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(FOR THE CANDIDATES ADMITTED

DURING THE ACADEMIC YEAR 2023 ONLY)

23UBY4N22

REG.NO. :

N.G.M.COLLEGE (AUTONOMOUS) : POLLACHI
END-OF-SEMESTER EXAMINATIONS : MAY-2025
B.Sc.-BOTANY **MAXIMUM MARKS: 50**
SEMESTER: IV **TIME : 2 HOURS**

PART - IV

BIOINFORMATICS

SECTION – A (10 X 1 = 10 MARKS)

ANSWER THE FOLLOWING QUESTIONS. (K1)

1. Adenine and guanine are ___________.
   a) pyrimidines b) purines c) aminoacids d) sugars
2. Protein coding sequences of a DNA are called -----------------------
   a) proteome b) genome c) exons d) introns
3. Multiple sequence alignment tool is ---------------------
   a) CLUSTAL X b) BLAST c) RASMOL d) GENMARK
4. RASMOL predicts the----------------- of protein.
   a) molecular weight b) atomic number c) tertiary structure d) All the above
5. Biomolecues are __________ compounds.
   a) inorganic b) organic c) aromatic d) aliphatic

ANSWER THE FOLLOWING IN ONE (OR) TWO SENTENCES. (K2)

6. What is DNA?
7. What are specialized databases?
8. Expand BLAST.
9. Define proteomics.
10. What is homology?

SECTION – B (5 X 8 = 40 MARKS)

ANSWER EITHER (a) OR (b) IN EACH OF THE FOLLOWING QUESTIONS.

11. a) Comment on the types of biomolecules.

(OR)

b) Describe the structure of DNA.

12. a) Brief the IT tools used in bioinformatics.

(OR)

b) Discuss the role of NCBI in Bioinformatics.

13. a) Explain the method of similarity searching.

(OR)

b) Write a short note on multiple sequence alignment.

14. a) Explain the methods of protein prediction.

(OR)

b) Discuss the biomolecular visualization tool which you have learnt.

15. a) Detail the steps involved in the construction of a phylogenetic tree.

(OR)

b) Bring out the databases and applications of phyogenetic analysis.

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