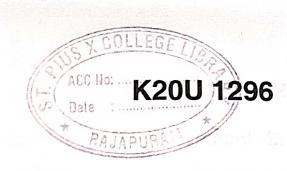


Reg. No. :



 $(4 \times 1 = 4)$

III Semester B.Sc. Degree (CBCSS – Sup./Imp.)
Examination, November 2020
(2014-'18 Admns.)
GENERAL COURSE IN MICROBIOLOGY
3A12 MCB: Biophysics and Bioinformatics

Time: 3 Hours Max. Marks: 40

SECTION - A

(Answer all th	ne four o	questions.)
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- FASTA program was designed by _____
- 2. A database for protein motifs/domain is _____
- 3. Sequences diverged from a common ancestor are known as _____
- 4. Hemoglobin represents _____ structure of proteins.

SECTION - B

(Answer very briefly on any seven questions out of ten.)

- 5. Genome mapping.
- 6. SWISS PROT.
- 7. Global sequence alignment.
- 8. Dialysis.
- 9. Molecular docking.
- 10. Phylip.
- 11. HITS.

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- 12. Entropy.
- 13. Clustal.
- 14. Omega loops.

 $(7 \times 2 = 14)$

SECTION - C

(Answer very briefly on any four questions out of six.)

- Information retrieval systems.
- 16. Secondary structure of proteins.
- 17. Representation of a phylogenetic tree.
- 18. Nucleosomes.
- 19. Laws of thermodynamics.
- 20. Genome databases.

(4×3=12

SECTION - D

(Answer any two questions out of four.)

- 21. Explain the methodology of phylogenetic tree construction.
- 22. Write a detailed account on genome sequencing and its applications.
- 23. Make a comparison of BLAST and FASTA.
- 24. Explain the Gibb's free energy concept and thermodynamics of biochemical reactions. (2x5=10)