PBL-1603220001050300   Seat No. _____

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

November / December - 2018

BI.503 : Proteomics

(New Course)

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.

1   Attempt the following :   14
(a) Answer the following short questions : (all compulsory) **4**
(1) What is DALPC and Mud PIT ?
(2) _____ technique involves use of an ion exchange column adjusted to one pH with buffer adjusted to second pH.
(3) Proteins can be separated by isoelectric focussing cannot be tested for biological activity. (True/False)
(4) SDS gel electrophoresis and IEF together make up the process of _____.

(b) Answer any **one** of the following questions.   **2**
(1) Size exclusion chromatography.
(2) Application of proteomics in systems biology.

(c) Answer any **one** of the following questions.   **3**
(1) What is the general principle of protein separation ?
(2) Difference between 2-DGE and multidimensional chromatography.

(d) Answer any **one** of the following questions.   **5**
(1) Proteomics technologies and its applications in biomarker discovery.
(2) Explain in details 2DGE, its principle and limitations.

2 Attempt the following :   **14**

    (a) Answer the following short questions : (all compulsory) **4**

        (1) What is the principle that allows us to use mass spectrometry to determine the molecular weight of a compound ?

        (2) Name different stains used in detecting proteins.

        (3) _____ are the algorithm for spot detection method.

        (4) In electrophoresis DNA migrates towards anode. (True/False)

    (b) Answer any **one** of the following questions.   **2**

        (1) What is Blocking Buffer ?

        (2) Why silver staining cannot be used to detect glycoprotein ? Give reason.

    (c) Answer any **one** of the following questions.   **3**

        (1) Method to determine protein sequence by complete hydrolysis.

        (2) Methods of quantitative proteomics based on Mass spectrometry.

    (d) Answer any **one** of the following questions.   **5**

        (1) Explain Mass spectrometry, its basic principle and instrumentation.

        (2) Identification of protein using data from peptide masses. Its advantages and limitations.

3 Attempt the following :   **14**

    (a) Answer the following short questions : (all compulsory) **4**

        (1) What is chromatography ?

        (2) List some protein interactions databases.

        (3) Proteolytic modifications of the polypeptide are an important process in the mechanism for protein sorting and transport. (True/False)

        (4) Define protein binary interactions and complex interactions.

(b) Answer any **one** of the following questions. 2

(1) What is Lumiere and Mappit ?

(2) What is FRET ?

(c) Answer any **one** of the following questions. 3

(1) What is Bacterial two hybrid system ?

(2) Explain Protein interaction with small molecules.

(d) Answer any **one** of the following questions. 5

(1) Explain the two-hybrid/protein complementation assays.

(2) Explain analysis of protein interaction data.

4 Attempt the following: 14

(a) Answer the following short questions : (all compulsory) 4

(1) _____ is a commonly used global gene expression profile method.

(2) Name some protein microarray detection method.

(3) Define Glycomics.

(4) O-linked β-N-acetylglucosamine (O-GlcNAc) is a modification of serine of threonine side chains of nuclear and cytoplasmic proteins (True/False)

(b) Answer any **one** of the following questions. 2

(1) Define Glycoproteomics.

(2) IMAC techniques and its importance in phosphoproteomics.

(c) Answer any **one** of the following questions. 3

(1) Quantitative analysis of phosphoproteomics. Explain.

(2) Biomarker discovery and technology for biomarker discovery. Explain.

(d) Answer any **one** of the following questions. 5

(1) Explain in detail about Glycoproteomic, its analysis, separation, detection and enrichment.

(2) Role of Proteomics in agriculture, Proteomics in industry.

5 Attempt the following :   14

   (a) Answer the following short questions : (all compulsory) **4**

      (1) What is the full form of PRIDE ?

      (2) What are the four categories of public proteomics data use ?

      (3) The first step for a functional analysis of a large protein list is to connect the protein name to a _____.

      (4) What is MIAPE ?

   (b) Answer any **one** of the following questions.   **2**

      (1) What kind of biological information is provided by proteomics for biological problems ?

      (2) List out all the post translation modifications.

   (c) Answer any **one** of the following questions.   **3**

      (1) What are the tools currently used in glycopeptide analysis utilizing a one-step strategy and explain its function.

      (2) Explain Pathway analysis of proteomic data.

   (d) Answer any **one** of the following questions.   **5**

      (1) Proteomics resources of Expasy.

      (2) Which are the Proteomics data repositories focusing on protein PTMs. List out and explain.

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