K16U 2118

Reg. No. : .....

Name : .....

III Semester B.Sc. Degree (CBCSS – Reg./Supple./Imp.) Examination, November 2016
(2014 Admn. Onwards)
GENERAL COURSE IN MICROBIOLOGY
3A12 MCB : Biophysics and Bioinformatics

Time : 3 Hours

Max. Marks : 40

SECTION – A

Answer **all** the questions.

1. The number of base pairs per turn in Z-form of DNA is _____
2. The characteristic bond in nucleic acid is _____
3. The Medical literature available in Entrez is _____
4. _____ is a bioinformatics tool for multiple sequence alignment. **(4×1=4)**

SECTION – B

Write notes on **any seven** questions out of ten.

5. What are primary databases ? Give one example.
6. What is entropy ? What happens to entropy when proteins denature ?
7. What are the differences between ribonucleotides and deoxyribonucleotides ?
8. Name any two phylogenetic tree construction programs.
9. What is FASTA ? What is its application ?
10. Compare EMBL and TrEMBL.
11. Why is Entrez useful in bioinformatics studies ?
12. What are hydrogen bonds ? Where do you find this ?
13. What is molecular docking ?
14. Compare global and local sequence alignments. **(7×2=14)**

P.T.O.

SECTION – C

Briefly explain **any four** questions out of six.

15. Write a short note on standard free energy change in biochemical reactions.

16. What are nucleotides ? How are they formed ? How many types of nucleotides are found in the cell ?

17. Write a brief account on drug designing.

18. What are the applications of multiple sequence alignment ?

19. Describe a few databanks specific to the databases of organisms.

20. Write a short account on channels and metabolic pumps in the cell membranes.

(4×3=12)

SECTION – D

Answer **any two** questions out of four.

21. Describe the tertiary structure of proteins.

22. Explain the methodology in BLAST.

23. Write a detailed account on the applications of Bioinformatics.

24. Describe the structure of DNA molecule. **(2×5=10)**
