LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034
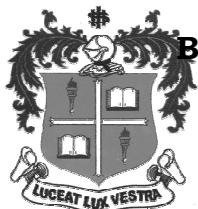
B.Sc. DEGREE EXAMINATION – **PLANT BIOLOGY & PLANT BIO-TECH.**

FIFTH SEMESTER – **APRIL 2013**

PB 5407 - BIOINFORMATICS

Date : 08/05/2013   Dept. No.   Max. : 100 Marks
Time : 1:00 - 4:00

Part –A   **(20 marks)**

Answer the following, each within 50 words.   **(10x2=20 marks)**

1. List any two advantages of World wide web.
2. Name two primary protein databases.
3. Differentiate local and global alignment.
4. Expand BLAST and FASTA.
5. What is six frame translation?
6. Provide the terms used to denote 5' and 3' splice sites.
7. Write any two post translational modifications of proteins.
8. What are the predominant secondary structures of proteins?
9. Mention any two applications of molecular modeling.
10. Define drug discovery.

Part B

Answer the following, each within <u>500 words.</u> Draw diagrams wherever necessary.

(5x7=35 marks)

11. a) What are secondary databases? Explain any two secondary databases.

        OR

   b) Write about primary, secondary and tertiary structure of protein.

12. a) Mention any three types of BLAST and add a note on database search using BLAST.

        OR

   b) Explain the steps involved in phylogenetic analysis.

13. a) Discuss the importance of restriction enzymes and the tool used for its prediction.

        OR

   b) Enumerate the applications of genome comparisons.
14. a) Compare pfam and PROSITE databases.

        OR
   b) Comment on protein visualization tools.

15. a) Summarize homology modeling of proteins.

OR

b) Give an account on any one biomedical journal database.

Part C

Answer any three of the following, each within <u>1200 words.</u> Draw diagrams wherever necessary.
(3x15=45 marks)

16. Write in detail about any three biological sequence databases.

17. Describe sequence alignment using Needleman-Wunch and Smith-Waterman algorithms.

18. Give a detailed account on repeat sequences, their identification and prediction.

19. Elaborate on the prediction servers for signal peptides, N-Glycosylation sites and O-Glycosylation

sites.

20. Evaluate drug discovery procedures and applications.

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