BB2510 Proteomics 6.0 credits

Proteomik

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

Establishment

Course syllabus for BB2510 valid from Spring 2020

Grading scale

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

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

Language of instruction

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

Intended learning outcomes

The aim of the course is to provide the students with an introduction to current methodologies and trends in the field of proteomics. The students should also obtain an overview and awareness of typical proteomics applications both from lectures and an introduction to proteomics lab work.

After completed course the student should be able to describe and discuss the possibilities and advantages, and the complexity and drawbacks of various proteomics technologies compare traditional methods with emerging technologies. The student should be able to suggest suitable approaches for specified applications and motivate the choice speculate and argue about the future of proteomics technologies. With the acquired knowledge, the students should be able participate in scientific discussions regarding proteomics technologies critically evaluate scientific results.

Course contents

Proteomics describes large-scale analysis of proteins in a biological sample. The aim of these studies is to determine the protein parts that are present in such samples and to define their concentrations, molecular states, structures, functions or connections. Today, there are different technologies being used and developed to study the different types of samples such as to find biomarker molecules that could help to diagnose diseases or even improve therapy of patients.

The objective of the course is to present current trends for global protein analysis and to demonstrate its principles, challenges and complexity. The course will therefore provide an overview of the different proteomics applications used today from planning the experiments to analyzing data.

The course is focused on different methods, technologies and strategies currently used within the field of proteomics in general and with an emphasis on biomarker discovery. The course provides theoretical information about proteomics and an introduction to lab work conducted in the different areas of proteomics.

The lectures will cover background and recent advances for proteomics methods, such as mass spectrometry, strategies using antibodies, and exemplify to role of bioinformatics. The lab work will provide an overview of proteomics technologies and cover elements introduced during the lectures.

Course literature

Principles of Proteomics by R.M Twyman, Garland Science, ISBN: 9780815344728 (second edition)
Reviews and scientific articles will be available on the course web
Handout are distributed at the lectures

Equipment

Computer

Examination

- ÖVN1 - Exercise, 1.0 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.

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

Other requirements for final grade

Passed grades in the written examination and in the oral part. Presence and participation in all the lab work activities. Completion of all mandatory online assignments and workshops.

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.