

B.Sc.-M.Sc. INTEGRATED PROGRAMME (BIOTECHNOLOGY)**SEMESTER V, ONLINE EXAMINATION 2021****PAPER CODE - BBT-CC14 TH****PAPER TITLE: GENOMICS AND PROTEOMICS***Time : Three Hours**Maximum Marks : 75*

Attempt all questions. All parts of a question must be attempted in continuation. Start answer of a fresh question on a new page. Cite examples and draw labelled diagrams wherever necessary

Question No. 1:**Q1 A: Answer/comment very briefly****[10 × 1=10]**

- i. How genomics and proteomics complement each other?
- ii. Arrange these forces in ascending order: Electrostatic forces, Van der Waals interactions, hydrogen bonds, disulfide bond.
- iii. List three differences in the sample buffer for SDS-PAGE and Native PAGE.
- iv. On what basis proteins are separated on 2D-PAGE.
- v. Mention full form of DDBJ, NCBI, EMBL and UCSC.
- vi. Draw the structure of any three hydrophobic amino acids.
- vii. What is proteome?
- viii. Mention different types of BLAST.
- ix. List three methods to determine the molecular mass of protein.
- x. List three gene/genome databases available on NCBI platform.

Q1 B Choose the correct answer from the given options:**[5 × 1=5]**

- i. The study of the full complement of proteins expressed by a genome is called:
 - a) Proteome
 - b) Proteomics
 - c) Genomics
 - d) Protein formation
- ii. Conserved gene order can be termed as _____
 - a) Ortholog
 - b) Synteny
 - c) Paralog
 - d) Microarray
- iii. Mitochondrial DNA is _____ in structure.
 - a) Circular
 - b) Linear
 - c) Ladder like
 - d) None of these
- iv. Tertiary structure includes on _____ bond.
 - a) Peptide
 - b) disulphide
 - c) Hydrogen
 - d) All of the above

- v. Which of the following is an example of Homology and similarity tool?
- a) BLAST
 - b) RasMol
 - c) EMBOSS
 - d) PROSPECT

Question No. 2:

Answer any TWO questions.

[2 x 7 ½ = 15]

- A.** Describe Maxam-Gilbert and Sanger methods of DNA sequencing in comparative manner.
- B.** What is genomics? Discuss different approaches of genome sequencing.
- C.** Discuss principle and technique of pyrosequencing.

Question No. 3:

Answer any TWO questions.

[2 x 7 ½ = 15]

- A.** Discuss a description on different types of Web based servers and softwares used for genome analysis.
- B.** Provide a detailed description of genbank, DDBJ and EMBL. What are the significance and implications of these database in functional and comparative genomics studies?
- C.** Discuss the components and utility of UCSC Genome Browser. Provide a brief discussion on tools on UCSC Genome Browser.

Question No. 4:

Answer any TWO questions.

[2 x 7 ½ = 15]

- A.** Discuss different levels of protein structure organization.
- B.** Discuss chemistry of hydrogen bonds in details. Highlights the role of hydrogen bonds in protein folding and stability.
- C.** Discuss the principle and application of gel filtration chromatography.

Question No. 5:

Answer any TWO questions.

[2 x 7 ½ = 15]

- A.** Discuss the principle of 2D gel electrophoresis. Highlights its application.
- B.** What is Proteomics? Discuss the significance of studying proteomics. Give an account of the steps in proteome analysis.
- C.** Discuss the principle and techniques of Mass spectroscopy used for protein sequencing and molecular mass determination.

It should be noted that 1 hour extra time will be provided to scan your answer sheets, build a PDF and upload it on E-mail: biotechnologyexam2020@gmail.com