Exam. Code : 206602
Subject Code : 8480

M.Sc. (Bioinformatics) Semester—II
STRUCTURAL BIOLOGY AND BIOINFORMATICS
Paper—BI-525

Time Allowed—3 Hours]   [Maximum Marks—75

SECTION—A   10×1.5=15

1. Explain following in *two* or *three* sentences each :

    (a) Crystal lattice

    (b) Dihedral angle

    (c) PFAM

    (d) DALI

    (e) A-DNA

    (f) CAFASP

    (g) Machine learning tools

    (h) Fold recognition

    (i) Chimera

    (j) RMSD.

SECTION—B   12×5=60

2. What is chemical shift ? Explain the principle of NMR for protein structure determination.

OR

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3. What is circularly polarized light ? Explain principle of CD for protein structure prediction.

4. What do you understand by protein folding ? Describe how protein structures have been classified in CATH.

OR

5. Describe major structural features of B-DNA. Explain methods used for RNA structure prediction.

6. Explain transition probability in HMM. Describe an algorithm based on nearest neighbor method for prediction of protein secondary structure.

OR

7. Describe algorithm of JPRED. Compare it with PHD.

8. What is threading in fold recognition ? Discuss steps involved in homology modeling.

OR

9. How do you evaluate a predicted protein structure ? Discuss the importance of protein structure visualization tools.

10. Explain methods used for structure-structure alignment of protein. Explain VAST.

OR

11. Describe DALI for protein structure alignment.