User Rules & Regulations
Core Facility for Mass Spectrometry and Proteomics (CFMP)
at the Center for Molecular Biology of Heidelberg University (ZMBH)

Last updated on the 4th of November 2026

§1 Definition and aims

1. The Core Facility for Mass Spectrometry and Proteomics (CFMP) is an infrastructure facility of the Center for Molecular Biology of Heidelberg University (ZMBH). It supports researchers on the Field of Focus 1 (FoF1) / Heidelberg and Mannheim Life Sciences campus with high-performance mass spectrometry for protein analysis and proteomics.

2. These User Rules & Regulations govern technical services, scientific collaborations, and method development at the CFMP. They are binding on all CFMP users. Every project has a technical service component; a project may additionally include a scientific collaboration component, as defined in §§6, 8, and 10.

3. Users receive an electronic copy of these User Rules & Regulations and the Service & Pricing List. Before using CFMP instruments or services, each user must sign an individual usage agreement confirming familiarity with and acceptance of both documents.

4. These User Rules & Regulations and the Service & Pricing List are intended to comply with the requirements of the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG) and the CellNetworks Core Technology Platform (CCTP). Matters not addressed here are governed by Heidelberg University's applicable Framework Usage Regulations for Core Facilities.

5. The CFMP is registered in the research infrastructure database of the German Research Foundation (DFG) with the following reference number: RI_00574.

§2 Responsibilities of the central service facility

1. The CFMP provides general technical advice, sample preparation and processing, mass spectrometry-based protein analysis, and routine processing of experimental data. Project-specific scientific input beyond these routine services constitutes an additional collaboration component (§6 and §10).

2. All services are performed by experienced CFMP personnel (full service). Routine technical services are listed in the current Service & Pricing List.

§3 Organization

1. The CFMP is managed by the core facility head.

2. The core facility head is accountable to the Scientific Advisory Board and the ZMBH directorate.

3. The Scientific Advisory Board approves the CFMP User Rules & Regulations and appoints a scientific coordinator from among its members.

4. The Scientific Advisory Board (§4) monitors the work of the CFMP under the supervision of the scientific coordinator (§5).

5. The names of the core facility head and the scientific coordinator are published on the CFMP website.

§4 Scientific Advisory Board

The Scientific Advisory Board supervises the activities of the CFMP to ensure its effective integration into the research environment of the FoF1 / Heidelberg and Mannheim Life Sciences campus. The scientific coordinator chairs the Board.

The Scientific Advisory Board consists of:

a) The scientific coordinator

b) One representative of the ZMBH

c) Two representatives of external institutes

The Scientific Advisory Board meets at regular intervals to discuss CFMP matters and review the head's statement of accounts. Decisions may also be taken by circular resolution. The Board establishes its own rules of procedure.

§5 Scientific coordination
The responsibilities of the scientific coordinator are:

a) Representing and communicating the needs of the ZMBH and CFMP users to the core facility head.

b) Acting as a knowledgeable and approachable contact for the core facility head on matters concerning the integration of the CFMP into the Heidelberg campus research environment.

c) Inviting members to regular Scientific Advisory Board meetings and to additional meetings when urgent matters arise.

d) Prioritizing the order of sample processing in times of high demand or in urgent cases.

§6 Provided services

1. The technical services offered by the CFMP are regularly updated to meet users' needs and are described in the current Service & Pricing List. Routine technical services comprise:
   a) General technical consultation on available services, sample suitability, and submission requirements.
   b) General advice on experimental requirements, such as protein amounts, sample volumes, compatible buffers, and standard measurement options. Developing a project-specific experimental strategy or selecting scientifically appropriate controls goes beyond this routine advice.
   c) Sample preparation using established procedures, including routine protein digestion, peptide purification, labeling, and enrichment, as agreed for the project.
   d) LC–MS analysis of peptide or protein samples using established acquisition methods and appropriate instruments.
   e) Routine data processing using established software and standard workflows: peptide/protein identification, database searching or library-based analysis as appropriate, standard false discovery rate control, quantification where applicable, technical quality control, and export of standard result tables. This includes a basic explanation of the files, software outputs, and routine workflow. Project-specific statistical modeling, biological interpretation, and publication figure development are excluded unless separately agreed as a scientific collaboration.

2. Users should contact the CFMP early to discuss sample suitability and avoid preventable errors. Before work begins, the CFMP and the user agree on the technical service scope, analytical approach, and estimated charges. Users must agree to cover the technical service costs. Where scientific contributions beyond routine services are anticipated, the user and the CFMP should confirm their intention to collaborate and their understanding of the expected scientific contributions and appropriate recognition, including co-authorship as described in §10. This may be documented through a brief e-mail exchange. The scope of the collaboration may evolve during the project and should be discussed as needed. If a project initially involves only routine services, a collaboration may be established when additional scientific input becomes necessary. In all cases, the technical service component remains payable.

3. The core facility head or their representative schedules services and projects. Routine technical services are normally processed on a first-come, first-served basis. As the ZMBH provides core funding for CFMP personnel and laboratory infrastructure, priority may be given to ZMBH research groups where necessary and operationally feasible. Priority may also be given to additional analyses required during journal peer review, particularly when needed to meet a revision deadline. Other exceptions may be made for objectively justified reasons, including efficient instrument use or the reproducibility of a measurement series. Additional

scientific work is scheduled according to available staff time and resources. Samples ready for LC–MS analysis are placed in the measurement queue. In cases of uncertainty, the scientific coordinator decides.

4. The core facility head or their representative may reject service requests for objectively justified reasons. The requester will receive an explanation and constructive feedback. The scientific coordinator must also be notified.

§7 Sample submission

1. CFMP staff register all samples electronically and assign each sample a unique identification number from a sequential numbering system.

2. Samples may be submitted by prior agreement in accordance with the guidelines on the CFMP website. Users must disclose any sample hazards before submission. Toxic, radioactive, or infectious samples cannot be processed. Potentially infectious material, including biofluids, must undergo inactivation in accordance with the established CFMP standard operating procedure (SOP) before processing by the facility. Inactivation must be documented and confirmed to the CFMP. Accepted formats are precipitated proteins or peptides, proteins or peptides in solution, and proteins in polyacrylamide gels.

3. Remaining samples remain the property and responsibility of the user. Refrigerated storage capacity is limited, and medium- or long-term storage is not available. Users who wish to recover remaining material must arrange collection within one month after completion of the service. Unless alternative arrangements have been agreed in advance, the CFMP may dispose of any remaining samples after this one-month period without further notice. Sample integrity cannot be guaranteed during storage.

§8 Costs

1. Every project includes a chargeable technical service component, including the agreed routine sample preparation, LC–MS measurements, and routine data processing defined in §6. The fees approved by the Scientific Advisory Board are set out in the Service & Pricing List. These charges remain payable when the project also includes scientific collaboration or method development. Co-authorship recognizes scientific contributions and does not replace payment; payment does not remove the obligation to recognize qualifying scientific contributions under §10. Funding for additional scientific work, including method development, must be agreed separately in writing. Where joint third-party funding covers technical services, the agreement must identify the budget from which those charges will be paid.

2. For comparative proteomics projects, users are strongly encouraged to submit at least four independent biological replicates per experimental condition where feasible. This is a planning recommendation, not a guarantee of adequate statistical power; the required sample size depends on biological variability, effect size, study design, and the intended analysis. Technical replicates do not replace independent biological replicates. Reduced pricing for projects with four or more biological replicates is subject to an agreed quotation and the discount conditions below. General advice on sample requirements is part of routine service; project-specific study design or power analysis may constitute a scientific contribution under §10.

3. For high-throughput or large-scale proteomics projects, pricing is agreed individually according to project complexity, sample numbers, and scheduling requirements. LC–MS analysis charges include both instrument measurements and routine data processing. Depending on project size and instrument utilization, these combined charges may be discounted by 25–50%. Sample preparation charges are excluded from the discount and remain payable in full. The quotation must identify the charges covered by the discount and the applicable rate.

§9 Data storage & security

1. Results are made available to the relevant research group members in a suitable form, for example by e-mail, iLab, or heiBOX.

2. Raw mass spectrometry data and the associated processing results generated during routine operations are stored on a server and made available to the relevant research group members on request.

3. Data are archived in cooperation with Heidelberg University's Computing Centre (Universitätsrechenzentrum, URZ) for 10 years.

§10 Publication of data

1. The CFMP follows the CCTP Publication Policy and the applicable DFG and Heidelberg University standards of good research practice.

2. Acknowledgment: All publications using CFMP services or data must acknowledge the facility and its support, including when technical services have been paid for or CFMP staff are co-authors. Routine technical services alone do not normally justify co-authorship. Directly involved staff should be named, with their agreement, and relevant facility software must be cited as appropriate.

   An example:
   We acknowledge the technical support of the Core Facility for Mass Spectrometry and Proteomics (CFMP, DFG RI_00574) at the Center for Molecular Biology (ZMBH), Heidelberg University. We thank [name(s)] for support with [specific contribution]. The CFMP is funded by the ZMBH and partially funded by the CellNetworks Core Technology Platform (CCTP) of Heidelberg University. The CCTP is funded in part by the Federal Ministry of Education and Research (BMBF) and the Ministry of Science Baden-Württemberg within the framework of the Excellence Strategy of the Federal and State Governments of Germany.

3. Co-authorship: Scientific contributions beyond the routine technical services defined in §6 constitute a collaboration component. Users must include the individual CFMP staff members whose genuine, identifiable scientific contributions are reflected in a publication as co-authors, in accordance with applicable authorship criteria. This obligation applies irrespective of charges paid for technical services. Authorship recognizes scientific work; it is not a fee, reward, or automatic entitlement based on facility access or position. Final authorship and author order must reflect actual contributions. Contributing CFMP staff must be given the opportunity to participate in manuscript drafting or substantive revision, approve the final version, and accept the responsibilities required by the publication venue.

   Examples of scientific contributions include:

- Experimental design and scientific guidance: Developing project-specific experimental strategies, selecting appropriate biological controls, resolving major design problems, and providing sustained scientific guidance. The scientific content of the contribution, rather than the number or duration of meetings, determines its relevance for authorship.

- Data analysis and interpretation: Selecting and justifying analysis parameters, normalization methods, statistical tests, and comparisons; assessing the validity and biological meaning of results; and taking scientific responsibility for these choices, including during peer review. Analyses performed using established or automated CFMP pipelines remain scientific contributions where they involve project-specific scientific judgment.

- Preparation of scientific outputs: Developing publication figures and supplementary materials that communicate the scientific findings, and scientifically curating, documenting, and validating datasets for deposition in repositories such as PRIDE.

- Method and software development: Developing or substantially adapting analytical methods, protocols, or software for the project, including R-based pipelines and web-based tools for exploring, interpreting, or visualizing datasets.

  These contributions warrant co-authorship when they constitute an identifiable scientific contribution to the publication and the applicable authorship criteria are met. Routine sample preparation, instrument operation, standard software instruction, and basic technical quality control are acknowledged as technical support. Automation or the use of established tools

does not, by itself, determine whether a contribution is technical or scientific.

For scientific collaborations, users must involve the contributing CFMP staff early enough to participate in preparing or substantively revising the relevant analyses, figures, and manuscript and to approve the final version before submission.

Patents and intellectual property: Patent inventorship is distinct from publication authorship and depends on the individual's contribution to the invention. Potential inventions, intellectual property rights, and disclosure arrangements must be addressed through the appropriate university procedures and collaboration agreement. Co-authorship does not itself establish inventorship or ownership.

§11 Type of use

1. All work is carried out by CFMP staff.

2. Internal use comprises services provided to members of Heidelberg University.

3. Services for external public institutions in Germany may be provided as non-economic cooperation where the applicable requirements of Heidelberg University's Framework Usage Regulations and state aid rules are met.

4. Alternatively, services for external public institutions in Germany may be provided as economic activities (contract research), subject to the applicable university agreements and pricing rules.

5. Services for external private users in Germany and for public or private users abroad may be provided under a cooperation agreement or as contract research, subject to the applicable university requirements. These administrative categories are distinct from the scientific collaboration component described in §§6, 8, and 10. The presence of scientific input does not by itself determine the administrative or state aid classification of a project.

Service & Pricing List
Core Facility for Mass Spectrometry and Proteomics (CFMP)
at the Center for Molecular Biology of Heidelberg University (ZMBH)

Last updated on the 4th of November 2026

The CFMP provides routine technical services and additional scientific support as described on its website and in these User Rules & Regulations. The service portfolio is adapted to the needs of research groups on the Heidelberg and Mannheim Life Sciences campuses. All prices below are in euros (€), excluding any applicable VAT. Technical service charges apply to both service-only projects and projects with a scientific collaboration component (§8).

		ZMBH	Basic price
Category	**Procedure**	**Price [€]**	**Price [€]**
LC-MS analysis	70 min	60	65
	105 min	76	83
	135 min	89	98
	165 min	103	113
	225 min	131	143
	285 min	158	173
	Intact protein mass determination	82	90
Consumables	Pre-Cast gel (we can help you set-up everything)	42	44
	Trypsin (20µg)	25	26
	LysC (20µg)	252	264
	H-Arginine (aliquot of 60.7 mg that can be used to prepare 0.5 L cell culture medium)	546	572
	H-Lysine (aliquot of 93.1 mg that can be used to prepare 0.5 L cell culture medium)	441	462
Services	In-solution digest and desalting (up to 100 µg, e.g. for TMT labeling)	53	55
	In-solution digest and desalting (up to 500 µg, e.g. for phosphoenrichment)	95	99
	In-solution digest and desalting (up to 1000 µg, e.g. in combination with PTMscan kits)	147	154
	In-gel digest setup (up to 10 samples)	90	110
	SP3 and desalting (up to 20µg)	42	44
	SP3 and desalting (up to 250µg)	73	77
	Dimethyl labeling (up to 10 samples)	53	55
	TMT 6plex (per replicate, see example)	158	165
	TMT 10/11 plex (per replicate, see example)	252	264
	Phosphoenrichment (up to 500 µg starting material)	26	28
	Protein concentration measurement (up to 10 samples)	105	110

Additional charges for external users apply according to the administrative categories in the table below, subject to the university's applicable agreements and pricing rules:

Type of service	**Cooperation[1] and contract research**	**Non-economic activity (cooperation)**	**Cooperation[1]**	**Contract research**
User	**Internal users[2]**	**External domestic public users**	**External domestic private and foreign private and public users**	**External domestic private and public and foreign private and public users**
	Use-related material expenses (DFG-compatible, e.g. DFG lump sum)	**Use-related material expenses** (DFG-compatible, e.g. DFG lump sum)	**Use-related material expenses** (DFG-compatible, e.g. DFG lump sum)	**Calculated individual full costs** (without depreciation)
Sum	**€**	**€**	**€**	
plus:				
Overhead 25 %	-	-	Applies	-
Overhead 60 %	-	-	-	Applies
Profit markup 5%	-	-	-	Applies
VAT, if applicable	-	Applies	Applies	Applies

[1] Cooperation in this administrative pricing table requires a significant scientific contribution and development effort by CFMP staff to solve a specific scientific problem. This classification does not waive technical service charges; eligibility and contractual terms must be established separately.
[2] Internal users are members of Heidelberg University.

Specification of procedures:

Pre-Cast Gel & Run (SDS-PAGE)
Samples are submitted as protein solutions in SDS sample buffer. This service includes electrophoretic separation on a commercial mini gel. The separation distance is agreed in advance. Gels are stained with a commercial colloidal Coomassie solution (approximately 3 h) and destained in water overnight.

In-Solution protein digest + peptide purification
Proteins are first digested with Lys-C in 8 M urea, followed by trypsin digestion after dilution to 2 M urea. Peptides are purified and desalted by solid-phase extraction and reconstituted in a solution suitable for nanoLC–MS analysis.

In-Gel protein digest
Users submit Coomassie-stained polyacrylamide gels. The service includes excision of bands or spots, reduction and alkylation of cysteine residues, and tryptic digestion. The service fee includes the project-specific time required to set up the digestion.

SP3 digest + peptide desalting
Proteins are captured on hydrophilic magnetic beads under organic-solvent conditions and washed to remove contaminants such as detergents and chaotropic reagents. The routine service covers protein inputs of 1–20 µg, as listed in the pricing table. Proteins are digested with trypsin in an aqueous buffer, and the resulting peptides are desalted using an in-house StageTip.

Dimethyl labeling
After proteolytic digestion, peptides are dimethyl-labeled using the appropriate reagents. Excess reagents are removed, and LC–MS/MS analysis is performed as described below.

TMT labeling
After proteolytic digestion, peptides are labeled with the appropriate TMT reagents. The reaction is quenched, excess reagents are removed, and labeled samples are pooled according to the agreed

experimental design. Peptides are fractionated by high-pH reversed-phase chromatography. Eight fractions are analyzed by LC–MS/MS as standard, unless otherwise agreed.

Phosphopeptide enrichment
After proteolytic digestion, phosphopeptides are enriched using Fe-NTA magnetic beads. The phosphopeptide-enriched fraction and a separate, unenriched aliquot for whole-proteome analysis are analyzed by LC–MS/MS, where included in the agreed project scope.

LC-MS/MS analysis
LC–MS/MS charges are based on the total instrument time, including sample loading, chromatographic separation and MS/MS acquisition, and column re-equilibration. For ZMBH users, the base charge is calculated at €27.50 per hour of instrument time plus €27.50 per sample for routine data processing (§6). For all other users, the corresponding rates are €30 per hour of instrument time and €30 per sample for routine data processing (§6). The table lists the applicable standard charges; the quotation specifies the charges for the agreed services, including any applicable surcharges or discounts. These are facility rates; eligibility for reimbursement depends on the relevant funding conditions.

Peptide samples are loaded directly onto the LC column and separated using an acetonitrile gradient suited to the sample. LC–MS/MS is performed using an appropriate available instrument. Routine systems include:

- UltiMate 3000 LC coupled to a Q Exactive HF mass spectrometer
- Vanquish Neo LC coupled to an Orbitrap Eclipse Tribrid mass spectrometer with ETD capability

Routine processing uses established workflows in appropriate software, for example MaxQuant, Proteome Discoverer, or DIA-NN. Standard identification and quantification results, where applicable, are provided in a suitable format together with basic explanations and technical quality control. Project-specific scientific analysis and publication figures are handled as described in §10. Raw data and associated processing results are archived under the arrangements in §9.

Intact protein mass determination
The intact mass of a protein is determined using a Q-TOF mass spectrometer following online LC desalting. Charge-state distributions are deconvoluted using the MaxEnt algorithm in Compass DataAnalysis 4.2 (Bruker), where appropriate for the data.