Exam.Code:0038
Sub. Code: 0990

1059

B.Sc. (Hons.) Biotechnology
Sixth Semester
BIOT- Sem-VI-IV-T: Genomics and Proteomics

Time allowed: 3 Hours　　　　Max. Marks: 67

***NOTE**: Attempt five questions in all, including Question No. 1 which is compulsory and selecting one question from each Unit.*

x-x-x

I. Answer briefly:

a) SGD
b) Clone contig
c) Proteome
d) Reproducibility of 2D PAGE
e) TEMED
f) Resolution (Mass spectrometry)
g) Zwitter ion
h) Quaternary structure of protein
i) Native PAGE
j) Van der waal interactions (10x1½)

UNIT – I

II. a) Discuss the Maxam and Gilbert method of DNA sequencing

b) Name and explain two Genome Assembly softwares. (7,6)

III. a) Discuss the Hierarchical and Shotgun method of Genome sequencing.

b) Site out the difference between the manual and automated method of DNA sequencing.

c) What is Pyrosequencing? (6,3,4)

UNIT – II

IV. a) Write a short note on ENSEMBL.

b) Name all Model Organism Genome databases and explain in detail any one. (6,7)

V. Write a short note on Fly base and UCSC genome Browser. (13)

P.T.O.

UNIT – III

VI. a) Discuss the Edman Degradation method of peptide sequencing.

b) What is the principle of Gel alteration Chromatography? Also mention its applications. (7,6)

VII. a) Write five Chemical properties of proteins.

b) Discuss the Physical interactions that determine the property of proteins (5,8)

UNIT – IV

VIII. a) Discuss the MALDI-TOF method of mass spectrometry for protein identification

b) Discuss the methods of solublisation and reduction of protein sample for 2-D PAGE. (8,5)

IX. a) How can we do the sequencing of peptide using Mass spectrometric data?

b) Discuss the ESI method of mass spectrometry for protein identification. (6,7)

x-x-x