# STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086 (For candidates admitted from the academic year 2019 – 2020 & thereafter)

SUBJECT CODE: 19BI/PC/MC34

## M. Sc. DEGREE EXAMINATION, NOVEMBER 2022 BIOINFORMATICS THIRD SEMESTER

**COURSE : CORE** 

PAPER : MOLECULAR MODELING AND COMPUTER AIDED DRUG

**DESIGN** 

TIME : 3 HOURS MAX. MARKS: 100

SECTION – A

### **ANSWER ALL QUESTIONS**

 $(20 \times 1 = 20)$ 

- 1. Define potential energy surface.
- 2. Define force field.
- 3. What is a coordinate system?
- 4. What are long range forces?
- 5. Brief about Verlet algorithm.
- 6. What are Gibbs free energy and change in Gibbs energy?
- 7. Define ensemble.
- 8. Define the periodic boundary conditions.
- 9. Why do we need to minimise energy?
- 10. What is the difference between dynamics and Monte Carlo simulation?
- 11. Define ADMET.
- 12. Define a pharmacophore?
- 13. What is *ab initio* modelling?
- 14. How a chemical library can be constructed?
- 15. Mention two protein visualization tools.
- 16. Differentiate leads and hits.
- 17. Expand QSAR.
- 18. How the modelled protein structure can be validated?
- 19. Write brief notes on any two molecular descriptors.
- 20. Justify the need for selecting a potential target for molecular docking.

#### **SECTION - B**

#### ANSWER ANY FOUR QUESTIONS

 $(4 \times 10 = 40)$ 

- 21. Explain the coordinate systems and detail their types.
- 22. Enumerate the significance of force fields and why different force fields are needed for effective structure analysis.
- 23. How molecular thermodynamic properties are explored during protein structure analysis?
- 24. List out the advantages of Monte Carlo simulation.
- 25. How effective the pharmacophore modelling in the field of drug discovery?.
- 26. Describe the ways of protein structure prediction methodologies.
- 27. Explain the methods involved in loop refinement and geometry optimization.

## ANSWER ANY TWO OF THE FOLLOWING IN DETAIL

 $(2 \times 20=40)$ 

- 28. Discuss in detail about Energy Minimization and their applications in structural bioinformatics.
- 29. Explain the concepts of molecular dynamics. Elaborate in detail the various algorithms involved.
- 30. Appreciate "structure based drug design" and explain various strategies.
- 31. How "molecular descriptors" are exploited in QSAR. Also elaborate the significance of QSAR.

\*\*\*\*\*