Technology Platform for Biological Mass Spectrometry located at the Biocentre of the Julius-Maximilians-Universität Würzburg

12 January 2026

Preface

Biological mass spectrometry (MS) is a key technology for proteome analysis in the fields of biochemistry, biology, pharmacy, and medicine. High-performance proteomics is enabled through state-of-the-art MS instrumentation equipped with high-resolution hybrid or tribrid mass analyzer technology. Operation of these high-end MS systems, typically coupled with ultra high-performance liquid chromatography (UHPLC), requires adequate resources and specifically trained personnel. Furthermore, sample preparation workflows, MS measurement methods and subsequent data analysis need to be tailored to the scientific question to be addressed. The Chair of Biochemistry II (Proteomics and Bioanalytical Mass Spectrometry) has a long-standing expertise in quantitative MS and functional proteomics. To foster proteomics research at the University of Würzburg, the Warscheid lab at the Chair of Biochemistry II has established laboratories to host a high-end MS technology platform at the Biocenter (Campus Hubland). The technology platform allows qualified operation of LC-MS systems by skilled personnel to ensure high performance, high-capacity utilization, and high data quality on a routine basis. Members of the technology platform also aid with proteomics experiment conception, MS data acquisition and analysis to support and foster interdisciplinary research across faculties, in particular Chemistry and Pharmacy, Biology and Medicine).

§1Terms of Usage

1) The terms of usage are **binding for all users** of the Biological Mass Spectrometry technology platform (bioMS). The bioMS platform is led by Prof. Dr. Bettina Warscheid, Chair of Biochemistry II.

2) The operation and usage of bioMS is generally based on scientific collaborations. There is no general right to resources, scientific knowledge, instruments, measurement times, data analysis and storage by potential users. The bioMS platform is not operated based on user fees alone (i.e. bioMS operates different to a core facility).

3) Access to the bioMS platform requires a short project outline and experimental plan how to address the scientific question of interest. The experimental design needs to be discussed and approved by the responsible scientific personnel of bioMS.

4) The scientific personnel at the Chair of Biochemistry II contribute to the acquisition, analysis, visualization and publication of the MS-based proteomics data. Therefore, contributions of the involved researcher should be adequately acknowledged, i.e. as co-author on peer-reviewed papers.

5) User fees are generally billed according to the guidelines of third-party funding agencies.

§2 User Duties

1) Users must comply with the general safety regulations for laboratories and the laboratory regulations of bioMS.
2) For human or mammalian sample material, the permission of usage by, e.g., the ethics committee must be provided.
3) Users need permission from the responsible personnel of the Chair of Biochemistry II to access bioMS. Users can only access or use the laboratories along with resources and equipment after permission and in presence of the responsible personnel of the Chair of Biochemistry II. Safety instructions must be followed.
4) Users are not allowed to make any changes in the configuration of instrument hardware and software, incl. measurement methods, without permission of the responsible personnel of bioMS.
5) Users are responsible for storage of their acquired MS data in accordance with the guidelines of the funding agency (e.g. DFG) and the Julius-Maximilians-Universität Würzburg. bioMS will generally store contact data and proteomics project-related data on their own file server. Search parameters allowing to repeat the raw data analysis are stored for a maximum of 10 years. For proteomics experiments, the responsible personnel of bioMS will provide the acquired MS raw files and result tables from database searches to users via file sharing.
6) Users are obliged to keep confidentiality about protocols, methods, research data, and knowledge of the Chair of Biochemistry II. User must not to confer such confidential information to a third party and can only use it for the purpose of the agreed usage.

§3 Access

1) Users must completely fill in the Sample Information And Processing (SIAP) form (available online at bioms.warscheidlab.de) and send it to the email address provided at the same URL. After approval, users can deliver samples to bioMS by mail or in person.
2) Samples must not be delivered before weekends or official holidays. General sample processing steps for LC/MS are performed by the responsible personnel of bioMS or by users after training. bioMS sample preparation protocols must be followed.
3) When the number of usage requests exceeds the available resources, access will be allocated based on the following priority order (earlier groups are granted priority):
    1. Existing collaboration partners
    2. Members of the biocenter
    3. Members of the University of Würzburg
    4. Other members of public higher-education institutions
    5. All remaining applicants (others)

§4 Pricing

1) Sample measurements are billed based on their MS measurement time and the pre-processing involved (see table below).
2) Blank injections - i.e., samples without peptides that are necessary for optimal analysis performance- are charged at €17.25 each. The decision to run blanks is made by the bioMS team.
3) Sample quality assessments, such as detecting contaminants or estimating sample quantity, will be performed when deemed necessary and billed accordingly (pre-analysis per sample). This determination is also made by the bioMS staff.

LC-MS analysis

1h LC-MS*	**100 €**
30 min LC-MS on Astral*	**100 €**
30 min LC-MS on Astral (+2 FAIMS voltages)	**160 €**
Intact protein analysis per injection	**25 €**
Pre-analysis per sample	**30 €**
Targeted MS method development	**750 €**

* all standard runs include ion-mobility separation with one compensation voltage using FAIMS

Sample preparation

Protein concentration measurements (BCA) pro sample set	**50 €**
Pre-cast gel	**40 €**
In-gel digestion per slice	**20 €**
In-gel digestion per lane (10 slices)	**100 €**
In-solution digestion per sample (SP3)	**15 €**
In-solution digestion per sample (urea)	**20 €**
Desalting per sample (stage-tipping)	**20 €**
Off-line fractionation per sample (stage-tip)	**5 €**
Off-line high pH RPLC fractionation (per sample)	**100 €**
Off-line peptide SEC fractionation (per sample)	**100 €**
Phosphopeptide enrichment (IMAC or TiO_2 cartridges)	**25 €**
Peptide enrichment (e.g. biotin-streptavidin)	**20 €**
Low-resolution complexome (sample prep. 30 slices)	**750 €**
High-resolution complexome (sample prep. 90 slices)	**1500 €**

Labeling methods

Dimethyl labeling per sample	**10 €**
TMT labeling (6-plex reagent)	**100 €**
TMT labeling (10/11-plex reagent)	**200 €**
Cross-linking (per sample)	**15 €**
Enrichable Cross-linking (per sample)	**35 €**

Data analysis

Standard data analysis is included.

Advanced Data analysis	
(e.g. cross-linking, PTM analysis, meta-analysis)	**100 € per hour**

Remark for DFG proposals

According to DFG-Vordruck 55.04 (07/24), a maximum cost of 100€ per measurement hour (without additional data analysis: 40€ / h) can be funded through a DFG proposal. The difference to the prices shown in the table are to be covered by the user. All items listed above are project specific costs in the sense of DFG-Vordruck 52.01.

Contact

bc2-wuebioms@uni-wuerzburg.de (Questions and inquiries)

Würzburg, **12 January 2026**

Prof. Dr. Bettina Warscheid (head)

Attachment

Responsible Technical and Scientific personnel and Available Resources

Date: 12 January 2026

Available instrumentation

Thermo Scientific Orbitrap Astral

with field-asymmetric ion-mobility separations (FAIMS) interface

coupled to Thermo Fisher Vanquish Neo UHPLC

Achieves very high sensitivity and throughput and is primarily used for data-independent analysis. It allows very short LC gradients with comparatively high quantification yields. Examples of applications include label-free quantification, complexomics, SILAC multiplexing.

Thermo Scientific Orbitrap Ascend (structural biology edition)

with FAIMS interface

MSn capabilities

CID, HCD and ETD fragmentation

high-mass option

coupled to Thermo Fisher Vanquish Neo UHPLC

Most versatile instrument for bottom-up and top-down proteomics as well as post-translational modification identification and localization. Complex multi-stage experiments (e.g. SPS-MS3 for TMT quantification) and advanced fragmentation techniques (e.g. EThcD) are possible. Examples of applications include: Precise localization of PTMs, TMT multiplexing, high-resolution intact mass (native MS).

Thermo Scientific QExactive Plus

Up to 70k MS resolution

CID & HCD capabilities

coupled to Thermo Fisher Ultimate 3000 UHPLC

Routine instrument for quality control and sample pre-analysis. Also performs well for targeted analyses. Examples of applications include: Identification of recombinantly purified proteins, targeted analyses of up to 50 transitions per run.

1) Head

Prof. Dr. Bettina Warscheid (Chair of Biochemistry II, BCII)

2) Scientific Supervision

Prof. Dr. Bettina Warscheid
Dr. Silke Oeljeklaus (BC II)
Dr. Julian Bender (BC II)

3) Personnel Responsible for Instrument Operation

Protein Mass Spectrometry

(i) *QExactive Plus (Thermo Fisher Scientific)*
Thomas Morgenbrodt (BC II), Hirak Das (BC II), Dr. Julian Bender (BC II)

(ii) *Synapt G1 High Mass (Waters, MS Vision)*
Dr. Julian Bender (BC II)

(iii) *Orbitrap Astral (Thermo Fisher Scientific)*
Thomas Morgenbrodt (BC II), Dr. Julian Bender (BC II)

(iv) *Orbitrap Ascend (Thermo Fisher Scientific)*
Thomas Morgenbrodt (BC II), Dr. Julian Bender (BC II)

4) Bioinformatics

(v) *Compute and file server*
Dr. Julian Bender (BC II)

(vi) *MS Data Analysis*
Dr. Silke Oeljeklaus (BC II), Dr. Julian Bender (BC II), Hirak Das (BC II)