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Reg. No. : ....

Name : ....

Second Semester M.Sc. Computational Biology Examination, June 2009
COB 523 : COMPUTATIONAL PROTEOMICS & METABOLOMICS

Time : 3 Hours   Max. Marks : 60

PART – A

Answer **all** questions, **each** carries **2** marks. Answer in **3-4** sentences only/or to point.

1. What is EIIP ?

2. Explain the term *propensity*.

3. Briefly explain X-ray crystallography.

4. Mention any two applications of molecular dynamics.

5. What is threading ?

6. What do you mean by metabolic profiling ?

7. What do you mean by the tertiary structure of protein ?

8. Explain the term *meander and cross over* in SCOP classification.

9. What do you mean by tertiary structure ?

10. List any four tools used for protein function prediction.   **(2×10=20 Marks)**

PART – B

Answer **any 8** questions. **Each** carries **5** marks.

11. Explain SCOP and CATH classification of protein.

12. What are the theories behind the purification and isolation of proteins ?

P.T.O.

13. Explain the term *molecular dynamics*.

14. Describe the features of GOR method for protein secondary structure prediction.

15. Explain the following terms

    a) Alpha helix

    b) Beta strand.

16. What are the key applications of metabolomics ? Discuss.

17. Predict which regions of the following peptide form alpha helices and beta sheets. Use Chau-Fasman algorithm.

    'FVNQHLCGSH'

18. Discuss homology modeling with reference to a popular tool.

19. Explain the following terms :

    a) Edmann degradation

    b) Metabolic profiling

    c) Metabolic fingerprinting

    d) Isoelectric focusing

    e) Western blotting.

20. Discuss in detail various facilities available in Protein Data Bank.   **(5×8=40 Marks)**

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