QP Code:PV25C002

Reg. No : .....

Name : .....

ST MARY'S COLLEGE (AUTONOMOUS), THRISSUR-20

III SEMESTER (CBCSS - VPG) DEGREE EXAMINATIONS, OCTOBER 2025

M. Voc. Applied Biotechnology

GEC3AB09 : PROTEOMICS AND METABOLIMUCS

2024 Admission Onwards

Time:3 Hours **Maximum Weightage:30**

Part A

*Short answer type questions: Answer **any four** questions. Weightage **2** for each question.*
(4x2 = 8 Weightage)

1. What are small ORFs?
2. Identify at least two proteomic data repositories.
3. Describe the difference between label-based and label-free quantitation strategies.
4. Explain the difference between Data Independent Analysis (DIA) and Data Dependent Analysis (DDA).
5. Explain lipidomics work flow.
6. Summarise targeted proteomics tool, skyline.
7. Evaluate the strengths and weaknesses of targeted metabolomics assays for clinical applications.

Part B

*Short essay-type questions: Answer **any four** questions. Weightage **3** for each question.*
(4x3 = 12 Weightage)

8. Define genome annotation.
9. Illustrate the workflow of tandem mass spectrometry (MS/MS).
10. Show how a metabolomics data repository can be used to compare datasets across studies.
11. What is retention time alignment, and why is it needed?
12. Examine the similarities and differences between MRM and PRM in terms of sensitivity and specificity.
13. Differentiate between the capabilities of MultiQuant, MarkerView, and LipidSearch.
14. Critically assess pathway-based analysis in interpreting metabolomics data.

Turn Over

Part C

*Essay-type questions: Answer **any two** questions. Weightage **5** for each question.*
(2x5 = 10 Weightage)

15. Name the major fragmentation modes used in tandem mass spectrometry.
16. Summarize how SEQUEST or X!Tandem identifies peptides from MS/MS data.
17. State the difference between targeted and untargeted metabolomics.
18. Differentiate between homology-based and *ab initio* gene prediction algorithms.

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