

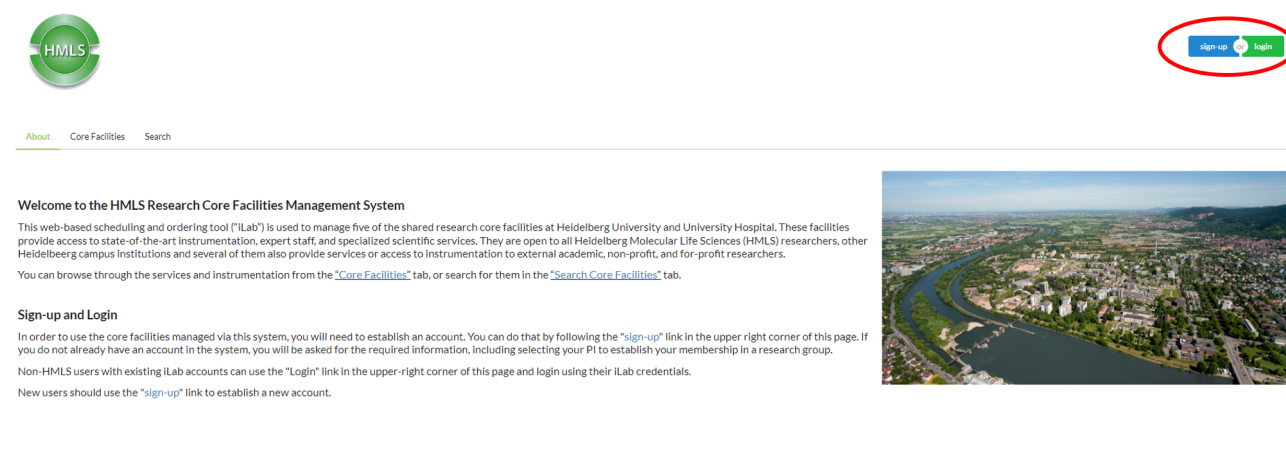
iLabs Sample Registration

Deep Sequencing Core Facility

June 28, 2024

1 Registration/Login to iLabs

Prior to starting the sample registration you need to register or login to iLabs here. If not set-up already you will need to create an account, activation may take up to 24 hours and the facility cannot speed this up since we have no influence on the registration process. Likewise we cannot see or reset.



Welcome to the HMLS Research Core Facilities Management System

This web-based scheduling and ordering tool ("iLab") is used to manage five of the shared research core facilities at Heidelberg University and University Hospital. These facilities provide access to state-of-the-art instrumentation, expert staff, and specialized scientific services. They are open to all Heidelberg Molecular Life Sciences (HMLS) researchers, other Heidelberg campus institutions and several of them also provide services or access to instrumentation to external academic, non-profit, and for-profit researchers.

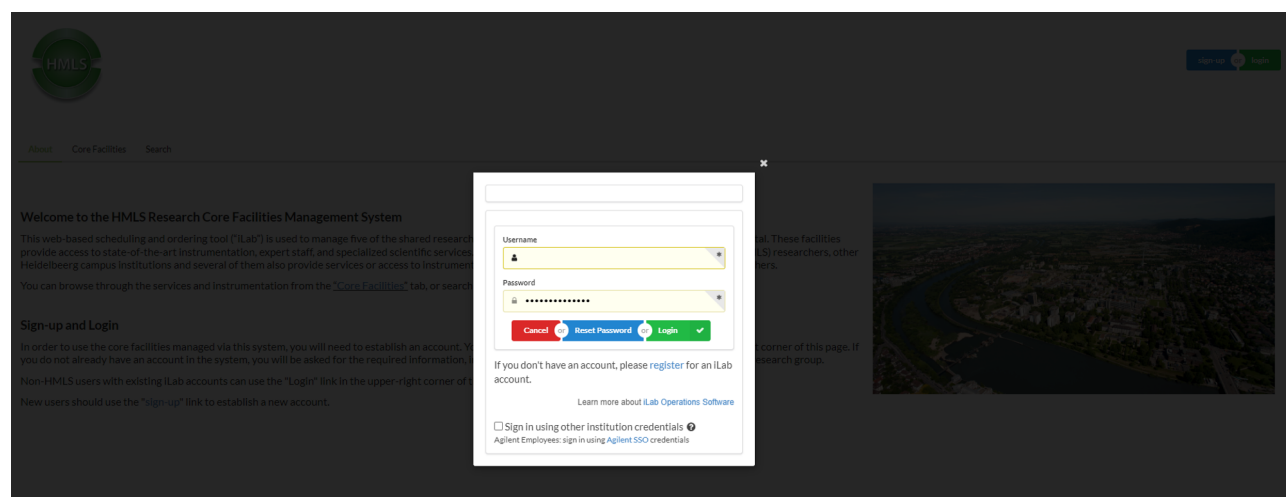
You can browse through the services and instrumentation from the "[Core Facilities](#)" tab, or search for them in the "[Search Core Facilities](#)" tab.

Sign-up and Login

In order to use the core facilities managed via this system, you will need to establish an account. You can do that by following the "[sign-up](#)" link in the upper right corner of this page. If you do not already have an account in the system, you will be asked for the required information, including selecting your PI to establish your membership in a research group.

Non-HMLS users with existing iLab accounts can use the "Login" link in the upper-right corner of this page and login using their iLab credentials.

New users should use the "[sign-up](#)" link to establish a new account.



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Username

Password

[Cancel](#) [Reset Password](#) [Login](#) ☒

If you don't have an account, please [register](#) for an iLab account.

[Learn more about iLab Operations Software](#)

☐ Sign in using other institution credentials 

Agilent Employees: sign in using [Agilent SSO](#) credentials

2 Select 'Request Services'

Agilent CrossLab | iLab Operations Software

Search... Go Blanka Berkl Help Sign Out

Deep Sequencing Core Facility

About Our Core Schedule Equipment **Request Services** View All Requests Reservations People Reporting Billing Administration

Dear Users,
Our facility will be closed between 10.08.2024 to 21.08.2024 due to staff holidays.
Thank you for your understanding!

[Overview of Services](#)

The Deep Sequencing Core Facility was established in September 2010 to provide the Neuenheimer Feld Campus with access to Next Generation Sequencing (NGS). We provide the possibility to construct libraries for sequencing with the focus not only on the „standard“ application but to help establish custom protocols which can be of benefit to the whole campus.

Sequencing is available on a variety of Instruments all based on the Illumina Sequencing by Synthesis technology. In addition to library preparation and sequencing we also can help you with planning your sequencing experiment and offer advice on your project.

[Facility Contact](#)

Scientists interested in using the facility are welcome to contact us by mail at:
deepseq@lab@bioquant.uni-heidelberg.de

Agilent CrossLab | iLab Operations Software

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About Our Core Schedule Equipment **Request Services** View All Requests Reservations People Reporting Billing Administration

User notes:

- Please read our [Users Terms and Conditions](#) and [Sample Submission Guidelines](#) before submitting samples.
- Depending on individual specifics, projects might take anywhere from 3 weeks to 2 months. Each user will be individually informed on their project progress.

Deep Sequencing Service Request (Library Prep+Sequencing) initiate request

Initiate this request if samples require processing for NGS before Sequencing can begin.
Note: User will always be charged for additional QC if samples fail Initial QC.

NGS Library Preparation Only initiate request

Standard library prep for RNA-Seq, Small RNA-Seq and genome sequencing - *price will vary based on sample quantity*.
Note: User will always be charged for additional QC if samples fail Initial QC.

NGS (Illumina) Sequencing Only initiate request

Initiate this request if samples have been prepared and are ready for sequencing.
Note: User will always be charged for additional QC if uploaded documentation and concentration measurements are deemed inadequate.

Sample QC initiate request

Please use this for if additional QC of samples is required prior to sample submission or sequencing, or you require such a service to check your samples prior to processing them for other protocols.

Spatial Transcriptomics initiate request

Initiate this request for Spatial Transcriptomics requests

[► Facility Services price list](#)

There are five types of services to choose from:

1. Library Prep and Sequencing: Select this if you need your samples to be prepared for sequencing and sequenced with us.
2. Library Preparation only: Select this if you need your samples to be prepared for sequencing on the Illumina platform but wish to sequence elsewhere. You will still be asked which instrument you wish to sequence on, as this can be important for the library preparation and subsequent pooling
3. Sequencing only: Select this if you have ready-to-load libraries
4. Sample QC: Select this if you need Qubit and/or Bioanalyzer/TapeStation measurements of samples
5. Spatial Transcriptomics: Select this if you would like to perform 10X Genomics Visium experiments

Also, on this page, you are able to consult the Core Facility prices. NOTE! Prices can change on a short notice!

3 Registering Your Sample(s)

Sample Registration Form: Library Prep and Sequencing_v2.33622

Please provide details for your project.
 Note: the information filed by the client hereafter shall be considered official confirmation of number of samples, type and sequencing requirements.
 Any further changes to these must be individually discussed with and accepted by Facility staff.

Please fill out the form below; click **Save completed form** button, then click **Submit request** to come at the bottom of the page to submit your request.

Sample ID (DeepSeq Lab Use)	Sample Name	Concentration (ng/ul)	Comments
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			

upload or download data to the grid from excel

Please confirm number of samples:
 How were your samples quantified? **QuickPipette**

Sample type: **Genome**

Required Library Type: **Genome**

Should the samples be barcoded? **Yes**

Should you samples be pooled? **No**

Note on Sequencing Options:
 Is a non-standard read output required (eg for 10x Genomics Libraries)? **No**

Please select instrument: **NextSeq 500**

Requested number of runs/lanes: **1**

Additional comments:

I agree to be billed, and pay the above mentioned contract. The contracted service will not be used as part of an „Auftragserforschung“ (eg Projekte der Baden-Württemberg Stiftung) or of any other further commercial interests.

I have read and agree to the [Usage Terms and Conditions](#)

Do you agree to the terms listed above?
☒ Yes
☐ No

Regardless of request type please enter your sample name(s) and their concentrations in the table. In the case of User Provided Libraries (Sequencing only), barcode sequences are also required.

The next step is to fill in the information as to what type of Library Preparation is required and what the origin of the sample is. These are drop down menus, so please look carefully. Afterwards please select the sequencing type required. This changes regularly, so it may be the case that the sequencing type requested is no longer available, in this case an alternative will be offered.

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: **10** %

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

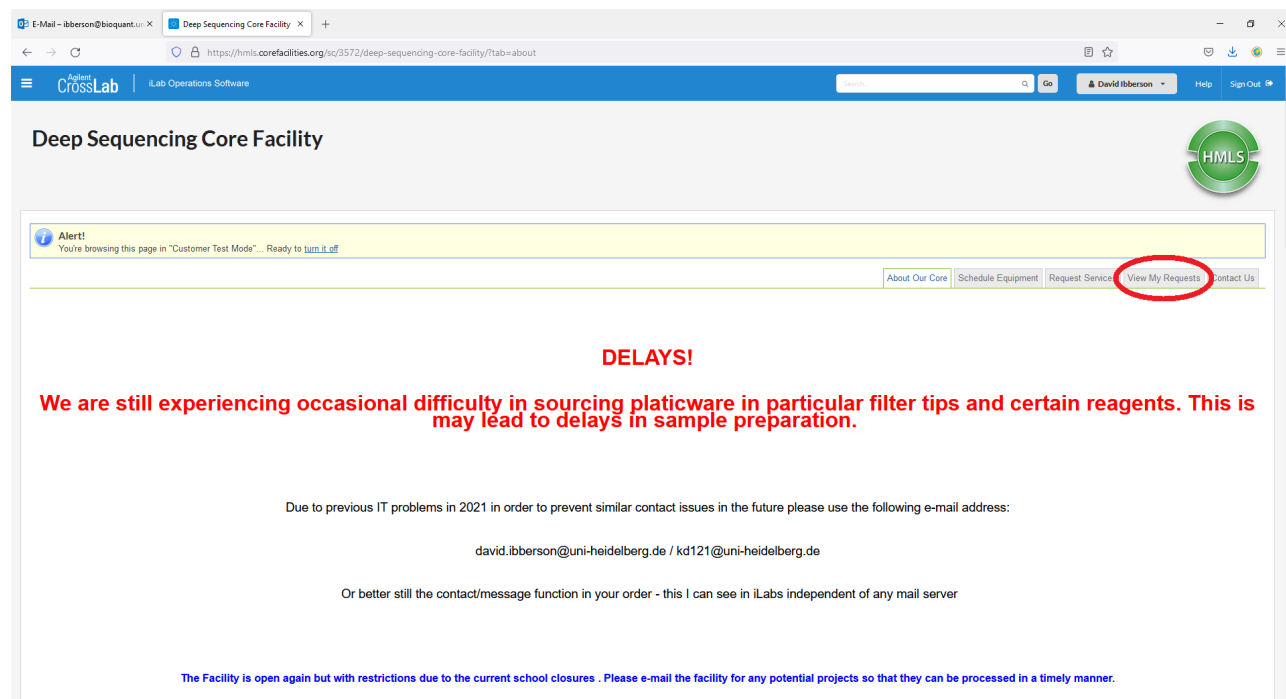
Skip approval? ☐

submit request to researcher (highlighted with a red circle)

Finally, please do not forget to click „save“ and „submit request“ otherwise we will not see the request.

After request submission, you will be provided with a cost estimate (which requires confirmation from yourself or PI). In addition, the order will be locked, so no changes can be made without confirmation by the facility.

4 Checking the progress of your sample submission



- You can keep track of the progress of your order by clicking on the tab „View My Requests”
- Upon clicking this, a list of your requests will become available
- By clicking the blue arrow on the left of your request, a drop down screen will open and here you can see the status of your request.