

B.Sc. DEGREE EXAMINATION, APRIL 2023
BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY
FOURTH SEMESTER

COURSE : ELECTIVE
PAPER : INTRODUCTION TO BIOINFORMATICS
TIME : 3 HOURS

MAX. MARKS: 100

SECTION – A

A. ANSWER THE FOLLOWING

18 Marks

I. Choose the correct answer

(5 x 1 = 5)

- 1) Which of the following is a protein sequence database ?
 - a) DDBJ
 - b) EMBL
 - c) PIR
 - d) GenBank
- 2) Which of the following is a sequence alignment tool ?
 - a) BLAST
 - b) PRINT
 - c) PIR
 - d) PROSITE
- 3) The term bioinformatics was coined by ?
 - a) J D Watson
 - b) Margaret Dayoff
 - c) Frederic Sanger
 - d) Pauline Hogeweg
- 4) Which if the following is a nucleotide sequence database ?
 - a) EMBL
 - b) SWISS PROT
 - c) PROSITE
 - d) TREMBL
- 5) The computational methodology that finds the best match between a receptor and a ligand are called ____
 - a) Molecular fitting
 - b) Molecular docking
 - c) Molecular affinity
 - d) Molecular matching

II. Fill in the blanks

(5 x 1 = 5)

6. RE base cutter is a tool used to locate sites of _____.
7. Swiss-Prot is a _____ sequence database.
8. GOR method is used to predict _____ structures in proteins.
9. Bioinformatics can be used to improve crops by creating _____ crops.
10. Virtual high-throughput screening allows one to identify _____ from a large collection of compound libraries.

III. State True or False

(4 x 1 = 4)

11. Genomics is the science which deals with mapping, sequencing and analysing of the gene.
12. Gene annotation is used to predict the function of a gene.
13. Proteomics is the study of protein expression, regulation and modification.
14. Sequin is a sequence submission tool.

IV. Match the following**(4 x 1 = 4)**

- | | |
|-------------------------|--------|
| 15. Primary database | BLOCKS |
| 16. Secondary database | SCOP |
| 17. Structural database | EMBL |
| 18. Composite database | OMIM |

V. ANSWER ANY SIX OF THE FOLLOWING QUESTIONS IN 50 WORDS EACH:**(6 x 3 = 18)**

19. Open reading frame
20. Accession number
21. Gap penalty
22. PubChem
23. DOTPLOT
24. Scoring matrix
25. Homology modelling
26. Systems biology
27. Pharmacophore

SECTION - B**ANSWER ANY FOUR OF THE FOLLOWING QUESTIONS IN ABOUT 200 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.****(4 x 6 = 24)**

28. Identify the three main branches in bioinformatics.
29. List the major secondary databases.
30. What is FASTA ?
31. Differentiate between global and local alignment.
32. Explain the Chou-Fasman method for protein secondary structure prediction.
33. Describe the term ADMET in the context of drug discovery process.

SECTION - C**ANSWER ANY TWO OF THE FOLLOWING QUESTIONS IN ABOUT 1000 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.****(2 x 20 = 40)**

34. Elaborate upon the important *in silico* tools and databases in NCBI.
35. Write an essay on multiple sequence alignment using CLUSTALW.
36. If the sequence of a protein named haemoglobin is given to you. How will you retrieve its nucleic acid sequence, amino acid sequence, find its 3D model and its important characteristics?
37. Write an essay on the role of structural bioinformatics in drug discovery.
