



Avinashilingam Institute for Home Science and Higher Education for Women
(Deemed to be University under Category 'A+' by MHRD (now MoE), Estd. u/s 3 of UGC Act 1956. Re-
accredited with A⁺⁺ Grade by NAAC. Recognised by UGC Under Section 12B)
Coimbatore - 641 043, Tamil Nadu, India

Continuous Internal Assessment II – April, 2025
Semester-II

Class: I PG
Major: Biotechnology

Max.marks:60
Time:2hours

23MBTC09–Bioinformatics

Course Outcomes:

After completing this course, the student will:

- CO1.** Explain the contents and layout of the important biological databases and to search and retrieve.
- CO2.** Apply bioinformatics tools for sequence alignment and to find the evolutionary relationships
- CO3.** Explain the theory behind the gene-finding tools, different types of genomics and proteomics
- CO4.** Understand the steps involved in the analysis of structures of biomolecules and predicting their secondary and tertiary structures with various bioinformatics tools.
- CO5.** Develop a protein model/design a drug and predict its structure and function with various tools.

Part– A

(6 x 1= 6)

Answer the following

1. What are the main criteria on which mass spectrometer used for? (CO4; K2)
(a) Composition in sample (b) Relative mass of atoms
(c) Concentration of elements in the sample (d) Properties of sample
2. What are the main criteria on which mass spectrometer used for? (CO4; K2)
(a) Composition in sample (b) Relative mass of atoms
(c) Concentration of elements in the sample (d) Properties of sample
3. Atomic coordinate files are the data files that specify __ molecular structures? (CO5; K1)
(a) 1 D (b) 2 D (c) 3 D (d) 4 D
4. All of the following are comparative modelling tools except (CO3; K3)
(a) MODELLER (b) SWISS MODEL (c) I-TASSER (d) HHPred
5. Lipinski's rule of five is used for (CO5; K3)
(a) Docking (b) similarity search (c) drug likeliness (d) MD simulation
6. Method of protein structure prediction used in the absence of homologous template (CO3; K2)
(a) Comparative modeling (b) Surface modeling
(c) Abinitio prediction (d) NMR method

Part– B

(3 x 6= 18)

Answer ALL questions.

Answer should not exceed 400 words or two pages

7. a) Comment on functional genomics. (CO2; K1)
Or
7. b) Discuss in brief about DNA microarray. (CO4; K3)
8. a) Write a note on energy minimization. (CO5; K2)
Or
8. b) What is lead optimization? Explain the steps involved in lead compound identification. (CO5; K2)
9. a) Discuss about the applications of Lipinski's rule of five. (CO5; K2)
Or
9. b) Give a detailed note on virtual screening. (CO5; K2)

Part– C

(3x 12 = 36)

Answer ALL questions.

Answer should not exceed 800 words or four pages

- 10.a) What are the methods developed for the prediction of protein secondary structure? (CO5;K3)
Or
10.b) Discuss in detail about the steps involved in homology modelling (CO3; K2)
- 11.a) Write a brief note on 2D gel electrophoresis? (CO3; K2)
Or
11.b) Give the features of mass spectroscopy. (CO3; K3)
- 12.a) Write down the steps involved in structure-activity relationship. (CO5; K3)
Or
12.b) Discuss the major features of RasMol. (CO4; K6)

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