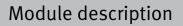
Module description

Module title					Abbreviation
Mass-Spectrometry and Proteomics					08-MBC-MSP-161-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		graduate			
Contents					
This module comprises a lecture, a seminar and a lab course. The lecture discusses the fundamental princip- les of the mass spectrometry of biomolecules. Topics to be covered in the lecture include ESI and MALDI ioni- sation techniques as well as the operating principles of TOF, Orbitrap and other mass analysers. The lecture al- so 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 modi- fications. The seminar covers the fundamental principles of the analysis of mass spectrometric data. It introdu- ces 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. After- wards, 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 affini- ty 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 ope- rate 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: In the semester in which the course is offered, no less than once a year 					
67 places.					
Additional information					
Workload					
150 h					
Teaching cycle					

8 83





Referred to in LPO I (examination regulations for teaching-degree programmes)

Module appears in

Master's degree (1 major) Chemistry (2016) Master's degree (1 major) Chemistry (2018) Master's degree (1 major) Biochemistry (2019) Master's degree (1 major) Chemistry (2024)

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