CB2110 Applied Proteomics 7.5 credits

Tillämpad proteomik

This is a translation of the Swedish, legally binding, course syllabus.

If the course is discontinued, students may request to be examined during the following two academic years

Establishment

Course syllabus for CB2110 valid from Autumn 2024

Grading scale

A, B, C, D, E, FX, F

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

A bachelor's degree equivalent to at least 180 ECTS, along with courses equivalent to at least 20 ECTS in life sciences and 10 ECTS in mathematics (or similar).

Language of instruction

The language of instruction is specified in the course offering information in the course catalogue.

Intended learning outcomes

The purpose of the course is to provide students with an introduction to current methods, challenges, and applications in the field of proteomics, with a focus on mass spectrometry-based analysis methods. Upon completion of the course, students should have a deep understanding of various advanced methods in the field of mass spectrometry-based proteomics and methods for protein analysis in complex systems. Students should be able to describe the principles behind these techniques and their specific applications in the field of biotechnology. Upon completion of the course, students should be able to:

1.Analyze and evaluate results from proteomics technologies (TEN1, LAB1)

- Critically assess the principles, strengths, and limitations of different proteomics technologies.
- Identify and discuss experimental design and data analysis with a focus on protein quantification.

2.Actively participate in scientific discussions within the field of Proteomics

- Engage in scientific discussions about proteomics technologies and their applications in life science. • Critically evaluate scientific results from proteomics experiments (TEN1, LAB1).

3.Analyze and interpret proteomics data from scientific articles and experimental studies.

- Assess and review research findings and subsequently analyze their reliability and relevance based on relevant statistical methods.

Course contents

This course introduces students to principles, techniques, and applications in proteomics. Students will learn the fundamentals of protein separation, identification, and quantification using mass spectrometry, as well as how these techniques can be applied in various areas such as medicine, biotechnology, and environmental science. The course will also cover data analysis and interpretation, as well as the integration of proteomics data with data obtained from other omics technologies. The sections included in the course are as follows:

- Introduction to proteomics
- Basic protein separation techniques and introduction to mass spectrometry
- Applied proteomics
- Protein identification and quantification
- Data analysis and integration with other omics technologies
- Biomarker identification and precision medicine
- Current challenges and future directions

Examination

- LAB1 - Computer Exercises, 2.5 credits, grading scale: P, F
- TEN1 - Written exam, 5.0 credits, grading scale: A, B, C, D, E, FX, F

Based on recommendation from KTH's coordinator for disabilities, the examiner will decide how to adapt an examination for students with documented disability.

The examiner may apply another examination format when re-examining individual students.

Ethical approach

- All members of a group are responsible for the group's work.
- In any assessment, every student shall honestly disclose any help received and sources used.
- In an oral assessment, every student shall be able to present and answer questions about the entire assignment and solution.