

3. Write short notes on **any three** of the following :
(3×5=15)

- (a) Genomics ethics
- (b) Environmental metagenomics
- (c) Post-translational modifications
- (d) Scope of bioinformatics

4. Differentiate between (**any three**) : (3×5=15)

- (a) Metagenomics and Epigenomics
- (b) Nucleotide database and Protein database
- (c) ChIP seq and Bisulphite sequencing
- (d) Genomics and Proteomics

5. (a) Describe the workflow of proteome analysis using 2-D gel electrophoresis. (8)

(b) What is NCBI BLAST? Describe its different types. (7)

6. (a) Discuss the role of epigenetics in stress adaptation in plants. (8)

(b) Discuss the objectives and applications of Human Microbiome Project. (7)

(1000)

[This question paper contains 4 printed pages.]

Your Roll No.....

Sr. No. of Question Paper : 5763

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Unique Paper Code : 2162014701

Name of the Paper : Genomics, Proteomics and Bioinformatics

Name of the Course : **Botany**

Semester : VII

Duration : 2 Hours

Maximum Marks : 60

Instructions for Candidates

1. Write your Roll No. on the top immediately on receipt of this question paper.
2. Question No. 1 is compulsory.
3. Attempt any **four** questions in all.
4. All parts of a question should be answered together.
5. Draw diagrams wherever required.

P.T.O.

1. (a) State whether the following statements are true or false (**any five**) : (1×5=5)

- (i) The term “epigenome” refers to the total set of genes in an organism.
- (ii) Cas9 endonuclease introduces double-stranded breaks in target DNA.
- (iii) X-ray crystallography is used to study the tertiary structure of DNA.
- (iv) PubMed database provides information on metabolic pathways.
- (v) DNA methylation is a reversible epigenetic modification.
- (vi) Entrez is a search system for accessing multiple biological databases.

- (b) Expand the following (**any five**) : (1×5=5)

- (i) sgRNA
- (ii) NCBI
- (iii) MALDI-ToF
- (iv) nLC-MS/MS
- (v) KEGG
- (vi) PDB

- (c) Fill in the blanks (**any five**) : (1×5=5)

- (i) A is any maximal consecutive run of spaces in a single sequence in a given alignment.
- (ii) is the study of the individuality of cells using omics approaches.
- (iii) CRISPR-Cas9 is derived from the natural immune system of
- (iv) The nucleotide sequence database maintained by NCBI is known as
- (v) In Edman sequencing, amino acids are removed sequentially from the terminus.
- (vi) is used to determine the 3D structure of proteins using diffraction patterns.

2. (a) Explain the complexity of the eukaryotic genome. Discuss the role of genomics in health. (8)

- (b) Define molecular phylogeny. With the help of a labelled diagram, explain the different parts of a phylogenetic tree. (7)