

MICROMON SANGER SEQUENCING

HOW TO PLACE A REQUEST USING THE ILAB OPERATIONS SOFTWARE

REACTION & SEPARATION – SAMPLES PROVIDED IN TUBES

LOGIN TO iLab

This guide assumes that you and your PI (or delegated lab group manager) already have a registered account in iLab. Please note that iLab is not configured for use on mobile devices.

Use the following access link:

monash.ilab.agilent.com/service_center/show_external/4451

At the top right, click the blue 'sign in' button.

- Select Monash if you are a Monash staff or student
- Select AAF if you belong to an academic institution or one of the listed government owned agencies.
- Select iLab if you are an external customer not on the AAF list.

You will be taken to your account homepage that will display all your active requests. At the top left-hand corner, click the three-line 'Menu' icon and the navigation panel will open. Click 'Core Facilities' and the range of Monash platforms will display for your selection.

On future logins, Micromon will be shown as a 'Frequently Used Core'.

NAVIGATING THE MICROMON PAGE

There are four tabs which will allow you to see Micromon contact information, make requests and view current and previous requests.

- About Our Platform
- Request Services
- View My Requests
- Contact Us (you can still contact us directly by regular email)

Select the REQUEST SERVICES tab which will display the page with the available Micromon services.

Find the Sanger sequencing item for tubes that you require:

- Sanger Sequencing (Sanger - Reaction & Separation)

and click the 'REQUEST SERVICE' button at the right-hand side.

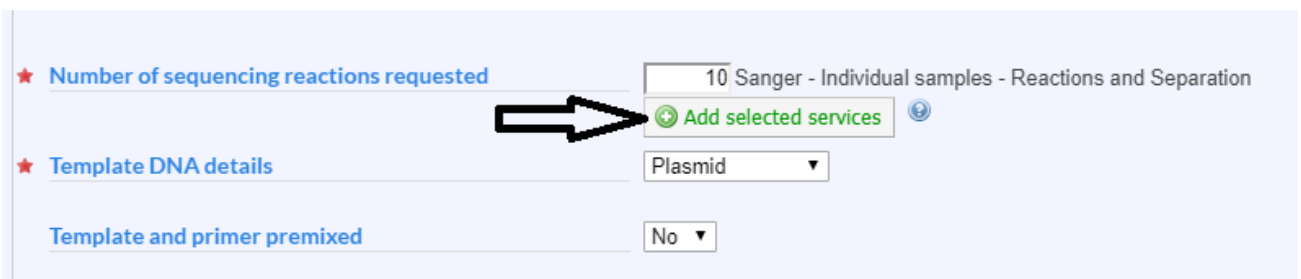
FORMS AND REQUEST DETAILS (1)

This will display the sequencing order form. For your first request in this system, please read the preamble at the top of the form which provides important information on sample submission.

Number of sequencing reactions requested

Insert the number of reactions that will be requested for processing.

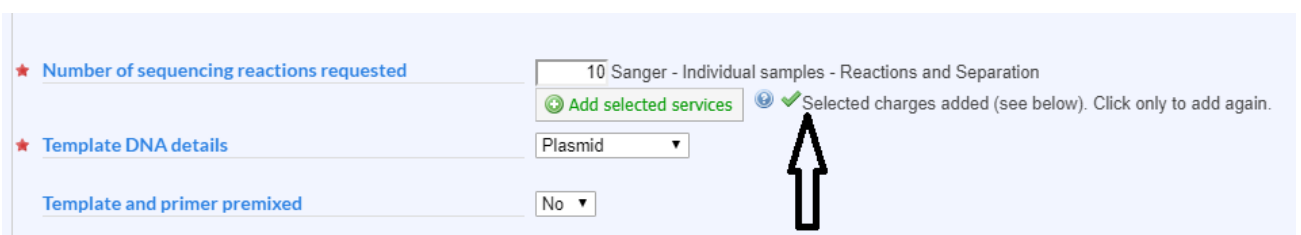
Then click the **ADD SELECTED SERVICES** button once in order to add the charge to your request. If successful, a green 'tick' will appear to the right of the button. If this button is accidentally clicked more than once, it will add another charge item to the charge section below the grid, but it can be deleted if this happens – no need to cancel the request.



★ **Number of sequencing reactions requested** 10 Sanger - Individual samples - Reactions and Separation
➕ Add selected services ⓘ

★ **Template DNA details** Plasmid ▼

Template and primer premixed No ▼



★ **Number of sequencing reactions requested** 10 Sanger - Individual samples - Reactions and Separation
➕ Add selected services ⓘ ✓ Selected charges added (see below). Click only to add again.

★ **Template DNA details** Plasmid ▼

Template and primer premixed No ▼

Template DNA Details

Select the relevant template type. If the PCR Product option is selected, an extra text box will appear in which you need to insert the size of the product. Please advise us if there are products of varying sizes, and these can be listed or a range shown.

Template and primer premixed

If you have opted to premix, select YES in the dropdown box. You do not need to complete the 'template' and 'primer' columns in the grid. Treat the first column of numbers in the grid as your tube labels and then just provide your filenames in the last column.

Special Protocol for Troubleshooting

Select YES at this option if you want us to use our special troubleshooting protocol on some or all your samples. If you select Yes for this option, a services box and button appear. Insert the number of samples requiring this protocol and 'Add Selected Services' as per the above process. The Troubleshooting Protocol is a Micromon customised one that utilises increased BigDye Terminator reagent, increased cycles, and the incorporation of the DNA relaxant, Betaine and is most effective in overcoming template DNA structural problems, and low copy number.

PeakTrace Basecaller

Select YES at this option if you want some or all of your samples re-analysed with this proprietary basecaller. If you select Yes for this option, a services box and button appear. Insert the number of files requiring this analysis and 'Add Selected Services' as per the above process. The AB Kb basecaller will be used by default unless you opt for re-analysis using the PeakTrace (enhanced basecaller).

Data Despatch

Select as relevant. For Monash users, a box containing a dropdown list will appear – please select your school/department indicating in what server directory we need to upload your data. Hudson users should select 'External'.

Sample grid

Insert details for all your templates and primers.

This can be done directly into the grid online if desired. The grid has unlimited rows, not just the ten displayed.

An alternative method for filling the grid is to download the grid template as a CSV file which can be opened in Microsoft Excel and filled offline. It can then be uploaded directly into the iLab grid using the displayed UPLOAD button. To take this option, see below the grid and click the link named '**upload or download data to the grid from excel**'.

When you have completed the form, click the '**SAVE COMPLETED FORM**' button. The form will minimise, and the charges for your order will be displayed. Note that you can reopen the form by selecting the 'View Form' link. Alternatively, you can save the form as a draft and submit it later.

COST (2)

The total cost of your order will be displayed. Prices for requests involving special quotes will be adjusted by Micromon staff following acceptance of the request.

PAYMENT INFORMATION (3)

Monash customer: enter your fund code or select your PAG from the dropdown list (you can also split code your charges).

External customer: enter your purchase order number or organisation account number or prepaid (if relevant). You must enter something so if any of these are not known, please enter TBC or similar. If you intend to pay the invoice using a corporate credit card, select the credit card option.

SEND THE REQUEST

When you are satisfied that your order is complete, click the **'SUBMIT REQUEST TO CORE'** button at the bottom of the page.

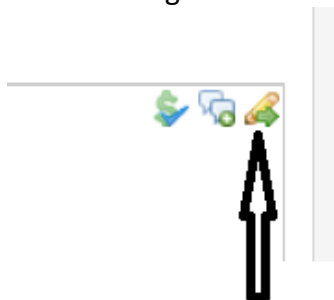
The request will then be Accepted by Micromon when your samples are received and the job commenced.

For external (non-Monash customers), if your PI (or delegated lab manager) has not set a spending threshold (limit) for you in iLab, each and every request you submit will be initially redirected to your PI for financial approval before the job can be commenced by Micromon. It is strongly advised that you ask your PI to set a spending threshold (see separate guide for this procedure) in order to avoid the financial approval step.

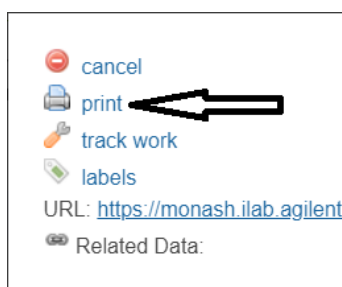
DELIVER YOUR SAMPLES TO MICROMON

Select the VIEW MY REQUESTS tab, and locate your active request.

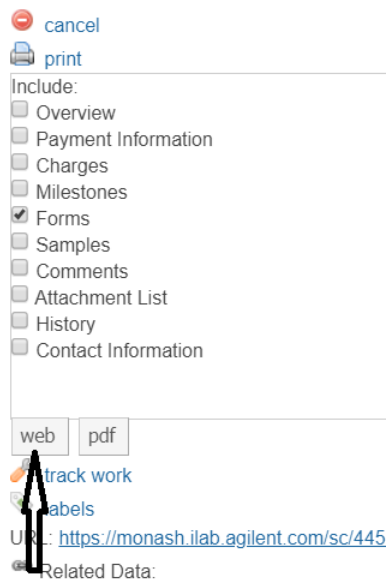
On the far right-hand side of your request item are three icons - click the 'pencil' icon



In the new window, select the PRINT option



In the new window, select the WEB tab (or the PDF tab if preferred)



Print to your desired printer and close the print window

The hard form is required by our staff to identify sample lots received by post and courier (a quality management system requirement), to match delivered samples with the online request, and as a workbench reference. The proposed future acquisition of tablets by our facility will remove the need for customers to bring hard copies but we are still exploring this option.

Deliver/send this print to the facility together with your samples. For those delivering samples in person to the facility, when you enter your name and number of samples in the facility receipt register, you will also be required to enter your unique iLab request number that is shown on your form. This CID or customer ID is unique per request to Micromon Genomics.

▼ Mar 22 (Mar 22 2019)	Mark Cauchi Micromon (Admin) Lab	MICM-MC-201 Sanger - Reaction & Separation
▶ Overview		
▶ Payment Information		

REQUEST STATUS

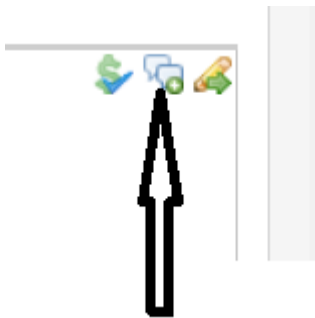
You can then check the status, follow the progress and check details of your request by selecting the VIEW MY REQUESTS tab. The status of your request is shown in the 'Status' column and you can check whether your request has been received and if completed. We will always send a notification email when the request is completed and the data is available for download.

To check request details, click the blue arrow on the left-hand side of the desired request, then the 'Forms and Requests' arrow.

The three icons at the far right-hand side will allow you to update your payment information e.g. fund code or purchase order, send a message to the Micromon facility, and print your form for local records if desired.

SENDING ADDITIONAL INFORMATION TO THE FACILITY

To send a request-related message to us via iLab, if desired, in the VIEW MY REQUESTS tab, at the far right-hand side, click the messaging icon.



In the box that opens, ensure you check this item

DNA Service<sequence@monash.edu> Phone: 0399054847

then type your message into the text box and 'Send'.

The text of your message shows up as a record under the 'Comments' section at the bottom of your displayed form as well as any responses by Micromon to your message.

Messages/comments can also be added and/or sent by clicking the 'Add Comment' link in this section.



Alternatively, simply send an email directly to sequence@monash.edu or call us on 9905 4847.