

1171

8

(iii) Protein disordered region

(iv) Genome Browsers

(4,4,4,3)

[This question paper contains 8 printed pages.]

**Your Roll No.....**

**Sr. No. of Question Paper : 1171**

**I**

Unique Paper Code : 2493010008

Name of the Paper : In-silico Tools in Proteomics  
and Genomics

Name of the Course : **B.Sc. (Hons.) Biochemistry**

Semester : V

Duration : 2 Hours

Maximum Marks : 60

**Instructions for Candidates**

1. Write your Roll No. on the top immediately on receipt of this question paper.
2. There are 6 questions in all.
3. Attempt any 4 questions.
4. Question no. 1 is compulsory.
5. All questions carry equal marks.

1. (a) Expand the following terms –

- (i) HTML
- (ii) OMIM
- (iii) DDBJ
- (iv) CDS
- (v) KEGG
- (vi) PDB
- (vii) PIR

(b) Comment on the following –

- (i) Sequence similarity is different from sequence identity

5. (a) What is Yeast two hybrid (Y2H) technique? What are its advantages?

(b) Discuss the current approaches employed in the drug discovery process emphasizing target identification, target validation, lead identification and lead optimization.

(c) Discuss the difference between local and global alignment with suitable examples.

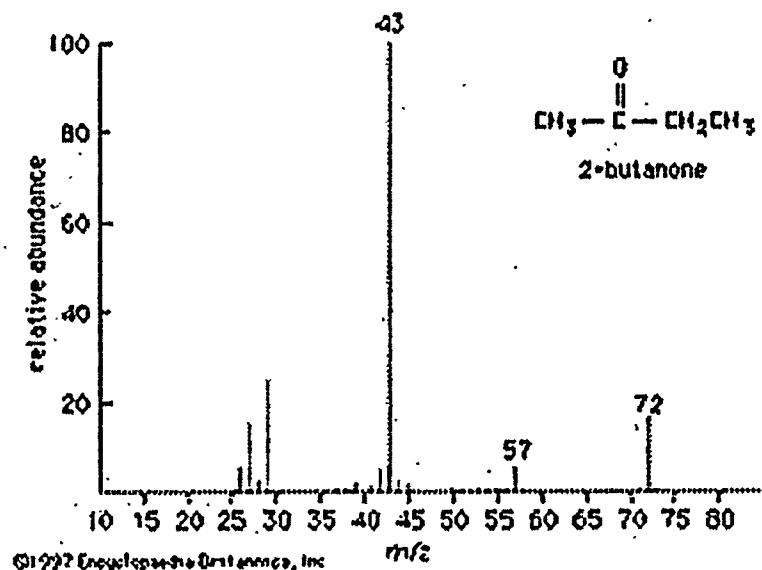
(5,5,5)

6. Write short notes on the following :

- (i) Role of AI in Genomics
- (ii) Human Genome Project

(b) You have a polynucleotide sequence. Describe the 6 reading frames that can be generated?

(c) Describe the principle of mass spectrometry. The figure above has mass spectrometry data for 2-butanone. Explain each of the peaks obtain in the spectra.



(6,3,6)

(ii) NCBI is a composite database.

(iii) Lipinsky's rule of 5 distinguishes drug-like and non-drug-like molecules

(iv) FASTA is a sequence file format

(c) Fill in the following blanks –

(i) \_\_\_\_\_ is a protein visualization tool.

(ii) Demis Hassabis and John M. Jumper won the 2024 Nobel Prize in Chemistry for their work on \_\_\_\_\_, an AI tool that predicts protein structures.

(iii) \_\_\_\_\_ tool can be used for predicting secondary structures in proteins.

- (iv) GLIMMER is a tool for predicting \_\_\_\_\_ in microbial DNA, especially the genomes of bacteria, archaea, and viruses.

(7,4,4)

2. (a) Differentiate between the following :

- (i) Primary and Secondary Databases
- (ii) Prokaryotic and eukaryotic genome organization
- (iii) Functional Genomics and Comparative Genomics
- (iv) Pairwise Sequence Alignment & Multiple Sequence Alignment

- (b) Describe Ramachandran plot. Explain how it is useful in protein modelling. (12,3)

3. (a) Describe Next Generation Sequencing (NGS).

What are its advantages and disadvantages?

- (b) Expand and describe BLAST. What is the difference between BLASTN and TBLASTN?

- (c) Describe any 2 applications of Bioinformatics.

(6,6,3)

4. (a) You have a protein of unknown function from a bacterium. You have made a knock-out mutant, but the bacteria die immediately without the corresponding gene. You have sequenced the protein. Describe the methods to predict the structure of the protein using in silico tools.