

HOW TO CREATE A NEXTGEN SEQUENCING REQUEST WITH THE ASU GENOMICS CORE

This guide assumes that you already have an account created on both the ASU iLab website (<https://asu.corefacilities.org/landing/261#/cores>). If you need assistance creating an account, please contact genomicshelp@asu.edu and we will be glad to help you!

STEP 1: GENERATING THE NGS REQUEST ON ILAB

When you log in, you should automatically be directed to the **About Our Core** tab; to generate your sequencing request, select the **Request Services** tab from the menu near the top of the screen (see the red arrow on the screen shot below for reference).

The screenshot displays the ASU Genomics Core iLab Operations Software interface. The top navigation bar includes the Agilent CrossLab logo, 'iLab Operations Software', a search bar, and user information for 'Payton Researcher'. The main header shows 'Genomics Core' and the ASU Arizona State University logo. A red arrow points to the 'Request Services' tab in the navigation menu. Below the menu, a list of request categories is shown with 'request service' buttons. The 'Illumina NGS Request (NGS)' button is highlighted with a green rectangle.

Request Category	Action
Consultation (Consultation)	request project
Illumina NGS Request (NGS)	request service
Microbiome NGS Request (Microbiome)	request service
Bioinformatics Analysis (NGS)	request service
Sanger Sequencing Request (Sanger)	request service
Machine Use / Sample QC Request (NGS)	request service
Training Request (Training)	request service

On the **Request Services** page, press the “request service” button for the Illumina NGS Request line item (see the green rectangle on the screen shot for reference.)

The form that appears (which you can see in the screen shot on the next page) will then need to be filled out. This form should be filled out with experimental detail as well as indicating the sample type, number of samples, run module, and bioinformatic analysis, along with whether or not you’re an ASU user and your method of payment for the order.

1) Forms and Request Details

1) Forms and Request Details

View Form: Next Generation Sequencing Requests - CF-327106-8

Data will be returned via an FTP server share to the email address associated with the user submitting this request form. The FTP link, username, and password can be shared by that user to any other relevant individual.

Data will be stored on our servers for six months following project completion.

Please provide a brief overview of your project

Please provide as much information as possible about your samples! If you are unsure about anything or have a project in mind that doesn't correspond well to this service request form, please contact us or leave a clarification/question in the project description section of this form.

In each of the sample entry grids, the rightmost green column refers to the number of library preparations you want per sample. This will usually be one, unless your experiment requires technical replicates. You can leave this column blank, or fill it out and press "process grid changes" to get an estimate of the cost of your project. For ready-to-load samples, there are two green columns, so that quality control on the "topsequator and qPCR" quantification can be selected separately. For pre-pooled samples, please enter in all your sample information, but only enter in the number of prep that you need (i.e., for an 80 amplicon pool enter a "1" in the first line of the grid and leave the others empty).

Sample Type

- RNA
- genomic or plasmid DNA
- amplicon or PCR DNA (1+1KB)
- library with adapters (needs CC)
- library with adapters (needs read)

Selecting a Run Module

The ideal run module for your experiment is dependent on the number of reads you require and the type of analysis you want to accomplish. Please contact the core if you are unsure about which run module to select or how many runs your project needs.

For reference:

- MiSeq v2 kits: 12-15 million reads
- MiSeq v3 kits: 22-25 million reads
- NextSeq 160 output kits: 120 million reads
- NextSeq High output kits: 400 million reads

- MiSeq v2 2x150 cycles
- MiSeq v2 2x250 cycles
- MiSeq v2 2x300 cycles
- NextSeq v2 1x75 cycles H
- NextSeq v2 2x75 cycles M
- NextSeq v2 2x75 cycles H
- NextSeq v2 2x150 cycles M
- NextSeq v2 2x150 cycles H
- Add selected services

Sample Multiplexing

Unless informed otherwise, we will load all of your samples at equal loading percentages, with 5% PhiX for quality control. If you have samples with low diversity (common with amplicon libraries) or conserved regions, please let us know so we can add the appropriate amount of PhiX control to ensure quality data for your samples. Additionally, if your experiment requires that some samples have more reads than others, please let us know either the number of reads you'd like us to target for each sample or the percentage of the run you'd like represented by each sample.

Sample Diversity

- High diversity (e.g. total RNA or genomic DNA)
- low diversity (e.g. mixed species amplicon pools)
- very low diversity (e.g. RADseq, amplicons containing constant regions)

Informatics

- If you require additional informatics analysis for your run, please fill out the bioinformatics request form below! If you are planning to do your own analysis and just need your FastQ files returned, please select the box below.
- Repeat FACS files only
- I would like the core to perform additional analysis

Please save your form! save completed form save draft of form lock and save form

After filling out the information and saving the completed form, the bottom half of the form will update with the costs and give you a menu to enter your payment information. Once that is done, you'll need to press the "submit request to core" button (highlighted in green below) to complete the iLab portion of the order.

2) 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)

3) Payment Information

Select an Account from the dropdown. All other tags are OPTIONAL unless directed otherwise.

% Account

- Select Account...
- Department Reporting Roll
- Please select one...
- Department Reporting
- Please select one...
- Audit Reporting
- Please select one...

100.0% %

100.0% Total Allocated

Split Charge

For internal use only. DO NOT enter credit card, account, or PO information. Contact okedcorebusiness@asu.edu for inquiries.

Skip approval?

submit request to researcher save draft request Cancel

When sequencing is complete, you'll receive an email from the bioinformatics team alerting you that your data is ready for download; you'll also receive an email from iLAB letting you know that your order is complete, and when you log in to your iLAB account you'll see the status marked as "Completed" under the "View My Requests" tab.

Please let us know if you have any questions or concerns about submitting samples at genomicshelp@asu.edu!