

**Avinashilingam Institute for Home Science and Higher Education for Women,
Coimbatore – 641043**

Continuous Internal Assessment Test – II -April 2025

Semester II

Class: I M.Sc.

Major: Bioinformatics

Time : 2 hrs

Max. Marks : 60

23MBIC10 – OMICs Technologies

Course Outcomes:

After completing this course, the student will

CO1: Outline genomics and genome database and genome browsers.

CO2: Plan experiments with the knowledge gained.

CO3: Illustrate key technologies involved in metabolomics.

CO4: Explain key technologies in proteomics.

CO5: Apply omics data in understanding and the management of disease.

Part – A

Choose the correct answer

(6X1=6)

1. Which enzyme is commonly used to cleave proteins at specific sites during sequencing

(CO4, K2)

a) DNA polymerase b) Trypsin c) Ligase d) Amylase

Which technique is used to separate protein fragments based on mass before sequencing

(CO4, K3)

a) SDS-PAGE b) Ion-exchange chromatography c) Mass spectrometry d) ELISA

3. The yeast two-hybrid system is based on the reconstitution of which transcription factor

(CO4, K4)

a) TATA-binding protein b) RNA polymerase c) Gal4 d) Lac repressor

4. Which molecule is used to specifically capture the target protein in Co-IP _____ (CO4, K3)

a) RNA b) Antibody c) DNA polymerase d) Histone

5. Which ionization technique is most commonly used in LC-MS _____ (CO4, K3)

a) Electron Ionization (EI) b) Matrix-Assisted Laser Desorption/Ionization (MALDI)
c) Electrospray Ionization (ESI) d) Fast Atom Bombardment (FAB)

6. In FRET, what happens when the donor fluorophore transfers energy to the acceptor fluorophore

(CO4, K3)

- a) The donor emits fluorescence, and the acceptor remains dark
b) The donor's fluorescence decreases, and the acceptor's fluorescence increases
c) Both the donor and acceptor emit fluorescence at the same intensity
d) The acceptor is completely degraded

Part - B
Answer the following
Answer should not exceed 400 words or two pages

3 x 6 = 18

7. a. Describe in amino acid sequence analysis by Edman degradation. (CO4, K2)
Or
7. b. Write about the database used to study protein -protein interaction. (CO4, K2)
8. a. Discuss about proteomic approaches to study post translational modification. (CO4, K3)
Or
8. b. Elaborate the mass spectral analysis. (CO4, K2)
9. a. Distinguish the Gene neighbor and gene cluster method. (CO4, K2)
Or
10. Explain about working principle of LC MS. (CO4, K2)
9. b. Explain about working principle of LC MS. (CO4, K2)

Part – C
Answer the following
Answer should not exceed 800 words or four pages

3 x 12 = 36

- 11.a. Give a detail account on Yeast two hybrid system to study protein -protein interaction. (CO4, K2)
11. b. Describe the principle and application of mass spectrometry. (CO4, K2)
- 12.a. Outline the steps involved in Coimmunoprecipitation and FRET. (CO4, K1)
Or
12.b. Illustrate the methods of protein sequencing (CO4, K3)
- 13.a. Explain in detail about Evolutionary genomics. (CO5, K3)
Or
13. b. Discuss in detail about comparative genomics. (CO5, K2)

Staff In charge: Mrs.S.Saraswathi

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