

**STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI –600 086**

**(For candidates admitted during the academic year 2009-10)**

**SUBJECT CODE: BY/PE/GP23**

**M. Sc. DEGREE EXAMINATION, APRIL 2010**

**BIOTECHNOLOGY  
SECOND SEMESTER**

**COURSE : ELECTIVE  
PAPER : GENOMICS AND PROTEOMICS  
TIME : 3 HOURS**

**MAX. MARKS: 100**

**SECTION – A**

**I CHOOSE THE CORRECT ANSWER: (1 x 5 = 5)**

1. The 3D coordinates of small molecules are deposited in  
a) PDB      b) HIC-UP      c) ZINC      d) CSD
2. FLY base is a  
a) Genome specific database   b) organism specific database   c) sequence specific database  
d) Structure database
3. The study of evolutionary relationship between organism is  
a) Homology   b) Phylogeny   c) Karyotyping   d) none of these
4. The type of alignment produced by BLAST program is  
a) global      b) global and local      c) local      d) none of these
5. Treatment of disease by use of genes or DNA sequence is  
a) gene therapy   b) rDNA therapy      c) vaccine therapy      d) DNA therapy

**II FILL IN THE BLANKS WITH THE APPROPRIATE ANSWER: (1 x 5 = 5)**

6. Highly conserved ungapped region in global multiple sequence alignment is \_\_\_\_\_.
7. \_\_\_\_\_ and \_\_\_\_\_ are the secondary structure database.
8. The ExPASy contains \_\_\_\_\_ tools.
9. \_\_\_\_\_ is a gene prediction tool.
10. \_\_\_\_\_ technique is used in Microarrays.

**III EXPAND THE FOLLOWING: (1 x 3 = 3)**

11. MALDI
12. KEGG
13. COGs

**IV STATE WHETHER TRUE OR FALSE: (1 x 5 = 5)**

14. Lower PAMs are used for the aligning distantly related sequences.
15. FASTA format for DNA/Protein sequence starts with lesser than symbol.
16. Transposons are moderately repeated sequence.
17. SDS is anionic detergent.
18. Curly brackets '{ }' used for non acceptable aminoacid in pattern regular expression.

**V. DEFINE IN ONE OR TWO SENTENCES (2 x 1 = 2)**

19. Junk DNA
20. DALI

**SECTION – B****ANSWER ANY FOUR QUESTIONS IN ABOUT 600 WORDS. (4 x 10 = 40)**

21. Explain in detail PDB.
22. Explain the algorithms used in BLAST and FASTA.
23. Write the applications of microarray in drug design.
24. What are the methods for protein secondary structure prediction?
25. Write the application of Bioinformatics in Human genome project.
26. What is whole genome shotgun sequencing?

**SECTION – C****ANSWER ANY TWO QUESTIONS IN ABOUT 1500 WORDS. (2 x 20 = 40)**

27. How the 3D structure of the protein is compared.
28. Discuss the genome organization of Eukaryotes.
29. Explain about substitution matrix.
30. Write notes on (i) Homology modeling  
(ii) Gap penalty.

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