JAQ-1603220001050300 Seat No. _____

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

November - 2019

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 :

(A) Answer the following short questions : **4**

(All Compulsory)

(1) Define differential proteomics.

(2) List different Quantification techniques in proteomics.

(3) _____ Chromatography is also known as Non-bonding method.

(4) Expand NEPHGE, IPG.

(B) Answer Any **One** of the following questions : **2**

(1) What are the techniques involved in proteomics study?

(2) Ion exchange chromatography?

(C) Answer Any **One** of the following questions : **3**

(1) Explain steps of Proteomics analysis.

(2) General principles of protein separation.

(D) Answer Any **One** of the following questions : **5**

(1) Proteomics technologies and its various applications.

(2) Explain origin and scope of proteomics.

2 Attempt the following :

(A) Answer the following short questions : **4**
(All Compulsory)

(1) _____ proteins are separated on the basis of their net charge irrespective of their mass.

(2) Defineampholytes.

(3) N terminal amino acid is identified using process Edman degradation. (True/False).

(4) How much time can Edman degradation take for sequence a larger peptide (30-40 residues)?.

(B) Answer Any **One** of the following questions : **2**

(1) What is Immunoblot?

(2) What is co-immunoprecipitation?

(C) Answer Any **One** of the following questions : **3**

(1) Explain the protein identification with antibody technique.

(2) Give a brief note on MALDI and ESI.

(D) Answer Any **One** of the following question : **5**

(1) Explain Edman degradation and its limitations.

(2) Explain MS and its application.

3 Attempt the following :

(A) Answer the following short questions : **4**
(All Compulsory)

(1) Protein interactions help in _____ of uncharacterised, hypothetical protein

(2) Affinity chromatography can be used to trap interacting proteins. (True/False)

(3) A labeled _____ is added to protein so the interactions can occur in physical methods.

(4) FRET

(B) Answer Any **One** of the following questions : **2**

(1) What is Affinity purification-mass spectrometry ?

(2) What is the Protein interaction Map?

(C) Answer Any **One** of the following questions : **3**

(1) Yeast two-hybrid system and its limitations?

(2) FRET its principle, advantages and limitation.

(D) Answer Any **One** of the following questions : **5**

(1) Explain methods to study protein-protein interactions.

(2) Explain library-based methods for binary interactions.

4 Attempt the following :

(A) Answer the following short questions : 4
(All Compulsory)

(1) _____ is a solid surface on which thousands of different proteins are immobilized in discrete spatial locations, forming a high-density protein dot matrix.

(2) What are the different methods that have been used for protein immobilization?

(3) ECL and RCA.

(4) RPAs allow for the determination of the presence of altered proteins that may be the result of disease. (True/False)

(B) Answer Any **One** of the following questions : 2

(1) Define Glycoproteomics.

(2) Functional protein microarrays.

(C) Answer Any **One** of the following questions : 3

(1) Explain protein synthesis of functional protein microarrays.

(2) Applications of proteomics in drug development.

(D) Answer Any **One** of the following questions : 5

(1) Explain in detail about analysis of phosphoprotein by mass spectrometry.

(2) Role of proteomics in drug development and disease diagnosis.
