

Single Cell RNASeq

SUBMISSION FORM

Date: _____

(Office use) Submission #: _____

(Office use) Case #: _____

Please ensure ALL sections on the front and back of this form are filled out completely (with exceptions noted)

PI: _____ Institution/Company Name: _____
PI E-mail Address: _____ Bill To/Accounts Payable: _____
PI Signature: _____
Samples submitted by: _____ Grant/P.O. No.: _____
Submitter e-mail address: _____ Funding Source: NIH NSF GLBRC
Telephone: _____ USDA Other

1) **Genome:** Human (GRCh38) Mouse (mm10) Custom (transgene, viral genome, alternative genome build, etc.)

a. If custom, please indicate what is needed: _____

2) **Submission type:** Cell Suspension Nuclei Suspension

3) **Cell type:** _____ Cell Culture Tissue Prep

4) **Cell suspension buffer:** _____

No additives that can inhibit reverse transcription (e.g. EDTA, DNase, surfactants, etc.)

5) **FACS performed:** Yes No

If yes, please coordinate separately with the [UWCCC Flow Cytometry Laboratory](#) to schedule time with the cell sorter at the WIMR or Biotechnology Center locations

6) **Targeted cells per sample to be sequenced:** _____

7) **Number of samples:** _____

8) **Library type:**

- Single Cell/Nuclei-Gene Expression - 3' 5'
- Single Cell-V(D)J Immune Profiling
- Single Nuclei ATAC-Seq
- Single Nuclei Multiome
- Visium Spatial Gene Expression
- Feature Barcoding - TotalSeq B TotalSeq C

9) **Date of experiment:** _____ **Estimated time of arrival:** _____

FOR OFFICE USE ONLY:

Submission # _____ Run # _____ Run Date _____ Bill Date _____ Order # _____

SEQUENCING OPTIONS (LEAVE THESE FOUR SQUARES BLANK - TO BE FILLED OUT BY UWBC STAFF)

MiSeq

of samples _____

of flowcells _____

NovaSeq6000*

of samples _____

of lanes _____

*MiSeq nano required for all full flow cells and lanes.

NovaSeq6000 (2x150 shared ONLY)

of samples _____

of reads per sample (in millions)** _____

** ±20% of stated value above

Use sample list to denote variable read requests.

Custom Sequencing Run

(scRNA, assymetric read lengths, etc)

Must be approved by DNA Sequencing Facility.

Must be purchased as a full flow cell.

Sequencer: _____

Parameters: _____

PLEASE FILL OUT THE BELOW SECTIONS

BIOINFORMATICS OPTIONS

Analysis to be done by (please choose one):

- Submitting lab
- UWBC Bioinformatics Resource Center (Please email brc@biotech.wisc.edu to inform them of your project.)
- Collaborator - Name _____ Email _____ UWNNetID _____

SAMPLE DISPOSAL

Full-length cDNA: Please choose one of the following options.

I will e-mail gecinfo@biotech.wisc.edu to arrange a time to pick up remaining full-length cDNA from the Gene Expression Center within two weeks of receiving notification of submission of libraries to the DNA Sequencing Center.

Please dispose of cDNA six weeks after library submission to the DNA Sequencing Center.

cDNA library: The DNA Sequencing Center stores dilutions of all libraries for 10 years. The stock cDNA library is stored for six months from submission date for sequencing. Please choose one of the following options.

I will e-mail nextgen-seq@biotech.wisc.edu to arrange pick up of cDNA stock libraries from the DNA Sequencing Center.

Please dispose of cDNA stock libraries after the six-month deadline.

I have read and understand the Illumina Sequencing Policy found on the [UWBC website](#) (please initial): _____