BB2510 Proteomics 6.0 credits

Proteomik

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

Establishment

Course syllabus for BB2510 valid from Autumn 2014

Grading scale

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

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

At least 150 credits from grades 1, 2 and 3 of which at least 100 credits from years 1 and 2, and bachelor's work must be completed. The 150 credits should include a minimum of 20 credits within the fields of Mathematics, Numerical Analysis and Computer Sciences, 5 of these must be within the fields of Numerical Analysis and Computer Sciences, 20 credits of Chemistry, possibly including courses in Chemical Measuring Techniques and 20 credits of Biotechnology or Molecular Biology.

Knowledge corresponding to the following courses, or similar, is required.

BB1010 Introduction to Biotechnology

BB1020 Cell biology with Immunology

BB1080 Biochemistry, Theory

BB1110 Gene Technology and Molecular Biology

BB1130 Analysis and Purification of Biomolecules

Language of instruction

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

Intended learning outcomes

The aim of this course is to provide the students with an introduction into methodologies in the field of proteomics. Therein, examples of current trends for global protein analysis will be presented from different perspectives in order to demonstrate complexity and terminologies of this field of research. The course will provide an overview of typical proteomics applications used today and present their use for different applications.

After having completed this course, the students shall be able to

- describe and discuss the possibilities offered by proteomics technologies
- judge and compare the various proteomics approaches
- suggest and reason for suitable strategies for specified projects.
- critically evaluate results from proteomic studies.
- participate in scientific discussions regarding proteomics technologies
- speculate and argue about coming trends of proteomics technologies.

Course contents

The course is focused on different methods, technologies and strategies currently applied in the field of proteomics. General concepts as well as an emphasis on biomarker discovery will be presented in order to demonstrate proteomic application, which span different areas in life science and biotechnology.

Disposition

The lectures will cover the different disciplines within proteomics by providing insights from researchers within the field as well as the perspectives of PhD students working with proteomics. Background on classical proteomics, such as 2D-gel electrophoresis or mass spectrometry, will be complemented by recent developments and strategies built on affinity proteomics, the high-throughput generation of binding reagents, data analysis as well as structural and interaction approaches.

Course literature

- Principles of Proteomics by R.M Twyman, Garland Science, ISBN: 9780815344728 (2013).
- Review articles and
- Handouts from presentations are distributed at each lecture.

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.

The examination consists an oral and a written part. The oral exam will in form of a panel discussion where groups of students will prepare arguments for a discussion on a given proteomic subject. One group will argue for the possibilities and advantages for a certain method or strategy and another group will then argue against this with drawbacks and limitations. It is important to see this part as not only an examination, but also as a learning activity to argument for your scientific perspective and to collect information from the lectures and other sources.

The written examination will mostly consists of questions, where the students are expected to describe and discuss the obtained knowledge about proteomics according to the aims of the course. The students will also be able to express your scientific opinion regarding various aspects of proteomics technologies. There is no right or wrong in the provided opinion, the students you will be able to demonstrate their knowledge about proteomics based on their argumentation.

Other requirements for final grade

A written examination (TEN1, 5 hp, grading scale A-F).

Participation in panel discussion (ÖVN1, 1 hp, Pass/Fail)

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.