

|  |  |  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|--|--|
|  |  |  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|--|--|



## GIET MAIN CAMPUS AUTONOMOUS GUNUPUR – 765022

B. Tech Degree Examinations, June - 2021

(Sixth Semester)

**BBTPC6020 – BIOINFORMATICS**

(Biotechnology)

Time: 2 hrs

Maximum: 50 Marks

**Answer ALL Questions****The figures in the right hand margin indicate marks.****PART – A: (Multiple Choice Questions)****(1 x 10 = 10 Marks)**

- Q.1. Answer ALL questions** [CO#] [PO#]
- a. Secondary structures prediction of proteins using statistical analysis is proposed by [3] [2]  
 (i) GCR (ii) Barton  
 (iii) Rost and Sandor (iv) Chou-Fasman
- b. How many best global alignments is possible between sequences AAAC and AGC, where the scoring scheme is +1 for match, -1 for mismatch and -2 for an alignment with a gap. [2] [2]  
 (i) 1 (ii) 2  
 (iii) 3 (iv) 4
- c. \_\_\_\_\_ database consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them. [3] [1]  
 (i) PROSITE (ii) Golden path  
 (iii) OMIM (iv) Gene cards
- d. Which of the following sets contains all aromatic residues? [2] [1]  
 (i) G, D, N, E (ii) I, V, L, M  
 (iii) R, K, H (iv) F, Y, W
- e. \_\_\_\_\_ is a web-based program that combines neural network with multiple sequence alignment [3] [2]  
 (i) PSI PRED (ii) PHD  
 (iii) Protparam (iv) pfam
- f. SSAP automatic structural alignment programme classifies the protein in \_\_\_\_\_ database. [1] [1]  
 (i) SCOP (ii) CATH  
 (iii) PDBSum (iv) PDBeFold
- g. In a protein sequence alignment, \_\_\_\_\_ refers to the percentage of matches of the same amino acid residues between two aligned sequences. [2] [2]  
 (i) sequence identity (ii) sequence homology  
 (iii) sequence similarity (iv) sequence non homology
- h. On average, what is the length of a typical domain? [4] [2]  
 (i) About 100 residues (ii) About 200 residues  
 (iii) About 500 residues (iv) About 900 residues
- i. The term sequence \_\_\_\_\_ which is the similar at same position of same amino acid along with similar in physiochemical properties such as size, charge, and hydrophobicity. [1] [2]  
 (i) Identity (ii) Similarity

- |   |               |   |   |
|---|---------------|---|---|
| (iii) Homology  | (iv) Xenology |   |   |
| j. Pharmacologically inactive compounds are called _____. |               | 4 | 2 |
| (i) Prodrug   | (ii) Predrug  |   |   |
| (iii) Postdrug  | (v) Biodrug   |   |   |

**PART – B: (Short Answer Questions)**

**(2 x 5 = 10 Marks)**

Q.2. Answer ALL questions

|  | [CO#] | [PO#] |
|--|-------|-------|
| a. Describe the uniqueness of Neural Network in protein structure prediction.  | 3     | 1     |
| b. Mention the applications of Needleman–Wunsch algorithm  | 2     | 2     |
| c. In protein secondary structure prediction various methods are used. Out of these two methods Chou & Fasman and PHD which one is good and why? | 3     | 1     |
| d. What does RCSB PDB stand for? What does it contain ?  | 1     | 2     |
| e. Explain the role of protein structure in Drug Designing.  | 4     | 2     |

**PART – C: (Long Answer Questions)**

**(6 x 5 = 30 Marks)**

Answer ANY FIVE questions

|  | Marks | [CO#] | [PO#] |
|--|-------|-------|-------|
| 3. Elucidate the characteristics and classification of biological database.  | (6)   | 1     | 2     |
| 4. Explain the significance, objectives, URLs, data formats of primary DNA database in detail.   | (6)   | 1     | 2     |
| 5. Explain the working of BLAST based on your knowledge of sequence alignment.   | (6)   | 2     | 1     |
| 6. Perform the Smith Watterman algorithm for the following sequences by Dynamic programming<br>Seq #1 TGAATTC<br>Seq #2 GATTC and the scoring rules are Match = 1, Mismatch = -2 and Gap penalty = -2. | (6)   | 2     | 1     |
| 7. What are Hidden Markov models? Explain how they are used to identify profiles in a protein sequence.  | (6)   | 3     | 2     |
| 8. Explain the Chou-fasman secondary structure prediction method. Detail about the algorithm.  | (6)   | 3     | 2     |
| 9. Summarize why Protein folding plays an important role in biotechnology.   | (6)   | 4     | 2     |
| 10. Illustrate in detail how the fold recognition and its library is very important in protein functional analysis and drug design.  | (6)   | 4     | 2     |

--- End of Paper ---