

Protein Structure Databases & Visualization Tools — Hands-on

Learn to find, evaluate, and visualize macromolecular structures with modern databases and viewers. Build clean, reproducible figure pipelines and validation reports ready for manuscripts.

Protein Structure Databases & Visualization Tools

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Session 1

Fee: Rs 6300 [Apply Now](#)

Structure Databases & Formats

Core resources, accessioning, and identifier mappings

[RCSB PDB](#) [PDBe](#) [AlphaFold DB](#) [EMDB](#) [UniProt](#)

File formats, annotations, and crosswalks

[PDB/mmCIF](#) [PDBx](#) [SIFTS](#) [FASTA](#)

Download automation & metadata filtering

[APIs](#) [CLI](#) [programmatic queries](#)

Session 2

Fee: Rs 8400 Apply Now

Viewers & Publication-Quality Figures

Interactive exploration and scene management

PyMOL **UCSF ChimeraX** **VMD** **Mol*** **NGL**

Representations, coloring, and annotations

cartoons **surfaces** **ligand highlighting** **ray tracing**

Reproducible figure pipelines & exports

sessions/scripts **SVG/PNG** **panels**

Session 3

Fee: Rs 11200 Apply Now

Validation & Quality Assessment

Geometry checks and statistics for reliability

Ramachandran **rotamers** **clashscore** **B-factors**

Tools & map fit for X-ray/cryo-EM models

MolProbity **EMRinger** **Q-score**

Best practices: provenance and reproducibility

checklists **versioning**

Session 4

Fee: Rs 14000 Apply Now

Mini Capstone: Structure Report

Assemble a complete structure dossier for a target

Theory + Practical

Scenes, figure panels, and validation summary

PyMOL/ChimeraX scripts **Mol* snapshots** **report templates**

Deliverables: figures, tables, README & manifest

PDF **CSV/TSV** **checksums**