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Oxford Nanopore launches Flongle for rapid, smaller DNA/RNA sequencing tests

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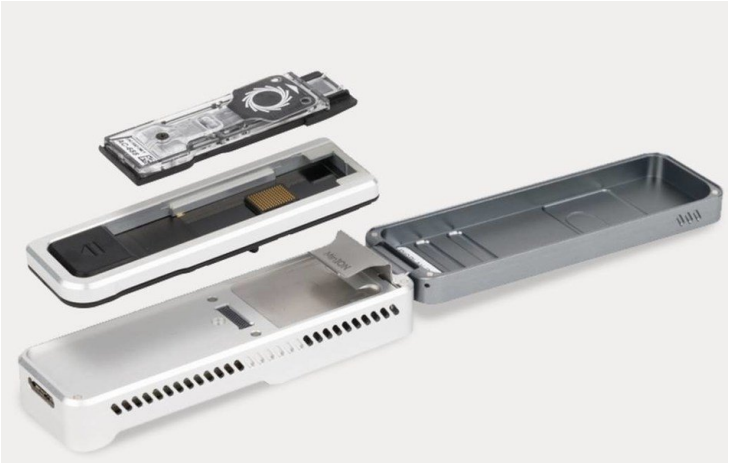

Oxford Nanopore has made Flongle starter packs available for purchase after initial testing in an early-access programme. Flongle introduces a new paradigm of smaller, on-demand DNA or RNA sequencing tests, with the potential to transform a range of applications where rapid insights are required at low cost.

Oxford Nanopore's goal is to enable the analysis of any living thing, by anyone, anywhere. Flongle is designed to bring this goal closer and to also allow low-cost sequencing at any time. With its compact format, Flongle opens up possibilities of on-demand testing in a broad range of locations, from scientific laboratories to farms and factories, healthcare settings, outdoor environments or classrooms.

Flongle is an adapter for the portable MinION and desktop GridION X5 sequencing devices. It uses the same core nanopore sequencing technology as other Oxford Nanopore devices, producing real-time data, direct sequencing and long reads. The small Flongle flow cells can currently produce as much as 1.8 Gb of sequence data with headroom for more than 3 Gb. This enables many sequencing experiment types, including small-genome sequencing, targeted panels/amplicon sequencing, metagenomics for the identification of viruses, bacteria or characterisation of microbiomes, or species ID. It can also be used for quality control for larger nanopore experiments.

At $90 per flow cell, Flongle allows on-demand sequencing at an affordable price point, without needing to wait for the large batches of samples that are often required to achieve low per-test costs on traditional sequencing devices. The workflow is fast and simple, with library preparation in as little as ten minutes and real-time data analysis.

Dr Matt Loose, from DeepSeq, School of Life Sciences, University of Nottingham, has been testing the Flongle as part of an early access programme. *"We've been using Flongle for testing and developing new protocols such as CRISPR/Cas9 selection for targeting select regions of the human genome, as well as working up new samples before running at scale on PromethION. We've been very happy with throughput and yield on early access flow cells and are looking forward to incorporating production-ready Flongle into our workflows. It will be really interesting to see how users apply Flongle in the field."*

Miten Jain, from the University of California, Santa Cruz, has also been trialling Flongle: *"Flongle-based sequencing is the best way to check a nanopore library. At UC Santa Cruz, we now routinely sequence native RNA and genomic DNA libraries on a Flongle Flow Cell before scaling them to our PromethION. We have observed that Flongle-based sequencing is a good predictor of library quality and its performance on the PromethION. Flongle also permits experimental tests at a more affordable scale and will be an integral part of our nanopore work going forward."*

Dr Justin O'Grady is a translational researcher from University of East Anglia, UK. He has been developing nanopore-based research methods for the rapid metagenomic characterisation of pathogens in clinical samples from patients with pneumonia or urinary tract infections. *"I am excited about how Flongle can help identify pathogens and antimicrobial resistance more quickly, and how such technologies could be used in settings much closer to patients in the future."*