Creating a NextGen Sequencing Core Service Request
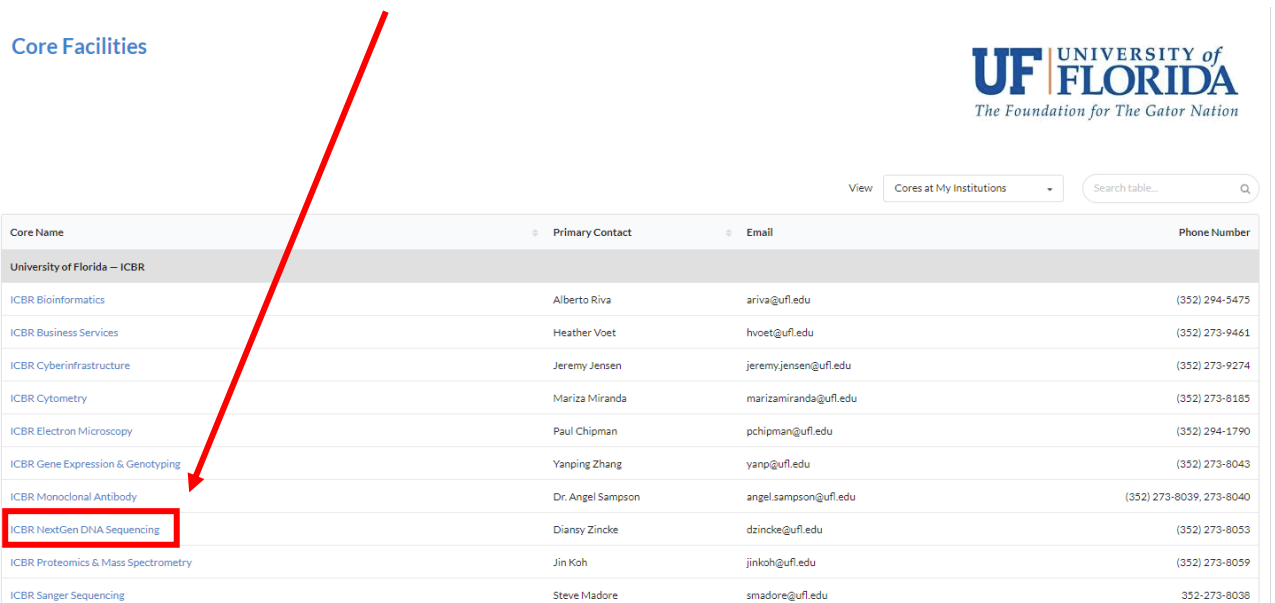
Step 1: Navigate to iLab from UF|ICBR website. Create an account and log in.
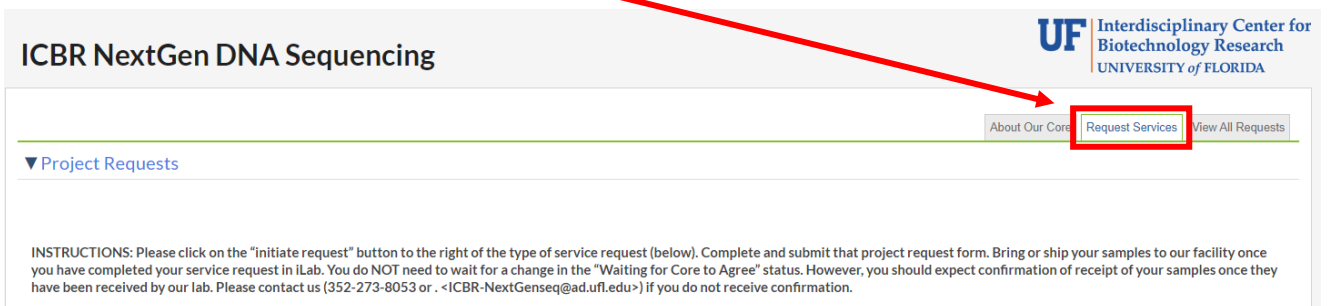

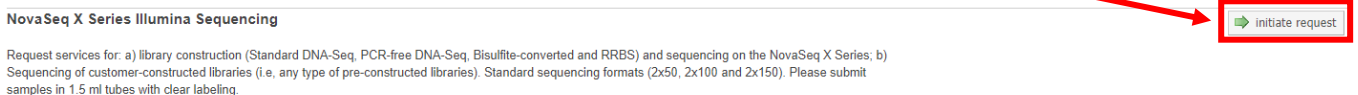****UF users should use GatorLink sign in****

Step 2: Select NextGen DNA Sequencing from Core Facilities.

Step 3: Navigate to "Request Services" tab. Scroll down to view services offered.

Step 4: Click "Initiate Request" for the desired service, after reviewing the provided description. Each sequencing platform has a different request form.

NovaSeq X Series Illumina Sequencing

Request services for: a) library construction (Standard DNA-Seq, PCR-free DNA-Seq, Bisulfite-converted and RRBS) and sequencing on the NovaSeq X Series; b) Sequencing of customer-constructed libraries (i.e, any type of pre-constructed libraries). Standard sequencing formats (2x50, 2x100 and 2x150). Please submit samples in 1.5 ml tubes with clear labeling.

➡ initiate request

Step 5: Type your name into the search bar. It should be accompanied by your lab/institution. Select your name and click "Proceed".

NovaSeq X Series Illumina Sequencing

person   search within: ◯ current customers ◯ this institution ◉ All

Chiara Licata   ICBR NextGen DNA Sequencing Core (UF) Lab   chiaralicata@ufl.edu   9045995036

➡ Proceed

✖ Cancel

Step 6a: Fill out the form with all the required information. See below for an example.

Please submit samples in 1.5-ml Lo bind tubes and label them with numbers in numerical order (Tube ID). Fill out the Library submission table and match the Tube IDs with the sample names.

★ Submission date: March 06, 2024 16:43

★ Please list the name, email, phone and address of the individual who should receive the data:
Chiara Licata, chiaralicata@ufl.edu, (352) 273-8050
2033 Mowry Road, Gainesville, FL 32610

Email is included

★ Is the PI a member of the UF Health Cancer Center (UFHCC)?
◯ Yes
◉ No

★ How would you like the data delivered?
◉ Shared on BaseSpace (preferred)
◯ Uploaded to HiperGator
◯ Delivered through Globus

Short organism name given

★ Organism (genus, species):   C. elegens

★ Type of Sample Material: Pre-constructed library(ies) ▾

★ Type of Library:
☐ Standard RNAseq (Directional or Non-Dir.)
☐ Ribo-depleted RNAseq
☐ Small RNAseq
☐ Single-cell RNAseq (3'- or 5' – 10X Genomics)
☐ Single-Cell V(D)J (10X Genomics)
☐ Single-Cell Cell Surface Protein Labeling (FBL 10X)
☐ Single-cell CNV (10X Genomics)
☐ Single-cell RNAseq (Rhapsody)
☐ 16S/ITS Metagenomics (Standard primers)
☐ 16S/ITS Metagenomics (QIAGEN phased primers)
☐ Sequence capture (e.g. ExoSeq)
☐ CITE-seq
☐ Split-seq
☐ TELL-seq
☐ Methyl-Seq (WGBS; RRBS)
☑ Standard DNA-Seq (e.g. Illumina DNA prep)
☐ PCR-free DNA-seq
☐ COVID-seq
☐ ChIPseq; HiC; 3C; 4C
☐ GBS; RADseq
☐ CLIPseq; RIPseq
☐ ATACseq
☐ PIPseq
☐ CUT&RUN
☐ Other seq

Type of material: pre-constructed libraries, gDNA, amplicons, etc.

★ Method(s) used to generate samples/libraries: NEB Ultra II DNA Library Pr

Brief description of sample prep

Suggested cluster density and PhiX% spike-in   5%

★ Do you require Qubit and TapeStation?
◉ Yes
◯ No

★ Concentration Method
◉ Qubit or equivalent
◯ Nanodrop or equivalent

Method used by your lab before submission

★ How many barcoded libraries?   8

★ Do you require pooling of individual libraries?
◉ Yes
◯ No

Select "No" if submitting a pool

★ qPCR quantification of individual samples:
◯ Yes
◉ No

★ qPCR quantification of final pool:
◉ Yes
◯ No

qPCR of final pool is required for partial lane requests

★ Does your run require custom sequencing primers?
◯ Yes
◉ No

★ Flowcell Type:
◯ 1.5B
◉ 10B
◯ 25B

★ Sequencing format:
◯ 2x50
◯ 2x100
◉ 2x150

★ Flowcell Lanes:
◯ Full Lane(s)
◉ Partial Lane
◯ Both

★ Partial Lane (%):   50 ▾

Based on specific library requirements and desired sequencing depth

Step 6b: Fill out the form with all the required information and upload documents.

Project Information (if applicable):	If you have **additional instructions for processing your samples** please tell us below. Also, tell us the name of the organism, method(s) used to isolate your sample, method(s) used to construct your library and **if you have any preferred clustering conditions (density, %PhiX, spike-in)** in the text box below:
	Libraries were constructed using the NEB Ultra II DNA Library Prep Kit. Expected average size is ~450 bp. Please pool equimolarly. Desired reads per library: 75 million. 5% PhiX spike-in.

Pooling conditions outlined

Sample Sheet Submission Instructions:
Please be sure to follow these directions when submitting your sample sheet.

Short_iLab_Submission_Guide.pdf ← Click to download instructions

Sample Sheet Template: NS-NovaSeqX-PreConstructed-Sample-Sheet.xlsx ← Click to download template **(REQUIRED)**

★ **Sample Sheet:**
Upload sample submissions following the provided template above based upon your selection of Sample Material.

🖇 please upload ← Upload template with all sample information filled out

Sample Image: Please upload file, gel image, bioanalyzer/tapestation or fragment analyzer traces. Indicate the volume of DNA loaded, marker sizes, and microgram/band sizes of marker loaded.

🖇 please upload ← Add sample image, if available; submit raw files when possible

It is required to use the provided template to upload sample information.

Step 7: Save draft or completed form, if finished. Add payment information and submit request to core. Use credit card option if alternative payment information is not available.

Please save your form! ➡ ✓ save completed form | 💾 save draft of form | 🔒 lock and save form

| 📄 Received Sample(S) | **description:** click to edit | **note:** click to edit | Not Started ▾ |
| 📄 Delivered Raw Data | **description:** click to edit | **note:** click to edit | Not Started ▾ |

Click to save request form

You have no issued vouchers to apply.

add service add charge add form add milestone sort manually add event
Build a quote, or add components to a new or running request using the 'add' links above.

Cost

Please provide the customer with a final quote for this request. The quote will be based on the services and charges you have added above and any "buffer" you have added. The "buffer" amount is for services or charges that you have not yet defined but that you expect to arise during the course of the request.

Add value or percent buffer:
as percentage ▾ amount: 0 %

Quote (total predicted cost):
$ 0.00 (automatic total of any services, charges or buffer added to this request)

Payment Information

Change to credit card, if necessary

Please enter the UF Chartfield ⓘ
UF Chartfield ▾ Select UF Chartfield... ▾

enter additional payment information

Skip approval? ☐ ⓘ

Click to submit request to core

✓ submit request to researcher | 💾 save draft request | ✗ Cancel

Step 8: Congrats! Your request is now submitted. You should receive a confirmation email from no-reply@ilabsolutions.com with a copy of your form and an NS-ID number. Please record this ID number to supply at sample drop off.

Step 9: Drop off your samples, with the NS-ID number, to the UF ICBR NextGen DNA Sequencing Core. The core can be found in CGRC Room 178.

If you are shipping your samples, please be sure to include your name, your institution/lab, and NS-ID. We recommend sending temperature-sensitive samples on dry ice, using overnight shipping. Please clearly address the package as follows:

UF ICBR NEXTGEN DNA SEQUENCING LAB
2033 Mowry Road
CGRC Building, ICBR Room 178
Gainesville, FL 32610
ATTN: Diansy Zincke, PhD

If you have any additional questions, please contact our core at (352) 273-8050, or email us at ICBR-NextGenseq@ad.ufl.edu. Thank you!