Post Graduate Diploma in Bioinformatics
Odd Semester Exam, 2025

Bioinformatics & Computational Biology Centre

Course No.: PGDBI-T1
(Fundamentals of Bioinformatics)

Full Marks: 70
Pass Marks: 30

Time: 3 hours

The figures in the right margin indicate full marks for the question.
Answer All questions

PART-I
(Marks : 20)

1. Choose the correct or the most appropriate alternative. 1x10=10

I. Disulfide bonds are found in which level of protein structure?

a. Primary b. Secondary

c. Tertiary d. Quaternary

II. Which model best explains the flexibility of the enzyme's active site during substrate binding?

a. Lock and Key Model

b. Induced Fit Model

c. Michaelis-Menten Model

d. Allosteric Model

III. In the Ramachandran plot, which secondary structure is most likely found in the top-left quadrant?

a. Alpha helix b. Beta sheet

c. Random coil d. Disordered loop

IV. Which database provides manually curated protein sequence and function information?

a. UniProtKB/Swiss-Prot

b. GenBank

c. EMBL

d. DDBJ

V. BLAST stands for:

a. Basic Local Alignment Search Tool

b. Biological Local Alignment Search Technique

c. Basic Linear Algorithm for Sequence Testing

d. None of the above

VI. In the Needleman-Wunsch algorithm, the optimal alignment is obtained by:

a. Random search

b. Local similarity

c. Dynamic programming

d. Linear regression

(d) PDB (e) NCBI

4. What is the basic principle of PCR? What do you mean by PCR primers ? Write various factors which need to be considered while designing PCR primers ? Explain the general procedure for in silico primer designing for PCR amplification of a desired gene of interest. 2+1+3+4=10

5. What are BLAST and FASTA algorithms? Compare their working principles and discuss their applications in pairwise sequence alignment. 10

6. Explain the difference between local and global sequence alignment. Describe the Needleman-Wunsch and Smith-Waterman algorithms with suitable examples. 10

7. Write short notes on the following: (any two) 2x5=10

a) Lipinski's rule of 5

b) ADME/Tox screening

c) Homology modelling

8. What do you mean by molecular docking? Name five softwares/tools used for molecular docking. What is the importance of molecular docking in CADD? What do you mean by QSAR? 2+2+3+3=10

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VII. Which parameter is related to drug absorption?

a. LogP b. TPSA

c. Rotatable bonds d. All of the above

VIII. What does the term "bioavailability" primarily refer to?

a. Drug solubility

b. Fraction of drug reaching systemic circulation

c. Drug's mechanism of action

d. Protein-binding ability

IX. Docking score primarily represents:

a. Solubility b. Binding energy

c. Molecular weight d. ADME profile

X. QSAR models correlate biological activity with:

a. Experimental procedures

b. Molecular descriptors

c. Target structures

d. Assay conditions

2. Answer the following questions 1x10=10

A. What is free energy?

B. What do you mean by isoelectric point of proteins?

C. Write the full forms of KEGG, PIR, MMDB & CATH.

D. What do you mean by tBLASTn ?

E. _____ alignment aligns two sequences from start to end, considering the full length of both sequences.

F. BLAST is slower than FASTA in performing sequence alignment. (**True/False**)

G. The technique used to compare two biological sequences and identify regions of similarity is called _____.

H. What is a combinatorial library?

I. What does a lower docking score usually indicate?

J. What is the main use of QSAR in drug discovery?

PART-II
(Marks-50)

3. Answer the following questions (any five) 10x5=50

1. What is Enzyme inhibition? Explain different types of enzymes inhibitors with examples. 2+8=10

2. Write notes on 4+6=10

   a. Laws of Thermodynamics

   b. Protein structures with examples and Ramachandran plot

3. Write very short notes on the following: 2.5x4=10

   (a) GenBank (b) PubMed