DEPARTMENT OF ONCOLOGY-PATHOLOGY

K7F2522, Proteomics by Mass Spectrometry: When and How, 3 credits (hec)

Proteomik med användning av mass spektrometri: När och hur, 3 högskolepoäng

Third-cycle level / Forskarnivå

Approval

This syllabus was approved by the The Committee for Doctoral Education on 2023-11-01, and was last revised on 2024-11-08. The revised course syllabus is valid from autumn semester 2024.

Responsible department

Department of Oncology-Pathology, Faculty of Medicine

Prerequisite courses, or equivalent

While no specific prerequisite courses are necessary for this program, a basic understanding at the university level of molecular biology, chemistry, biochemistry, and omics technologies is recommended to fully benefit from the course.

Purpose & Intended learning outcomes

Purpose

The aim of this course is to give an overview of mass spectrometry based proteomics for researchers who would like to apply these techniques in their own research and/or understand how proteomics data is generated to be able to analyse proteomics data.

Intended learning outcomes

After completing the course, the student will be able to

-Define and apply common proteomics terminology
-Recognize the principles of the most common proteomics techniques
-Describe the mass spectrometry based proteomics workflow: Experimental design, sample preparation and selection of techniques
-Understand the basic principles of MS based proteomics from sample preparation to

generation of the protein data matrix to such an extent that he/she will be able to utilize proteomics core facilities or collaborate with proteomics researchers.
-Evaluate the quality of protein and peptide identifications.
-Give examples on how modern proteomics is applied to clinical research and to evaluate when proteomics research could be beneficial to incorporate in research projects.
-Design your own research project by mass spectrometry based proteomics.

Course content

Practical Laboratory Exercise: Practical laboratory exercise utilizes mass spectrometry-based proteomics to teach sample preparation, demonstrate sample acquisition and analysis, and provide a foundation for basic data interpretation.

Skills Acquisition and Project Presentation: The skills acquired during the course will be applied to write and orally present a brief proteomics research project.

Focus of the Course: This course emphasizes proteomics technologies and applications. For proteomics data analysis, we recommend our KI doctoral course "Omics Data Analysis: From Quantitative Data to Biological Information”

Lectures and workshops on:

-Overview of proteomics

-The proteomics workflow

-Basic of separation sciences: Protein and peptides

-Sample preparation for proteomics

-Introduction to Mass spectrometry

-Quantitative proteomics methods

-Global and targeted proteomic

-Experimental design

-Plasma proteomics

-Protein Identification statistics

-Proteogenomics

-Biological validation

-Clinical applications

-Single cell proteomics

-Data Analysis & Bioinformatics

Forms of teaching and learning

The course contains lectures, seminars, and a practical laboratory exercise using proteomics techniques. The students will plan their own project as a case study as well make an oral laboratory report.

Language of instruction

The course is given in English

Grading scale

Pass (G) /Fail (U)

Compulsory components & forms of assessment

Compulsory components:

Attendance at lectures and the practical laboratory exercise.

Attendance at the examination seminar and submission of the written examination assignment.

Additional written assignments can be used to compensate for absence.

Recommended preparation: Students are advised to read the literature listed below before the course begins.

Forms of assessment:

Students are required to present a proteomics project (preferably related to their research) covering various aspects of the proteomics workflow. This will be presented orally and submitted as a written exam.

Students are expected to deliver an oral laboratory report as a group.

Course literature

Access to Materials: PowerPoint presentations related to the lectures will be accessible on the learning platform canvas during the course.

Recommended Reading: It is advisable to review the following literature before the course to maximize your learning experience:

An Introduction to Mass Spectrometry-Based Proteomics, Steven R Shuken, J Proteome Res. 2023 Jul 7;22(7):2151-2171. doi: 10.1021/acs.jproteome.2c00838.

The pros and cons of peptide-centric proteomics, Mark W Duncan, Ruedi Aebersold, Richard M Caprioli, Nat Biotechnol. 2010 Jul;28(7):659-64. doi: 10.1038/nbt0710-659.