

# How to initiate a request at iLAB

[https://www.zmbh.uni-heidelberg.de/Central\\_Services/Mass\\_Spectrometry/default.html](https://www.zmbh.uni-heidelberg.de/Central_Services/Mass_Spectrometry/default.html)



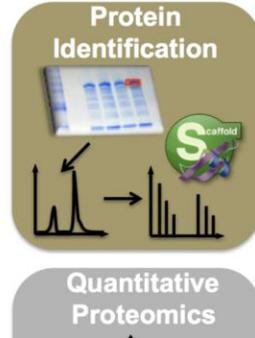
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Welcome to the **Core Facility for Mass Spectrometry & Proteomics (CFMP)** at the ZMBH

Our mission is to provide researchers of the Heidelberg Life Science Campus state-of-the-art high-performance mass spectrometry services. These services include all aspects of protein characterization and qualitative and quantitative proteomics:

- Protein identification from 1D and 2D-gels
- Quantification based on label-free (spectral co-isotope labeling (SILAC & reductive dimethyl labeling))
- Detection and localization of posttranslational modifications
- Deciphering the interactome of target proteins



Dear customer,

as of 1st  
submit  
you make  
MS-service

ms-service

Please follow the registration procedure.  
You will get your login details within 24 hours.

Once you have got your login details you can start a request.

[About Our Core](#) [Schedule Equipment](#) [Request Services](#) [View My Requests](#) [Contact Us](#)

## ▼ Service Projects & Quote Requests

Please note: An initial project consultation is **mandatory** for all projects unless a similar project has already been triggered in our facility.

### Discussion of projects (Discussion)

Discussion of projects

[request project](#)

### Sample Submission CFMP Project (MS-Analysis)

Please initiate this request **only** if you have already worked with our facility on a similar project. If not please contact us by mail to have an initial project consultation at [ms-service@zmbh.uni-heidelberg.de](mailto:ms-service@zmbh.uni-heidelberg.de).

[request service](#)

### Training Request for MALDI-TOF MS (Training)

[request service](#)

#### ZMBH Home

#### Home

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Project number 20-103

In this example there are several projects with their project numbers

To see the detailed information of one project click on the triangle

The screenshot shows the Agilent CrossLab iLab Operations Software interface. The top navigation bar includes the Agilent CrossLab logo, the text 'iLab Operations Software', a search bar, a 'Go' button, the user name 'Thomas Ruppert', and a 'Help' link. Below the navigation bar are several tabs: 'About Our Core', 'Schedule Equipment', 'Request Services', 'View My Requests', and 'Contact Us'. The main content area displays a list of projects with columns for 'date', 'TOR', 'services', 'status', 'cost', 'tax', and 'total'. Three projects are visible:

date	TOR	services	status	cost	tax	total
Jun 11 (Jun 11 2020)	Thomas Ruppert Ruppert, Thomas (Heidelberg) Lab	20-103 Sample Submission... MS-Analysis	Waiting for Core to Begin	€1,428.00 (€1,428.00)	€0.00	€1,428.00
Apr 29 (Apr 29 2020)	Thomas Ruppert Ruppert, Thomas (Heidelberg) Lab	20-82 Sample Submission... MS-Analysis	Processing Sample delivered	€864.00 (€864.00)	€0.00	€864.00
Apr 20 (Apr 20 2020)	Thomas Ruppert Ruppert, Thomas (Heidelberg) Lab	20-79 Sample Submission... MS-Analysis	Processing Sample delivered	€714.00 (€928.00)	€0.00	€928.00

Below the project list, there are sections for 'Overview', 'Payment Information', and 'Forms and Request Details'. The 'Forms and Request Details' section includes an 'Upload Samples' button and a 'Review Uploaded Samples' table:

Sample Id	NUMBER	Experiment	Fraction N°	Instrument	Comment	Well number	Plate name
14628	1	300ul/min shiny					✗
14629	2	350ul/min shiny					✗

Blue arrows point from the text annotations to the project list and the detailed view section.

# An overview

The screenshot shows the Agilent CrossLab iLab Operations Software interface. At the top, there is a navigation bar with 'About Our Core', 'Schedule Equipment', 'Request Services', 'View My Requests', and 'Contact Us'. A sidebar on the left contains a tree view with categories like Owner, Institution, Payment Number, etc., and filter options. The main content area displays a request overview for 'Thomas Ruppert' on 'Apr 20 2020', including details on sample submission, processing, and payment. Below this, there is a section for 'Review Uploaded Samples' with a table listing sample IDs, numbers, experiments, and well numbers. The table shows six samples, all with a red 'X' in the 'Plate name' column. Below the table is a 'View Form' section for 'CFMP form A' with fields for 'Sample delivered', 'Sample cut', 'Sample digested', 'Sample measured', and 'Data analysis'. At the bottom, there is a 'Comments' section with 'add comment', 'Attachments & URLs', and 'add attachment' buttons.

Sample Id	NUMBER	Experiment	Fraction N°	Instrument	Comment	Well number	Plate name
14628	1	300ul/min shiny					X
14629	2	350ul/min shiny					X
14630	3	300ul/min 2h					X
14631	4	300ul/min shiny					X
14632	5	350ul/min shiny					X
14633	6	300ul/min 2h					X

samples



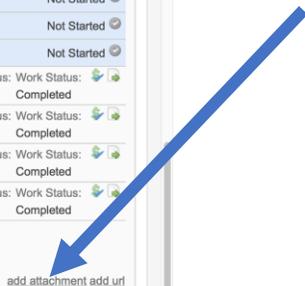
Organism, proteolytic enzymes, PTMs



Communication by email



Uploading any type of file like gel images, excel files, pdf and so on.



If it is a gel based analysis, upload a gel image before bringing the samples

# in more detail

Apr 20 Thomas Ruppert 20-79 Processing €714.00 €0.00 €928.00  
(Apr 20 2020) Ruppert\_Thomas (Heidelberg) Lab Sample Submission... Sample delivered (€928.00)  
MS-Analysis [Complete](#) Thomas Ruppert

► Overview

► Payment Information [update payment inform](#)

► Forms and Request Details

▼ Upload Samples

Please fill in only one generic sample under sample number, like "1", and click "Confirm". We then fill out the precise sample names etc. for you.

Select Submission Type

submit individual samples

Select Services

Sample preparation

Dimethyl Labeling

In-Gel Digest

In-Solution Digest

Gradient length

LC-MS analysis: 25 min separation

LC-MS analysis: 60 min (1 h) separation

LC-MS analysis: 120 min (2 h) separation

LC-MS analysis: 180 min (3 h) separation

LC-MS analysis: 240 min (4 h) separation

Other services

Intact Protein Mass Determination

Purity Control of Synthetic Peptides

MALDI Measurement

Enter Sample Information

You can upload samples by entering your information directly into the grid below. Alternatively, you can download an Excel template, enter your sample information and then upload your file to the grid.

via grid entry

via excel upload

To edit samples please go to 'Review Uploaded Samples' section

[clear out grid](#)

NUMBER	Experiment	Fraction N°	Instrument	Comment
1				
2				
3				
4				
5				
6				
7				
8				
9				
10				

[Confirm Samples](#)

► Review Uploaded Samples

If you don't know how the analysis should be done, simply fill in „1“

# After uploading the samples you can review and edit the entries

Upload Samples

Review Uploaded Samples

Edit Print

Sample Id	NUMBER	Experiment	Fraction N°	Instrument	Comment	Well number	Plate name
14628	1	300ul/min shiny					✗
14629	2	350ul/min shiny					✗
14630	3	300ul/min 2h					✗
14631	4	300ul/min shiny					✗
14632	5	350ul/min shiny					✗
14633	6	300ul/min 2h					✗

View Form: CFMP form A Completed

Sample delivered	description:	note: click to edit	Not Started
Sample cut	description:	note: click to edit	Not Started
Sample digested	description:	note: click to edit	Not Started
Sample measured	description:	note: click to edit	Not Started
Data analysis	description:	note: click to edit	Not Started

In the column „number“ only numbers are allowed

Use the column experiment for a more detailed description

Next step:  
form A

View Form: CFMP form A Completed

Please fill in details about your project here.

Request creation date: April 20, 2020 16:45

Related Projects/discussions:

short description: Anzahl Identifizierungen in Abhängigkeit von der Flußrate und Gradientenlänge; HeLa

upload a excel file with sample names:

Taxonomy or database: H. sapiens (human)

Modification(s):

- Acetylation (N-term)
- Carbamidomethyl (C)
- Carbamylation (N-term)
- Crosslinker
- Deamidation (NQ)
- N-Hexosylation (ST)
- O-Hexosylation (ST)
- Methylation (N)
- Myristoylation (N-term Gly)
- NEM (C)

If it is a follow up experiment you can indicate the previous experiments

A short description is always helpful especially with complex experiments

which organism?

And all the rest is filled out when you bring the samples