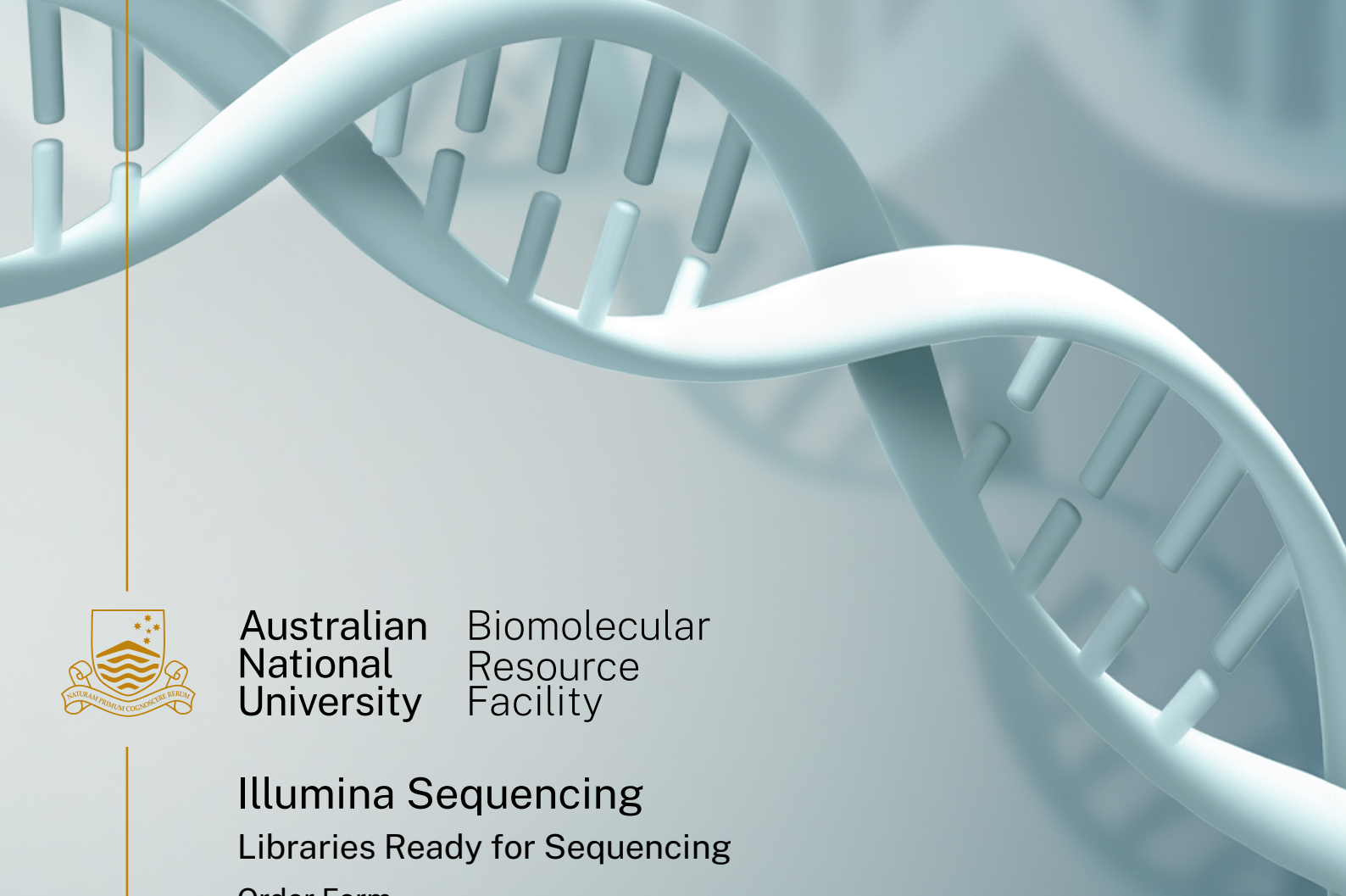


Australian National University

Biomolecular Resource Facility

Illumina Sequencing

Libraries Ready for Sequencing

Order Form

NCRIS National Research Infrastructure for Australia

An Australian Government Initiative

BIOPLATFORMS AUSTRALIA

1. Contact & Billing Information

Customer Information

Full Name

Address

Phone

Email

PI (or lab head) Information

Full Name

Phone

Email

Signature (digital)*

Date

Billing Information

GLC Charge Code (ANU Customers Only)

Purchase Order/Work Order, or Email Address (Non-ANU Customers Only)

*Please use the Adobe E-Sign tool, or type initials. By signing you acknowledge and accept BRF charges, terms and conditions.

2. Sequencing Information

Please fill in the following section, using the **dropdown menus** to select which sequencing kit is required for your project (choose only one instrument per order form). Use the dropdown menu under "Data Delivery" to choose how you would like the sequencing data to be delivered. Under the "Read Lengths" section, enter your chosen read lengths e.g. 150 bp paired-end, 100 bp single-end etc.

For more information on data output and compatible read lengths, please email the BRF at brf@anu.edu.au

Data Delivery

MiSeq i100

Reagent Kit

Read Lengths

NextSeq 2000

Reagent Kit

Read Lengths

NovaSeq X Plus

Reagent Kit

Read Lengths

3. Library Pool Information

Please fill in the following sections for your library pool(s). If you are submitting a pool for a MiSeq or NextSeq 2000 run, you will only need to fill in 1 of these sections. If you are submitting multiple pools for sequencing on separate flow cell lanes (NovaSeq X Series), fill in a section for each pool.

1 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

2 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

3 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

4 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

5 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

6 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

7 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

8 **Name:** _____ **Concentration:** _____ **Prep. kit:** _____

Species/Origin: _____

Additional Information

If you have additional information about your libraries and sequencing configuration, please provide it here:

_____

4. Required Documentation

In addition to this submission form, we require a fragment analysis of your libraries such as an Agilent TapeStation or Bioanalyzer report, or similar. Alternatively, if you are unable to provide a fragment analysis report, we can accept a fluorometric quantification for your libraries (e.g Qubit).

We require a sample sheet detailing the indexes (barcodes) of your libraries. If you are unsure of how to correctly format a sample sheet, we can accept a list of the samples names with their corresponding barcodes in their forward-strand orientation.

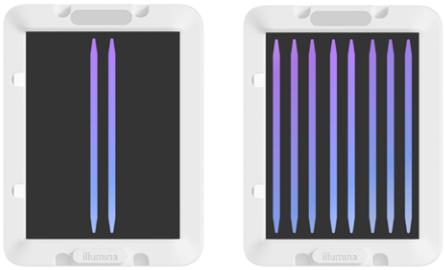
After filling in this form, please email it to the BRF at brf@anu.edu.au, along with your fragment analysis report and sample sheet (or barcode list). You do not need to print a copy of this form for submission.

5. Library Requirements

The Illumina MiSeq and NextSeq 2000 use flow cells with a single lane, meaning only one library pool can be sequenced per run. The Illumina NovaSeq X Series uses flow cells with multiple lanes, meaning multiple library pools can be sequenced per run. Users also have the option to load a single library pool across all lanes, attributing the total data output to that library pool.

MiSeq i100

NextSeq 2000



NovaSeq X Series

Each Illumina sequencer requires different amounts of DNA for a sequencing run:

- **Illumina MiSeq i100**: at least 50 µL of ~2 nM DNA
- **Illumina NextSeq 2000**: at least 25 µL of ~2 nM DNA
- **Illumina NovaSeq X Series**: at least 40 µL of ~2 nM DNA per lane

For the NovaSeq X Series, users have the option to load multiple library pools onto separate lanes of the flow cell e.g. one library on all lanes, two libraries on four lanes each, eight libraries on one lane each etc.

1.5B flow cells on the NovaSeq X Series feature 2 lanes. 10B and 25B flow cells have 8 lanes.

The NovaSeq X Series can run 2 flow cells simultaneously. If you are submitting libraries for 2 sequencing runs, you will need to fill this form for one run and a second form for the second run.

Custom primers: if your libraries require custom sequencing primers for the sequencing run, these will need to be submitted with the libraries. There can be up to four custom sequencing primers required for the sequencing run (Read 1, Read 2, Index 1 and Index 2) - please provide ~30 µL of each primer at 100 µM in separate tubes. Do not combine any of these primers into single tubes.

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Website

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CRICOS Provider Code: 00120C