

# Proteomics

Programme course

6 credits

Proteomik

TFKE57

Valid from: 2017 Spring semester

**Determined by**

Board of Studies for Chemistry, Biology  
and Biotechnology

**Date determined**

2017-01-25

## Main field of study

Chemical Biology

## Course level

Second cycle

## Advancement level

A1X

## Course offered for

- Protein Science, Master's Programme
- Chemical Biology, M Sc in Engineering
- Protein Science, Master's programme

## Entry requirements

Note: Admission requirements for non-programme students usually also include admission requirements for the programme and threshold requirements for progression within the programme, or corresponding.

## Prerequisites

Admission to advanced level studies in Chemical Biology. Protein chemistry, gene technology and biological measurements. Basic knowledge of analytical chemistry and bioinformatics is also recommended.

## Intended learning outcomes

The aim of the course is to provide a broad knowledge of methods and applications within proteomics. Many of the basic methodological principles (genetic, biochemical, analytical chemical and bioinformatic) have been introduced in earlier courses, but here the student learns how these principles are used within a currently very expansive research area: Global characterisation of the proteome with regard to protein abundance, function, regulation, interactions and localisation in different cell types. Transcriptomics is also discussed. To pass the course, the student should be able to

- describe the relevance and distinctive character of proteomics
- describe and discuss principles and applications of modern methods and strategies to analyse the transcriptome and the proteome
- identify proteins and peptides using mass spectra and genome databases
- summarise the contents of selected original proteomics literature, interpret its message and review it critically

## Course content

Quantitative mRNA-analysis with DNA microarrays and other methods. Multi-dimensional protein separation methods (2DGE, 2DLC). Identification of cellular protein contents using enzymatic cleavage, MS- and MS/MS-analysis and genome databases. Protein quantification based on isotope labelling and MS. Analysis of post-translational modifications. Analysis of protein interactions using affinity chromatography, Y2H methodology and protein microarrays. Characterisation of changes of the cellular protein contents following changes in the environment, for e. g. identification of disease biomarkers. Metaproteomics. Human Proteome Atlas.

## Teaching and working methods

The course consists of lectures, seminars, demonstrations, and two home assignments.

## Examination

UPG2	Presentation	1 credits	U, G
UPG1	Hand-in assignments	1 credits	U, G
TEN1	Written examination	4 credits	U, 3, 4, 5

## Grades

Four-grade scale, LiU, U, 3, 4, 5

## Department

Institutionen för fysik, kemi och biologi

## Director of Studies or equivalent

Magdalena Svensson

## Examiner

Karin Enander

## Education components

Preliminary scheduled hours: 36 h

Recommended self-study hours: 124 h

## Course literature

Twyman, R. M.; "Principles of Proteomics" 2nd edition. Originalartiklar.

## Common rules

Regulations (apply to LiU in its entirety)

The university is a government agency whose operations are regulated by legislation and ordinances, which include the Higher Education Act and the Higher Education Ordinance. In addition to legislation and ordinances, operations are subject to several policy documents. The Linköping University rule book collects currently valid decisions of a regulatory nature taken by the university board, the vice-chancellor and faculty/department boards.

LiU's rule book for education at first-cycle and second-cycle levels is available at [http://stydokument.liu.se/Regelsamling/Innehall/Utbildning\\_pa\\_grund-\\_och\\_avancerad\\_niva](http://stydokument.liu.se/Regelsamling/Innehall/Utbildning_pa_grund-_och_avancerad_niva).