction

Library preparation

Sequencing

ElysION | Fully automated, sample-to-answer device

wers to your biological questions

Analyse

Scientist

EPI2ME™

- Pre-configured workflows
- No bioinformatics skills needed
- Run locally or in the cloud
- Choose between real-time or post-run analysis

Bioinformatician

Command-line tools

- Access the latest algorithms
- Open-source tools developed by Oxford Nanopore or Nanopore Community
- Run pre-configured EPI2ME workflows

nanoporetech.com/analyse

Data analysis

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. Our streamlined library preparation kits are easy to automate, with protocols available for a range of liquid handlers — find out more at **nanoporetech.com/automation**.

	Native DNA		
	Ligation Sequencing Kit	**Rapid Sequencing Kit**	**Ultra-Long Sequencing Kit**
Prep time	60 min	10 min	200 min + 1 x O/N incubation
Input	~1 µg gDNA or 100–200 fmol for amplicons	~200 ng gDNA or 50 ng for amplicons	6M cells
Multiplexing options	✓	✓	
Read length	Equal to fragment length	Random distribution, dependent on input fragment length	N50 >50 kb
PCR required			
Methylation included	✓	✓	✓
Product range highlights	Output optimised	Speed optimised	Ultra-long reads optimised

Amplified DNA	Targeted	RNA	
Rapid PCR Barcoding Kit	**16S Barcoding Kit**	**cDNA-PCR Sequencing Kit**	**Direct RNA Sequencing Kit**
15 min + PCR	25 min + PCR	225 min + PCR	135 min
1–5 ng gDNA	10 ng gDNA	10 ng poly-A+ RNA or 500 ng total RNA	300 ng poly-A+ RNA or 1 µg total RNA
✓	✓	✓	In development
~2 kb	Full-length 16S gene (~1.5 kb)	Enriched for full-length cDNA	Equal to RNA length
✓	✓	✓	
			✓
Low input optimised	Oxford Nanopore devices also offer adaptive sampling, a unique on-device target enrichment methodology that requires no upfront library enrichment (see page 10)	Optimised for identification and quantification of full-length transcripts	Detect modified bases for free

View all kits nanoporetech.com/prepare

MinION Mk1D

Your personal, portable DNA and RNA sequencer

A sequencer for everyone — empowering individual researchers, labs, and those new to DNA/RNA sequencing to perform in-house sequencing and take control of their timelines with a cost-effective, personal device. Weighing only 130 g and running off a laptop, MinION Mk1D generates tens of gigabases of real-time data in the field or lab.

Indicator lights inform the user of run status and progress

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

Sensor chip works with custom ASIC for control and data acquisition

Specification

Weight	Size	Compatible with
130 g	W 55 mm | H 13 mm | D 125 mm	MinION Flow Cells

Order now store.nanoporetech.com

GridION

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

A flexible, self-contained, benchtop nanopore sequencer, running up to five MinION Flow Cells 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.

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

Onboard compute and data analysis offering real-time basecalling and adaptive sampling

Q

GridION Q, part of the locked-down Q-Line range of devices for applied applications, also available. Find out more at **nanoporetech.com/q-line**.

Sample added to flow cell here

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

Specification

Weight	Size	Compatible with
14.4 kg	W 370 mm | H 220 mm | D 365 mm	MinION Flow Cells

Order now store.nanoporetech.com

PromethION 2 Solo and PromethION 2 Integrated

Low-cost access to high-output PromethION sequencing

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

Specification

Weight	Size	Compatible with
1.5 kg	W 110 mm | H 87 mm | D 152 mm	PromethION Flow Cells

High-resolution touchscreen display allowing complete device control

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

PromethION 2 Integrated

Specification

Weight	**Size**	**Compatible with**
10.6 kg	W 225 mm | H 180 mm | D 430 mm	PromethION Flow Cells

Order now store.nanoporetech.com

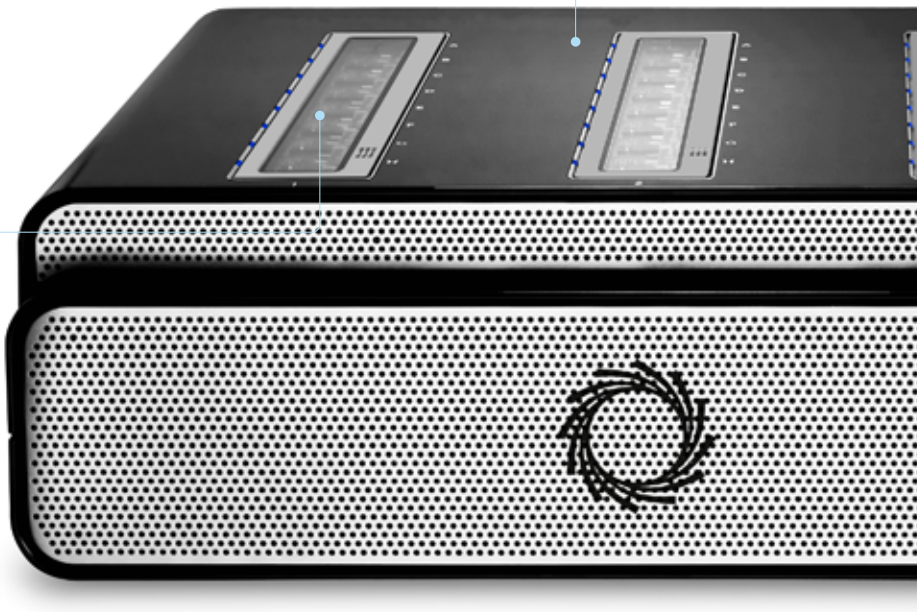
PromethION 24

A flexible DNA/RNA high-throughput nanopore sequencer

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*.

Sequencing Unit

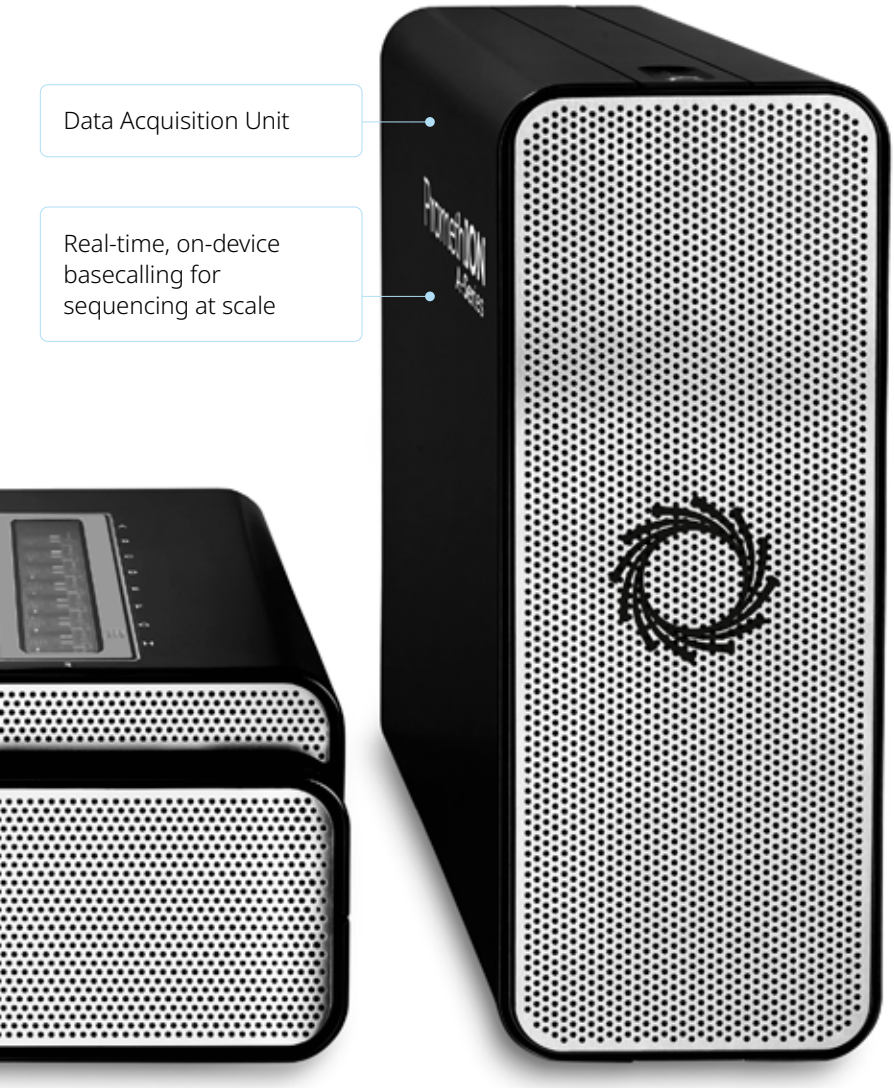
Twenty-four flow cells can be operated individually or together for flexible, on-demand sequencing



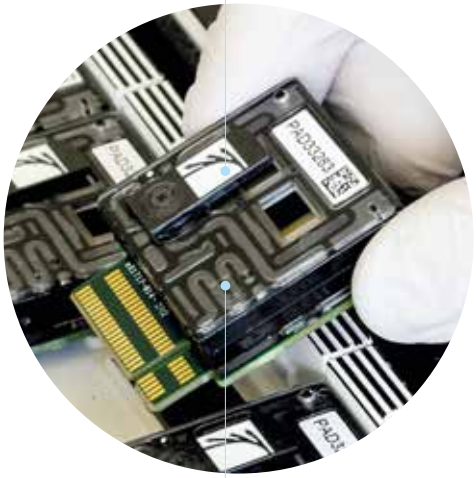
* PromethION 48, offering double the number of flow cell positions, available by request.

Data Acquisition Unit

Real-time, on-device basecalling for sequencing at scale



Sample added to flow cell here



Each flow cell comprises up to 2,675 active channels

Specification

	Weight	Size	Compatible with
Sequencing Unit	28 kg	W 590 mm | H 190 mm | D 430 mm	PromethION Flow Cells
Data Acquisition Unit	26 kg	W 178 mm | H 440 mm | D 470 mm	

Order now store.nanoporetech.com

ElysION

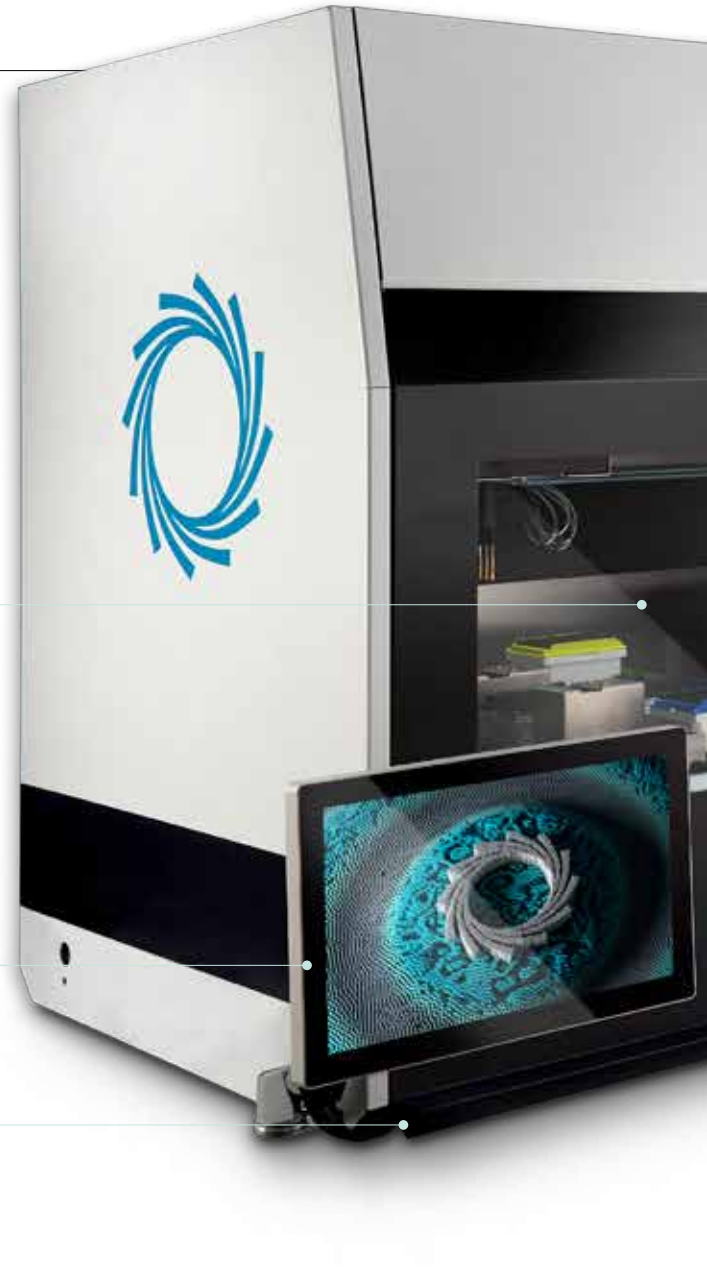
Bring streamlined genomics into your lab

ElysION provides a hands-free, simplified genomic workflow that goes from sample to data analysis. This benchtop device automates the entire sequencing workflow — sample extraction and library preparation to flow cell loading, sequencing, and data analysis — into one seamless solution to generate ultra-rich data with minimal hands-on time.

Integrated MinION Mk1D or PromethION 2 Solo, plus powerful compute with pre-installed basecalling and analysis software

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

Onboard data analysis with integrated EPI2ME software and verified end-to-end workflows



Automated sample-to-answer nanopore sequencing on single device

Prepare
Library prep directly from sample or nucleic acids

Sequence
Flow cell loading, sequencing, and basecalling

Analyse
Local analysis with EPI2ME

Wash
Flow cell washing for reuse or return

Benchtop design offering easy installation into any lab

Standalone, fully integrated device with the latest generation compute and high-capacity, high-performance data storage

Specification

Weight	Size	Compatible with
188 kg	W 1,190 mm | H 1,094 mm | D 782 mm	MinION or PromethION Flow Cells*

*Device dependent

Discover more nanoporetech.com/elysion

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

Raw data straight off ASIC

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 output file formats suitable for analysis using a range of downstream analysis tools, 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

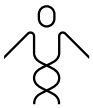
Visualise sequencing progress and performance in real time. Quality check your run, and if there's a problem with the library, stop sequencing, wash the flow cell, and start again

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

More information nanoporetech.com/analyse

Intuitive analysis with EPI2ME

The EPI2ME desktop application makes powerful genomic data analysis accessible to all scientists, regardless of bioinformatics expertise. Using an intuitive interface, users can navigate a growing range of open-source, best practice workflows that can be run on an Oxford Nanopore sequencing device*, laptop, desktop computer, cluster, or cloud service.



Human genomics

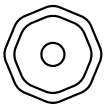
All-in-one variant detection, including SNPs, SVs, CNVs, STRs, and methylation

Genome assembly

Plasmid and bacterial genome assembly and annotation

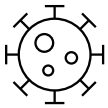
Cancer genomics

Somatic variation detection from paired tumour/normal data



Single cell & transcriptomics

Comprehensive analysis of full-length transcripts



Microbiology & infectious disease

Real-time metagenomic species identification and pathogen analysis workflows

Targeted sequencing

Variant calling in amplicon sequences

Explore the full range of EPI2ME workflows and view example reports at **nanoporetech.com/epi2me**.

EPI2ME

* GridION or PromethION devices with integrated compute only.

Detailed interactive reports

Intuitive interface

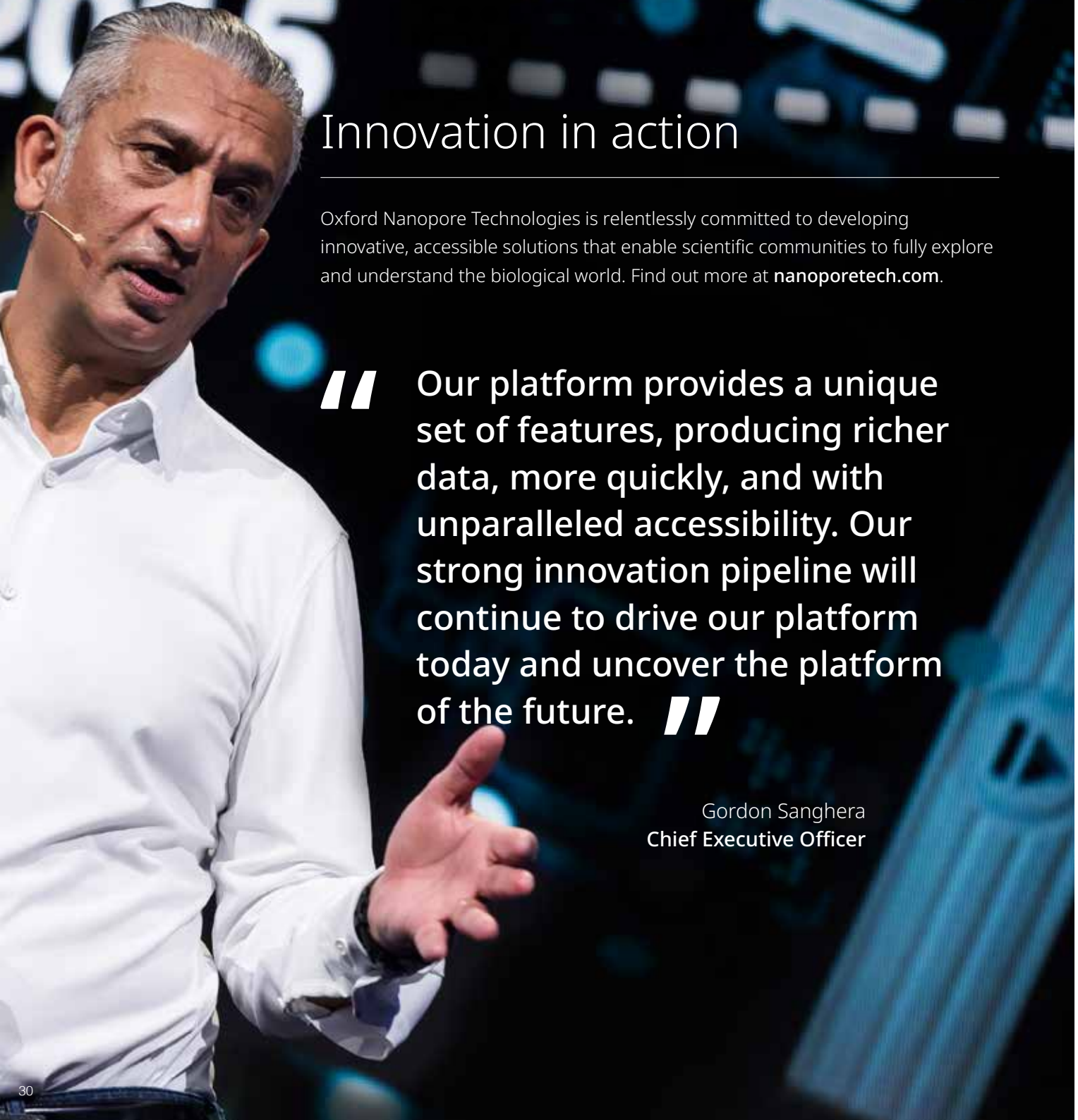
Run locally or in the cloud

No bioinformatics experience required

Preconfigured, open-source workflows

Compatible with macOS, Windows, and Linux

More information nanoporetech.com/analyse



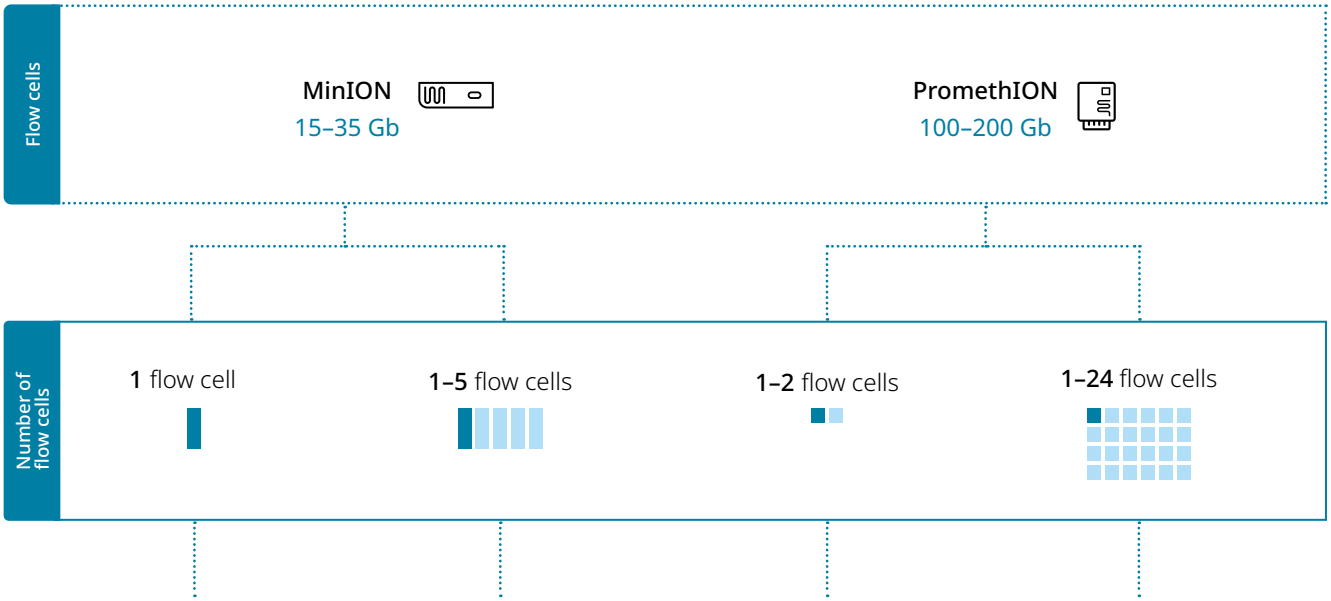
Innovation in action

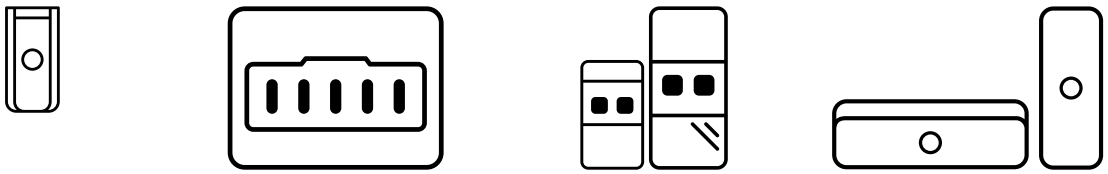
Oxford Nanopore Technologies is relentlessly committed to developing innovative, accessible solutions that enable scientific communities to fully explore and understand the biological world. Find out more at **nanoporetech.com**.

"Our platform provides a unique set of features, producing richer data, more quickly, and with unparalleled accessibility. Our strong innovation pipeline will continue to drive our platform today and uncover the platform of the future."

Gordon Sanghera
Chief Executive Officer

One technology. Any scale





MinION

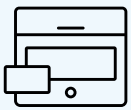
- MinION Mk1D

GridION

- GridION
- GridION Q

PromethION

- PromethION 2 Solo
- PromethION 2 Integrated
- PromethION 24



Full workflow automation — from sample to answer — available with ElysION.

Discover more nanoporetech.com

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