

Sequencing Core at CTRII Tulane University

RNA-Seq Sample Submission Form

Please complete this form before submitting samples to the CTRII at Tulane University. We cannot accept samples unless accompanied by this form.

1. Contact Information

PI Name		PI Email	
Post Doc/Student/Tech		Email	
Institution/Department		Phone	
Address			
City		State	Zip Code

2. Experiment and Sample Information

2.1 If you are submitting RNA samples for sequencing library preparation, please provide RNA extraction information below.

- a. RNA extraction reagent: Kit _____ (Cat No. _____)
- b. DNase treated? Yes No
- c. gDNA elimination column applied? Yes No

2.2 Desired Library Prep. The optimal quantity of starting material is listed below. If sufficient RNA quantity and concentration is not available, please consult the Core personnel before submitting.

- | | |
|---|--|
| <input type="checkbox"/> mRNA Seq | ≥ 1ug total RNA (0.1ug to 4ug) in 50ul water/TE buffer or less |
| <input type="checkbox"/> Small RNA Seq | ≥ 1ug total RNA (1ug to 5ug) in 5ul water/TE buffer |
| <input type="checkbox"/> Total RNA Seq | ≥ 1ug total RNA (0.1ug to 4ug) in 10ul water/TE buffer or less |
| <input type="checkbox"/> Total RNA Seq (Require ribo-depletion or Globin-depletion) | ≥ 1ug total RNA (0.1ug to 4ug) in 10ul water/TE buffer or less |
| <input type="checkbox"/> Total RNA Seq (Require DNase treatment & ribo-zero or globin-zero) | ≥ 2ug total RNA (0.1ug to 4ug) in 10ul water/TE buffer or less |
| <input type="checkbox"/> RNA Access Seq | ≥ 1ug total RNA (0.1ug to 4ug) in 10ul water/TE buffer or less |
| <input type="checkbox"/> Other | |

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2.5 Choose sequencing run options below

Select Output Level

- P2 (100 cycle kit): 400M Single Reads, 800M Paired-End Reads, 40 Gb Output per Flow Cell
- P2 (200 cycle kit): 400M Single Reads, 800M Paired-End Reads, 80 Gb Output per Flow Cell
- P2 (300 cycle kit): 400M Single Reads, 800M Paired-End Reads, 120 Gb Output per Flow Cell
- P3 (100 cycle kit): 1.1B Single Reads, 2.2B Paired-End Reads, 110 Gb Output per Flow Cell
- P3 (200 cycle kit): 1.1B Single Reads, 2.2B Paired-End Reads, 220 Gb Output per Flow Cell
- P3 (300 cycle kit): 1.1B Single Reads, 2.2B Paired-End Reads, 330 Gb Output per Flow Cell

Select read type and length

- Single Read 100 cycles (1x100)
- Single Read 200 cycles (1x200)
- Paired End Read 200 cycles (2x100)
- Paired End Read 300 cycles (2x150)

Paired-end sequencing allows users to sequence both ends of a fragment and generate high-quality, alignable sequence data. Paired-end sequencing facilitates detection of genomic rearrangements and repetitive sequence elements, as well as gene fusions and novel transcripts.

Single-read sequencing involves sequencing DNA from only one end, and is the simplest way to utilize Illumina sequencing. This solution delivers large volumes of high-quality data, rapidly and economically. Single-read sequencing can be a good choice for certain methods such as small RNA-Seq or chromatin immunoprecipitation sequencing (ChIP-Seq).

CUSTOM: (Please provide complete description)

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2.6 Data analysis/bioinformatics options

- On your own
- Primary analysis done by the Center
- Slug analytics or done by the Center (See price sheet for details)

If done in house, list groups or pairwise analysis below from the samples listed in 2.3

2.7 Data Delivery Format

- User supplied external hard drive – minimum of 100GB required
- Tulane Box Account
- Illumina BaseSpace Transfer – BaseSpace account required

3 *Payment Information*

Please attach a copy of the quote received from the Sequencing Core at CTRII Tulane University to this form. Sample submission will not be accepted unless a quote for services has been generated prior to submission.

CLIENT INFORMATION

Name of Principal Investigator:

Lab Location:

Phone Number:

Email Address

Account Manager

Contact information:

Tulane University Account Number

Other (Please provide billing contact information for invoicing)

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4 *Sample Drop off or by Shipping*

Email or call to schedule a time for sample drop off.

[Submit to CTRII Tulane University](#)

Contact	Kejing Song	ksong1@tulane.edu 504-988-0453
Contact	Genevieve Pierre	gpierre@tulane.edu
Hours of operation for sample drop off	9:00am to 4:30pm Monday – Friday, excluding University holidays.	
Location/ Shipping Address	Center for Translational Research in Infection and Inflammation Tulane University School of Medicine JBJ 345 333 S. Liberty St J. Bennett Johnston 345 New Orleans, LA 70112	

5 *Required Signatures*

Please have both the Principal Investigator (PI) that will be paying for the Sequencing Services and the Research/Technician/Student/ Post-Doc preparing the samples sign below acknowledging that all of the information provided on the form is correct. Signature of this form acknowledges that the PI and Technician/Student/Post-Doc have agreed to all sample submission, quality, quantity, project scheduling, and researcher financial responsibility requirements. Signature of this form authorizes the Sequencing Core at CTRII Tulane University to order all consumables necessary for the researcher’s sequencing project and confirms that the PI is financially responsible for items ordered for their project and all labor cost associated with the project.

Principle Investigator Signature _____ Date _____

Technician/Student/Post-Doc Signature _____ Date _____

6 *Data and Sample Retrieval*

All data from sequencing run will be deleted from our servers 30 days after your project is complete. Please submit an external hard drive to collect your data.

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Please pick up original RNA samples submitted along with constructed libraries no later than 30 days after your data is available. If you do not pick up your samples and libraries, they will be destroyed.