

Structural Bioinformatics and Protein Modelling

3 + 1 (optional) days hands-on course, 3 ECTS Credits

OVERVIEW

The combination of the information from a protein structure with the tools of structural bioinformatics provides much deeper understanding and new valuable insights in biochemical and molecular biology research, both in academia and industry. By using the tools of structural bioinformatics we may answer questions like: How can I use structural information to increase the stability of my protein at higher temperatures or different pH? How to use structural information in drug discovery? How can I make an amino acid sequence alignment and relate it to the 3D structure? What is the best way to plan an amino acid replacement in the protein of interest?

Advances in high-throughput techniques in structural biology have resulted in thousands of three-dimensional structures of proteins and their complexes with various ligands, including substrate analogues and inhibitors. All this information will be available for you, when you master the principles of structural bioinformatics, and it will help you to dramatically increase the throughput of your own research.

AIM

The course aims at providing the participants with basic understanding of modern structural bioinformatics and homology-based protein modelling. After finishing the course the participants will be able to:

- Use Internet-based structural bioinformatics tools to analyse three-dimensional structures of a proteins and a protein-ligand complexes and perform homology-based modelling.
- Understand the general principles behind protein crystallisation and X-ray crystallography, assess the requirements and take active part in the planning and the subsequent development of this type of projects.

The course will also serve as a meeting point and will provide networking opportunities with people from Sweden, Denmark and Europe.

COURSE OUTLINE

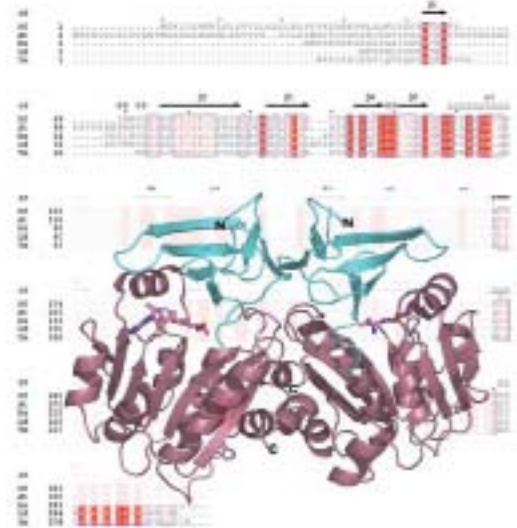
- An overview of the crystallography techniques used in structure determination of proteins and protein-ligand complexes.
- An overview of the general principles of protein

structure, function and dynamics, forces that stabilise proteins and control protein-protein and protein-ligand interactions.

- An overview of the basic requirements for three-dimensional structure prediction and homology-based modelling.

Computer tutorials during the course will include:

- Hands-on training in the use of industry-standard structure visualisation and homology modelling programs.



COURSE PROGRAM

Day 1

Morning: Overview of X-ray crystallography and protein crystallisation. Basics of protein structure, classification of structures.

Afternoon: Structural databases (PDB, PDBSUM, CATH, SCOP, DALI); Graphics tools for analysis of structures: JalView, SwissPDB Viewer. Structure-based sequence alignment; Symmetry and the biological unit in PDB. How to view electron density; criteria for structure quality.

19.00 Course dinner

Day 2

Morning: Secondary structure prediction; homology modelling; quality of a homology model.

Afternoon: Simple modelling; effect of mistakes in sequence alignment; model optimisation and quality check.

“excellent to outstanding” in the recent international evaluation of research at Lund University, RQ -08.

Day 3

Morning: Advanced modeling: difficult cases. Overview of homology modelling with Schrödinger software.

Afternoon: Modelling and model analysis using Schrödinger software.

Day 4 (Optional)

For those who are interested there is a possibility to add an extra day.

Morning: General discussion. Overview of software alternatives, future trends in homology modelling. Visit to MAX-lab and lunch.

Afternoon: Private discussion of own projects with course tutors.



Professor Salam Al-Karadaghi

LECTURERS

Professor Salam Al-Karadaghi is responsible for organizing the course. He is also one of the lecturers. Professor Al-Karadaghi has published more than 60 scientific papers in the field of protein structure and function and has contributed to 41 entries in the Protein Data Bank, PDB. Outside the university Al-Karadaghi has been involved in structure-guided design projects with several companies such as Active Biotech, Biovitrum and Leo Pharma.

Dr. Björn Walse is a founder and CEO of SARomics AB offering R&D support to pharmaceutical and biotechnology industries within the areas of structural biology and in silico drug discovery. Previously Björn was responsible for managing structural chemistry activities in drug discovery projects in the therapeutic areas of cancer, autoimmunity and inflammatory diseases at Active Biotech in Lund.

BIOCHEMISTRY AND STRUCTURAL BIOLOGY AT LUND UNIVERSITY

The Department of Biochemistry and Structural Biology represents one of the strong and expansive research fields at Lund University. The Department's focus is within the areas of three-dimensional structure, function and dynamics of key enzymes and macromolecular assemblies. It uses world-class experimental facilities and its research has been classified as

WHAT IS STRUCTURAL BIOINFORMATICS?

Learn more about the fascinating world of structural bioinformatics and how it can facilitate your research on <http://www.proteinstructures.com/>, a site that is managed by professor Al-Karadaghi.

WHO SHOULD ATTEND?

Scientists from industry and academia and persons responsible for R & D or persons just looking for new ideas for product development will benefit from the course.

There are no formal requirements on academic qualifications, however in order to be able to absorb as much as possible from the course content it is advisable that the participants have a background in chemistry/biochemistry/molecular biology or are involved in R & D work within the area. Participants with other backgrounds can expect to get a broad overview of principles and tools in proteins structure, modelling and design, which can inspire to new understanding and insights.

SCHEDULE AND FEE

September 20–22, 2010

The course will take place at the Chemistry Centre, Lund University. Course fee is 12.400 SEK, VAT exclusive. Those who are interested can add Day 4 (23/09). The fee for Day 4 is 4.100 SEK, VAT exclusive. The course fee comprises diploma, course literature, coffee, lunch and course dinner.

Each day will include morning (9-12) and afternoon (13.15-17) sessions. Lunch will be at 12, coffee will be served at 10 and 15. Morning sessions will be mostly lectures, while afternoon sessions will be focused on computer tutorials.

Registration deadline: August 16, 2010. The registration is binding. Substitution of participants is allowed at any time and without charges, but it is advisable that such should take place at the start of the course.

For information about the course and application please contact Mirka Fahlander at Lund University Commissioned Education (Ph. +46-46-222 0777 or mirka.fahlander@education.lu.se).

For more information about the course and structure-related research please contact professor Salam Al-Karadaghi at the Department of Biochemistry and Structural Biology, Lund University (Ph. +46-46-222 4512 or salam.al-karadaghi@mbfys.lu.se).

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COURSE ORGANISER

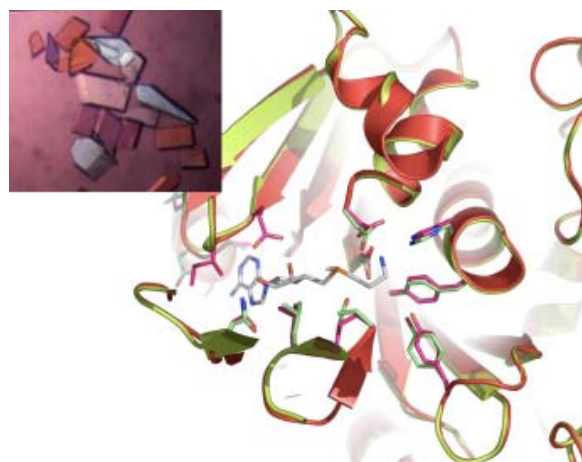
Professor Al-Karadaghi has been involved in several projects of biomedical interest. His academic projects include studies of the molecular mechanisms of iron homeostasis in mitochondria, chlorophyll synthesis, as well as structure and function of enzymes from *Plasmodium falciparum*, the causative agent of malaria. Through his activities in SARomics Biostructures AB, a company in which he is one of the co-founder, Professor Al-Karadaghi has been involved in structure-guided design projects with Biovitrum AB, Active Biotech AB, Leo Pharma A/S, and some other companies.

Professor Al-Karadaghi has extensive teaching experience. He is responsible for and teaches at the course Structural Bioinformatics at Lund University. The course is focused on structural bioinformatics, protein modelling and structural aspects of drug design.

BIOCHEMISTRY AND STRUCTURAL BIOLOGY AND THE CENTRE FOR MOLECULAR PROTEIN SCIENCE AT LUND UNIVERSITY:

OUTSTANDING RESEARCH AND WORLD-CLASS FACILITIES
The Departments of Biochemistry and Structural Biology and Biophysical Chemistry, has in 2005 established the Centre for Molecular Protein Science (CMPS). CMPS brings together protein scientists involved in fundamental research on proteins, with a strong focus on molecular structure, function and dynamics.

Modern structural biology relies on advanced instrumentation and CMPS is uniquely equipped in this regard. The conditions for X-ray crystallography, the main technique for protein structure



determination, are ideal, with convenient access to MAX-lab, the Swedish National Laboratory for Synchrotron Radiation Research. MAX-lab has several beamlines dedicated to structural studies of proteins. A modern crystallisation laboratory equipped with nano-drop robotics for screening and optimisation of protein crystallisation conditions is also placed at MAX-lab. CMPS scientist also operate three nuclear magnetic resonance (NMR) laboratories with eight state-of-the-art NMR-instruments. These large-scale facilities put CMPS scientists at the very fore-front of research in structural biology.