Module title			Abbreviation
Mass-Spectrometry and Proteomics			08-MBC-MSP-152-m01
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

This module comprises a lecture, a seminar and a lab course. The lecture discusses the fundamental principles of the mass spectrometry of biomolecules. Topics to be covered in the lecture include ESI and MALDI ionisation techniques as well as the operating principles of TOF, Orbitrap and other mass analysers. The lecture also provides an introduction to CID and ETD fragmentation techniques, peptide and protein separation methods as well as the analysis of mass spectrometric data (protein databases, FDR, GO terms, etc.). It gives an overview of quantitative proteomics with a special focus on different stable isotope quantification methods (e.g. SILAC, N15 labelling, iTRAQ) and provides an insight into the mass spectrometric analysis of post-translational modifications. The seminar covers the fundamental principles of the analysis of mass spectrometric data. It introduces students to different software packages and gives them the opportunity to independently develop solutions to a range of problems. In the lab course, students will use affinity purification to isolate a protein complex from yeast. They will then use 1D-SDS-PAGE to separate that complex and will proteolytically cleave it in the gel. Afterwards, students will use nano-LC-MS/MS to analyse the peptides thus obtained and will conduct a data analysis to identify specific interaction partners and post-translational modifications.

Intended learning outcomes

Students have learned the theoretical foundations of mass spectrometry protein and proteomic analysis. They have learned how to use proteomic data analysis software tools. Students have become proficient in the affinity purification of protein complexes and have learned the steps involved in the preparation of samples for mass spectrometry protein analysis, e.g. SDS-PAGE and in-gel digestion. They have gained an insight into how to operate a nanoHPLC-coupled mass spectrometer.

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)

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)
Language of assessment: German and/or English
Assessment offered: Once a year, winter semester

Allocation of places

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.

Additional information

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Workload

150 h

Teaching cycle
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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)