N	am	^	
Τ.	am	C	•

Enrolment No:



UPES

End Semester Examination, May 2025

Course: Structural Biology and Biophysical Chemistry Program: INT-BMSC-MICROBIOLOGY

Course Code: HSMB3012O

Semester: VIth **Duration: 3 hours** Max. Marks: 100

Instructions: Carefully read and attempt all the questions.

S. No.	Section A	Marks	COs
	Short answer questions/ MCQ/T&F (20Qx1.5M= 30 Marks)		
Q1.	At the folding transition midpoint (Tm), what is the Gibbs free energy	1.5	CO1
	difference (ΔG) between folded and unfolded states?		
	A. Positive B. Negative		
	C. Zero D. Undefined		
Q2.	Charged amino acids are most commonly found:	1.5	CO1
	A. Inside the hydrophobic core B. On the surface of proteins		
	C. In disulfide bridges D. At the N-terminal only		
Q3.	Protein folding is thermodynamically favorable because:	1.5	CO2
	A. Enthalpy decreases and entropy increases		
	B. Enthalpy increases and entropy decreases		
	C. Enthalpy decreases and entropy of the solvent increases		
	D. Both enthalpy and entropy increase		
Q4.	Recall the reason for glycine occupying a wider region in a	1.5	CO
	Ramachandran plot compared to other amino acids.		
	A. Its side chain restricts rotation		
	B. It lacks a side chain beyond a hydrogen atom		
	C. It forms extra hydrogen bonds		
	D. It is always charged		
Q5.	Which of the following is not an advantage of CD spectroscopy?	1.5	CO2
	A. Requires small amounts of protein		
	B. Non-destructive and fast		
	C. Suitable for detecting protein folding		
	D. Provides atomic-resolution structure		
Q6.	NMR spectroscopy primarily detects nuclei that have:	1.5	CO2
	A. High molecular mass		
	B. A magnetic moment and non-zero spin		
	C. UV absorbance		
	D. Free electrons		
Q7.	The phase problem in X-ray crystallography refers to the:	1.5	CO2
	A. Difficulty in obtaining high-resolution crystals		
	B. Loss of amplitude during detection		

	C. Inability to directly measure phase information from diffraction data		
	D. Decay of crystals under X-rays		
Q8.	Describe the primary reason for using cryo-cooling (e.g., liquid	1.5	CO2
C - ·	nitrogen) during X-ray data collection.		
	A. Increase signal intensity		
	B. Prevent water evaporation		
	C. Reduce radiation damage to the crystal		
	D. Enhance diffraction resolution		
Q9.	In an XFEL experiment, why are extremely short X-ray pulses	1.5	CO1
	important?		
	A. They improve sample cooling		
	B. They outrun radiation damage before it destroys the sample		
	C. They decrease signal intensity		
	D. They increase crystal size		
Q10.	XFEL sources are particularly powerful for studying:	1.5	CO
	A. Very large crystals only		
	B. Single molecules and nanocrystals		
	C. Only metal complexes		
	D. Only surface topographies		
Q11.	Identify the detector revolutionized Cryo-EM by increasing resolution	1.5	CO
	and sensitivity.		
	A. Photographic film B. CCD camera		
	C. Direct Electron Detector (DED) D. CMOS sensor		
Q12.	Efficient FRET requires that:	1.5	CO
	A. Donor emission spectrum overlaps acceptor absorption spectrum		
	B. Donor absorption spectrum overlaps acceptor absorption spectrum		
	C. Acceptor emits at a longer wavelength than the donor absorbs		
	D. Donor and acceptor are separated by > 100 nm		
Q13.	Fluorescence emission typically occurs at a longer wavelength than	1.5	CO2
	absorption because of:		
	A. Excited state instability		
	B. Vibrational relaxation before photon emission		
	C. Higher energy of emitted photons		
	D. Stronger absorption		
Q14.	In a Jablonski diagram, fluorescence occurs when an excited electron	1.5	CO
	returns from:		
	A. Ground state to excited state		
	B. Excited singlet state to ground singlet state		
	C. Triplet state to ground state D. Excited state to a vibrational state		
Q15.	During an EPR experiment, if no signal is detected, a logical	1.5	CO2
~	explanation could be:	1.0	
	A. The sample contains no unpaired electrons		
	B. The magnetic field is too high		
	z. me magnetic note to then	1	

MD simulation, you see that water molecules near the protein ce are highly ordered. What does this most likely indicate? atter evaporation rmation of clathrate structures rmation of a hydration shell stability in the simulation D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for protein interactions. B. Internal loops	1.5 1.5 or 1.5	CO
ce are highly ordered. What does this most likely indicate? atter evaporation rmation of clathrate structures rmation of a hydration shell stability in the simulation D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.	1.5	СО
rmation of clathrate structures rmation of a hydration shell stability in the simulation D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.		
rmation of clathrate structures rmation of a hydration shell stability in the simulation D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.		
rmation of a hydration shell stability in the simulation D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system amic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for protein interactions.		
D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.		
D simulations, periodic boundary conditions are mainly used to: mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.		
mit simulation time crease the size of the system imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for- protein interactions.		
crease the size of the system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for protein interactions.	or 1.5	СО
imic an infinite system and avoid edge effects crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for protein interactions.	or 1.5	СО
crease the number of atoms artificially ify the regions in the RNA secondary structure NOT preferred for -protein interactions.	or 1.5	CO
ify the regions in the RNA secondary structure NOT preferred for protein interactions.	or 1.5	CO
-protein interactions.	or 1.5	CO
-protein interactions.		
-		
D. Hiteriai 1000s		
lige loops D. Multibranch loops		
	1.5	CO
-		
* * *		
· · · · · · · · · · · · · · · · · · ·	1.5	CO
-		
ey are unstable and never found in functional KivAs		
i i f	Il the correct statement about the G-U wobble base pair in RNA. destabilizes the secondary structure completely is forbidden in stems and loops is less stable than Watson-Crick pairs but tolerated in RNA forms only in DNA tify the TRUE statements about RNA pseudoknots. ney are formed by simple hairpin loops ney involve base pairing between two completely adjacent regions ney result from base-pairing between a loop and a complementary ence outside the loop ney are unstable and never found in functional RNAs	destabilizes the secondary structure completely is forbidden in stems and loops is less stable than Watson-Crick pairs but tolerated in RNA forms only in DNA tify the TRUE statements about RNA pseudoknots. ney are formed by simple hairpin loops ney involve base pairing between two completely adjacent regions ney result from base-pairing between a loop and a complementary ence outside the loop

	Section C (2Qx15M=30 Marks)		
Q1.	Design an experiment to investigate protein-protein interactions within a cellular environment. Evaluate the chosen technique and analyze its limitations.	5 + 10	CO4
Q2.	Plan an experimental approach to examine the influence of different buffers on protein stability and explain the underlying principle with the aid of an illustrative diagram.	7 + 8	CO4
	Section D		
	(2Qx10M=20 Marks)		
Q1.	Differentiate between synchrotron radiation and XFEL and describe the concept of bunching as it applies to XFEL.	5 + 5	CO3
Q2.	Explain the concept of Larmor frequency. Describe the working principle of NMR spectroscopy and evaluate its advantages over X-ray crystallography for structural studies.	3 + 7	CO3