LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

B.Sc. DEGREE EXAMINATION – PLANT BIOLOGY & PLANT BIO-TECH.

FIFTH SEMESTER – NOVEMBER 2009

PB 5404 - BIO-INFORMATICS

Date & Time: 31/10/2009 / 9:00 - 12:00   Dept. No.   Max. : 100 Marks

PART A

I Choose the correct answer   **(5 x 1 = 5)**

1. _____ structure contains more than one polypeptide chain.
  a) Primary   b) Secondary   c) Tertiary   d) Quarternary

2. _____ is the software used for multiple sequences.
  a) GENSCAN   b) PUBMED   c) REPEAT MASKER   d) CLUSTALW

3. Splice sites are predicted using _____.
  a) netgene2   b) nebcutter2.0   c) signalp   d) pfam

4. DIP is a _____ database.
  a) protein sequence   b) protein structure   c) protein family   d) protein interaction

5. _____is a journal database.
  a) PUBMED   b) RASMOL   c) SOPMA   d) GENSCAN

II State whether the following statements are True or False: **(5 x 1 = 5)**

6. Secondary structure refers to the formation of a regular pattern of twists or links.
7. DOTPLOT is used for multiple sequence alignment.
8. GENSCAN is for restriction site identification.
9. MOLMOL is a tool used for structural visualization.
10. Homology modeling is used for primary structure prediction.

III Complete the following: **(5 x 1 = 5)**

11. _____ is a collection of information in the form of data, in a machine readable format.
12. _____ is a program that performs global multiple sequence alignment.
13. ORF stands for_____.
14. FSSP database stands for _____.
15. _____ is a collective term that refers to theoretical methods and computational techniques to model or mimic the behavior of molecules.

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IV Answer the following, each in about 50 words   (5 x 1 = 5)

16. Define nucleosome.
17. What is a Pairwise alignment?
18. What is meant by TypeII restriction endonuclease?
19. Define Ramachandran plot.
20. Define Swiss model server.

PART B

V Answer any FIVE of the following, each in about 350 words   (5 x 8 = 40)

21. What is a biological database? Write a note on NCBI.
22. Explain the translation of mRNA into protein.
23. Explain Needleman & Wunsch algorithm.
24. What is FASTA? Discuss the different types of FASTA programs.
25. Write a note on genomic databases.
26. Write a note on gene prediction.
27. Write a note on the software used to study the physical properties of proteins.
28. Discuss about the applications of Drug discovery.

PART C

VI Answer the following, each in about 1500 words   (2 x 20 = 40)

29. (a) Draw and explain the different levels of proteins
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OR

   (b) Discuss about restriction site identifications.

30. (a) Explain the secondary structure prediction of proteins.

OR

   (b) Explain in detail about any one online journal database.

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