Exam.Code:0038
Sub. Code: 0990

2072
B.Sc. (Hons.) Biotechnology
Sixth Semester
BIOT- 604-T: Genomics and Proteomics

Time allowed: 3 Hours Max. Marks: 67

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

x-x-x

I. Answer briefly:

a) SGD

b) Scaffold

c) Bonding interactions

d) SDS

e) β-mercaptoethanol

f) MALDI-TOF

g) pI

h) Tertiary structure of protein

i) Sedimentation analysis

j) Gel filtration (10x1½)

UNIT - I

II. a) Discuss the Chain termination method of DNA sequencing.

b) Which genome sequencing method is preferred for small genome sizes and why? (6,7)

III. Write a detailed note on the different types of Genome sequence assembly softwares. (13)

UNIT - II

IV. a) Write a short note UCSC genome browser.

b) Explain the Drosophila genome database. (6,7)

V. What is significance of software tools for genome analysis? Explain any one tool used for genome analysis. (13)

P.T.O.

UNIT - III

VI. a) How is Edman degradation used for determining covalent structures?

b) Discuss the principle and applications of NATIVE PAGE. (7,6)

VII. a) Write a note on the physical interactions that determine the property of proteins.

b) How is SDS PAGE used for determination of protein sizes? (6,7)

UNIT - IV

VIII. a) How is mass spectrometry used for protein identification?

b) Write a note on the analysis of proteome. (7,6)

IX. a) Is reproducibility an issue with 2D PAGE? If yes, how can it be addressed?

b) Discuss the sample preparation and solublization of proteins for 2D PAGE. (5,8)

x-x-x