



QP CODE: 25047255



25047255

Reg No :

Name :

M.Sc DEGREE (CSS) EXAMINATION, NOVEMBER 2025

Third Semester

M Sc BIOINFORMATICS

Core Course - BT010302 - PROTEOMICS & CADD

2019 ADMISSION ONWARDS

1A35E46A

Time: 3 Hours

Weightage: 30

Part A (Short Answer Questions)

*Answer any **eight** questions.*

Weight 1 each.

1. What is the basic principle of mass spectrometry?
2. Write a short note on any open source molecular visualization system
3. How do you determine the domain of a protein?
4. Write a short note on a database that presents classification of 3-D protein folds.
5. What is 3D-PSSM? Explain its use.
6. Evaluate the applications of Ramachandran plot.
7. What are the characteristics of a good drug?
8. What are pharmaceutical and pharmacokinetic phases of drug action?
9. How do you define LogP of a chemical compound?
10. Why flexibility is important in docking?

(8×1=8 weightage)

Part B (Short Essay/Problems)

*Answer any **six** questions.*

Weight 2 each.

11. Elaborate on PIR and its major databases.
12. Give your views on significance of backbone flexibility in computational protein design.
13. Describe the main protein fold classes based on the secondary structure proportions.
14. Describe the important steps involved in homology modelling.
15. Explain how recent developments in deep feature learning methods helps in protein function prediction.





16. Explain the main cellular targets for drug action.
17. Write a short essay on drug discovery pipeline.
18. What are hit and lead identification stages in virtual screening?

(6×2=12 weightage)

Part C (Essay Type Questions)

*Answer any **two** questions.*

Weight 5 each.

19. Explain the principle and applications any two main methods used for protein structure determination.
20. Explain the types of interatomic interactions involved in protein conformation.
21. Give a comparative account of traditional and modern methods of drug discovery.
22. Explain the methodology of 3D QSAR.

(2×5=10 weightage)

