

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

T2 EXAMINATION-2016

B.Tech BIOINFORMATICS – 2nd SEMESTER

COURSE CODE: 10B11BI211

MAX. MARKS: 25

COURSE NAME: Structural Biology

MAX. TIME: 1.5 HOURS

Note: All questions are compulsory. Attempt ALL questions.

1. A. Imagine you are given a α/β protein structure that has four beta strands and three alpha helices; explain as to how will you identify its active site region. [2.5]
B. Explain in detail with examples as to how enzymes evolve in nature. [2.5]
2. A. Define Levinthal's paradox. [2.5]
B. Imagine a protein (100 residues long) that can form a maximum of six disulfide bridges in its final native confirmation. Explain with the help of diagrammatic pathway as to how this hypothetical protein would fold and what could be its intermediate state and what possibly could be the rate limiting step in reaching its final native conformation. [2.5]
3. A. Compare and contrast the characteristics of a disulfide bond and a salt bridge. [2.5]
B. How are hydrophobic interactions formed in a protein? [2.5]
4. A. What form of DNA would you expect to see in desiccated shrimp eggs and in the spores of *Clostridium tetani*? [2.5]
B. In high salt concentration, the DNA changes from B form to the Z form. Explain stepwise the specific molecular events in the sugar phosphate backbone that lead to this conformational change? [2.5]
5. A. Given that the atomic size of K^+ and Na^+ are highly similar, explain as to why the K^+ channel cannot transport Na^+ . [2.5]
B. Define Hydropathy Scale and explain the algorithm (using a flowchart) as to how it is used in predicting transmembrane helices in a given protein sequence. [2.5]