Structural Bioinformatics of Membrane Proteins & Ions — Hands-on

Learn practical structural bioinformatics workflows for membrane proteins and ion binding systems. From topology annotation and embedding in lipid bilayers to analysis of channels, transporters and ion coordination sites, you will work with experimental and predicted structures to assess stability, dynamics and druggability in realistic membrane environments.

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Session Index

Session 1

Fee: Rs 12320 Apply Now

Classes, Topology & Databases

Membrane protein classes and architecture

channels, transporters and receptors | **alpha helical vs beta barrel** | **single pass vs multi pass proteins**

Topology prediction and annotation concepts

transmembrane segment prediction ideas | **inside outside orientation thinking** | **signal peptides and**

targeting motifs

Structural resources for membrane proteins and ions

specialised membrane protein databases | channels and transporter repositories | annotated ion binding site resources

Session 2

Fee: Rs 16520 Apply Now

Modeling, Embedding & Lipid Environment

From sequence to membrane protein models

using homology and AI predictions | validating TM segment placement | handling loops and disordered termini

Embedding proteins into bilayer models

membrane plane orientation concepts | bilayer building tools and workflows | coarse views of lipid composition

Lipid environment, interfaces and hot spots

protein lipid interaction regions | annular vs non annular lipids ideas | cholesterol and cofactor interaction concepts

Session 3

Fee: Rs 20720 Apply Now

Channels, Transporters & Ion Coordination

Pores, pathways and gating views

identifying channels and cavities | constriction sites and bottlenecks | open, closed and intermediate conformations

Ion binding sites and coordination geometry

common ion binding motifs **coordination numbers and distances** **filters and selectivity determinants concepts**

Transport cycles and conformational changes (concepts)

rocker switch and alternating access ideas **capturing conformational ensembles overview** **relating structure snapshots to function**

Session 4

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Dynamics, Stability, Druggability & Reporting

Membrane protein dynamics and stability views

flexible loops and gating elements **tilt, rotation and packing changes** **links to MD level analysis concepts**

Druggability, ligandability and docking in membranes

binding site identification on membrane proteins **allosteric pockets and lipid exposed grooves** **constraints and caveats for docking setups**

Figures, tables and project ready documentation

topology and membrane embedding schematics **pore profiles and ion site panels** **checklists for membrane protein studies**