

Biostructural Technologies

Programme course

6 credits

Biomolekylär strukturanalys

TFKE35

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

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

Organic chemistry 2 or similar. Biochemistry 1 or similar.

Intended learning outcomes

The course aims at providing the basic theoretical framework for NMR spectroscopy and x-ray crystallography, which is the foundation for structural analysis of proteins and other biomolecules in organic chemistry and structural biology. After completed course, the student should be able to:

- Master and explain important concepts, methods and theories in the determination of molecular structure and dynamics.
- Illustrate and shed light on theoretical concepts with examples from biomolecular analysis.
- Interpret, assess and evaluate experimental results.
- Propose and motivate an optimal strategy for solving a given problem within structural biology or bioorganic chemistry.

Course content

The NMR part of this course comprises: The NMR phenomenon, resonance, chemical shift, spin-spin couplings (weak and strong), dipolar couplings, nuclear spin relaxation, especially the nuclear Overhauser effect. Dynamic NMR, chemical exchange. Two dimensional NMR spectroscopy, COSY, TOCSY, NOESY. Heteronuclear experiments, HSQC. Analysis of onedimensional and multidimensional spectra. Procedures for structural and dynamical characterization of proteins.

The crystallography part of this course comprises: protein crystallization, including concepts such as unit cell, asymmetrical unit, space group, Miller index, Bragg's law and Evald sphere. Furthermore, the entire process of solving a protein structure starting from a protein crystal will be treated, including concepts such as resolution, electron density maps, R-factor, B-factor, heavy metal derivatization and molecular replacement.

Teaching and working methods

Lectures, seminars, demonstrations.

Examination

KTR1	Written test	1.5 credits	U, 3, 4, 5
TEN1	Written examination	4.5 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

Patrik Lundström

Education components

Preliminary scheduled hours: 36 h

Recommended self-study hours: 124 h

Course literature

Additional literature

Books

Gale Rodes, (2000) *Crystallography made Crystal Clear* 2nd edition

P. Lundström, (2012) *NMR Spectroscopy – Principles and Applications to Proteins*.

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.