

**Chapter 6 Chapter questions**  
**Proteins: Three Dimensional Structure**

Study exercises 1, 3, 4, 5, 7, 11, 12, 13 and chapter problems 4, 5, 6, 8, 9.

- 1) What is it about the peptide backbone that allows it to form defined secondary structures? *There are a limited number of rotations that can be formed due to the nature of the peptide bond. Specifically, the psi and phi bonds and how they are predicted to turn in respect to the peptide bond.*
  
- 2) Explain why glycine occurs every 3rd residue in a collagen helix. *Space. The pitch of the helix is much tighter than that found in the alpha helix. The small side chain of glycine is the only amino acid that will fit when the triple helix of collagen is formed.*
  
- 3) A primary structure of a protein
  - a) Is the association of proteins with its subunits
  - b) Is the linear sequence of amino acids \*\*\*\*
  - c) Is the ordered structure of peptide backbone such as an helix or a  $\beta$  pleated sheet
  - d) Is detected only by a polyclonal antibody
  - e) None of the above
  
- 4) The force stabilizing the alpha helix is?
  - a) Hydrogen bonds in the nearby chains
  - b) Hydrogen bonds in the same chain\*\*\*\*
  - c) Salt bridges
  - d) The decrease in entropy of water
  - e) Water under the bridge
  - f) Disulfide bonds between cysteines
  - g) Hydrophobic interactions
  
- 5) The proline limits the phi and psi bonds possible in an alpha helix. This is due to?
  - a) The increase in flexibility of the peptide bond
  - b) The small size of proline R group
  - c) The cyclic nature of the side group of proline \*\*\*\*
  - d) The decreased steric hindrance due to the small side group of proline
  
- 6) A gene is mutated such that the amino acids glycine and alanine are now glutamate and leucine respectively. What are the potential results of each of these mutations? Assume that the mutations are not near each other in the primary sequence. *The glycine-glutamate change is very significant. Not only in size but most importantly because of the change in hydrophobicity. Before the mutation the glycine was most likely founding the interior of the protein or in a local hydrophobic enviroment. Now the charge of the carboxyl group will not allow the same conformation. The amino acid is now likely to be found shifted to the surface of the protein. The alanine and leucine change is less dramatic and considered conserved. That is the hydrophobic nature of the amino acids has*

*not been significantly altered. Other than slight shifts due to size, one would not expect a large structural change.*

7) A protein that is normally an alpha helix at low pH is distorted and curves or bends at a neutral and higher pH. Why? The only unique feature about the primary sequence is that every fourth amino acid is glutamate. *To best understand this question you have to consider the nature of the alpha helix. If every fourth aa is a glutamate, then they will generally be lined up on one side of the helix. As the pH increases the side chains will become unprotonated and an ionic clash will result. The bend is due to the amino acids trying to "get away" from each other.*

- 8) A secondary level of protein structure
- a) Is the linear sequence of amino acids
  - b) Is the association of proteins with its subunits
  - c) Is the ordered structure of amino acids such as an  $\alpha$  helix or a  $\beta$  pleated sheet. \*\*\*\*\*
  - d) Is detected only by a polyclonal antibody