QP Code: UV25DR013

Reg. No : ....
Name : ....

ST MARY'S COLLEGE (AUTONOMOUS), THRISSUR-20

I SEMESTER (FYVP) DEGREE REGULAR EXAMINATIONS, NOVEMBER 2025

BIO1MN101 : Biological Systems and Basics of Bioinformatics

2025 Admission Onwards

(Credits: 4)

Time: 2 Hours **Maximum Marks: 70**

Section A

*Answer **all**. Each question carries **3** Marks.* ***(Ceiling: 24 Marks)***

1. Identify the function of Mitochondria.
2. Define Golgi apparatus.
3. Mitochondria act as the “powerhouse of the cell".Explain.
4. Describe the structure and function of the chloroplast envelope.
5. Apply the concept of central dogma to explain how genetic information leads to protein synthesis.
6. Explain the significance of initiation factors in translation control.
7. Inspect the role of CDK protein kinase in metabolic pathways.
8. Compare and contrast different data retrieval systems.
9. Why data standardization is essential among NCBI, DDBJ, and EMBL?
10. Evaluate the importance of STS, EST and VAST in constructing genetic maps.

Section B

*Answer **all**. Each question carries **6** Marks.* ***(Ceiling: 36 Marks)***

11. State the difference between genetic maps and physical maps.
12. State the structure and functions of prokaryotic and eukaryotic cells.
13. Compare Rasmol and Pymol in visualizing three dimensional stuctures.
14. Apply your knowledge to explain what happens when apoptotic regulation fails in cancer cells.
15. Describe the role of peroxisomes in protecting the cells from oxidative damage.
16. Compare and contrast the role of primary and secondary structural databases in addressing three dimensional bimolecular structures.

Turn Over

17. Differentiate between the regulation mechanisms at G1/S and G2/M checkpoints.

18. Analyze the interplay between cyclins, CDKs, and checkpoint proteins in ensuring proper cell cycle control.

Section C

Answer ***any one*****.** ***(1x10=10marks)***

19. Describe the different stages of mitosis with neat labeled diagrams and explain the significance of each.

20. Analyze the algorithmic steps involved in BLAST and explain how it finds sequence similarity efficiently.

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