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

14 March 2025

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 Würzburg Biological Mass Spectrometry technology platform (WueBioMS). WueBioMS 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 of the bioMS platform contributes 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 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. 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.

6) 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.

7) 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 Pricing

1) Sample measurements are billed based on sample running time. The current price per measurement hour for academic labs is 69.00 € per 30 min on the Orbitrap Astral and 69.00 € per 60 min on all other instruments. This includes basic data analysis and interpretation by the bioMS contributors.

2) Blanks (i.e. injections without peptides between samples) are billed with 17.25 € per blank.

Contact

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

Attachment

Responsible Technical and Scientific personnel and Available Resources

Date: 14.03.2025

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), Johannes Zimmermann (BC II), Dr. Julian Bender (BC II)

   (ii) *Synapt G1 High Mass (Waters, MS Vision)*
   Daniel Wendscheck (BC II), 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), Johannes Zimmermann (BC II)

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