



**Karolinska
Institutet**

Course syllabus for

Proteomics and Bioinformatics, 7 credits

Proteomik och bioinformatik, 7 hp

This course has been cancelled, for further information see Transitional provisions in the last version of the syllabus.

Course code	4BI028
Course name	Proteomics and Bioinformatics
Credits	7 credits
Form of Education	Higher Education, study regulation 2007
Main field of study	Biomedicine
Level	AV - Second cycle
Grading scale	Excellent, Very good, Good, Satisfactory, Sufficient, Fail, Fail
Department	Department of Medical Biochemistry and Biophysics
Decided by	Programnämnden för biomedicinprogrammen
Decision date	2008-10-28
Revised by	Programme committee for study programmes in biomedicine
Last revision	2017-11-30
Course syllabus valid from	Spring 2008

Specific entry requirements

Bachelor's degree or vocational degree worth at least 180 ECTS credits (120 credits) in biomedicine, biotechnology, cellular and molecular biology, medicine or equivalent.

Objectives

After the course the student should

- understand the importance of protein structure and function in a physiological context
- have an insight into methods available for the identification of unknown gene products in a high-through-put manner
- have a basic knowledge about theory and practice within bioinformatics and the use of these methods within biomedical research
- be able to set up a proteomics investigation
- be able to use bioinformatics tools
- be able to critically choose between methods to solve proteomics and bioinformatics problems
- be able to apply a scientific approach to proteomics and bioinformatics problems

Content

The relationships between protein function and structure in a global mode. Protein structural determination with techniques as sequence analysis, mass spectrometry analysis, X-ray crystallography and NMR. Identification of unknown proteins with 2-dimensional gel electrophoresis and mass spectrometry. Determination of protein-protein interactions. Overview of front-line techniques within the field of proteomics. Microarray techniques. Databases and handling of sequence data, pair-wise alignment, multiple alignment, the portals SRS and Entrez, DNA patterns and motives, protein patterns and motives, profiles, predictions, computer modelling and a presentation of non-sequence related bioinformatics problems like enzymatic databases, 2D-gel databases, handling of microarray data and gene ontology data. A short background to algorithms behind the used computer programs will be given.

Teaching methods

The teaching is given as introductory lectures and demonstrations. In parallel a project work is performed within a research group with focus on proteomics with the use of bioinformatics tools, where the students together with the supervisor will design the project. At the end of the course the project will be presented both orally and in written form for all other course participants. Beside the project work the students have to solve a number of assignments within bioinformatics.

Examination

The presentation of the project work (both a written report and an oral presentation) will be performed as an examination. All students have to take an active part in the final discussions.

Compulsory attendance

Attendance during the project work and the final presentation is compulsory. Absence from these compulsory parts may be compensated in agreement with the course director, judged on a case-to-case basis. However, attendance to all lectures/demonstrations is strongly recommended.

A student who does not pass the presentations on their first occasion is offered a maximum of five additional opportunities to presentation. If a student has not passed the presentation after a total of four attempts then it is recommended that the student retake the whole course at the next opportunity. Following this the student is permitted to another two presentations. A student who fails the presentation on six occasions is not permitted to do the examination again or to retake the course.

Transitional provisions

The course has been **cancelled**.

Other directives

The course will be evaluated in accordance with the guidelines established by the Board of Higher Education.

The course language is English.

Literature and other teaching aids

Higgs, Paul G.; Attwood, Teresa K.

Bioinformatics and molecular evolution

Oxford : Blackwell, 2005. - 365 p.

ISBN:1-4051-0683-2 (pbk.) LIBRIS-ID:9119432

[Library search](#)

Proteomics : from protein sequence to function

Pennington, Stephen R.; Dunn, Michael J.

Oxford : BIOS, 2001 - xxii, 313 s.

ISBN:1-85996-296-3 LIBRIS-ID:6501825

[Library search](#)