Sr. No	Lecture Title	Description	Category	Duration
	Segment 4: 3D Structure Visualization & Evaluation			
1	Chimera	• Introduction to UCSC Chimera and its uses. • Visualization and analysis of a protein 3D model using Chimera. • Comparing and analysis of more than one protein structure for research purposes.	3D Structure Visualization	25:23:00
2	PyMol	• Introduction to PyMol. • Defines parameters to visualize and analyze the protein 3D model. • Commands used in PyMol to visualize and manipulate protein 3D model.	3D Structure Visualization	40:48:00
3	WhatCheck	• Introduction to WhatCheck, a protein model evaluation tool. • Utilization of WhatCeck tool for protein model evaluation. • Analysis and implication of results for protein structure evaluation.	3D Structure Evaluation	8:40
4	ProCheck	• Introduction to ProCheck, a protein model evaluation tool. • Utilization of ProCheck to check quality of protein model based on certain parameters. • Interpretation of results to select the best model.	3D Structure Evaluation	12:36
5	ERRAT	• Introduction to ERRAT, a protein model evaluation tool. • Procedure to evaluate experimentally determined protein model. • Analysis and interpretation of results to evaluate the best model.	3D Structure Evaluation	6:44
6	Verify3D	• Introduction to Verify3D, a protein model evaluation tool. • Procedure to evaluate a protein model using the web server of Verify3D. • Interpretation and analysis of the results provided by Verify3D	3D Structure Evaluation	8:31

7	RAMPAGE	• Introduction to RAMPAGE, a protein model evaluation tool. • Procedure to evaluate protein model based on Ramachandran plotting by RAMPAGE. • Interpretation of Ramachandran plotting to select the best model.	3D Structure Evaluation	3:29
8	PROSA	• Introduction to ProSA server. • Procedure to evaluate protein model predicted using different methods. • Analysis of three different structures of the protein predicted from three different tools for their comparative analysis.	3D Structure Evaluation	10:05
9	SAVES	• Introduction to SAVES tool and its purpose. • Procedure to evaluate a predicted protein model using Saves server. • Analysis of Ramachandran plot generated by the SAVES server for the predicted query protein structure.	3D Structure Evaluation	5:31