[this question paper contain ..... printed pages]

Your roll No.....

Serial No.	:	7910
Unique Paper Code	:	2163010022
Name of the Paper	:	PLANT GENOMICS, PROTEOMICS AND BIOINFORMATICS
Name of the Course	:	Botany
Semester	:	VIII

Duration: 2 Hours Maximum Marks: 60

Instructions for Candidates

a) Write your Roll No. on the top immediately on receipt of this question paper.

b) Question No.1 is compulsory.

c) Attempt any four questions in all.

d) All parts of the question must be answered together.

e) Draw diagrams wherever required.

1. (a) State whether the following statements are true or false (any five): 1x5=5

i. Metagenomics studies cultured microorganisms only.
ii. Histone acetylation generally represses gene expression.
iii. Non-coding DNA has no biological function.
iv. KEGG is a protein structure database.
v. 2-D gel electrophoresis separates proteins by charge and size.
vi. UniProt is a database for protein sequence and functional information.

(b) Expand the following (any five): 1x5=5

i. HMP
ii. FASTA
iii. SNP
iv. PDB
v. TAIR
vi. BLAST

P.T.O.

(c) Fill in the blanks (Attempt any five): (1 × 5 = 5 marks)

I. The technique used to identify DNA–protein interactions is _____.
II. The study of genetic material recovered directly from environmental samples is known as _____.
III. In two-dimensional gel electrophoresis (2-DE), isoelectric focusing separates proteins based on their _____.
IV. The _____ database contains three-dimensional structural data of biomolecules.
V. Cross-database querying in NCBI is enabled by _____.
VI. Highly repetitive DNA sequences present in the genome are referred to as _____ DNA.

2. Write short notes (any three): 3x5=15

i. Explain the principles and applications of genome editing.
ii. Define the concept of metagenomics with diagram.
iii. Describe the principles and steps involved in protein-microarray analysis.
iv. Explain the concept of post-translational modifications with suitable examples.

3. Differentiate between (any three): 3x5=15

i. Coding DNA and non-coding DNA.
ii. Two-dimensional (2D) gel electrophoresis and SDS-PAGE.
iii. Primary and secondary biological databases
iv. Structural genomics and functional genomics.

4. **(a)** Describe the technique of nano liquid chromatography–tandem mass spectrometry (nLC–MS/MS) and critically evaluate its applications in modern proteomics. (8 marks)

(b) Explain the principle and applications of MALDI-TOF mass spectrometry. (7 marks)

5. **(a)** The NCBI is a widely used bioinformatics resource. Discuss the major tools and databases hosted by NCBI. (8 marks)

(b) Define sequence alignment. Explain the concepts of local, global, and multiple sequence alignment with the help of suitable diagrams. (7 marks)