23105488

QP CODE: 23105488

Reg No : .....

Name : .....

B.Sc DEGREE (CBCS) REGULAR / REAPPEARANCE EXAMINATIONS, MARCH 2023

Sixth Semester

CORE COURSE - BO6CRT12 - BIOTECHNOLOGY AND BIOINFORMATICS

Common for B.Sc Botany Model I, B.Sc Botany Model II Food Microbiology, B.Sc Botany Model II Environmental Monitoring and Management, B.Sc Botany Model II Horticulture and Nursery Management & B.Sc Botany Model II Plant Biotechnology

2017 Admission Onwards

06AAFCF1

Time: 3 Hours Max. Marks : 60

Part A

*Answer any **ten** questions.*

*Each question carries **1** mark.*

1. What is agar?
2. What is meant by sub culturing?
3. What is indirect organogenesis?
4. Write the aim of anther culture.
5. What do you mean by secondary metabolites?
6. Name an entrapping technique used to protect cells from mechanical damage.
7. What is rDNA technology?
8. Write short note on Agarose.
9. What is DNA fingerprinting?
10. How many basepairs are there in human genome as per the results of Human Genome Project?
11. What is meant by bioinformatics?

12. What is PIR?

(10×1=10)

Part B

*Answer any **six** questions.*

*Each question carries **5** marks.*

13. Describe briefly on different sterilization methods used in tissue culture technique.
14. Comment on somaclonal variations.
15. Briefly describe the procedure of somatic hybridization.
16. Restriction endonucleases are generally called ‘molecular scissors’. Comment on this statement.
17. Briefly describe the procedure of PCR.
18. Give an account on UV trans-illuminator.
19. Write the difference between GenBank and DDBJ.
20. Write about different softwares used in sequence alignment.
21. Briefly explain molecular phylogeny.

(6×5=30)

Part C

*Answer any **two** questions.*

*Each question carries **10** marks.*

22. Write an essay on various aseptic techniques followed in plant tissue culture.
23. Describe the various steps in recombinant DNA technology.
24. Explain the procedure of DNA sequencing by Sangers dideoxy method.
25. Explain sequence analysis. Comment on various sequence analysis tools in bioinformatics.

(2×10=20)