Biopharma

Nanopore sequencing solutions

for cell and gene therapies

Oxford Nanopore Technologies

WHAT YOU'RE MISSING MATTERS

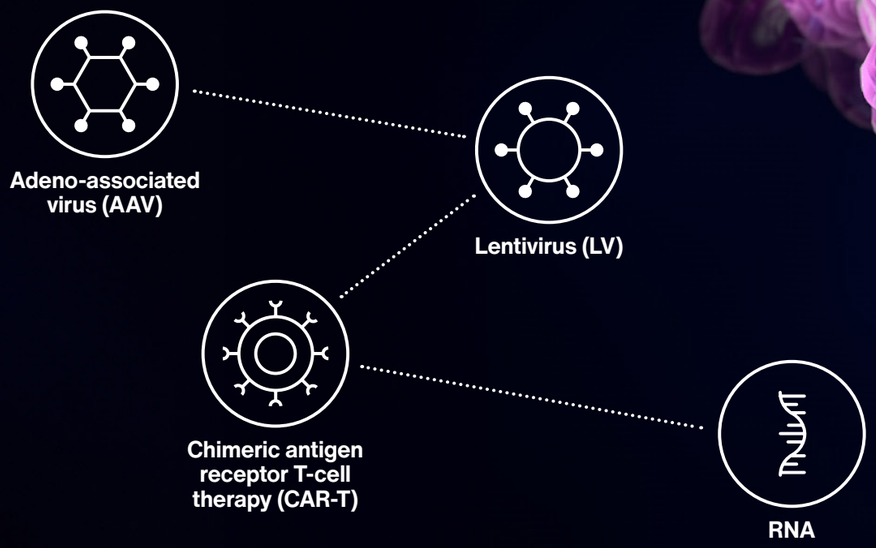
Nanopore sequencing solutions for cell, gene, and RNA therapies

Next-generation sequencing (NGS) is now an essential tool across the drug development value chain; however, the requirement of traditional NGS technologies for nucleic acid fragmentation and amplification erases critical sample information. Nanopore sequencing from Oxford Nanopore Technologies overcomes these limitations to reveal the true biology of your samples and uncover what you've been missing.

Nanopore sequencing delivers:

- Accurate, rich data — for comprehensive insights
- Any read length — from short to ultra-long (>4 Mb)
- PCR free — no amplification bias and built-in methylation detection
- Scalable devices — portable to ultra-high throughput
- Real-time analysis — immediate access to actionable insights

Our industry-leading solutions for the development of cell, gene, and RNA therapy drug modalities provide the data you need to develop better and safer drugs, while reducing risk.



Plasmid sequencing

Plasmids are an essential starting material for cell, gene, and RNA therapies and erroneous constructs can cost significant time and money. Traditional Sanger sequencing has many limitations, including the exclusion of the plasmid backbone and the inability to resolve repetitive regions, dimers, and deletions, plus the requirement for vector-specific primers.

Oxford Nanopore Technologies has developed an easy-to-implement whole-plasmid sequencing workflow that overcomes all of these challenges to deliver complete confidence in your production processes.

Sanger sequencing

Gene insert
- No mutations

Partial plasmid sequence

Nanopore sequencing

Promoters
- Compatible with host organism

Gene insert
- Correct orientation
- No mutations

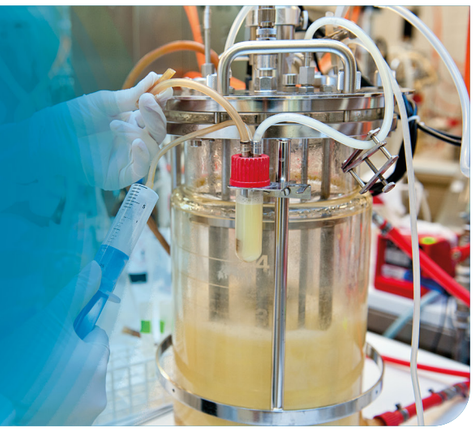
Complete plasmid sequence

Resistance genes
- Correct sequence
- Not already present in host organism

Backbone
- No mutations
- Suitable for storage and future use

Why nanopore sequencing?

- Whole plasmid sequence verification, including insert orientation, resistance genes, promotors, and backbone — without primers or complicated primer walking
- Resolve repetitive regions, dimers, and deletions
- Simple end-to-end workflow with rapid, same-day turnaround time — up to 96 samples per run
- In-house process — less downtime plus increased data and intellectual property security



Gene therapy

Accurate quality control (QC) of AAV vectors is crucial to ensure that correct, error-free AAV genomes are packaged into capsids. However, critical features such as inverted terminal repeats (ITRs) are often overlooked due to the inherent limitations of traditional short-read sequencing technologies.

Long nanopore sequencing reads can span entire AAV genomes, enabling complete characterisation of ITRs and easy identification of truncated genomes, contamination, and mutations. Transgenes and promoters of interest can also be identified to support the verification of AAV vectors.

Short-read sequencing

Ambiguous data caused by incomplete AAV coverage

Nanopore sequencing

Long sequencing reads deliver complete AAV coverage

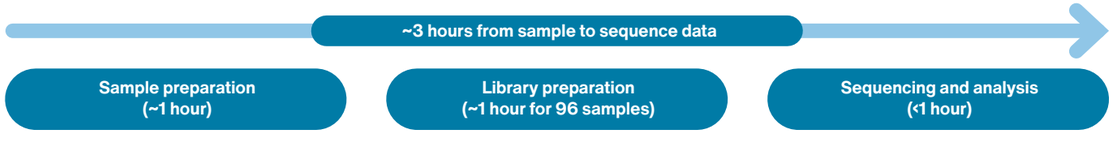
Why nanopore sequencing?

- Reduce failure risks through whole AAV genome validation — ITR to ITR
- Map truncation hotspots across vector genomes
- Shorten QC testing time with unbiased, amplification-free identification of vector and contaminants in a single assay

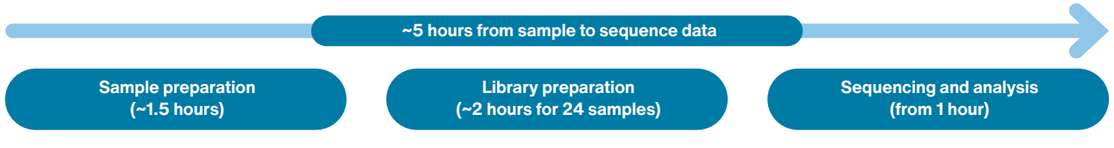
Streamlined, end-to-end AAV workflow

Nanopore sequencing acts as a rigorous QC tool by facilitating the generation of full-length, end-to-end reads of the AAV genomes and the plasmids used to create them.

Plasmid validation: check the integrity of AAV plasmid vectors prior to transgene insertion



AAV QC: check the integrity of single-stranded and self-complementary AAV vectors



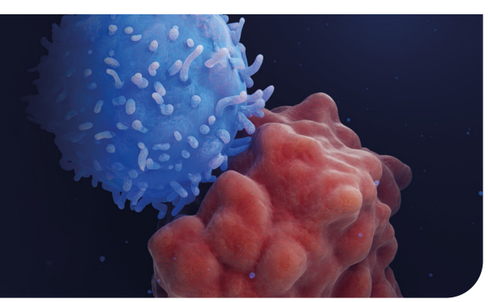
Cell therapy

An essential step in CAR-T engineering is the integration of engineered chimeric antigen receptor (CAR) genes into the genomes of T cells. To advance the safety and efficacy of CAR-T cell therapy, it is important to fully understand the genomic context of gene insertions, including orientation, sequence conservation, and copy number.

Traditional short-read sequencing techniques can overlook insertion events in repetitive regions of the genome; however, long, accurate nanopore sequencing reads provide comprehensive characterisation of integration events, irrespective of genomic location or context.

Why nanopore sequencing?

- Comprehensive insertion site analysis (ISA) and copy number analysis
- Reduced QC time
- Whole-genome or targeted sequencing approaches



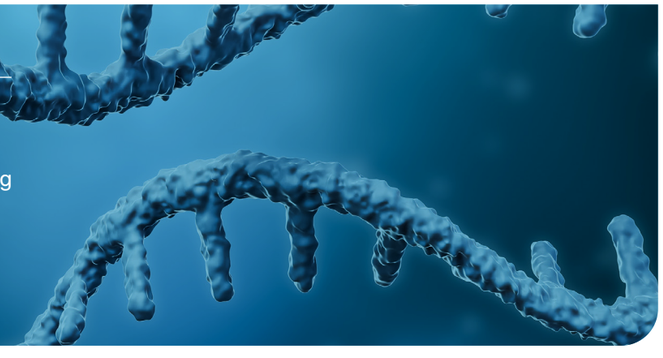
RNA therapy

RNA has quickly become a key drug modality to treat complex indications such as infectious diseases and cancer. Until recently, sequence-based analysis of RNA required its conversion to complementary DNA (cDNA), a process that introduces bias and erases all information on modified bases, which are known to play a key role in RNA expression and stability.

Nanopore sequencing is the only technology that enables direct sequencing of native RNA, without amplification or conversion to cDNA. This delivers unbiased analysis of RNA molecules, including base modifications — providing comprehensive insights for biopharma research and manufacturing.

Why nanopore sequencing?

- Directly sequence RNA for accurate and unbiased identity, integrity, and poly(A) tail length testing
- Determine the length distribution of RNA molecules
- Detect RNA base modifications



About Oxford Nanopore Technologies

Founded in 2005, Oxford Nanopore Technologies has developed a new generation of sequencing technology. It is the only sequencing technology that offers real-time analysis, in fully scalable formats from pocket to population scale, that can analyse full-length native DNA or RNA.
The technology is used in over 120 countries worldwide to deliver rapid, comprehensive genomic insights to users across academic, healthcare, environmental, and industrial settings.

The company is headquartered in Oxford, UK, with satellite offices around the world.

Your partner for cell and gene therapies

- Strong IP position with over 1,350 patents and applications
- Easy, robust, and scalable protocols and end-to-end workflows
- Rapid, local, field-based support
- Global presence with offices across North America, Europe, and Asia
- Robust supply chain
- Proven technology backed up by over 8,600 peer-reviewed publications

Contact us today to discuss your drug development requirements, or visit **nanoporetech.com/biopharma** for more information.

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