



# Real-time, on-demand sequencing in the palm of your hand





Nanopore sequencing technology is advancing at an unprecedented pace, promising a future where portable sequencing will be routine in surveillance and many other fields.

Jana Batovska, La Trobe University

MinION ~5 kb amplicon run basecalling all done at 34.28 Gb, I'll take that :) **77** 

Dr. John Tyson, University of British Columbia

# Immediate access to gigabases of data

MinION and MinION Mk1C allow you to sequence anything, anywhere — from the bench to the field — with real-time analysis providing immediate access to actionable results. The same DNA and RNA sequencing workflows are available across Oxford Nanopore devices, offering unrestricted read lengths, from short to ultra-long, and complete scalability to suit your needs.



\* 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.

Delivering tens of gigabases of data, MinION devices are suitable for a wide range of investigations, including:

- Low-pass large genomes (e.g. human)
- Complete microbial genomes
  and metagenomes
- Medium to high plex targeted sequencing
- Quantitative species identification
- Full-length isoform characterisation
  and quantification
- Base modifications as standard (e.g. methylation)

All the benefits of real-time nanopore sequencing in a portable, low-cost device



### Any length read

Short to ultra-long reads (>4 Mb) to suit your requirements – complete genomic characterisation; SNVs, SVs, repeats, phasing, and transcript isoform resolution

### **High yields**

As much as 50 Gb\* data suitable for all applications - from whole genomes and transcriptomes to highthroughput targeted analyses



#### **Real time**

Immediate access to actionable results – from pathogen and antimicrobial resistance identification to fusion transcripts





#### Portable

#### Accessible

required

#### Direct

bias and detect base modifications (e.g. methylation)

\* 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.

Sequence samples at source for faster access to meaningful results





Low-cost, affordable devices with no capital investment or complex IT infrastructure



Study native DNA and RNA, not a copy – eliminate amplification





# 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.

# Choose your MinION Starter Pack



Starter Pack	Enhanced Starter Pack		
1	1		
1	4		
1	1		
1	1		
Included	Included		
76487-168	76521-796		

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

# Choose your MinION Mk1C plan

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.

Integrated, real-time compute with preinstalled basecalling and analysis software

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

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

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

MinION Flow Cells can deliver tens of gigabases of data



Specification Size W 140 mm | H 30 mm | D 114 mm

Weight

420 g

	Starter Pack	Enhanced Starter Pack	CapEx <sup>†</sup>	
MinION Mk1C device	1	1	1	
Flow cells (R9.4.1)	6	12	-	
igation Sequencing Kit (LSK-110)	1	2	-	
Wash kits	1	1 1		
Software licence and device warranty*	12 months	12 months	12 months	
Community Support	Included	Included Included		
/WR Cat. No.	76487-170	76521-798	76487-172	

\* Extended warranties available.

<sup>†</sup> Device purchase.

Enquire for pricing, and training and support services.



MinION Mk1C COVID Starter Pack also available for simple, scalable, and rapid sequencing of SARS-CoV-2 samples. Discover more at vwr.com.



#### Prepare

- Streamlined library preps in as little as 10 minutes
- High DNA/RNA yields from low input amounts
- Sample multiplexing for maximum throughput
- · Application-specific kits (e.g. SARS-CoV-2 and 16S sequencing)

#### Sequence

- Sequence what you need, when and where you need it
- Read lengths determined by your sample and experimental needs
- MinION devices sequence DNA and RNA directly - meaning no amplification bias and retained modification information (e.g. methylation)
- Adaptive sampling on-sequencer target enrichment; reject or accept reads on a strandby-strand basis

#### Analyse

- · Real-time results for time-critical applications such as pathogen identification
- User controlled run time stop sequencing when sufficient data generated, wash and reuse flow cell
- Portable data analysis using MinION Mk1C or combine MinION with a laptop
- Output raw signal or basecalled .fastg files for use in custom analysis pipelines

#### **Applications include:**

- Rapid metagenomic species identification and antibiotic resistance profiling
- Accurate high-coverage microbial genome assemblies (DNA and RNA)
- Enhanced large genome analysis (e.g. cancer samples) through accurate mapping of structural variation, repetitive regions, and phasing
- Quantify and characterise RNA splice variants, isoforms and fusion transcripts

# Streamlined library preparation for all applications...

A comprehensive range of library preparation kits are available, including direct, amplificationfree DNA and RNA approaches that minimise potential bias and retain base modification information. Multiplexing (barcoding) options allow multiple samples to be analysed in a single sequencing run, maximising data generation while minimising costs.

	DNA		RNA			
Kit	Ligation	Rapid / Field	PCR	PCR cDNA	Direct cDNA	Direct RNA
Prep time	60 min	10 min	60 min + PCR	165 min	270 min	105 min
Input	1,000 ng ds DNA	From 50 ng HMW gDNA	100 ng dsDNA	1 ng RNA	100 ng poly-A <sup>+</sup> RNA	500 ng poly-A <sup>+</sup> RNA
PCR required	No	No	Yes	Yes	No	No
Output	•••	•••	•••	•••	•••	• • •
Multiplexing	Yes	Yes	Yes	Yes	Yes	In dev.

#### Also available

- New: Ligation Sequencing Kit (Q20+) our latest chemistry, optimised for modal raw read accuracy of Q20+ (99%+)
- Ultra-Long DNA Sequencing Kit optimised for ultra-long DNA fragments and reads
- Field Sequencing Kit all the benefits of rapid sequencing plus ambient shipping and storage
- Cas9 Sequencing Kit streamlined, PCR-free enrichment of long targeted regions, retaining base modifications
- Application-specific library preparation kits (e.g. SARS-CoV-2 and 16S sequencing)
- Automatable workflows

# ...and end-to-end analysis workflows

EPI2ME and EPI2ME Labs offer a rapidly growing number of streamlined, best practice analysis pipelines.

#### EPI2ME:

Simple, real-time data analysis workflows accessed through the cloud or locally using MinION Mk1C\*.

#### EPI2ME Labs:

Interactive tutorials and workflows allowing you to explore your data and develop your bioinformatics skills

#### Workflows include:

- SARS-CoV-2 analysis
- Metagenomic species ID
- Antimicrobial resistance profiling
- 16S-based microbial ID
- Plasmid sequencing
- Structural variation analysis
- Variant calling
- Clone validation
- Reference alignment

\* Local EPI2ME workflows on MinION Mk1C coming soon.

For a full list of kits, including sample multiplexing options, visit vwr.com

# workflows





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