

JADAVPUR UNIVERSITY

Dept. of Pharmaceutical Technology

M. Pharm 1st year, 2nd semester, 2024

Sub: Bioinformatics and Computational Technology

Time: 3hrs.

Full Marks: 75

Answer **ANY FIVE** of the following questions

1. Write down the difference between protein and peptide. Briefly describe GRAVY value. Describe the properties of side chains in amino acids. 2+3+10 = 15
2. Elaborate on any two tools of EXPASY for primary structure analysis. How does physicochemical characterization help in primary structure prediction? 7+8 = 15
3. Write short notes on the following- 5x3 = 15
 - a. Protein informatics and significance of protein data
 - b. Schematically represent structure based drug design, and define molecular docking.
 - c. Steps involved in secondary structure analysis.
4. Write down the operating procedure of the ProtParam tool of EXPASY. Briefly describe the following:
 - a. GOR method of secondary structure analysis of proteins.
 - b. Chou and Fasman method of secondary structure analysis of proteins.
 - c. Advantages and disadvantages of ProtParam programme. 6+(3x3) = 15
5. Describe briefly about pairwise and multiple sequence alignment. Difference between FASTA and BLAST tool. Describe about FASTA and BLAST tool used for pairwise sequence alignment. (4+3)+3+5 = 15
6. Docking is a “hand-in-glove” analogy or “lock-and-key” analogy - justify. Describe conformationally important amino acids. Write names of four protein-ligand docking software applications. 5+5+5 = 15
7. Define the following terms – Gene sequence, Chaperone protein, Nucleotides and Nucleosides, Hereditary and Inheritance. Discuss the term Bioinformatics and cite its applications. Discuss the Human Genome Project and its significance. (2x4)+4+3 = 15