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(April)

BIOTECHNOLOGY

(Honours)

(Genomics, Proteomics and Computer Application)

Marks : 56

Time : 3 hours

The figures in the margin indicate full marks for the questions

Answer Question No. **1** which is compulsory and any **four** from the rest

1. Write notes on the following : 2+2+2+2+4=12

    (a) Batch processing of data

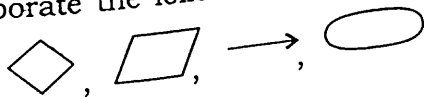   (b) Peptide bond

    (c) Gene editing

    (d) α-helix

    (e) Data mining concept

(2)

2. *(a)* Discuss the salient features of the human genome project.   8

(b) What is C-value paradox?   3

3. *(a)* Discuss the basic contexts of a C-program.   5

(b) Describe the various parts and code of the following C program :   6

```
# include <stdio.h>
int main() {
/* my first program in C*/
printf ('Hello, world! \n");
return θ;
}
```

4. *(a)* What is an oligopeptide? How is it different from a polypeptide? Explain your answers with suitable diagrams.   4

(b) Differentiate between α-helix and β-sheet protein conformations. How do they contribute to the secondary structure of a protein molecule?   4+3=7

5. *(a)* Define sequence tagged sites. How do they contribute to the human genome project?   2+3=5

(3)

(b) Define flowcharts. Discuss their applications in mapping evolutionary characteristic of organism.   3

(c) Elaborate the following symbols :   3

◇, ▱, →, ⬭

6. Define the following with suitable examples :   4+4+3=11

(a) SWISS PROT

(b) MEDLINE and PubMed

(c) Bankit and Sequin

7. *(a)* Describe and discuss how transcriptomics can be used to improve diagnosis and treatment of disease.   7

(b) What are ESTs, Contigs and SNP?   4

8. Describe the role of computers in the automation of bioreactors.   11

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