



Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

SLUkurs

Syllabus

PNSo158 Protein crystallisation and X-ray data collection, 3.0 credits

Syllabus approved

2017-11-21

Subjects

Biology/Chemistry

Education cycle

Third cycle

Grading scale

Pass / Failed

The requirements for attaining different grades are described in the course assessment criteria which are contained in a supplement to the course syllabus. Current information on assessment criteria shall be made available at the start of the course.

Language

English

Prior knowledge

The course is primarily intended for PhD students at SLU, but will be open for other researchers at SLU, and PhD students from other universities as space allows. It is expected that the student has basic knowledge about protein composition and structure. Prior experience of protein crystallisation and X-ray crystallography is not required.

Objective, including learning outcomes

The course aims to provide comprehensive introduction and hands-on training of protein crystallisation, X-ray data collection and data processing.

At the end of the course the student will be able to

- Propose suitable strategies, e.g. recombinant expression system, and methods for preparation of proteins for crystallisation experiments and subsequent structure studies.
- Set up protein crystallisation screening experiments, evaluate the results, and perform optimization of crystallisation conditions.
- Manipulate protein crystals (e.g. ligand soaking), handle and prepare for transportation and X-ray data collection (e.g. cryo-protection, capture crystals in loops, flash cool, put in transportation dewar).
- Use a synchrotron beam line for testing crystal diffraction and collecting X-ray diffraction datasets, including selection of suitable parameters and data collection strategies.
- Perform diffraction data processing (e.g. indexing, integration, scaling, post-refinement), extract statistics, and analyze and evaluate the quality of the diffraction data.
- Use diffraction data to solve structures by molecular replacement and calculate electron density maps (other phasing techniques will be mentioned, but not covered in depth).
- Document and describe methods and results of protein preparation, crystallisation and x-ray diffraction for scientific articles on protein structure studies.

Content

The course will consist of three elements:

- 1) Literature study corresponding to one full day of studies.
- 2) One scheduled course week at SLU, Uppsala, focusing on protein preparation and crystallisation, where lecture(s) are followed by hands-on laboratory exercises. Students are encouraged to bring own proteins to work on during practicals.
- 3) One scheduled course week at MAX IV, Lund, including hands-on X-ray data collection at a synchrotron beamline, practical data processing, structure solution, evaluation of diffraction data and electron density. Lectures will cover mostly practical, and briefly theoretical aspects of X-ray crystallography.

Requirements for examination

Active participation in the scheduled activities during both course weeks, satisfactory performance at laboratory exercises and computer practicals, and approved final examination.

Additional information

The course is organized in collaboration with MAX IV.

The number of students will be limited to 15. PhD students at SLU will have precedence.

Responsible department

Department of Molecular Sciences