Semester: 8	
Course: Major V	
Paper Title: Structural Biology + Protein folding and Structure	
Paper code: C4BT230852T/C4BT230852P	**Credits: 4 (3+1)**
Hours/week: 3 + 3	
Category: Core/MDC/SEC/VAC: Core	
Theory / Practical / Composite: Composite	
No of Modules: Theory – 1	

Course Overview:

This course provides a comprehensive understanding of the principles and emerging applications of x-ray crystallography, SAXS, negative stain and cryo-electron microscopy to determine the three-dimensional structure of biological macromolecules and their complexes experimentally. Students will learn how to corroborate structural observations with functional observations through their studies and presentations of cutting-edge research papers in the section of structure-function paradigm.

In practical module, students will learn the protein crystallization techniques. They will measure ΔG to understand the stability of a protein and learn to determine chaperone activity. They will also be exposed to the software required for structure determination techniques.

COURSE OUTCOME:

THEORY

CO1. Understand the importance of determine biological macro molecular structures experimentally.

CO2. Learning of the crystallization principles and techniques.

CO3. Analyze and integrate the x-ray diffraction pattern through different software with structures of protein assemblies, protein-DNA, protein-RNA complexes.

CO4. Describe the techniques of SAXS to figure out functionally relevant domain motions of proteins.

CO5. Describe the principles and techniques of Cryo-EM to determine the structure of molecular assemblies.

CO6. Analyze the structure function relationship through studies of cutting-edge research papers from high impact publications.

PRACTICAL

1. Explain the principles regarding spectrofluorimetric methods for protein stability.
2. Perform quantitative estimation of protein aggregation to determine chaperone activity using spectrophotometer.
3. Perform protein crystallization using vapour diffusion techniques.

Syllabus

Unit/Module	CONTENT	Hours / Number of Classes	Co Mapping	Cognitive Level
	UNIT I Protein crystallography: Principle of crystallizations and crystal growth, X-ray scattering by atoms and UNIT cells of crystals, Review of Fourier transforms, Bragg's Law, point groups, Bravais lattices, indexing of lattice planes, space groups,	3 classes/week	**CO 1 to CO2**	**K1 to K6**

	Phasing- Isomorphous replacement, Molecular replacement, Difference electron density maps-2Fo-Fc, Fo-Fc, omit maps, Refinement, model accuracy.			
	Unit II **Small and Wide-Angle X-ray Scattering SAXS & WAXS**: Brief overview on principles and applications.		**CO 3**	**K1 to K6**
	Unit III **Cryo-electron microscopy of biological macromolecules and complexes:** Introduction to electron microscopy and structural biology, the electron microscope and image formation process, negative staining and cryo-electron microscopy, sample preparation, image reconstructions and available software.		**CO 4**	**K1 to K6**
	Unit IV **Structure – function Paradigm:** Recent developments		**CO 1 to CO6**	**K1 to K6**
Practical [40 marks]	1. Hands on experiments on crystallization, freezing and mounting. 2. Software handling for data collections and refinements. 3. Calculation of ΔG of a protein by fluorimetric measurement. 4. Chaperone activity of a protein by aggregation assay.			
Text books:	1. Crystallography made crystal clear by Gale Rhodes: Chapter 1-7 2. Atomic and Nuclear Physics by SN Ghoshal: Chapter- X-rays 3. Crystallization of Nucleic Acids and Proteins: A Practical Approach by Arnaud Ducruix and Richard Giegé: Chapters: Crystallization of protein.			
Web Resources:	Relevant Research Papers			
Evaluation:	**Theory** CIA- 10; Assignment – 02; Attendance – 03; Semester Exam- 45; **Practical:** CA (38 marks)**;** Attendance (2 marks)			
Question Paper Structure: Compulsory objective questions of 5 marks with choice; And 4 questions of 10 marks (Any 4 from 6).				

COURSE OUTCOMES (COS) AND COGNITIVE LEVEL MAPPING

Course Outcome	Cognitive Level (KO)
CO1 Remember the concepts of experimental structure determination of biomacromolecules, and crystallization of biomacromolecules	**K1 – K3**
CO2 Interpret diffraction data using different software	**K1 – K3**

CO3 Evaluate applications of SAXS	**K4 – K6**
CO4 Evaluate applications of Cryo-electron microscopy.	**K1 – K3**
CO5 Perform crystallization and stability assays.	**K1 – K4**
CO6 Analyze applications through the study of research papers.	**K4 – K6**