Paper / Subject Code: 30002 / BIOINFORMATICS - I

1T00415 - T.E.(BIOTECHNOLOGY)(Sem V) (CBSGS) / 30002 - BIOINFORMATICS - I

Q.P.Code: 37863

(3 Hours) Total Marks: 80 NB: (1) Question **No.1** is **compulsory** (2) Attempt any **three** questions out of remaining **five** questions (3) Each question carries **equal** marks (4) Illustrate answers with sketches wherever required 1. Write Short Notes on: (20)a) PAM b) DDBJ c) NCBI d) CLUSTAL W 2. a) Describe different steps of homology modelling (10)b) Describe the applications of Bioinformatics. (10)3. a) Explain different 3D- protein structure viewers. (08)b) Explain Needleman - Wunsch algorithm with an example (12)4. a) Explain dot matrix alignment with example. (10)b) Explain Markov chains and Hidden Markov models. (10)5. a) Explain the different classification databases based on the type of data. (10)b) Explain amino acid substitution matrices. (10)6. Explain the following in detail (20)a) KEGG b) TrEMBL c) Chao-Fasman Algorithm d) Types of Biological data

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