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 2011

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.

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 student should also obtain an overview and awareness of typical proteomics applications.

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
- suggest suitable approaches for specified applications and motivate the choice
- speculate and argue about the future of proteomics technologies
- participate in scientific discussions regarding proteomics technologies
- critically evaluate scientific results

Course contents

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 lectures will cover background and recent advances for both classical proteomics methods, such as 2D-gel electrophoresis and mass spectrometry, and strategies based on high-throughput antibody generation, bioinformatics and structural approaches.

Course literature

- **Principles of Proteomics** by R.M Twyman, Garland Science, ISBN: 1859962734
- distributed review articles
- handouts from all lectures

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 of two parts, one oral and one written. The oral exam will be based on a panel discussion where you in groups will prepare a discussion on a given subject. One

group will argue for the possibilities and advantages for a certain method or strategy and another group will then argue for the drawbacks and limitations. It is important to see this part as not only an examination, but also as a learning activity.

The written exam consists of discussion type questions, where you are expected to show that you have obtained the knowledge according to the aims of the course. You will also be able to express your opinion regarding various aspects of proteomics technologies. Opinions cannot be right or wrong but the way the argumentation is done will reveal your knowledge.

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.