



Avinashilingam Institute for Home Science and Higher Education for Women

Deemed to be University Estd. u/s 3 of UGC Act 1956, Category A by MHRD (now MoE)

Re-accredited with A++ Grade by NAAC. CGPA 3.65/4, Category I by UGC

Coimbatore - 641 043, Tamil Nadu, India

Master's Degree Examination – May 2025

II Semester

Class : I P.G.
Major : Biochemistry

Time: 3 Hours
Max. Marks: 100

23MBCC08 Concepts of Bioinformatics for Biochemistry

Course Outcomes:

- CO1: Explain the basic principles of experimental methods for determination of the structure of macromolecules
CO2: Explain the types of data available from the most common sequence and structuredatabases
CO3: Apply bioinformatic tools for sequence alignment and prediction of secondary andtertiary structure prediction
CO4: Analyse the different tools available for various sequence and structure analysis
CO5: Predict different protein molecules with various bioinformatics tools

Part A

10 x 1 = 10

Choose the Correct Answer

1. What does the "KEGG" database primarily contain? CO1K1
a. Protein structures b. Genetic variations
c. Metabolic pathways d. Organism-specific genomes
2. Find a database that contains information related to the functional annotation of genes? CO1K2
a. Gene Ontology b. UniProt c. KEGG d. BLAST
3. Which of the following algorithms is used for pairwise sequence alignment? CO2K1
a. Smith-Waterman b. ClustalW c. BLAST d. Needleman-Wunsch
4. Mention the scoring matrices that is used for protein sequence alignment? CO2K2
a. BLOSUM b. PAM c. Both BLOSUM and PAM d. Smith-Waterman
5. Which of the following is typically used to check the specificity of a primer? CO3K1
a. Gel electrophoresis b. BLAST search
c. Primer melting curve analysis d. Electrospray ionization
6. Find a tool that is used to search protein sequence databases for matches to a query sequence? CO3K2
a. BLASTp b. ClustalW c. Phyre2 d. Prosite
7. Which one of the following shows the application of microarray technology? CO4K1
a. Identifying disease biomarkers b. Analyzing protein-protein interactions
c. Determining the three-dimensional structure of proteins
d. Performing genome-wide sequencing
8. Mention the technique that is most commonly used for identifying and characterizing proteins in proteomics? CO4K2
a. Polymerase chain reaction (PCR) b. Western blotting
c. Mass spectrometry (MS) d. DNA microarrays
9. Which of the following file formats can RasMol read to display molecular structures? CO5K1
a. FASTA b. PDB c. CSV d. XML

10. Identify a technique that is used in CADD to screen large databases of compounds for potential drug candidates? CO5K2
- a. Mass spectrometry b. Molecular docking
 c. Gel electrophoresis d. PCR amplification

Part B

5 x 6 = 30

Answer ALL questions

Each answer should not exceed 400 words or two pages

- 11.a. Discuss on the biological databases for the structural classification of proteins CO1K2
 (or)
- 11.b. Explain the model organism database and its importance. CO1K3
- 12.a. Write a note on alignment tool - BLAST and its types. CO2K3
 (or)
- 12.b. Briefly explain dot plot and its applications. CO2K4
- 13.a. Outline on the prediction of secondary structure of RNA. CO3K4
 (or)
- 13.b. Explain the tools for peptide cleavage and mapping with example. CO3K3
- 14.a. Define structural genomics. Explain the present status and future prospects. CO4K4
 (or)
- 14.b. Illustrate principle and applications of 2D gel electrophoresis. CO4K2
- 15.a. Discuss the importance of ADME studies for the 3D structural analysis of biomolecules. CO5K3
 (or)
- 15.b. Explain the method of prediction of ligand binding to a biomolecule. CO5K4

Part C

5 x 12 = 60

Answer ALL questions

Each answer should not exceed 800 words or four pages

- 16.a. Explain in detail on the literature and mapping databases. CO1K3
 (or)
- 16.b. Write in detail the aim, scope, branches and applications of bioinformatics. CO1K2
- 17.a. Differentiate global and local alignment algorithms. CO2K4
 (or)
- 17.b. Write on the types, methods and software for the phylogenetic tree analysis. CO2K3
- 18.a. Summarize on primer designing and probes to analyse nucleotide sequence. CO3K2
 (or)
- 18.b. Describe the prediction of secondary structure of proteins in sequence analysis. CO3K4
- 19.a. Illustrate on the principle and applications of DNA microarray. CO4K4
 (or)
- 19.b. Explain the principle and applications of MALDI-TOF. CO4K3
- 20.a. Elaborate the molecular visualization tools – RasMol and Deep View. CO5K4
 (or)
- 20.b. Explain in detail the steps in the computer aided drug design and its applications. CO5K4
