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**N – 1355**

Reg. No. : .....

Name : .....

**Sixth Semester B.Sc. Degree Examination, April 2022**

**First Degree Programme under CBCSS**

**Botany**

**Core Course**

**BO 1642 – MOLECULAR BIOLOGY, GENERAL INFORMATICS AND  
BIOINFORMATICS**

**(2018 Admission)**

Time : 3 Hours

Max. Marks : 80

(Draw diagrams wherever necessary)

**SECTION – A**

Answer **all** questions. **Each** question carries **one** mark.

1. What are computer softwares?
2. What is cyber addiction?
3. What is ORF?
4. What is plagiarism?
5. What is a database? Name one nucleic acid database.
6. Name the bond that connects nucleotides in a polynucleotide chain.

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7. Enzyme involved in relieving the super coiling in DNA.
8. What is monocistronic mRNA?
9. Give an example for a left-handed double helical DNA.
10. What is exon?

**(10 × 1 = 10 Marks)**

### SECTION – B

Answer any **eight** of the following. **Each** question carries **two** marks.

11. What are computer peripherals?
12. Explain the concept of Operating System in a computer.
13. Expand and explain what is http.
14. Name the applications where you would use methods like Clustal and PHYLIP.
15. Differentiate pair wise sequence alignment and multiple sequence alignment.
16. Write a brief account on any one protein sequence database you have studied.
17. What is data mining in bioinformatics?
18. Describe the applications of RasMol.
19. What is the difference of the 5' end of eukaryotic mRNA with that of prokaryotic mRNA?
20. What is wobble hypothesis?
21. What is spliceosome?
22. What is Pribnow box?
23. What is the central dogma in molecular biology?

24. Explain the role of Sigma factor in transcription.
25. What is the role of DNA polymerase I in DNA replication?
26. Differentiate between nucleoside and nucleotide.

**(8 × 2 = 16 Marks)**

### SECTION – C

Answer any **six** of the following. **Each** question carries **4** marks.

27. What is INFLIBNET? Add a note on its significance.
28. Describe the basic features and applications of MS-EXCEL.
29. Differentiate local sequence alignment from global sequence alignment.
30. SWISS-PROT is an annotated protein sequence database. Explain.
31. What is BLAST? Give two applications where you would use BLAST.
32. What were the major proposals in Chargaff rule?
33. Explain the semi discontinuous replication of DNA.
34. Write a brief note on the different classes of transposable genetic elements.
35. What is tRNA charging? Describe the process of tRNA charging.
36. What is genetic code? What are the important features of the genetic code?
37. What is ribozyme? Give two examples for ribozymes.
38. Compare the molecular composition of ribosomes in prokaryotes and eukaryotes.

**(6 × 4 = 24 Marks)**

## SECTION – D

Write an essay on any **two** of the following. **Each** question carries **15** marks.

39. Describe the internet as a knowledge repository and explain how it is useful in teaching and learning.
40. What is phylogenetic tree? How do we build a phylogenetic tree? Give the name of any one tool used.
41. What is multiple sequence alignment? Add a note on tools used for sequence alignment.
42. Describe the processes involved in the maturation of pre-mRNA in eukaryotes.
43. Compare and contrast the structure of RNA and DNA.
44. Write an account on the operon model for the regulation of gene expression in prokaryotes.

**(2 × 15 = 30 Marks)**

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