LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

 **B.Sc.** DEGREE EXAMINATION – **MATHS & PHYSICS**

 THIRD SEMESTER – NOVEMBER 2010

 **PB 3208 / 3204 - BIOINFORMATICS - I**

 Date : 12-11-10 Dept. No. Max. : 100 Marks

 Time : 9:00 - 12:00

**PART- A (20 marks)**

**Answer All the questions:**

**I. Choose the correct answer: (5x1=5)**

1. Transcription process occurs in the

1. Cytoplasm b) Mitochonderia c) Nucleus d) Lysosomes

2. NCBI is

1. National centre for Bioinformatics Information
2. National centre for Biochemical Information
3. National centre for Biotechnology Information
4. National centre for Biological Information

3. are compared in pair wise alignment

a) More than 2 sequences b) Only 2 sequences

 c) Both of the above d) None of the above

4. Secondary structure prediction method is

1. Chou and Fasman b) GRAIL c) HMM d) FITG

5. RSCB is

1. Research collaboratory for structural Bioinformatics
2. Research structurally for collaboratory Bioinformatics
3. Research collaboratory for schematic Bioinformatics
4. Research conservative for structural Bioinformatics

**II. State whether the following statements are true or false: (5x1=5)**

1. Genes are located in Chromosomes.
2. EMBL is a Nucleotide sequence database.
3. PUBMED is a disease based database.
4. Rasmol is the best viewer for micromolecular structure.
5. The tool protparam is used for primary structure analysis.

**III. Complete the following: (5x1=5)**

11. Human somatic cells contain \_\_\_\_\_\_\_\_\_\_ pairs of chromosomes.

12. The human Genome project was completed in the year \_\_\_\_\_\_\_\_\_\_\_\_.

13. The alignment of two sequences is called \_\_\_\_\_\_\_\_\_\_\_ alignment

 14. GOR stands for \_\_\_\_\_\_\_\_\_\_.

 15. The physical properties of the protein are calculated using\_\_\_\_\_\_\_\_\_\_\_\_ tool.

**IV. Answer the following each within 50 words only: (5x1=5)**

 16. Define the central dogma of molecular Biology.

 17. What is DDBJ?

 18. What is paralogs?

 19. Give any two examples of Gene prediction methods.

 20. Define SOPMA.

**PART- B**

**Answer the following, each answer within 350 words only. Draw necessary diagrams.**

 **(5x7=35)**

 21. a) Explain the structure of DNA and its fuctions?

Or

 b) Explain the ultra structure of Nucleus.

 22. a) State the applications of Human Genome Project.

Or

 b) Explain any two protein sequence databases.

 23. a)How do you perform pair wise and multiple sequence alignment?

Or

 b) What is OMIM? Mention its Significance.

 24. a) Explain the algorithm of BLAST.

Or

 b) Examine any two secondary structure prediction tools.

 25. a) What is PDB? Mention its Significance?

Or

 b) Describe any one of molecular visualization tool.

 **PART – C**

**Answer any three of the following, each answer within 1200 words. Draw necessary diagrams. (3x15=45)**

 26. Elaborate the different levels of protein structures.

 27. Give an account on NCBI.

 28. Discuss the methods of Sequence alignments.

 29. How do you predict secondary structure of proteins?

 30. Discuss the softwares used in identifying the physical properties of protein sequences.

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