

BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE, PILANI
BIO F417, BIOMOLECULAR MODELING
FIRST SEMESTER 2016 – 2017
MID-SEMESTER EXAM (CLOSED BOOK)

Full marks: 50 DATE: 03.10.16 DURATION: 90 Mins.

- **Answer to the point**
 - **Irrelevant and verbose answer may attract penalty**
 - **Steps in each calculation carry marks**
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1. Write notes on: **i)** Hydrophobic collapse model **ii)** helical wheel diagram **iii)** Major groove of DNA **iv)** Internal coordinates **v)** solvent accessible surface area **[2X5=10]**

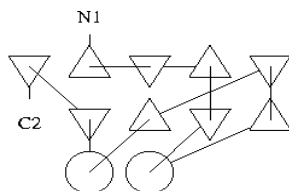
2. **a)** Show with proper diagram *cis* and *trans* orientation of proline residue. **[2.5]**

b) With the help of proper diagram explain the fact that *trans* peptide bonds are more stable than *cis* peptide bond. **[2.5]**

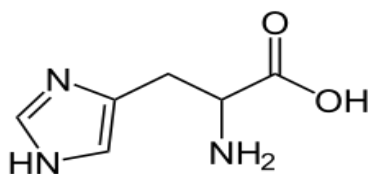
c) What are rotamers? Does it depend on mainchain conformation? Justify your answer. **[2]**

d) What is “Ramachandran plot”? How does it useful in protein modeling. **[3]**

3. **a)** Schematically represent (with standard secondary structure representation) following TOPs carton. **[3]**



b) Draw the smile representation of following amino acid and list down few unique characteristics features of this amino acid. **[3+2]**



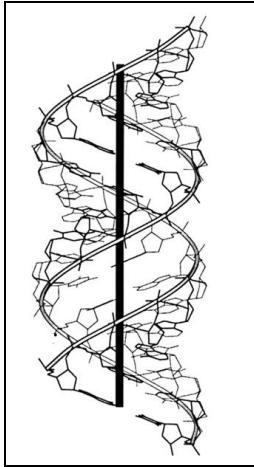
c) What are the distinguishing features of β -turns and γ -turns **[2]**

4. **a)** Why does Z-DNA conformation is rare in nature? **[2]**

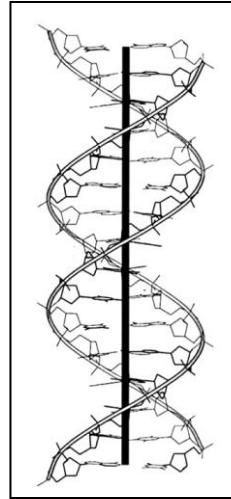
b) Schematically represent one form of G-quadruplex indicating (separately) schematic hydrogen bonding scheme. **[3]**

c) Draw the standard coordinate frame of DNA double helical structure **[2]**

d) What structural change will you perform to convert conformation (i) to conformation (ii) of following double helix DNA. **[3]**



(i)



(ii)

- 5. a)** Which type of interaction gives specificity of protein-DNA interaction and which are giving stability of a given protein-DNA interaction? [2]
- b)** List down the common features of perfect funnel landscape of protein folding. [3]
- c)** List down the common structural motifs of RNA structure. [2]
- d)** What is the reason for intrinsic negative propeller twist and around 32° twist of DNA double helix? [3]
