

Online Workshop on Homology Modeling and Protein Structure Analysis: From Sequence to Structure

Empowering Bioinformaticians to Build Tomorrow's Structural Insights

08-10 June 2026, 6:30 PM IST

Course Overview

This intensive 3-day workshop provides participants with a practical understanding of protein structure prediction and bioinformatics-based modeling. Through guided tutorials and exercises, learners will explore the full pipeline—from sequence analysis and template selection to 3D model building, validation, and structural interpretation.

Key Features

- Expert-led training sessions
- Access to cloud-based modeling tools
- Certificate of Participation upon completion
- Post-workshop resources and learning materials
- Ideal for students, researchers, and professionals in life sciences, biotechnology, or bioinformatics

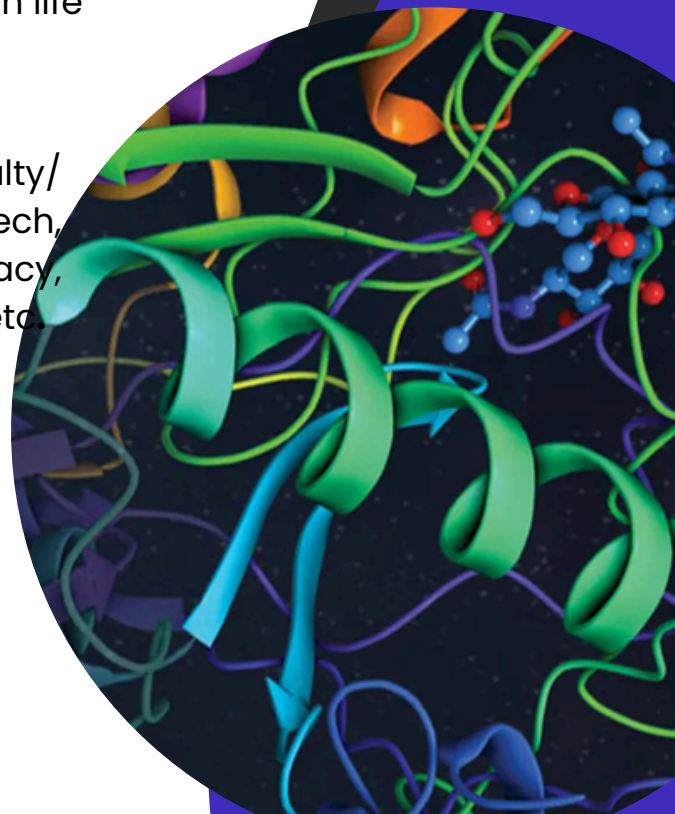
Who can Join?

Graduate / Postgraduate / Research scholars/ Faculty/ Industrialist in the field of Life Sciences (ZBC, Biotech, BioChem, MicroBio etc.), MBBS/MD/MS, Pharmacy, Chemical Sciences, Medicine, Medical Professionals etc.

Fee & Features

₹799 (India) | \$55 US (International)

- E-Certificate to Participants
- Online by Google Meet Platform
- Hands-on Live Sessions
- Interaction with Resource Person
- Lecture PPTs and Recordings to Participants



Course Module

Module 1: Foundations of Protein Structure and Homology Modeling

- Overview of protein structures (primary → quaternary levels).
- Concept & applications of homology modeling.
- Steps in homology modeling (alignment → model building → refinement).
- Template selection: sequence identity and structure quality.
- Key databases & tools: **PDB, UniProt, BLAST.**

Module 2: Building and Validating a Homology Model

- Hands-on practice using **SWISS-MODEL** and **Phyre2.**
- Model validation with **Ramachandran Plot** and **ProSA.**
- Troubleshooting and optimization tips.

Module 3: Structural Analysis and Applications

- Identifying **active sites and functional domains.**
- **Binding pocket** and **ligand site** detection.
- Visualization and comparative structural analysis using **PyMOL, CastP, IntePRO, JPred,** and **PSIPRED.**



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