



HDP-003-006503

Seat No. _____

B. Sc. (Bioinformatics) (Sem. V) (CBCS) Examination

November / December – 2017

BI - 502 : Proteomics & Image Analysis

(New Course)

Faculty Code : 003

Subject Code : 006503

Time : $2\frac{1}{2}$ Hours]

[Total Marks : 70

- Instructions :** (1) All questions are compulsory.
(2) The right side figure indicates total marks of the question.

PART - A (20 Marks)

- 1 The first proteomics laboratory was founded by which university?
- 2 Why is proteomics data analysis necessary?
- 3 Chromatography based techniques fall under which proteomic application?
- 4 Mass spectrometry is used for Structural analysis. True or false
- 5 What is key to peptide identification and what provides it?
- 6 Based on what is the data displayed as a 3-D map?
- 7 SRM stands for -
- 8 Which is the first step for a functional analysis of a large protein list ?
- 9 Why is liquid chromatography coupled to mass spectrometry approach designed?
- 10 Name the approach that does not require prior knowledge of is required to define peptide selection criteria during the LC-MS analysis.

- 11 Name Highly specific databases developed for signal transduction processes.
- 12 What is Qualitative Data Analysis?
- 13 Principles of Qualitative Data Analysis
- 14 The test used when the two groups under comparison are independent of each other is _____.
- 15 Scatterplot is used for Quantitative data analysis of what kind of data?
- 16 What is the purpose of ion source?
- 17 One who won the nobel prize in Chemistry for his work in mass spectrometry.
- 18 Which technique was adopted to reduce the sample complexity in top-down proteomics?
- 19 Datasets are submitted to PRIDE _____.
- 20 Name the proteomic repository of sharing raw/processed MS data.

PART - B

- 1 (a) Explain any **three** : **6**
 - (1) List of proteomics tools
 - (2) Goals of analyzing proteomics data.
 - (3) Applications of 2DPAGE
 - (4) Pattern recognition
 - (5) SILAC
 - (6) Edge detection

- (b) Explain any **three** : **9**
- (1) Proteomics databases
 - (2) Proteomics tools
 - (3) Use of mean, median, standard deviation for analyzing data.
 - (4) Image filtering
 - (5) Explain any one High throughput technique
 - (6) Steps involved in SDS - PAGE
- (c) Attempt any **two** : **10**
- (1) Give the overview of proteomics techniques
 - (2) Evolution and applications of proteomics.
 - (3) Proteomics data analysis: types of data, methods used for analysis, statistical measures used and goals of analyzing data.
 - (4) Give the schematic representation of Conventional methodology for protein analysis.
 - (5) Image Processing methods
- 2** (a) Explain any **three** : **6**
- (1) Tandem mass spectrometry.
 - (2) Which are the major barriers being commonly confronted in the analysis of proteinprotein interaction analysis?
 - (3) Why is vacuum required for a mass spectrometer?
 - (4) Xenobiotic
 - (5) Subtractive Genomics Approach.
 - (6) How does a time-of-flight mass analyzer work?

- (b) Explain any **three** : **9**
- (1) Schematic representation of the mass spectrometric process.
 - (2) What are the various scoring functions that are used to compare mass spectra?
 - (3) Applications of mass spectrometry
 - (4) K-means clustering
 - (5) Subtractive Genomics Approach
 - (6) Applications of proteomics in Drug development.
- (c) Attempt any **two** : **10**
- (1) Explain general workflow for MS-based high-throughput bottom-up and top-down proteomics.
 - (2) Experimental approaches for protein-protein interactions
 - (3) Supervised learning methods
 - (4) Tools used for proteomics data analysis
 - (5) Types of Mass Spectrometry.
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