

**M. Sc. Bioinformatics Sem.-II (C.B.C.S.) (2013 Course) / Advanced
Diploma in Bioinformatics Sem.-II (C.B.C.S.) (2013 Course) :
SUMMER - 2019
SUBJECT : GENOMICS & PROTEOMICS**

Day : Friday
Date : 12/04/2019

S-2019-1467

Time: 02.00 PM TO 05.00 PM
Max Marks. 60

N.B.

- 1) **Q. 1 and Q. 5 are COMPULSORY.** Out of the remaining questions solve any **TWO** from each section.
- 2) Figures to the right indicate **FULL** marks.
- 3) Both the sections should be written on **SAME** answer sheets.
- 4) Draw neat labeled diagram **WHEREVER** necessary.

SECTION – I

- Q.1** Define with diagrammatic representation: (10)
- a) Gene
 - b) Genome
 - c) Nucleosome
 - d) Nucleotides
 - e) GC rich regions
- Q.2** Answer the following : (Any TWO) (10)
- a) Explain any one conventional DNA sequencing method.
 - b) Explain the concept of genome assembly in brief.
 - c) Describe ion torrent sequencing principle in detail.
- Q.3** Write short notes on : (Any TWO) (10)
- a) Genome Annotation
 - b) ORF prediction Tool
 - c) Drug target identification
- Q.4** Write on pharmacokinetics classification, comparative screening, ADMET & Toxicity screening (10)
- OR**
- Describe briefly on any four genome alignment methods.

SECTION - II

- Q.5** Give reasons? (10)
- a) Proteomics is more complicated than genomics.
 - b) Protein folding is a complicated process.
 - c) Why there is a need to validate computational analysis?
 - d) More advanced protein separation techniques required.
 - e) PPI is a need of a hour.
- Q.6** Answer the following: (Any TWO) (10)
- a) Differentiate between ion – exchange & affinity chromatography.
 - b) Write a note on 2D – PAGE.
 - c) Describe briefly proteomics field.
- Q.7** Write short notes on : (Any TWO) (10)
- a) Protein sequencing method (Any one)
 - b) Mass spectrometry
 - c) Protein engineering
- Q.8** Explain DIP & InterpreTS server in detail. (10)
- OR**
- Explain the working principles of BIND, MINT, GRID, and Yeast two hybrid method.

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