

## AFLYST 18/12 pga. få tilmeldte - Protein Biochemistry

Title	AFLYST 18/12 pga. få tilmeldte - Protein Biochemistry
Semester	F2024
Master programme in	Medicinal biologi / Molekylær biologi / Chemical Biology / Molecular Health Science
Type of activity	Laboratory Course
Teaching language	English
Study regulation	Read about the Master Programme and find the Study Regulations at <a href="https://ruc.dk">ruc.dk</a>  Læs mere om uddannelsen og find din studieordning på <a href="https://ruc.dk">ruc.dk</a>

## REGISTRATION AND STUDY ADMINISTRATIVE

Registration	<p>Sign up for study activities at <a href="#">stads selvbetjening</a> within the announced registration period, as you can see on the <a href="#">Studyadministration homepage</a>.</p> <p>When signing up for study activities, please be aware of potential conflicts between study activities or exam dates.</p> <p>The planning of activities at Roskilde University is based on the recommended study programs which do not overlap. However, if you choose optional courses and/or study plans that goes beyond the recommended study programs, an overlap of lectures or exam dates may occur depending on which courses you choose.</p>
Number of participants	<p>The Master Programme/Institute reserves the right to cancel the course if fewer than 8 students are registered for the course.</p> <p>There is a maximum of 20 students at this course.</p>
ECTS	5
Responsible for the activity	René Jørgensen ( <a href="mailto:renejoe@ruc.dk">renejoe@ruc.dk</a> )
Head of study	Lotte Jelsbak ( <a href="mailto:ljelsbak@ruc.dk">ljelsbak@ruc.dk</a> )
Teachers	
Study administration	INM Registration & Exams ( <a href="mailto:inm-exams@ruc.dk">inm-exams@ruc.dk</a> )
Exam code(s)	U60177

## ACADEMIC CONTENT

### Overall objective

This aim of this course is to teach students the pathway from gene sequence to a 3D protein structure along the exploration of primary, secondary, tertiary and quaternary structure of an unknown protein sequence. At each step of this pathway multiple choices e.g. for cloning (vectors/tags), purification (strategies) and structure analysis (three main methods) are explained and compared, some of which are also actively explored during lab days. Teaching aims on the thorough understanding of pros and cons of each method introduced to allow the students choosing the most appropriate method applied to solve a given experimental problem.

The course is a mixture of lectures, practical exercises, excursions and student presentations.

### Detailed description of content

### Course material and Reading list

Pensum in this course are lecture notes and articles provided during the course.

### Overall plan and expected work effort

- Lectures: 20 hours
- Preparation: 30 hours
- Experimental sessions: 25 hours
- Experimental evaluation and report writing: 40 hours
- Exam: 25 hours

**Total for this 5 ECTS course is 140 hours**

### Format

### Evaluation and feedback

The course includes formative evaluation based on dialogue between the students and the teacher(s).

Students are expected to provide constructive critique, feedback and viewpoints during the course if it is needed for the course to have better quality. Every other year at the end of the course, there will also be an evaluation through a questionnaire in SurveyXact. The Study Board will handle all evaluations along with any comments from the course responsible teacher.

Furthermore, students can, in accordance with RUCs 'feel free to state your views' strategy through their representatives at the study board, send evaluations, comments or insights from the course to the study board during or after the course.

### Programme

The course consists of a series of lectures and experimental sessions, and a mini-project about protein structure, stability and function. Some of the lectures will be "case stories" where you will get introduced to a specific research area in protein biochemistry by a leading expert.

In the experimental sessions, you will be introduced to a method or technique in protein biochemistry and obtain experimental data that you need to analyze using theory from the lectures. For the experimental session, you will need to hand in a report based on the experiment.

At the end of the course, you will do a mini-project in groups where you will apply the knowledge that you have learned. Each group will present its mini-project at the end of the course.

## ASSESSMENT

Overall learning outcomes

After completing the course, the student is able to:

- select and use bioinformatic tools to explore the primary and secondary structure of proteins
- analyze structural bioinformatics and modelling of unknown proteins
- demonstrate techniques in protein cloning and purification
- analyze the experimental secondary structure investigation of proteins
- evaluate 3D structure determination based on X-ray crystallography NMR and Electron microscopy
- design experiments for preparation of protein crystals for crystallographic studies
- analyse complex data structures with relevant mathematical and statistical models/programs.

Form of examination

The course is passed through active and satisfactory participation.

Active participation is defined as:

The student must participate in course related activities (e.g. workshops, seminars, field excursions, process study groups, working conferences, supervision groups, feedback sessions).

Satisfactory participation is defined as:

- e.g. oral presentations (individually or in a group), peer reviews, mini projects, test, planning of a course session .

Assessment: Pass/Fail.

Form of Re-examination

Samme som ordinær eksamen / same form as ordinary exam

Type of examination in special cases

Examination and assessment criteria

The course is passed through active and satisfactory participation.

Active participation is defined as:

The student must participate in course related activities, lectures, Experimental sessions and report writing

Satisfactory participation is defined as:

- Groups of students will write reports based on experiments carried out during the course and a miniproject, which will be evaluated in an oral exam like setup, where the students will present their project.

Here the student should be able to

- Identify a protein from its primary sequence
- Find physiochemical information about the protein based on its primary sequence

- Suggest a strategy for expression and purification of the protein
- Solve the protein structure (in silico)
- Discuss potential methods and techniques to elucidate a hypothesis chosen by the students.

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