

Sample submission

In all cases, contact the Facility before you send any sample, to discuss your needs and to determine the best approach to prepare and analyze your samples.

To optimize an efficient completion of your project, we ask you to observe the following procedure:

1. Contact the Facility at an early stage

- This will allow you to explain your biological questions, and us to advise on the best way to prepare your samples and give hints to the experimental design like controls, number of replicates, etc..
- We recommend you familiarize yourself with the recommendations on [sample preparation](#) and sample submission guidelines before the meeting.
- Please, familiarize yourself with the CFMP user regulations.
- If you have questions regarding the procedure, the sample processing or sample submission, please contact Marcin Luzarowski:
m.luzarowski@zmbh.uni-heidelberg.de

2. Send a request via iLab management software

The iLab software from iLab Solutions is a platform to organize projects by a project number, containing information about the number of samples to be processed and how they should be processed. It is a container for additional information like gel images, publications relevant for the project, email correspondence and the user fee, which is accounted for the specific project.

The iLab software is used by several core facilities on the campus. To use services of the CFMP you have to **register to iLab**.

3. Make an appointment to hand over the samples

Sample submission and processing will only be possible after **initiating a request in iLab**. Vials have to be marked clearly so that description on the vials match the sample list submitted to iLab. It must be easy to identify the sample (container or vials labeled with iLab project number, numbers indicated on gel images).

Now you are ready to make an appointment with the member of the CFMP:

- Sabine Merker: s.merker@zmbh.uni-heidelberg.de
 - Protein identification of gel separated proteins
 - Identification of interaction partners from Co-IP experiments
 - Analysis of proximity labeling (BioID) experiments
- Nicole Lübbehusen: n.luebbehusen@zmbh.uni-heidelberg.de
 - Molecular weight determination of intact proteins
- Ute Bach: u.bach@zmbh.uni-heidelberg.de
 - Proteome analysis

4. Sample shipping guidelines

- **Notification and Shipping:**

Please inform us in advance when sending your samples, allowing us to anticipate their arrival and store them appropriately. For samples shipped on dry ice, dispatch them on Mondays to ensure timely delivery before the weekend. Send your samples to the following address:

Universität Heidelberg
Zentrum für Molekulare Biologie der Universität Heidelberg (ZMBH)
Core Facility for Mass Spectrometry and Proteomics
Dr. M. Luzarowski
Im Neuenheimer Feld 345 (1.OG)
69120 Heidelberg

- **Sending In-Solution Samples:**

Ensure proper labelling of tubes with the ID numbers from the iLab form. Proteomics samples undergo processing using the SP3 protocol. Prepare 10 µg of proteins per sample in 100 µl of an appropriate buffer (e.g., 50 mM Tris pH 8.0 for RIPA buffer or 50 mM TEAB pH 8.5 for Urea lysis buffer). If using a custom buffer, specify the composition during project discussions and upload it to iLab. Seal tubes securely and send on dry ice in bags or boxes, noting the project number and your name for efficient processing.

- **Sending SDS-PAGE Gel:**

Use a zip bag or a supermarket-bought sandwich bag sealing machine (approx. €20) and VWR plastic foil (Cat No: 129-2157). Place the gel between two layers of foil, ensuring no liquid leaks. Use a few drops of water or 0.1% acetic acid (100 – 200 µl) to keep the gel moist during transit; excessive liquid may damage the gel. Secure the gel between rigid cardboard sheets, avoiding sticking the foil to the cardboard. Place the protected foil in a padded envelope, and include a short notice with the project number, your name, and a gel image indicating bands of interest.

These guidelines help us efficiently process and analyze your samples. Thank you for your cooperation!