DEPARTMENT OF MEDICINE, HUDDINGE

H7F6059, Protein Structure, Function and Disease, 4.5 credits (hec)

Proteinstruktur, funktion och sjukdom, 4,5 högskolepoäng

Third-cycle level / Forskarnivå

Approval

This syllabus was approved by the The Committee for Doctoral Education on 2025-01-27, and is valid from autumn semester 2025.

Responsible department

Department of Medicine, Huddinge, Faculty of Medicine

Prerequisite courses, or equivalent

Completed Master studies in the field of biochemistry, biotechnology, biomedicine, biophysics, chemical neuroscience or related subjects.

Purpose & Intended learning outcomes

Purpose

The course deals with the molecular properties of proteins concerning their molecular structure and implementation in biology as well as protein misfolding and the relation to neurodegenerative diseases. It covers the general architecture of proteins, the relation of structure to function and mechanisms of regulations of protein function. It includes recent insights into the molecular mechanisms of protein aggregation and the link to neurodegenerative diseases. Moreover, it gives an overview about recent developments within methods for protein structure and dynamics determination, in particular X-ray crystallography, electron microscopy and nuclear magnetic resonance. The course will also train the participants to prepare scientific presentations and critically assess research literature.

Intended learning outcomes

At the end of the course the students are expected to be able to:
- Understand how protein architecture is related to protein function

• Explain how protein dynamics, catalysis, binding sites and cofactors determine the protein structure-function relationship
• Identify and discuss control mechanisms of protein function, including competitive binding and cooperativity of ligands, post-translational modification and enzyme reactions
• Understand the principles and apply some tools for sequence alignment, homology modeling and structure prediction methods from protein sequence
• Show up-to-date knowledge of the working principles for major methods for protein structure and dynamics determination as well as microscopic nucleation mechanisms underlying protein aggregation

Course content

The course is divided into two parts.
The first part of the course is based on the course book “Protein Structure and Function” and related research articles and consists of:

- Protein structure (from primary to quaternary structure, protein stability and protein flexibility, etc.)
- From structure to function (binding sites, catalysis, cofactors, etc.)
- Control of protein function (mechanisms of regulation, binding ligands, post-translational modifications, etc.)
- Deriving protein function from sequence (sequence alignment, homology modeling, structure prediction, etc.)

The second part is based on lectures from the course directors and from invited specialists in the field, including

- Neurodegenerative disorders and protein misfolding
- Molecular mechanisms of protein aggregation
- Recent developments in protein structure and dynamics methods, including:

- X-ray crystallography
- Electron microscopy
- Nuclear magnetic resonance

Forms of teaching and learning

The course consists of
• Student presentations of research articles related to Chapters in the course book. If suitable examples from the student’s own research can be included.
• Questions for student presentations by students (two students are assigned as “opponents” for each presentation) and audience
• Written tasks, including practical of bioinformatics tools, related to the content of the Chapters, which are handed in before each session
• Presentations by several invited specialists of the field

Language of instruction

The course is given in English

Grading scale

Pass (G) /Fail (U)

Compulsory components & forms of assessment

Compulsory components

Attendance of lectures, student presentations and exercise sessions is compulsory. Absence needs to be compensated for by a written task related to the lecture subject in agreement with the course director. Further, the students need to submit written tasks and perform one scientific presentation about a research article.

Forms of assessment

The course content will be examined by written tasks as well as student presentations and oral examination of the topic by the course directors.

Course literature

Mandatory reading:
1. Gregory A Petsko, Dagmar Ringe
Protein Structure and Function
Oxford University Press Inc
ISBN: 9780878936632
224 pages
2. Additional lecture material (will be provided)