Name:

Enrolment No:

UPES

End Semester Examination, May 2025

Course: Analytical Techniques for Biosimilars **Semester: VIIIth**

Program: B.Tech - Biotechnology **Duration: 3 hours**

Course Code: HSBT4013 **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.	**NMR spectroscopy primarily detects nuclei that have:** A. High molecular mass B. A magnetic moment and non-zero spin C. UV absorbance D. Free electrons	1.5	CO1
Q2.	**List the critical quality attribute often monitored through peptide mapping in biologics.** A. pH of formulation buffer B. Thermal stability C. Oxidation, deamidation, and glycosylation sites D. Hydrophobicity index	1.5	CO2
Q3.	**The shape of a molecule can be inferred from:** A. Its extinction coefficient B. Its sedimentation coefficient and diffusion coefficient C. Its isoelectric point D. Its crystal lattice structure	1.5	CO1
Q4.	**Analytical ultracentrifugation (AUC) is primarily used to study:** A. Protein crystallization B. RNA sequencing C. Size, shape, and interactions of macromolecules in solution D. Enzyme-substrate kinetics	1.5	CO2
Q5.	**Define void volume in SEC.** A. The volume of the mobile phase only B. The total volume of the column C. The volume at which the smallest molecules elute D. The volume not accessible to any solute (elution of the largest molecules)	1.5	CO3
Q6.	**A common application of SEC in protein biophysics is to:** A. Determine enzyme activity B. Assess oligomeric state or aggregation C. Identify phosphorylation sites D. Map epitope binding	1.5	CO2
Q7.	**Identify the attributes typically measured in an ion mobility separation before MS analysis.** A. UV absorbance	1.5	CO1

	B. Arrival time distribution (ATD) C. Heat of desorption D. Isotopic ratio		
Q8.	**IM-MS is particularly useful in structural biology because it provides information about:** A. Protein solubility B. Collisional cross-section (CCS) and conformational heterogeneity C. Nucleotide sequences D. Protein melting temperature	**1.5**	**CO1**
Q9.	**……. labeling strategy is commonly used in antibody arrays for detection.** A. Bioluminescence B. Radiolabeling C. Fluorescent or chemiluminescent tags D. Gel electrophoresis	**1.5**	**CO3**
Q10.	**Identify the application that is not typical of antibody array mapping.** A. Cytokine profiling B. Kinase activity measurement C. Biomarker discovery D. Protein expression profiling	**1.5**	**CO2**
Q11.	**In HDX-MS, which type of protein region typically shows slower deuterium uptake?** A. Disordered loop regions B. Surface-exposed domains C. Hydrogen-bonded, structured regions (e.g., α-helices, β-sheets) D. Post-translationally modified residues	**1.5**	**CO2**
Q12.	**In HDX-MS, increased deuterium uptake typically indicates:** A. Highly structured regions B. Regions with slow exchange C. Flexible or solvent-exposed regions D. Protein denaturation artifacts	**1.5**	**CO1**
Q13.	**Differential Scanning Calorimetry (DSC) is primarily used to measure:** A. Molecular weight of proteins B. Optical activity of biomolecules C. Heat changes associated with thermal transitions D. Molecular vibrations	**1.5**	**CO2**
Q14.	**The area under the DSC thermogram peak corresponds to:** A. Molecular weight B. Heat capacity C. Enthalpy change (ΔH) D. Entropy change (ΔS)	**1.5**	**CO2**
Q15.	**Identify the region of the infrared spectrum is most useful for identifying functional groups.** A. Near-IR (14000–4000 cm^{-1}) B. Fingerprint region (4000–1500 cm^{-1}) C. Mid-IR (4000–400 cm^{-1}) D. Far-IR (400–10 cm^{-1})	**1.5**	**CO2**
Q16.	**…… structural change is typically observed in CD spectra upon protein denaturation.** A. Shift from α-helix to β-sheet signals B. Increase in near-UV signal	**1.5**	**CO1**

	C. Loss of characteristic secondary structure peaks D. Intensification of 222 nm peak		
Q17.	**Which of the following is not an advantage of CD spectroscopy?** A. Requires small amounts of protein B. Non-destructive and fast C. Suitable for detecting protein folding D. Provides atomic-resolution structure	**1.5**	**CO2**
Q18.	……. is the smallest repeating unit that, when replicated throughout space, forms the entire crystal lattice.	**1.5**	**CO1**
Q19.	**Describe the primary reason for using cryo-cooling (e.g., liquid 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	**1.5**	**CO2**
Q20.	**Primary sequence of the protein be determined by -** A. Tandem MS/MS B. MALDI-TOF MS C. Edman Degradation D. All the above	**1.5**	**CO1**
	Section B **(4Qx5M=20 Marks)**		
Q1.	Discuss miller indices. Draw miller indices for 110 and 101.	**5**	**CO3**
Q2.	Illustrate the workflow of hydrogen deuterium exchange technique.	**5**	**CO1**
Q3.	Describe pression motion in NMR and what is the effect of increasing the magnetic field on precession motion.	**5**	**CO2**
Q4.	Discuss and describe the role of HILIC in determining glycosylation's on antibody.	**5**	**CO4**
	Section C **(2Qx15M=30 Marks)**		
Q1.	Propose an experimental method based on mass spectrometry to compare the conformational states of the purified antibody. **(10 marks)** Explain the technique used with the help of a diagram. **(5 marks)**	**15**	**CO2**
Q2.	Draw a working model for X-ray diffraction. **(5 marks)** Discuss and draw the workflow for determining a three-dimensional structure using X-ray crystallography. **(10 marks)**	**15**	**CO4**
	Section D **(2Qx10M=20 Marks)**		
Q1.	Two purified antibodies were tested for thermal stability. Propose an experimental method for determining thermal stability along with its working principle.	**10**	**CO3**
Q2.	Describe MALDI-TOF. **(7 marks)** Outline the role of MALDI-TOF for finding the biosimilarity. **(3 marks)**	**10**	**CO4**