2316 20

Class –M.Sc.-II (Sem)BIF

Subject – Structural Biology & Bioinformatics

Paper – BT-525

Time Allowed : 3 hrs. **Maximum Marks : 75**

SECTION- A

Attempt all questions. Each carries 1.5 marks.

1.5×10=15

1. Bragg's Law.
2. Chemical shift
3. CAFASP
4. Pymol
5. Threader
6. Sugar puckering
7. Graph theory
8. Z-DNA
9. SOPM
10. Dihedral angles

SECTION- B

Attempt any five questions. Each carries 12 marks.

12×5=60

1. Explain the principle of mass spectrometry. Discuss its applications.

Or

2. Explain the principle of X-ray Diffraction and NMR. Discuss their application in protein structure determination.

3 Discuss the methods used for RNA structure prediction.

Or

4. What do you understand by protein folds? Discuss the classification of protein structure in CATH.

5. What is GOR? Discuss different types of GOR and their features.

Or

6. What is neural network? Discuss the principle and algorithm of PHD for protein secondary structure prediction.

7. What is Homology modeling? Write the steps for template selection, Loop modelling and side chain Modelling. How is the accuracy of modelled structure measured?

Or

8. Discuss Threading and Fold Recognition methods for protein structue prediction.

9. Write short note on structure visualization tools and its significatnce. Explain Rasmol and SPDBV.

Or

10. (a) Write a note on Ramachandran plot.
    (b) Write a note on Motifs and Domains.

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