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| Module title | | Abbreviation |
| Mass-Spectrometry and Proteomics | | o8-MBC-MSP-152-mo1 |
| Module coordinator | | Module offered by |
| holder of the Chair of Biochemistry | | Chair of Biochemistry |
| ECTS | Method of grading | Only after succ. compl. of module(s) |
| 5 | numerical grade | -- |
| Duration | Module level | Other prerequisites |
| 1 semester | graduate | -- |
| Contents | | |
| <p>The module "Mass Spectrometry and Proteomics" includes a lecture, which teaches the basics of mass spectrometry of biomolecules. There, inter alia, the gentle ionization ESI and MALDI, and the functional principles of different mass analyzers such as TOF and Orbitrap are discussed. The lecture part gives an introduction to the mass spectrometric fragmentation techniques CID and ETD, its separation techniques for peptides and proteins, as well as to the analysis of mass spectrometric data (protein databases, FDR, GO terms, etc.). Furthermore, an overview of the field of quantitative proteomics is given; especially different methods of quantification by stable isotopes (SILAC, N¹⁵-Labeling, iTRAQ, etc.) will be discussed. Finally, the lecture gives insights in the mass spectrometric analysis of posttranslational modifications. The seminar part of the module imparts fundamentals of mass spectrometric analysis data. To this end, the participants will be introduced to different software packages and then work independently on exemplary data sets to find solutions for different tasks. In the practical part of the module, participants will isolate a protein complex from yeast by affinity purification. This complex is separated by 1D-SDS-PAGE and proteolytically cleaved in the gel. The peptides obtained are analyzed by nanoLC-MS / MS. Finally data analysis is conducted with the aim of identifying specific interaction partners and post-translational modifications.</p> | | |
| Intended learning outcomes | | |
| <p>On a broad basis, participants are taught the theoretical foundations of mass spectrometric analysis of proteins and proteomes. In the seminar, participants learn how to use data analysis software in the field of proteomics. In the practical part, students will learn affinity purification of a protein complex, and typical steps of sample preparation for mass spectrometric protein analysis, such as SDS-PAGE and in-gel digestion. Participants get an insight into the operation of a nanoHPLC-coupled mass spectrometer.</p> | | |
| Courses (type, number of weekly contact hours, language — if other than German) | | |
| V (2) + S (1) + P (2) Module taught in: German or English | | |
| Method of assessment (type, scope, language — if other than German, examination offered — if not every semester, information on whether module is creditable for bonus) | | |
| <p>a) written examination (approx. 45 to 90 minutes) or b) log (20 to 30 pages) or c) oral examination of one candidate each (20 to 30 minutes) or d) oral examination in groups of up to 3 candidates (15 to 30 minutes per candidate) or e) presentation (20 to 40 minutes) Assessment offered: Once a year, winter semester Language of assessment: German and/or English</p> | | |
| Allocation of places | | |
| <p>Biochemie (Biochemistry), Master's: 6 places. Places will be allocated according to the number of subject semesters. Among applicants with the same number of subject semesters, places will be allocated by lot. A waiting list will be maintained and places re-allocated by lot as they become available.</p> | | |
| Additional information | | |
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| Referred to in LPO I (examination regulations for teaching-degree programmes) | | |
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| Module appears in | | |
| Master's degree (1 major) Biochemistry (2015) | | |



Master's degree (1 major) Biochemistry (2017)