

(i) Printed Pages : 2

Roll No.

(ii) Questions : 9

Sub. Code :

1	7	9	8	9
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Exam. Code :

0	0	3	8
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**B.Sc. (Hons.) (Biotechnology) 6th Semester
(2056)**

GENOMICS AND PROTEOMICS

Paper : BIOT-604-T

Time Allowed : Three Hours]

[Maximum Marks : 67

Note :— Attempt five questions in all. Q. 1 is compulsory and attempt any one question from each unit.

1. Answer briefly:

- (a) Automated sequencing
- (b) Bis acrylamide
- (c) Hydrogen bonds
- (d) VISTA
- (e) FlyBase
- (f) NCBI genome
- (g) Van der waal interactions
- (h) Disulphide bonds
- (i) Clone contig
- (j) Native PAGE.

1.5×10=15

UNIT-I

- 2. (a) Write a note on the Sanger sequencing method. 6
- (b) Discuss the methodology and applications of Pyrosequencing. 7

3. (a) Explain any two genome sequence assembly software. 6
(b) Elaborate on the computational tools for genome sequencing projects. 7

UNIT-II

4. (a) Explain the construction and applications of ENSEMBL. 7
(b) Discuss the construction and features of Yeast genome database. 6
5. (a) Elaborate on the UCSC genome browser for genome analysis. 7
(b) What is the significance of web-based servers and software for genome analysis? Cite examples to support your answer. 6

UNIT-III

6. (a) Write a note on the chemical properties of proteins. 6
(b) Elaborate on the role of short-range interactions and electrostatic forces on stabilizing protein structure. 7
7. (a) Explain the use of gel filtration for determination of sizes. 6
(b) How is Edman degradation used for determining covalent structures of proteins? 7

UNIT-IV

8. (a) Discuss the sample preparation, solubilization and reduction of 2D PAGE. 7
(b) Explain the principle behind the separation of proteins based on pI. 6
9. Write a detailed note on principle and methodology of mass spectrometry-based methods for protein identification. 13