

# Gandhi Institute of Engineering and Technology University, Odisha, Gunupur (GIET University)



B. Tech (Sixth Semester) Examinations, April 2025

**21BBTPC36002 / 22BBTPC36002 – Bioinformatics**

(Biotechnology)

Time: 3 hrs

Maximum: 70 Marks

**Answer ALL questions**  
(The figures in the right-hand margin indicate marks)

## PART – A

(2 x 5 = 10 Marks)

Q.1. Answer **ALL** questions

- |  | CO # | Blooms Level |
|--|------|--------------|
| a. What are the submission tools of Gen Bank? What are the data not accepted by Gen Bank         | CO1  | K1           |
| b. Convert the given molecular marker into MSA<br>TCYGIFVL<br>TCGIFVL<br>SCYGIFVLSG<br>ACGIFVLSG | CO2  | K2           |
| c. Explain the option of BLAST and FASTA   | CO2  | K1           |
| d. What is phylogenetic? How many rooted and unrooted trees can be obtained using 7 OUT.         | CO3  | K2           |
| e. Draw the flow chart of molecular docking  | CO4  | K1           |

## PART – B

(15 x 4 = 60 Marks)

Answer **ALL** the questions

- |  | Marks | CO # | Blooms Level |
|--|-------|------|--------------|
| 2. a. Explain the layer of PIR database  | 8     | CO1  | K1           |
| b. Write the storing and retrieving method of EMBL database  | 7     | CO1  | K2           |
| (OR)   |       |      |              |
| c. Write retrieving method and submission tools of PDB database  | 8     | CO1  | K2           |
| d. Write the storing method and submission tools of DDBJ database  | 7     | CO1  | K2           |
| 3.a. Find the optimal alignment and alignment score between two sequence GCATGCA and GATTACA by using Needleman-Wunch algorithm (Assume Match= 1, Mismatch = -1 and Gap= -1)       | 8     | CO2  | K2           |
| b. Expand BLOSUM. Find the BLOSUM value of all amino acid of the given block<br>GGI<br>TGM<br>SGM<br>SGW<br>GGM  | 7     | CO2  | K2           |
| (OR)   |       |      |              |
| c. Find the optimal alignment and alignment score between two sequence GGATCGA and GAATTCAGTTA (Assuming match =5, Mismatch = -3 and gap = -4) By using Smith -Waterman algorithm. | 8     | CO2  | K2           |
| d. Define PAM. Find the PAM value of all amino acid of the given MSA<br>ACGCTAFKI<br>GCGCTAFKI   | 7     | CO2  | K2           |

ACGCTAFKL  
GCGCTGFKI  
GCGCTLFKI  
ASGCTAFKL  
ACACTAFKL

4.a. Design a phylogenetic tree by using NJ method

8 CO3 K2

	A	B	C	D	E
A		22	39	39	41
B			41	41	43
C				18	20
D					10
E					

b. Suppose there are 20,000 amino acid in the database of which 2000 are serine and there are 5000 amino acids in helical conformation of which 500 are serine. calculate the type of information

7 CO3 K2

(OR)

c. Find the no. of valid shifts of the given Test sequence- 31415926535 and pattern sequence 26 using Rabin Karp algorithm

8 CO4 K2

d. Which two sequences are very close to each other justify it by using Hamming distance method

7 CO4 K2

ADIKLAAIKL  
ADSKLAAIKA  
KILASDPQWE

5.a. Explain the computational method of Drug design

8 CO5 K2

b. Explain different windows of Cn 3D

7 CO5 K2

(OR)

c. Explain molecular Dynamic Simulation. Write the process of studying the dynamic behaviour of protein by AMBER package.

8 CO5 K2

d. How do you predict the 3D structure of proteins by homology modelling

7 CO5 K2

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