

MGI DNBSEQ Standalone Sequencing Service Request Form

User Information

User Name:	User E-mail:
Tel no:	Department or School:
Supervisor's Name:	Account no. to be Charged:
User's Signature:	Date:

Sequencing Requirement

Instrument	<input type="checkbox"/> DNBSEQ-G400 <input type="checkbox"/> DNBSEQ-T7	
Data Output	<input type="checkbox"/> Whole flow cell <input type="checkbox"/> Sequenced with other samples: _____ Gb (in the increments of 12 Gb) [#]	
Library Type	<input type="checkbox"/> RNA-seq <input type="checkbox"/> Whole Genome Sequencing <input type="checkbox"/> Whole Exome Sequencing <input type="checkbox"/> ChIP-seq <input type="checkbox"/> ATAC-seq <input type="checkbox"/> Amplicon Sequencing <input type="checkbox"/> Metagenomic Sequencing <input type="checkbox"/> Small RNA-seq <input type="checkbox"/> Whole Genome Bisulfite Sequencing <input type="checkbox"/> Others: _____	
Sequencing Configuration (please leave this section blank if "Sequenced with other samples" is chosen)	Sequencing Kit	<u>DNBSEQ-G400</u> <input type="checkbox"/> SE50 <input type="checkbox"/> SE50 (Small RNA) <input type="checkbox"/> SE100 <input type="checkbox"/> SE400 <input type="checkbox"/> PE100 <input type="checkbox"/> PE150 <input type="checkbox"/> PE200 <u>DNBSEQ-T7</u> <input type="checkbox"/> SE50 <input type="checkbox"/> PE100 <input type="checkbox"/> PE150
	Primers	<input type="checkbox"/> MGI <input type="checkbox"/> App-A <input type="checkbox"/> App-C <input type="checkbox"/> App-D <input type="checkbox"/> TM <input type="checkbox"/> STOmics <input type="checkbox"/> Custom Primers
	Read Type & Indexing	<input type="checkbox"/> Single Read <input type="checkbox"/> Paired-End <input type="checkbox"/> Single-indexed <input type="checkbox"/> Dual-indexed
	Read length	Read 1: _____ Read 2: _____ Index 1: _____ Index 2: _____
Supervisor's Signature*:		Date:

[#] For pooled samples, PE150 is used for sequencing and users cannot designate the sequencer model to be used.

* Supervisor please read and sign for terms and conditions in the next page as well.

For Official Use Only

Request Form Submission Date:		Library Received Date:	
Sequence Kit Ordered Date:		Sequence Kit Arrival Date:	
Sequence Kit Charge:		Service Charge:	Total Charge:
DNB Concentration (by Qubit ng/ µL)	Library 1	Date:	Concentration:
	Library 2	Date:	Concentration:
	Library 3	Date:	Concentration:
	Library 4	Date:	Concentration:

For Official Use Only

Sequencing Results	Start date:	Finished date:	Raw data delivery:
Folder name			
Lane 1	DNB number:	R1 Q30%:	R2 Q30%:
Lane 2	DNB number:	R1 Q30%:	R2 Q30%:
Lane 3	DNB number:	R1 Q30%:	R2 Q30%:
Lane 4	DNB number:	R1 Q30%:	R2 Q30%:
Remarks: _____			

Terms and Conditions

General policy

1. BioCRF does not accept any sample with potential biohazard.
2. This service is for Research Use Only. The reagent has not been approved, cleared, or licensed by the United States Food and Drug Administration or any other regulatory entity whether foreign or domestic for any specific intended use, whether research, commercial, or diagnostic.
3. BioCRF will order and reserve reagents for this project once the PI has submitted this service request form. PI is responsible for the cost of expired reagents (reagents guaranteed shelf life is 3 months) due to delays in sample submission (i.e. sample quality control issues).
4. BioCRF makes no representations and extends no warranties of any kind, either express or implied. The results are provided by BioCRF to user “as is”.

Sample submission and quality policy

A sample goes into queue only after the reagent cost and sample are received. If a sample does not pass our incoming QC, we will not process the sample until incoming QC is met. BioCRF is not responsible for the performance of a sample sequenced on the MGI sequencing machine. The following items are required for sample submission:

- a) Bioanalyzer or Fragment Analyzer traces of all libraries submitted.
- b) Library quantification using Thermo Fisher Scientific Qubit3.0 or above or KAPA library quantification kit.

Results and data distribution policy

After checking instrument performance and invoicing the work, a summary report generated is sent to the user. BioCRF is not responsible for backups of customer data after distribution.

Supervisor’s Signature: _____

Date: _____