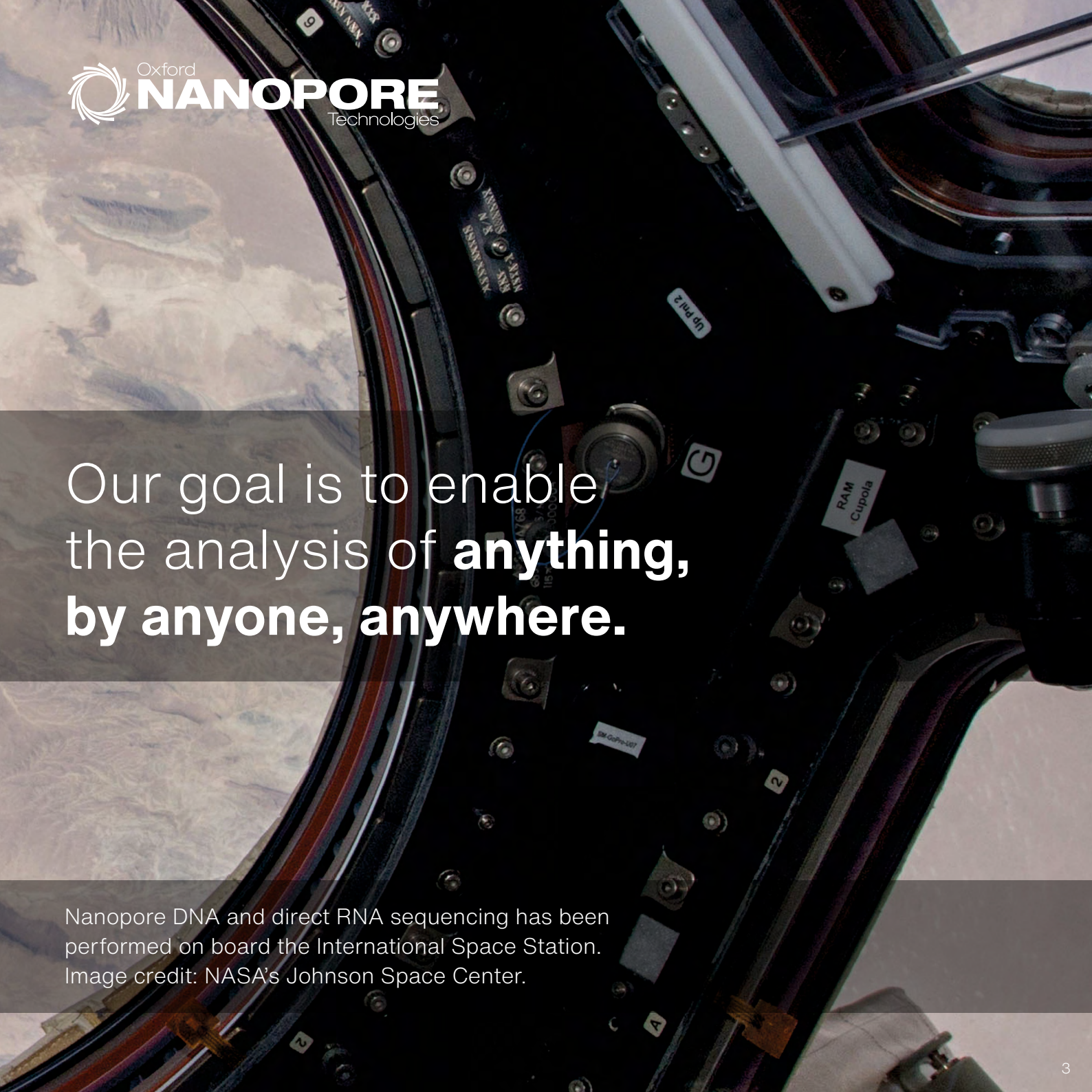
Product


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

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.

Discover the benefits of nanopore technology

Any read length, from short to ultra-long (longest >4 Mb*)

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

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-output benchtop sequencing with GridION™ and PromethION™

Direct sequencing

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

Streamlined library preparation

- Rapid 10-minute (DNA) library prep
- Automatable kit formats
- High DNA and RNA yields from low input amounts
- Maximise throughput with barcoding

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

On-demand sequencing

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

* 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 sequencing by synthesis [SBS])[1]

SNPs & phasing

Detect SNPs in regions inaccessible to SBS sequencing and generate chromosome-scale phaseblocks

Indels

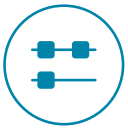
Detect the same variants as existing technology while exploring new biology

Assembly

Generate highly contiguous, chromosome-scale scaffolds

Methylation

Identify base modifications (e.g. 5mC, 5hmC, 6mA, m6A) alongside nucleotide sequence — no additional sample prep required



Splice variation

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

Gene expression

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

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

A complete and streamlined workflow — real-time an

PREPARE

Manual preparation

Automated preparation

nanoporetech.com/prepare

SEQUENCE

Compatible with **Flongle**

MinION Mk1B

GridION

PromethION 2 Solo/Integrated

PromethION 24/48

nanoporetech.com/sequence

swers 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

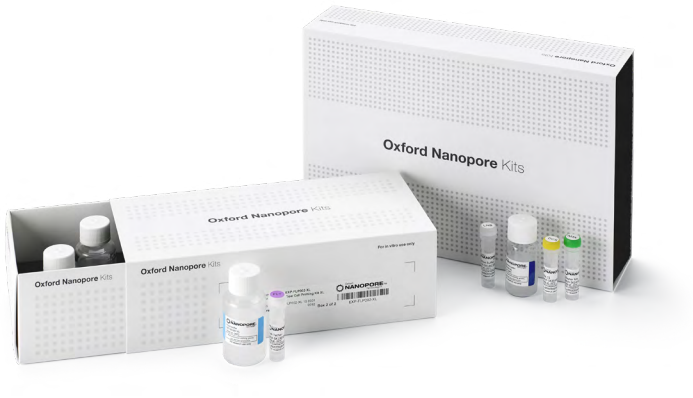
- Access the latest algorithms
- Open-source tools developed by Oxford Nanopore or Nanopore Community
- Run pre-configured EPI2ME workflows

nanoporetech.com/analyse

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 **nanoporetech.com/prepare**.

	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	400–1,000 ng gDNA	From 100 ng gDNA	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 16)	Detect modified bases for free with the Direct RNA Sequencing Kit	

View all kits nanoporetech.com/prepare

Get more from your flow cells

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.

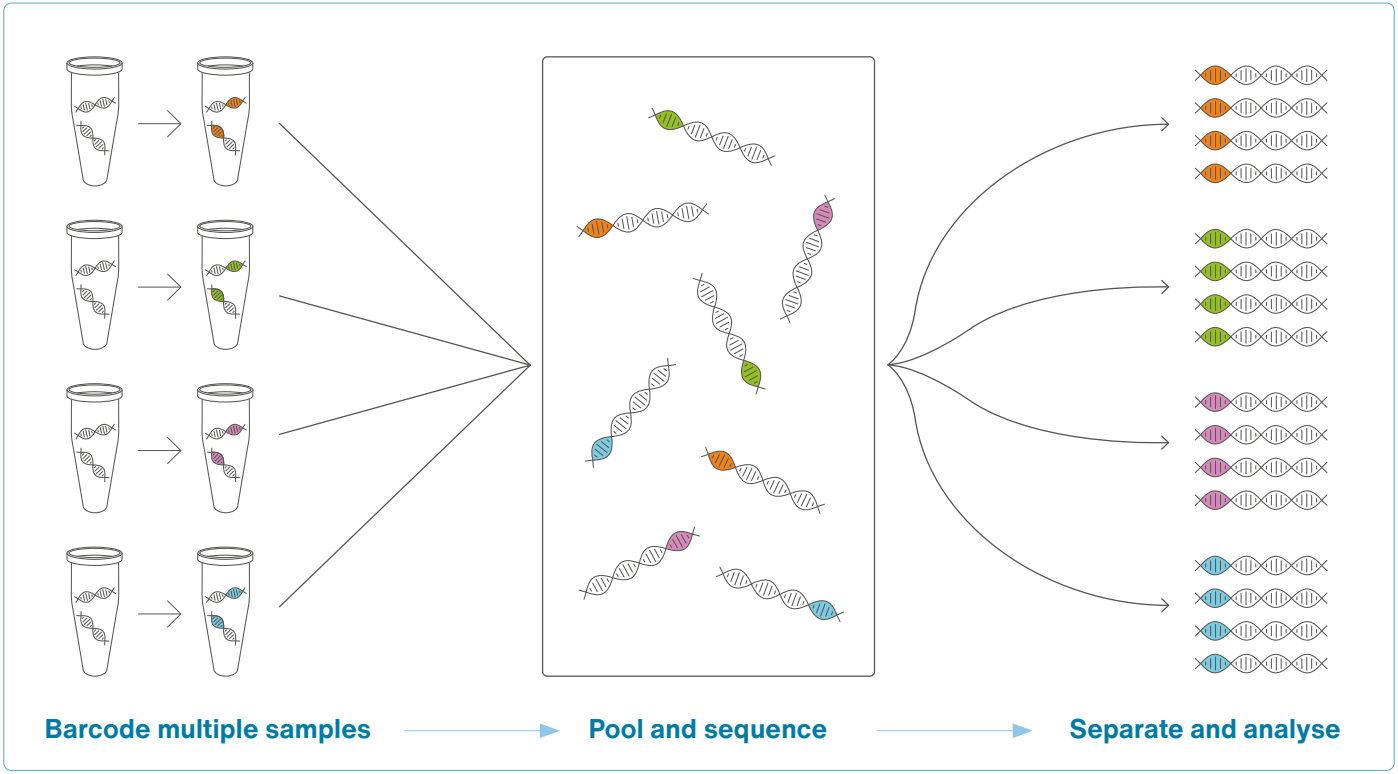
- Native Barcoding Kits and Rapid Barcoding Kits for PCR-free approach
- Rapid PCR Barcoding Kit for low input amounts

Flow cell reuse

The wash kit allows reuse of flow cells after short sequencing runs, meaning multiple libraries can be run sequentially on the same flow cell.

Sample recovery

Nanopore flow cells allow libraries to be recovered after sequencing, enabling rare or precious samples to be resequenced for maximum data output.



Easily automate your workflow

Automated library preparation

Automation of library preparation improves the overall consistency of results, supporting robust and standardised workflows, which enables increased sample throughput for medium- and large-scale projects, such as large cohort studies. Our streamlined library preparation kits are easy to automate, and protocols are available for a range of liquid handlers.

Open platform development

Alongside in-house development of automation scripts, we work with automation platform vendors and customers to design, develop, and test scripts that can be used as part of your workflow. View our rapidly expanding range of automation scripts at **nanoporetech.com/automation**.

Oxford Nanopore qualified	Vendor developed	Customer developed
Developed and verified in house at Oxford Nanopore Benchmarked against manual library preparation performance to ensure highly robust sequencing results	**Designed, developed, and tested by automation vendors** Results shared with Oxford Nanopore to verify robust and acceptable performance — against both manual and automated libraries	**Customer developed to suit specific needs** Scripts with variations from protocols published by Oxford Nanopore Customers post results, enabling public assessment of performance

Get expert advice and support from our dedicated Automation Solutions Team: **register.nanoporetech.com/automation**

Nanopore sequencing — how it works

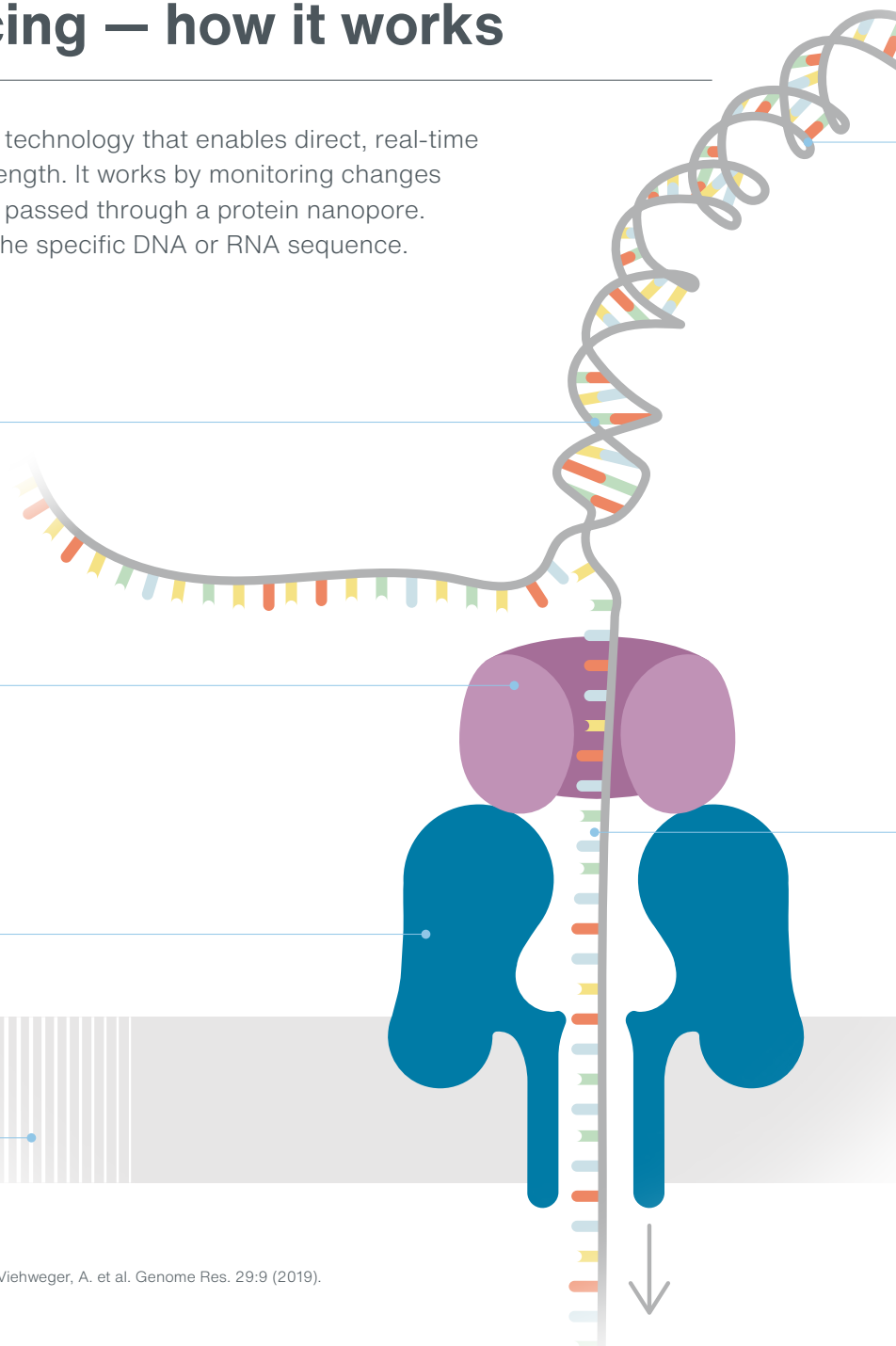
Nanopore sequencing is a unique, scalable technology that enables direct, real-time analysis of DNA or RNA fragments of any length. It works by monitoring changes to an electrical current as nucleic acids are passed through a protein nanopore. The resulting signal is decoded to provide the specific DNA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

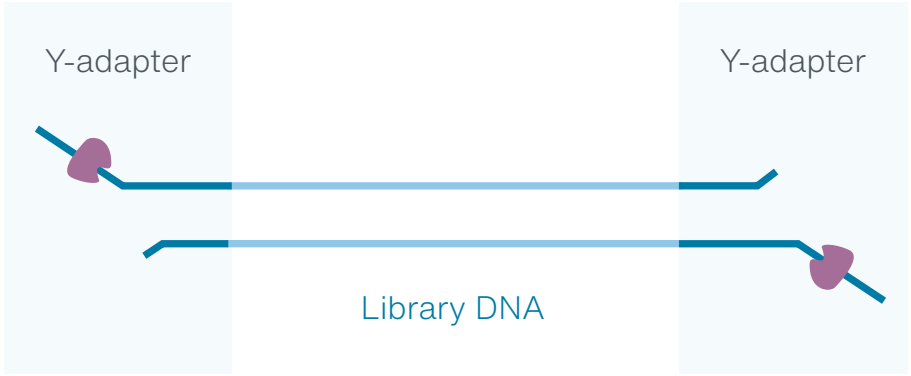
Nanopore reader
DNA or RNA fragments pass through a nano-scale hole. The fluctuations in current during translocation are used to determine the DNA or RNA sequence (see page 30).

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

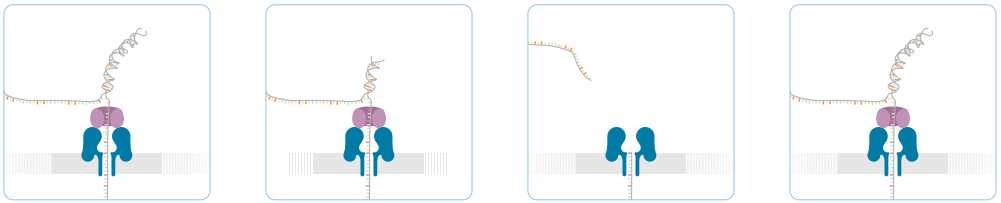


1. Internal data generated using the Ultra-Long DNA Sequencing Kit. 2. Viehweger, A. et al. Genome Res. 29:9 (2019).

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)

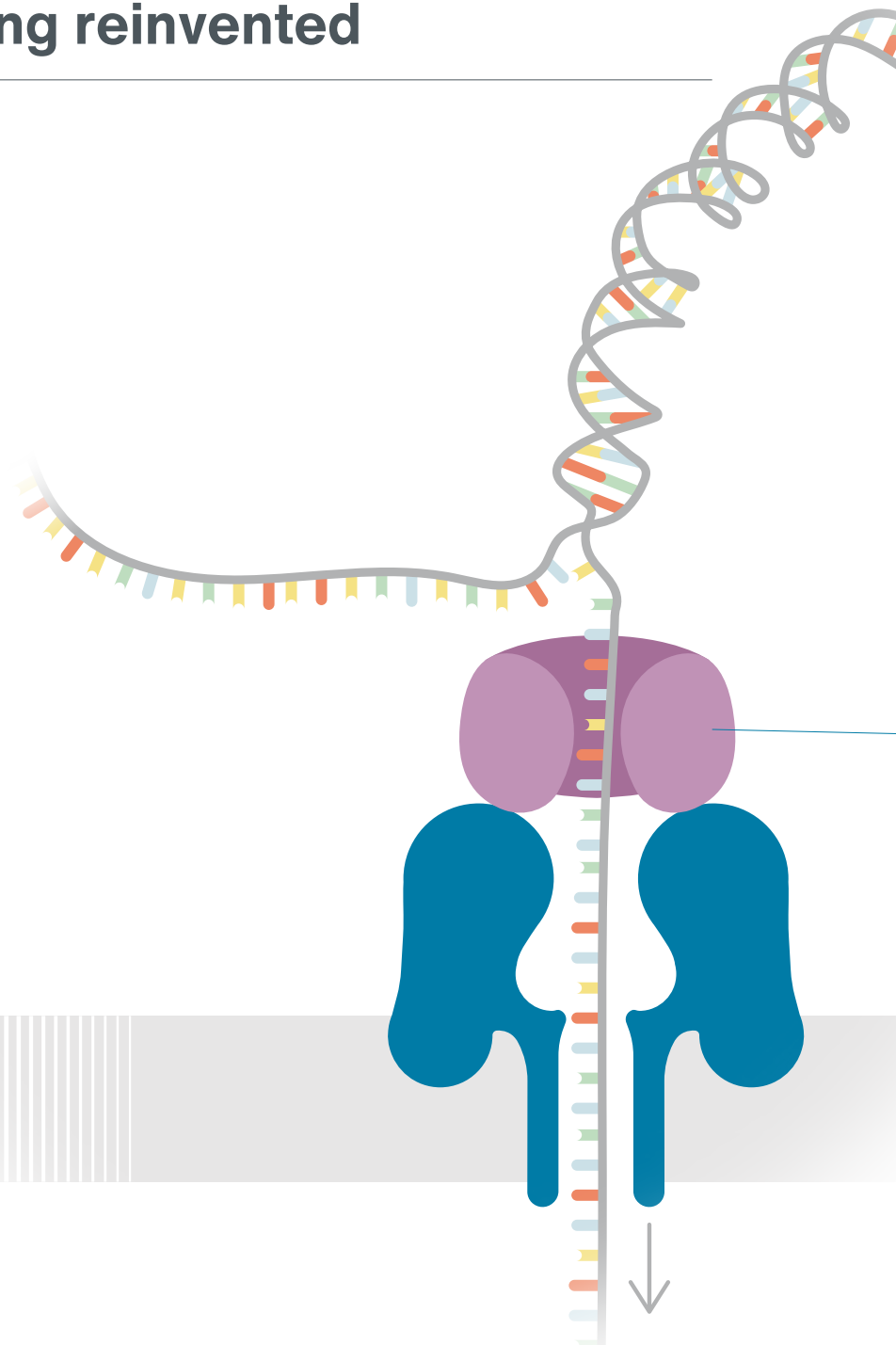
Next molecule (or second strand)...

Targeted sequencing reinvented

Adaptive sampling

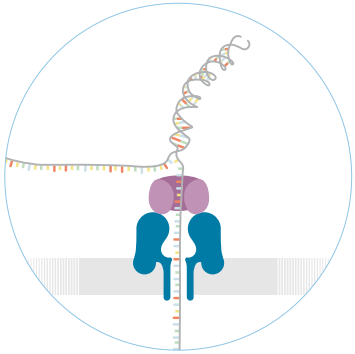
Adaptive sampling is a unique, on-device approach to targeted sequencing, which requires no upfront library enrichment steps. Using real-time basecalling, DNA fragments can be accepted or rejected for further sequencing based on their initial sequence composition. Furthermore, adaptive sampling can be 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

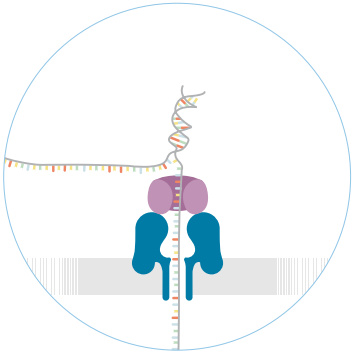


Region of interest

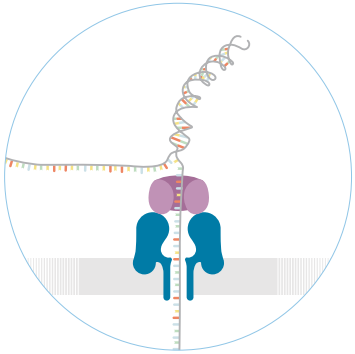
Strand is sequenced and analysed in real-time



Region of interest found. Sequencing continues

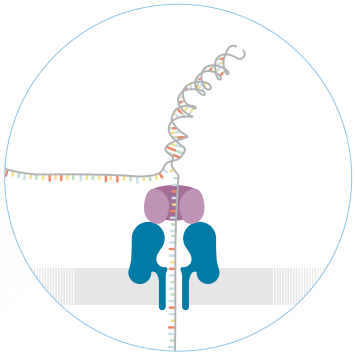


Nanopore completes sequencing, available for next strand

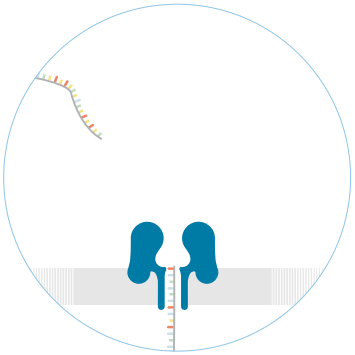


No region of interest

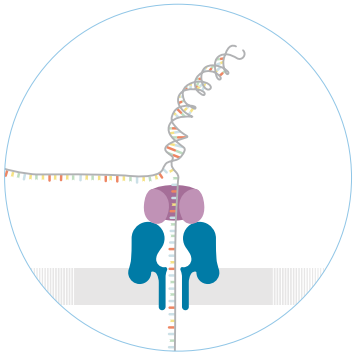
Strand is sequenced and analysed in real-time



Sequence seen is not in region of interest. Strand ejected. Nanopore available for next strand



Subsequent strand sequenced (shown here with region of interest)



Flongle

Adapting MinION and GridION devices for smaller rapid tests and analyses

Flongle is an adapter for MinION or GridION devices 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.

Reusable adapter that allows docking of smaller flow cell

Same MinION device

Specification

Weight
20 g

Size
W 105 mm | H 23 mm | D 8 mm

Compatible with
MinION and GridION devices

Order now store.nanoporetech.com

MinION Mk1B

Your personal, portable DNA and RNA sequencer

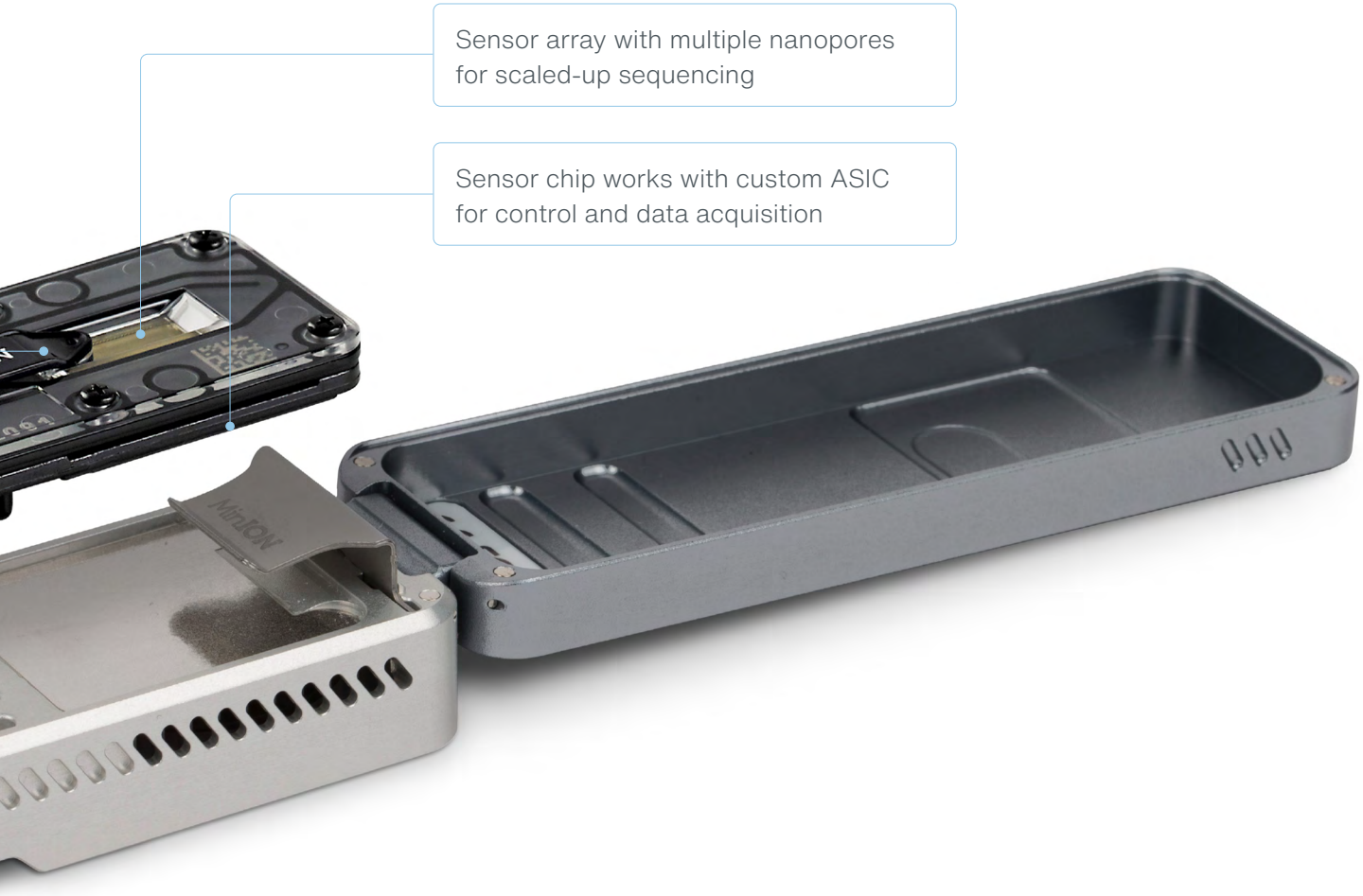
Get complete control and creativity over when, where, and how often you sequence. MinION Mk1B provides the power of nanopore sequencing in an accessible, fully portable device. Weighing only 100 g and running off a laptop, MinION Mk1B generates tens of gigabases of real-time data in the field or lab.

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
87 g (103 g with flow cell)

Size
W 105 mm | H 23 mm | D 33 mm

Compatible with
MinION and Flongle 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 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.

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

Onboard data analysis offering real-time basecalling and adaptive sampling

NANOPORE Service Certified

Service provider certification is available for the GridION

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

Specification

Weight
14.4 kg

Size
W 370 mm | H 220 mm | D 365 mm

Compatible with
MinION and Flongle 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

NANOPORE Service Certified

Service provider certification is available for PromethION devices

Specification

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

PromethION 2 Integrated

High-resolution touchscreen display allowing complete device control

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

Specification

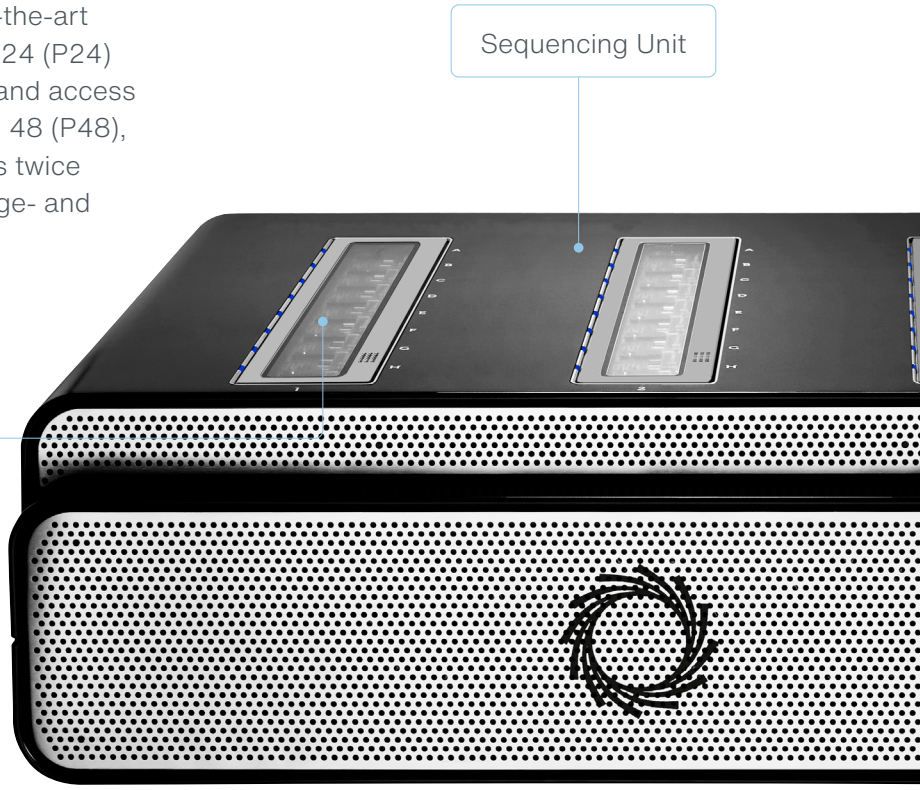
Weight	**Size**	**Compatible with**
10.6 kg	W 180 mm | H 225 mm | D 430 mm	PromethION Flow Cells

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 (P24) provides single or multiple users with on-demand access to terabases of sequencing data. PromethION 48 (P48), our most powerful sequencing device, delivers twice the capacity and output of P24 — ideal for large- and production-scale sequencing projects.



NANOPORE Service Certified

Service provider certification is available for PromethION devices

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

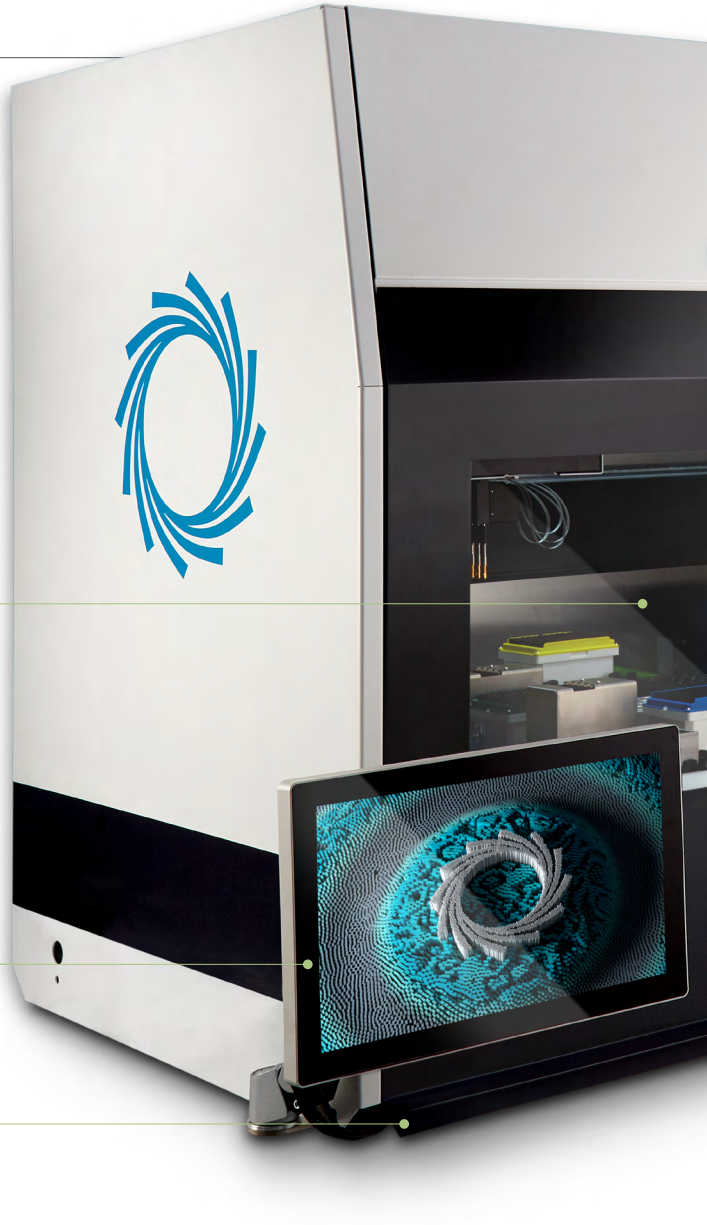
Your automated, sample-to-answer sequencing solution

ElysION™ provides a hands-free, simplified genomic workflow that goes from sample to data analysis. This benchtop device integrates 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



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

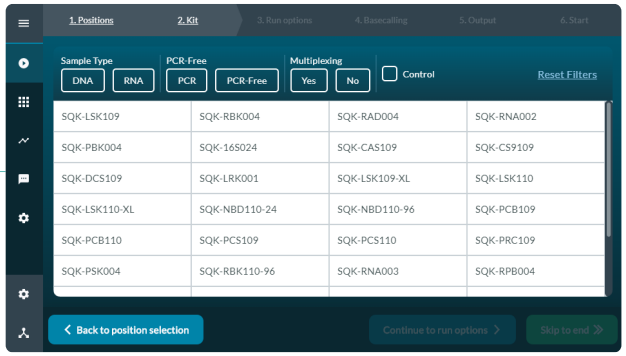
The facility of nanopore technology to sequence native DNA and RNA without the requirement for amplification or reverse transcription, allows the retention and detection of base modifications (e.g. methylation) alongside nucleotide sequence

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

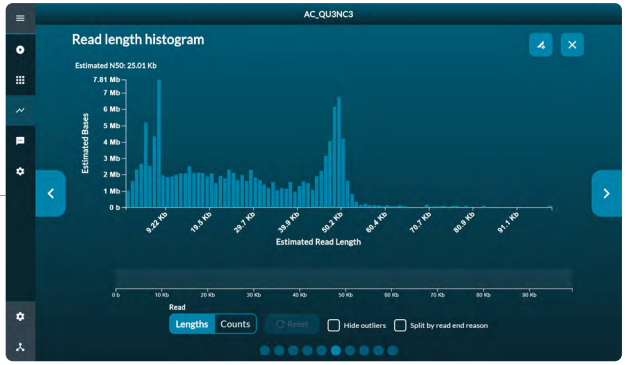
MinKNOW™, the device control and primary analysis software for all nanopore devices, provides easy experimental setup and real-time visualisation of sequencing performance.

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

Data analysis workflows include:

- Human variation: SVs, SNVs, and methylation
- Somatic variation: tumour/normal sequence data
- Plasmid and amplicon assembly
- Metagenomic species identification
- Infectious diseases: SARS-CoV-2, smallpox, influenza, etc
- Single cell and transcriptomics

	EPI2ME
Location	Local, distributed, or in the cloud
Access	Intuitive graphical interface*
Configurability	Pre-configured
Reporting	Detailed output, shareable reports
Focus	Seamless real-time or post-run analysis
Operating systems	Windows, Mac, Linux
Bioinformatics expertise	● ○ ○

* All EPI2ME workflows can also be executed from the command line.

More information nanoporetech.com/analyse

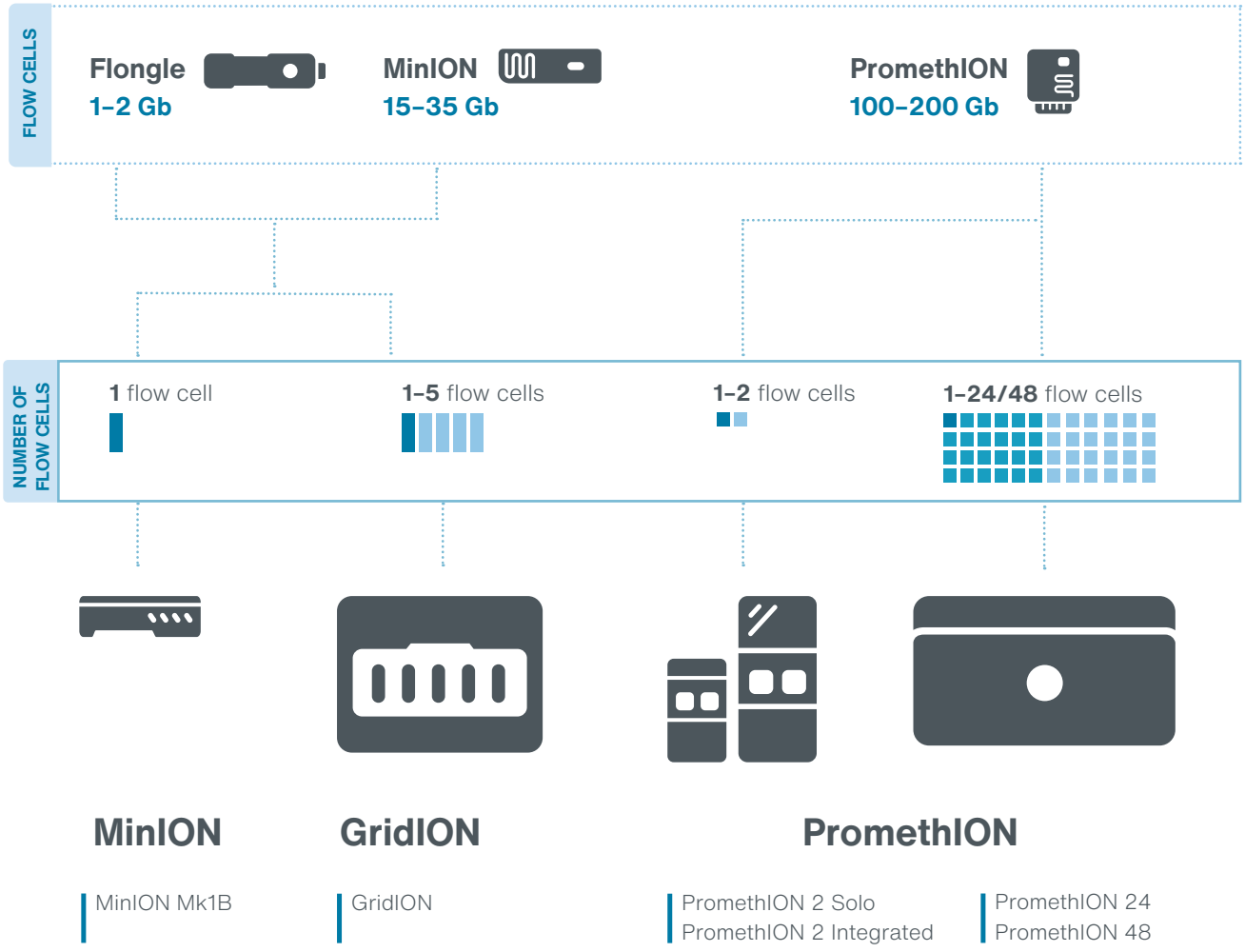
Innovation in action

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**.

> ***"Innovation is at the heart of everything we do, and it generates highly differentiated products and drives continuous improvement to deliver value to our users"***

Clive Brown
Chief Technology, Innovation, and Product Officer

One technology. Any scale



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