



K22U 1328

Reg. No. :

Name :

**II Semester B.Sc. Degree (CBCSS – O.B.E – Regular / Supplementary /
Improvement Examination, April 2022
(2020 Admission Onwards)**

**CORE COURSE IN LIFE SCIENCES (ZOOLOGY) AND COMPUTATIONAL
BIOLOGY**

2B02 ZCB : Fundamentals of Computational Biology and Bioinformatics

Time : 3 Hours

Max. Marks : 40

PART – A

Answer **all** the questions. **Each** question carries **1** mark.

1. Expand RCSB.
2. Who is considered as the pioneer of Bioinformatics and Computational Biology ?
3. The molecular sequences that produce due the horizontal gene transfer during evolution is known as _____
4. Name the algorithm used to find the global alignment of molecules sequences.
5. The English alphabet “E” stands for which amino acid ?
6. The search engine used for the retrieval of the data from NCBI is _____
(6×1=6)

PART – B

Answer **any 6** questions. **Each** question carries **2** marks.

7. INSDC
8. Homologous sequences
9. PAM
10. Molecular clock hypothesis
11. Gap penalty
12. Kimura-2 parameter model
13. ExPASy server
14. Travelling salesman’s problem
(6×2=12)

P.T.O.



PART – C

Answer **any 4** questions. **Each** question carries **3** marks.

15. Differentiate between similarity and identity. Discuss the term alignment score and E-value in the context of similarity search.
16. What do you mean by progressive alignment ?
17. Outline the file format of PDB.
18. Discuss various types of BLAST programs.
19. What do you mean by boot strapping ? Discuss the applications of bootstrapping.
20. Compare Genomics and Proteomics. Outline the applications of these fields.

(4×3=12)

PART – D

Answer **any 2** questions. **Each** question carries **5** marks.

21. Classify databases and outline various types of biological databases with suitable examples.
22. What is molecular phylogenetics ? Elaborate various methods used for the constructions of phylogenetic trees.
23. Outline the history, objectives, scope and applications of the human genome project.
24. Prioritise the scope of DNA computing and outline the principle, shapes and junctions used for the constructions of DNA computers.

(2×5=10)