

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

T3 EXAMINATION, 2015

B.TECH – II SEMESTER

COURSE NAME: STRUCTURAL BIOLOGY

MAX.MARKS:35

COURSE CODE: 10B11BI211

MAX.TIME: 2 HRS

Note: All questions are compulsory. Carrying of mobile phones during examinations will be treated as a case of unfair means. Each question carries 5 Marks.

1. The sequence below forms an α -helix. The residues underlined contribute to the biological function of this peptide, whereas those in **bold** do not. If you had to design this helix as a novel sequence, yet retain the structure, what amino acids would you change and why? Label the residues as helix stabilizing or unimportant. (5 Marks)

NH₂-**L** **I** **R** **F** V G R L L A Y F G D T I-COOH

2. Consider the structures of the four Watson Crick base pairs that form in a duplex B-form DNA. (5 Marks)
- Draw the structures of these four base pairs.
 - Label which atoms lie in the DNA major groove and which atoms lie in the minor groove.
 - Label all the potential hydrogen bond donating atoms and all the hydrogen bond accepting atoms in each of the two grooves of all four base pairs.
3. HyD crystalline protein is known to be involved in cataract formation in the eye. Cataracts form when several proteins in the eye create a very large insoluble multi-protein complex. There is a point mutation that changes the Arginine normally found at position 14 to a Cysteine. Children with this mutation develop cataracts. The overall 3D confirmation of the protein does not change despite the mutation. In the wildtype and this mutant of HyD crystallin protein there is also a Cysteine at position 110. (5 Marks)
- What type of interaction could form between these two amino acids?
 - How do you think the interaction between them in question (a) would lead to the development of a cataract?
4. Prof. G. N. Ramachandran explored the hard sphere contacts that limit protein main-chain conformations. How would you recognize a helix and a beta strand on a Ramachandran diagram? (5 Marks)
5. The structure of the 129-amino acid cytokine, IL-4, was determined independently by two different groups. The first group used X-ray crystallography method and the second group used NMR method. Both used the same protein, and all the structures had the same fold in which a short, two-stranded antiparallel β -sheet is packed against a four-helix bundle. (5 Marks)
- The refinement statistics of the X-ray structure has a resolution of 2.25 Å, number of reflections is 8085, data completeness is 93%, and R-factor is 0.218. Why would you consider this structure for deposition to the PDB?
 - Three loops had high B-factor in the x-ray solved structure. How does this affect the conformation of the loops in the final refined structure?
 - Reason as to whether one would be able to view these three loops in the NMR solved structure or not.
6. What is the approximate molecular weight of a protein with 682 amino acid residues in a single chain? (5 Marks)
7. Daenerys Stormborn Targaryen can command her dragon Drogon to spit fire on the Sons of Harpy when she says "Darcarys". In order for Drogon's fire glands to work optimally the ~200 residue long protein "Dragonfire" needs to withstand high temperatures. According to legends, Dragonfire has the property to generate extreme heat once it gets cleaved from its precursor form. While the precursor protein is prone to destabilize under high heat. How do you think the protein Dragonfire is able to withstand high temperatures? List all scientific possibilities only. (5 Marks)