LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

B.Sc. DEGREE EXAMINATION – MATHEMATICS & PHYSICS

THIRD SEMESTER – NOVEMBER 2009

PB 3208 / 3204 / 3202 - BIOINFORMATICS - I

Date & Time: 13/11/2009 / 9:00 - 12:00   Dept. No.   Max. : 100 Marks

PART A

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

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

2. The synthesis of mRNA from DNA is termed as _____.
   a) replication   b) transcription   c) translation   d) renaturation

3. _____ is a software used to view 3D structure.
   a) DDBJ   b) PDB   c) RASMOL   d) PIR

4. _____ is a nucleotide division of NCBI.
   a) Genbank   b) EMBL   c) SWISSPROT   d) SOPMA

5. _____ discovered a restriction enzyme from *Haemophilus influenzae*.
   a) Hamilton Smith   b) Michael Smith   c) Antoine Smith   d) Denver Smith

II State whether True or False. If false, give reasons   **(5 x 1 = 5)**

6. Vacuoles convert fatty acid into acetyl-coA.
7. DDBJ exchanges information with EMBL and Genbank.
8. Swiss Model Server is similar to homology modeling.
9. VMD is Visual Molecular Dynamic Programming.
10. Dotmatrix analysis is a method of Pairwise sequence alignment.

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

11. _____ is independent of a nucleus.
12. _____ is a protein sequence database.
13. MEME stands for_____ .
14. _____ cuts the DNA at a unique sequence.
15. _____ is designed to produce high quality graphics for print publication.

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

16. Define tRNA.
17. What is a sequence database?
18. What is meant by tFASTx?
19. Give a short description of GRAIL1.
20. Define Ramachandran plot.

PART B

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

21. Draw and explain the structure of an eukaryotic cell.
22. Explain the translation of mRNA into protein.
23. What is a biological database? Write a note on NCBI.
24. What is FASTA? Discuss the different types of FASTA programs.
25. Draw a repeat sequence for ABRACADABRACADABRA
                            ABRACADABRACADABRA
26. Give an account on gene prediction.
27. Write notes on the software used to study the physical properties of proteins.
28. Discuss about protein structure analysis.

PART C

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

29. (a) What are proteins? Discuss its classification, chemical composition and its
        different structural levels.

OR

   (b) Discuss about EMBL and DDBJ. Write a short note on Genbank.

30. (a) Define structural visualization. Write a note on the software's used to visualize.

OR

   (b) Explain the secondary structure prediction of proteins.

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