

**M.Sc. Bioinformatics - 2nd Semester**  
(2721)

**Paper: BI-525 Structural Biology & Bioinformatics**

**Time allowed: 2 hrs.**

**Max. Marks: 75**

**Note: There are EIGHT questions of equal marks. Candidates are required to attempt any FOUR questions.**

**Section A**

1. A) Explain the principle of CD spectroscopy. Discuss its application.  
B) What are post translational modifications? Explain application of mass spectroscopy in post translational modifications.
2. What is the principle of mass spectroscopy? Explain its application in peptide mapping.

**Section B**

3. What are triplex and G-quadruplex? Discuss a method for prediction of RNA structure.
4. Explain Levinthal paradox. Discuss classification of protein structure in SCOP.

**Section C**

5. What are secondary structures of protein? Discuss SOPM and CASP.
6. Explain Hidden Markov Model. Discuss its application in bioinformatics.

**Section D**

7. What is fold recognition method? Discuss its application in prediction of protein tertiary structure. Explain its merits and demerits.
8. Discuss algorithm of VAST and DALI.

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