



CENTRE FOR Tropical Bioinformatics and Molecular Biology

Long-read Sequencing for Research in the Tropics : Round 2

After the great success of our Nanopore sequencing grants in 2019 the Centre for Tropical Bioinformatics and Molecular Biology is pleased to launch a follow up competition for 2020! The center is once again offering its members the chance to win access to **free long read sequencing** using an Oxford Nanopore sequencer. This time the focus will be broader and a wider variety of sequencing options are on offer.

Nanopore sequencing is a type of single molecule nucleic acid (DNA or RNA) sequencing that offers ultra-long reads, rapid operation and relatively high total throughput. Oxford Nanopore develops a range of instruments for nanopore sequencing including the MinION, which is highly portable (phone sized), inexpensive and flexible -making it particularly suited to molecular biology in the tropics. The main cost of sequencing for this technology is the price of flow cells (disposable, per run) and reagents for preparing libraries. This situation has recently improved with the release of small sized “Flongle” flow cells which are around 1/10th the price, and provide around 1/10th the sequencing output of a full sized flow cell. In this grant round we are offering access to both types of flow cell (Flongle, and full-size).

Access grants details

CTBMB has four full size flow cells and 12 Flongle cells available as well as reagents for preparing DNA sequencing libraries. These will be used to support small pilot sequencing projects using the MinION. Applications are encouraged from all CTBMB members including those with no prior nanopore experience. If you are unsure whether the system is appropriate for your research you should first explore examples listed here <https://nanoporetech.com/applications> or seek advice from ctbmb@jcu.edu.au.

Assessment criteria;

- The project leader should be a member of the CTBMB. Non-members can submit a membership application online via <https://forms.gle/283UUmvfTd5qh1s19>
- MinION sequencing should offer significant enhancements to the project compared with other sequencing platforms (eg in terms of cost-effectiveness, overall quality of the final result, unique findings only possible with long read technology, portability)
- Project outcomes should be clearly identified and feasible, for example;

- Validation of a method that will have high utility if successful
- Direct outcomes that could not have been achieved with other technologies
- Realistic, small proof of concept projects that support future grant applications
- Projects should be self-sufficient other than the MinION sequencer, flow cell and sequencing kit. These requirements include basic lab facilities and expertise to prepare DNA (e.g., high molecular weight DNA extraction).
- The project must be feasible with the resources available. For example, a Flongle flowcell should generate data that is sufficient to assemble the genome of a bacterial isolate, whereas at least one full flow cell would be needed for a small eukaryotic genome. Direct RNA sequencing, amplicon sequencing, metagenomic sequencing or multiplexing are also possible but require additional kits which can be purchased directly from Oxford Nanopore.
- Flow cells have a limited shelf life so it is important that projects are able to **start sequencing as soon as possible**.
- Access grant awardees should aim to present results at the CTBMB conference in 2021 (COVID restrictions permitting)

Submission and assessment process:

Grant applications should be a single page or less. Submit your application by email to CTBMB@jcu.edu.au no later than 4th December 2020.

Applications will be assessed by the CTBMB executive team and applicants will be notified of the outcome by 17th December 2020.