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Ministry of Human Resource Development Government of India

Latest Methods in X-ray Crystallography : Lecture Series and Practical Course at JNU

Overview

X-ray crystallography is today the most suitable and most powerful technique to analyse the structure-functionrelationship of biological macromolecules, as proteins and nucleic acids. Only the three-dimensional structure at high resolution is providing the information required to understand the function of biomolecules. Overall in several fields of biological research and biotechnology this information is required, for example in structure based drug discovery, for site directed mutagenesis to optimize enzymes for distinct applications in biotechnology, to analyse receptor–ligand interactions ect. . Today approx. 110.000 structures are deposited in the protein data bank and particular the new and upcoming synchrotron- and free-electron-laser radiation sources will open new routes in structural biology in the near future.

In terms of the course it is indented to convey participating students and scientits the theoretical background of X-ray crystallography in terms of series of lectures to understand also latest procedures applied in X-ray crystallography. The lectures will be accombined by tutorials and a pratical course, hands on, to mediate the potential of the methods and to gain experience in applying them. A particular focus will be directed towards teaching methods and technques about the new radiation sources and latest methods for diffraction data collection, as serial crystallography and time resolved measurements.

Topics of Lectures

- 1. Introduction to protein structure analysis
- 2. The protein data bank and how to use it
- 3. Crystallization, precipitants and phase diagram, crystal morphology, crystal symmetry and space groups, crystallogenesis
- 4. X-rays, X-ray sources, conventional X-ray souces, synchrotron radiation and free-electron-laser radiation sources
- 5. X-ray diffraction, Bragg's law, reciprocal lattice and Ewald-sphere construction
- 6. Diffraction data collection, single crystal approach and serial crystallography
- 6. X-ray diffraction by electrons, fourier analysis and synthesis
- 7. Protein structure determination by X-ray diffraction
- 8. The crystallographic phase problem
- 9. Patterson map, molecular replacement (MR)
- 10. Multiple isomorphous replacement (MIR)





- 11. Multi-wavelength anomalous diffraction (MAD)
- 12. Calculation of electron densities
- 13. Interpreation of electron densities
- 14. Refinement of protein structures, R-factors
- 15. Crystallography and the drug discovery processstudying protein-ligand interactions

Module	Latest Methods in X-ray Crystallography : Lecture Series and Practical Course at JNU
You Should Attend If	For students and scientits interesting in the theoretical background and latest development of X-ray crystallography. Introduction to new radiation sources and latest methods for diffraction data collection, such as serial crystallography and time resolved measurements.
Fees	The participation fee for taking the course is as follows: Participants from abroad : US \$ 500 Industry/ Research Organizations: INR 10,000/- Faculty from Indian Academic Institutions: INR 2000/- Ph.D. Students: INR 1000/- M.Sc. Students of JNU other recognized Universities: Free The above fee includes all instructional materials, computer use for tutorials and assignments, laboratory equipment usage charges, free internet facility during lecture and practical session. The participants will be provided accommodation on payment basis if available in the university hostels.

Teaching Faculty



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