12
RN11

Roll No. ....

94084

B. Sc. Bio-Tech 5th Sem. (N. S.)
Examination – November, 2017

GENOMIC & PROTEOMICS

Paper : BT-504

Time : Three Hours] *[Maximum Marks : 40*

Before answering the questions, candidates should ensure that they have been supplied the correct and complete question paper. No complaint in this regard, will be entertained after examination.

Note : Attempt *five* questions in all. Question No. **1** is *compulsory*. Attempt at least *one* question from each Unit.

1. Answer the following in about 20 words : 1 × 10 = 10

   (a) What is transcriptome ?

   (b) Which is the first bacteria whose genome has been completely sequenced ?

   (c) How many bases are there in human sequenced genome ?

   (d) Who hosts the UCSC ?

   (e) Name any browser which can scale the whole chromosome along with annotations.

(f) Which bonds are responsible for secondary structure of proteins ?

(g) What do you mean by data mining in genomics ?

(h) What is 2 D-PAGE ?

(i) Name the major components of mass spectrometry.

(j) Name the first sequenced protein.

UNIT – I

2. Explain in detail the DNA sequencing method by Maxam and Gilbert. How does it differ from the Sangers Method for DNA sequencing ? $7\frac{1}{2}$

3. Describe the following w. r. t. DNA sequencing :

(a) Chain termination sequencing. 4

(b) Shotgun sequencing. $3\frac{1}{2}$

UNIT – II

4. Describe various selected model organismal genomes. $7\frac{1}{2}$

5. Write notes on the following :

(a) VISTA 4

(b) UCSC genome browser. $3\frac{1}{2}$

UNIT – III

6. Describe in detail the chemical properties of proteins. Also write the various physical interactions that determine the properties of proteins. $7\frac{1}{2}$

7. Write notes on the following :

   (a) Non covalent bonding in proteins. $3\frac{1}{2}$

   (b) Determination of covalent structures in proteins. 4

UNIT – IV

8. Explain the use of mass spectrometry from the identification of proteins. $7\frac{1}{2}$

9. Write notes on :

   (a) Sample preparation for 2 D PAGE. 4

   (b) De novo sequencing using mass spectrometric data. $3\frac{1}{2}$
