

HOW TO CREATE A MICROBIOME 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 either Jason (jason.steel@asu.edu) or genomicshelp@asu.edu and we will be glad to help you!

STEP 1: GENERATING THE SANGER 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 shows the ASU Genomics Core website interface. The top navigation bar includes the Agilent CrossLab logo, 'iLab Operations Software', a search bar, and user information 'Payton Researcher'. The main header shows 'Genomics Core' and the ASU logo. A red arrow points to the 'Request Services' tab in the secondary navigation menu. Below the menu, a list of services is displayed with 'request service' buttons. The 'Microbiome NGS Request (Microbiome)' button is highlighted with a green circle.

Service	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 Microbiome 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, DNA extraction, “mock communities” or controls 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 (see bottom of list to add items to this request)

View Form: Microbiome NGS Form Visible 3 Not Star 1 Save Progress

Who would you like the completed data sent to? Contact: PI
 Demultiplexed data will be returned via a secure FTP server

Additional Emails
 Email 1:
 Email 2:

SEQUENCING PROJECT INFORMATION
 Number of samples:

Sample quality, quantity and purity are essential for library construction and sequencing.
 Sample concentration of genomic DNA should be between 10 - 500 ng/μL.
 Sample purity A260/280 ratio of 1.8 or above is recommended.
 Intact high molecular weight DNA is recommended for sequencing. Partially degraded DNA may affect in library construction and sequencing.
 A minimum of 30 μL per sample will be required.

Would you like DNA extraction? (Select 2)

Are you including samples with "mock communities" and/or negative controls? (Select 2)

For each sample, we will need the following information:

Sample ID	16S	18S	ITS	Sample Volume (μ)	Sample concentration	ratio (260/280)	Special Instruction
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							

upload or download data to the grid from excel

Would you like Bioinformatic Analysis? (Select 2)

Do you agree to the terms? Yes

Material Return Terms:
 End user acknowledges that any all wet lab materials will be kept for 2 months after project completion and that they must request any materials be returned before that date.
 End user acknowledges that any all data that resides on the Genomics Core servers materials will be kept for 3 months after project completion and that they must download any data before that date.

Please save your 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:
 amount: %

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:
 Department Reporting Split
 Please select one...
 Department Reporting
 Please select one...
 Audit Reporting
 Please select one...
 100.0% Total Allocated

For internal use only. DO NOT enter credit card, account, or PO information. Contact:

Ship approval?

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!