(FOR THE CANDIDATES ADMITTED DURING THE ACADEMIC YEAR 2021 ONLY)

21UBY509

REG.NO. :

N.G.M.COLLEGE (AUTONOMOUS) : POLLACHI
END-OF-SEMESTER EXAMINATIONS : NOVEMBER-2023
COURSE NAME: B.Sc.-BOTANY **MAXIMUM MARKS: 70**
SEMESTER: V **TIME : 3 HOURS**

PART - III

BIOINFORMATICS

SECTION - A (10 X 1 = 10 MARKS)

ANSWER THE FOLLOWING QUESTIONS.
MULTIPLE CHOICE QUESTIONS. (K1)

1. Which of the following is not an output device?
   a) printer b) joystick c) projector d) speaker

2. Choose the correct keyword in C _____.
   a) word b) go to c) breaker d) for

3. PIR stands for_____.
   a) Protein Information Resource b) Protein Information Repository
   c) Protein Identification Resource d) Protein Information Record

4. BLASTN is used for
   a) protein query sequence b) nucleotide query sequence
   c) rna query sequence d) translated sequence

5. Which of the following compound has desirable properties to become a drug?
   a) fit drug b) fit compound c) lead d) target

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

6. Name any two input devices.
7. Define: program.
8. Expand: FTP.
9. Define: Phylogeny.
10. Expand: CAD.

SECTION – B (5 X 4 = 20 MARKS)

ANSWER EITHER (a) OR (b) IN EACH OF THE FOLLOWING QUESTIONS.
(K3)

11. a) Enlist the components of a computer.

(OR)

b) Comment on high level languages.

(CONTD……2)

12.a) Interpret the tags used in HTML

(OR)

b) Indicate the features of C program.

13.a) Recall about LAN and WAN.

(OR)

b) Outline the bibliographic resources available for biology.

14.a) Explain the methods involved in sequence alignment.

(OR)

b) Write about ENTREZ.

15.a) Prioritize the Ab initio model of protein prediction .

(OR)

b) Discuss about lead compound .

SECTION - C (4 X 10 = 40 MARKS)

ANSWER ANY FOUR OUT OF SIX QUESTIONS
(16th QUESTION IS COMPULSORY AND ANSWER ANY THREE QUESTIONS
(FROM Qn. No : 17 to 21) (K4 (Or) K5)

16. Explain the features of operating system.

17. Elaborate the types of storage devices .

18. Enumerate the structure of C program.

19. Discuss about biological databases.

20. Write the methods involved in pairwise alignment.

21. How to use RASMOL to visualize protein structure?

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