Name:	
Enrolment No:	

UPES
End Semester Examination, December 2024

Course: Structural Biology   **Semester: VII**th
Program: INT-BMSc Microbiology   **Duration: 3 hours**
Course Code: HSMB8009   **Max. Marks : 100**

Instructions: Carefully read and attempt all the questions.

S. No.	Section A Short answer questions/ MCQ/T&F (20Qx1.5M= 30 Marks)	Marks	COs
Q1.	Identify the server used for determining the extinction coefficient of protein. 　　A.　ProtPapram　　　　　B.　Protscale 　　C.　Peptide cutter　　　　D.　Protein weight	1.5	CO1
Q2.	The CHARMM and AMBER force fields are primarily used for: 　　A.　Quantum mechanics calculations 　　B.　MD simulations of biological macromolecules 　　C.　Statistical analysis of molecular data 　　D.　Crystallographic structure determination	1.5	CO2
Q3.	Identify the most difficult region in the protein tertiary structure to model- 　　A.　Helices　　　　　　B.　sheets 　　C.　Side-chains　　　　D.　loops	1.5	CO1
Q4.	All proteins consist of secondary structures. **True or False**	1.5	CO2
Q5.	PLIP web tool can be used for the analyses of - 　　A.　Protein-protein　　　B.　Protein-DNA 　　C.　Protein-Ligand　　　　D.　Protein-RNA	1.5	CO1
Q6.	If the wavelength of the X-ray is greater than the interplanar spacing "d" then _____. 　　A.　Diffraction cannot occur. 　　B.　Diffraction occurs at higher angles. 　　C.　Diffraction occurs at lower angles. 　　D.　The crystal planes move apart.	1.5	CO1
Q7.	A diffraction peak in an XRD pattern represents _____. 　　A.　The number of atoms in the unit cell 　　B.　The interplanar spacing of the crystal lattice 　　C.　The temperature of the crystal sample 　　D.　The speed of the X-ray beam	1.5	CO1
Q8.	Databases such as CATH and SCOP are used to identify_____. 　　A.　The structural family to　　　B.　The generic family to 　　　　which a protein belongs.　　　　　which a protein belongs. 　　C.　homologous proteins　　　　D.　analogous proteins	1.5	CO1
Q9.	A strong negative peak at 222 nm in a CD spectrum indicates:	1.5	CO3

	A. A beta-sheet structure B. An alpha-helical structure C. A random coil structure D. Protein aggregation		
Q10.	In MD simulations, equilibration refers to: A. The process of setting up the initial coordinates of molecules B. The period during which the system is allowed to reach a steady state C. The production phase of the simulation D. The calculation of the potential energy	1.5	CO2
Q11.	Using shorter wavelength light for diffraction results in – A. Increased Resolution B. No-change in Resolution C. blurred Image D. Decreased Resolution	1.5	CO2
Q12.	Identify the secondary protein structure database? A. PDB B. Pubchem C. Chembank D. SCOP	1.5	CO1
Q13.	Proteins with similar structures but different function may result from A. Codominant evolution B. Dominant evolution C. Divergent evolution D. Convergent evolution	1.5	CO2
Q14.	In Bragg's Law, θ is: A. The angle of reflection B. The angle of incidence between the X-ray and the crystal plane C. The angle between two diffracted beams D. The refractive index	1.5	CO2
Q15.	Protons diffract more than the electrons. **True or False**	1.5	CO2
Q16.	Chemical shift in an NMR spectrum represents _____. A. The interaction of nuclei with unpaired electrons B. The shielding or deshielding of nuclei by surrounding electrons C. The motion of nuclei in a magnetic field D. The nuclear spin relaxation process	1.5	CO1
Q17.	A strong negative peak at 222 nm in a CD spectrum indicates: A. A beta-sheet structure B. An alpha-helical structure C. A random coil structure D. Protein aggregation	1.5	CO2
Q18.	Primary sequence of the protein can be determined by? A. MALDI-TOF MS B. Nextgen sequencing C. Sanger Sequencing D. All the above	1.5	CO1
Q19.	Identify the computational method to predict the three-dimensional structure of the protein. A. X-ray crystallography B. NMR C. Cryo-EM D. Threading	1.5	CO1
Q20.	_____ proteins are soluble in water.	1.5	CO1
	Section B		

		(4Qx5M=20 Marks)		
Q1.		Examine the role of protein-protein interactions in cellular processing with suitable example.	5	CO3
Q2.		Compare the differences between energy minimization and equilibration in MD simulations.	5	CO4
Q3.		Compare difference between real space and reciprocal space? Write the vector equation to convert real space into reciprocal space.	5	CO4
Q4.		Describe Synchrotron? List its advantages?	5	CO2

Section C
(2Qx15M=30 Marks)

Q1.	Illustrate the process of homology modeling. (7) In what conditions should this method be used? (3) Elucidate the differences between the homology modeling and ab initio modeling? (5)	15	CO4
Q2.	Discuss the advantages of 3D NMR over 2D NMR? (10) Explain with an example. (5)	15	CO2

Section D
(2Qx10M=20 Marks)

Q1.	Explain Force Field? List the parameters included in formulating the Force Field. Give examples of two popular force fields.	10	CO3
Q2.	Classify and explain the types of protein-protein interactions. Propose an in-vitro method to identify protein-protein interactions.	10	CO3