

Faculty of Science

KEMM25, Chemistry: Structural Biochemistry, 15 credits

Kemi: Strukturbiokemi, 15 högskolepoäng Second Cycle / Avancerad nivå

Details of approval

The syllabus was approved by Study programmes board, Faculty of Science on 2018-12-19 to be valid from 2018-12-19, autumn semester 2019.

General Information

The course is an elective second-cycle component of a Master of Science (120 credits) degree in Chemistry and Molecular Biology, and compulsory for a degree of Master (120 credits) of Science in Protein Science.

Language of instruction: English

Main field of studies Depth of study relative to the degree

requirements

Molecular Biology A1N, Second cycle, has only first-cycle

course/s as entry requirements

Chemistry A1N, Second cycle, has only first-cycle

course/s as entry requirements

Protein Science A1N, Second cycle, has only first-cycle

course/s as entry requirements

Learning outcomes

The aim of the course is to enable students to acquire a specialised understanding of proteins, focusing on structure and the connection to biological function. The course deals with both the principles determining these properties and the methods, mainly X-ray crystallography, that is used to study them in modern molecular protein science.

Knowledge and understanding

On completion of the course, the students shall be able to

- account for the three-dimensional structure, stability, interaction and dynamics of proteins
- account for the relations between structures of enzymes and enzyme complexes and their modes of functioning
- describe the principles behind three important methods in structural biochemistry: X-ray crystallography, Small Angle X-Ray Scattering and neutron crystallography
- account for how the information about the three-dimensional structure of proteins can be used in drug design

Competence and skills

On completion of the course, the students shall be able to

- use electronic databases and computer-based tools for the analysis of protein sequences and structures
- perform advanced homology modelling of proteins and discuss potential modifications of the structure and function of a protein
- perform simple protein crystallisation experiments

Judgement and approach

On completion of the course, the students shall be able to

- interpret and critically assess protein structures deposited in public databases with regard to resolution, quality and information content
- interpret and critically assess the research literature on protein structure and function

Course content

Lectures (7.5 credits): Polypeptide conformations. The secondary and three-dimensional structure of proteins, structural classes and structure databases. Prediction and modelling of protein structure. The stability and dynamics of of proteins, interaction in proteins: packing and electrostatics. Ligand bonding and structure-based design of drugs. Principles of X-ray crystallography and other methods such as Small Angle X-Ray Scattering, neutron scattering, NMR etc

Bioinformatics (4 credits): Exercises in relevant computer-based methods to study protein structures and dynamics. Searching in sequence and structure databases, and advanced homology modelling of proteins.

Laboratory and computer exercises in structural biochemistry (3.5 credits): The exercises cover all stages of a typical structure determination using X-ray crystallography: crystallisation, data collection, computing, structure determination, model construction, refinement and validation. A few exercises are carried out as demonstrations.

Course design

The teaching consists of lectures, computer exercises and laboratory sessions. Compulsory participation is required in computer exercises, laboratory sessions and associated elements.

Assessment

The assessment is based on a written exam at the end of the course, a computerbased mid-course exam in bioinformatics and compulsory components throughout the course.

Students who fail an assessment will be offered another opportunity for assessment soon thereafter.

The examiner, in consultation with Disability Support Services, may deviate from the regular form of examination in order to provide a permanently disabled student with a form of examination equivalent to that of a student without a disability.

Subcourses that are part of this course can be found in an appendix at the end of this document.

Grades

Marking scale: Fail, Pass, Pass with distinction.

For a grade of Pass on the whole course, the student must have passed the final exam, the mid-course exam in bioinformatics, the lab reports and the compulsory components.

The grades awarded for the exam are Fail, Pass and Pass with Distinction. The grades awarded for the mid-course exam in bioinformatics are Fail and Pass. The grades awarded for the compulsory components in structural biochemistry are Fail and Pass.

The final grade is determined by the aggregated result of the computer-based midcourse exam and the final written exam.

Entry requirements

To be admitted to the course, students must meet the general entry requirements for higher education and requirements for English proficiency corresponding to English 6 from Swedish upper secondary school, and have passed 90 credits in science courses including courses equivalent to:

- KEMA20 General Chemistry 15 credits, or KEMA10 General Chemistry 7.5 credits and KEMA12 Inorganic Chemistry- Basic Course 7.5 credits, KEMA01 Organic Chemistry- Basic Course 7.5 credits and KEMA03 Biochemistry- Basic Course 7.5 credits, and
- MOBA02 Chemistry of the Cell 15 credits

Students who have obtained the equivalent knowledge by other means may also be admitted to the course.

Further information

The course may not be included with the full number of credits in a degree together with KEMM15 Structural Bioinformatics 15 credits.

Subcourses in KEMM25, Chemistry: Structural Biochemistry

Applies from H19

1901 Structural Biochemistry, 7,5 hp Grading scale: Fail, Pass, Pass with distinction

1902 Bioinformatics, 4,0 hp Grading scale: Fail, Pass

1903 Structural Biochemistry, Compulsory Elements, 3,5 hp

Grading scale: Fail, Pass