UPES
End Semester Examination, December 2024

Course: Structural Biology   Semester: Vth
Program: B.Tech. Biotechnology   Duration: 3 hours
Course Code: HSBT3006   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.	Template based protein modeling techniques is called as _____.
	    A. X-ray crystallography B. NMR
	    C. Cryo-EM D. Homology modeling
		1.5	CO1

Q2.	Primary sequence of the protein can be determined by?
	    A. Tandem MS/MS B. Nextgen sequencing
	    C. Sanger Sequencing D. All the above
		1.5	CO2

Q3.	Identify the server used for determining the molecular weight of protein.
	    A. ProtPapram B. Protscale
	    C. Peptide cutter D. Protein weight
		1.5	CO1

Q4.	Identify the servers used for predicting the secondary structure of the protein.
	    A. J-Pred B. Sci-Pred
	    C. Protein-Pred D. I-Pred
		1.5	CO1

Q5.	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

Q6.	Identify the key limitation of MD simulations.
	    A. They cannot simulate molecular motions
	    B. They are only applicable to gaseous systems
	    C. They are limited by computational resources and timescales
	    D. They do not require force fields
		1.5	CO1

Q7.	Fibrous proteins are soluble in water. **True or False**	1.5	CO1

Q8.	Identify the web tool used for the analyses of Protein-ligand interactions.
	    A. CLIP B. ProtParam
	    C. PLIP D. ProtScale
		1.5	CO1

Q9.	Identify the correct statements regarding Bragg's Law.
	    A. It is only valid for amorphous solids.
	    B. It can be used to determine the structure of crystalline solids.
	    C. It explains the scattering of light by particles in a liquid.
		1.5	CO1

	D. It is derived from the principles of quantum mechanics.		
Q10.	The characteristic X-rays used in XRD are typically generated by: A. Bremsstrahlung radiation B. Radioactive decay C. Electron transitions in heavy atoms (e.g., Cu or Mo targets) D. Gamma-ray sources	**1.5**	**CO1**
Q11.	PyMOL is written in which programming language? A. Python B. Java C. C++ D. MATLAB	**1.5**	**CO1**
Q12.	The CD can be used for determining – A. Secondary Structures B. Gibbs Free energy C. Enthalpy D. All of the above	**1.5**	**CO3**
Q13.	Phylogenetic trees generated from MSA data are useful because they: A. Show the exact mutation rates for each residue B. Illustrate evolutionary relationships among sequences C. Improve alignment accuracy D. Increase computational speed	**1.5**	**CO2**
Q14.	Using longer wavelength light for diffraction results in – A. Increased Resolution B. No-change in Resolution C. Sharper Image D. Decreased Resolution	**1.5**	**CO3**
Q15.	_____ is a protein structure database. A. PDB B. Pubchem C. Chembank D. SCOP	**1.5**	**CO1**
Q16.	Proteins with different structures but same function may result from A. Codominant evolution B. Dominant evolution C. Divergent evolution D. Convergent evolution	**1.5**	**CO4**
Q17.	Identify the role of the magnetic field in NMR. A. To align the nuclei in specific energy states B. To excite the nuclei to higher energy levels C. To increase the temperature of the sample D. To create a diffraction pattern	**1.5**	**CO1**
Q18.	Identify the main challenge in Cryo-EM sample preparation. A. Maintaining vacuum during imaging B. Preventing sample crystallization during freezing C. Increasing the conductivity of the sample D. Adding heavy metal stains for contrast	**1.5**	**CO1**
Q19.	Electrons diffract more than the protons. **True or False**	**1.5**	**CO2**
Q20.	CD is often combined with thermal denaturation studies to: A. Measure protein melting temperature (T_m) B. Study protein aggregation kinetics C. Determine protein solubility D. Analyze protein degradation pathways	**1.5**	**CO2**

	Section B (4Qx5M=20 Marks)		
Q1.	Classify the proteins based on their functions.	**5**	**CO4**
Q2.	List the role of protein-protein interactions in the cell.	**5**	**CO1**
Q3.	Discuss the help of a flowchart, explain the basics of Molecular Dynamics (MD) simulations	**5**	**CO3**
Q4.	Discuss the method used for representing the orientation of atomic planes in a crystal? Write the steps involved to represent the orientation of atomic planes.	**5**	**CO2**
	Section C (2Qx15M=30 Marks)		
Q1.	Describe force fields used for MD simulation. (7) List the parameters included in its formulation. (6) Give two popular examples. (2)	**15**	**CO3**
Q2.	Discuss and draw the workflow for determining a three-dimensional structure using Cryo-EM.	**15**	**CO4**
	Section D (2Qx10M=20 Marks)		
Q1.	Describe the steps involved in determining the Miller indices of a crystal. Draw the Miller indices for 210 and 101.	**10**	**CO3**
Q2.	Discuss the components of PDB file format? List the components responsible for its visualization and labeling. Describe "HETATM" in PDB file.	**10**	**CO4**