Indraprastha Institute of Information Technology Delhi (IIITD)

Department of Computational Biotechnology

BIO211 – Cell Biology and Biochemistry

ASSIGNMENT-3 (December 02, 2022)

Instructions:

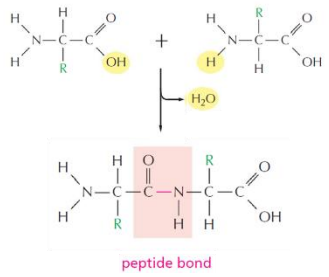
1. You have to submit a single PDF file having all the answers.
2. Use your roll no. as file name.
3. You have to submit the assignment by ~~next Sunday, 11 December 2022~~ Dec 15, 2022.

The main objective of this assignment is to understand one of the important aspects related to the structure of protein.

You now know that the primary structure of a protein is defined as the sequence of amino acids it is composed of. The different amino acids residues in a polypeptide are linked together by amide linkage, known as peptide bond. This polypeptide sequence determines the shape that the protein adopts, according to the spatial limitations on the arrangement of the atoms in the protein, the chemical properties of the component amino acid residues, and the protein's environment.

To add to this information, find out the answers to the following questions:

1. Describe the formation of peptide bond. [2 marks]



A peptide bond is formed between two amino acids when the carboxyl group of one amino acid reacts with the amino group of the other, releasing a molecule of water (also known as a condensation reaction).

2. Describe the nature of peptide bond. Is peptide bond rotatable? [3 marks]

A peptide bond (CO-NH) has a rigid planar structure. This happens due to interaction between electrons of the double bond of carbonyl group and those of the C-N bond, such that the latter acquires partial double-bond properties.

No, peptide bond is not rotatable.

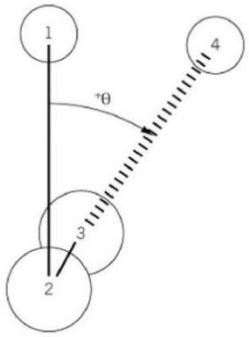
3. What are the two possible conformations of the planar peptide bond? What is the difference between the two conformations? Which of these conformations is more favorable? [3 marks]

There are two possible conformations of the planar peptide bond: cis and trans.

In the trans conformation, the Cα atoms of adjacent amino acids are on opposite sides of the peptide bond, whereas in the cis conformation the Cα atoms are on the same side of the peptide bond.

In most cases, the trans isomer is favored over the cis isomer. The cis isomer places the R groups of the two connected amino acids in close proximity to each other. This results in a steric clash, a non- bonded interaction in which electrons involved in a bond get too close to electrons involved in an adjacent bond. In the trans isomer of the peptide bond, the steric clash is avoided, and the R groups are held far apart. However, cis forms can occur in peptide bonds that precede a proline residue. In such cases, the cis form is more stable than usual since the proline side-chain offers less of a hindrance.

4. What are torsional angles? [2 marks]



Torsion angles within a molecule are defined by four atoms connected by three bonds.

5. How many torsional angles are present in the main chain of any polypeptide? Describe each of those torsional angles. [4 marks]

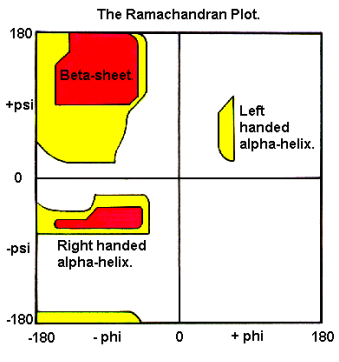
The backbone of a protein has three different torsion angles.

i. The phi-angle (φ) - around the N-Cα bond
ii. The psi-angle (ψ) - around the Cα-C bond
iii. The omega-angle (ω) - around the peptide bond between C and N.

6. What determines the conformation of the backbone of a polypeptide? [2 marks]

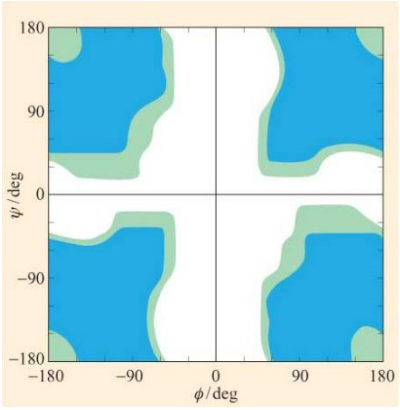
The structure of a protein is mainly formed by the φ- and ψ-angles. The ω-bond has a slightly double-bond character and is therefore almost always 180 degrees.

7. What is Ramachandran plot? Also comment on its application. [5 marks]



The Ramachandran plot is a plot of the torsional angles - phi (φ) and psi (ψ) - of the residues (amino acids) contained in a peptide. The plot was developed in 1963 by G. N. Ramachandran. Plotting the torsional angles in this way graphically shows which combination of angles are possible. The torsional angles of each residue in a peptide define the geometry of its attachment to its two adjacent residues by positioning its planar peptide bond relative to the two adjacent planar peptide bonds, thereby the torsional angles determine the conformation of the residues and the peptide. Many of the angle combinations, and therefore the conformations of residues, are not possible because of steric hindrance. By making a Ramachandran plot, protein structural scientists can determine which torsional angles are permitted and can obtain insight into the structure of peptides.

8. Find out how the Ramachandran plot for a polypeptide chain containing glycine residues looks like. What can you say about the conformations that glycine can adopt? Why does glycine differ from the other residues with respect to its conformations? [4 marks]

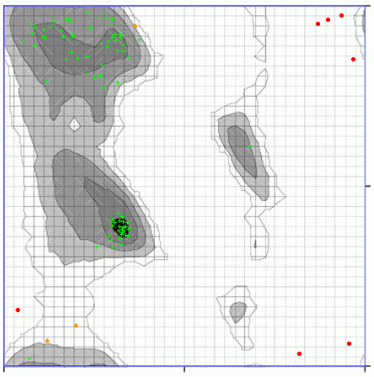


Ramachandran plot for poly-L-glycine. 'Allowed' conformations are within the blue or green areas, with those that are 'outer limit' conformations in the latter. The remaining conformations, in the white area, are 'forbidden'.

Glycine is the simplest amino acid that contains a hydrogen as its side chain. It is less sterically hindered and has much greater conformational freedom than any other amino acid residues. Therefore, glycine can adopt phi and psi angles in all four quadrants of the Ramachandran plot.

9. Functional properties of any protein are dependent on its tertiary structure. The 3D coordinates of a protein structure are generally saved in PDB format. In the absence of an experimentally solved protein structure, computational approach is used to predict the 3D structure model. Ramachandran plot is one of the most commonly used method for evaluating the correctness of the modelled protein structures.

Use the provided .pdb file of a modelled protein and generate the Ramachandran plot using the PDBsum service (http://www.ebi.ac.uk/thornton-srv/databases/pdbsum/Generate.html). Upload the given .pdb file and provide your e-mail ID. The link to the results page will be shared with you once ready. Provide the plot obtained and briefly discuss the results. Do you think it can be a reliable structure that can be used for other studies? [5 marks]



Black Dark Grey Grey Light Grey represent Highly Preferred Conformations. Delta >= -2
White with **Black Grid** represents preferred conformations. -2 > Delta >= -4
White with Grey Grid represents questionable conformations. Delta < -4
Highly Preferred observartions shown as GREEN Crosses: 85 (89.474%)
Preferred observations shown as BROWN Triangles: 3 (3.158%)
Questionable observations shown as RED Circles: 7 (7.368%)
Not Shown: 2
Total: 95

Yes, this modelled structure can be used for further studies.