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PROTEIN STRUCTURE AND FUNCTION

REVIEW THE CONCEFTS 0 2 0 6 Theorem of the polypeptide chain. The tertiary structure of a protein is the various spatial arrangements that result from folding localized regions of the polypeptide chain. The tertiary structure of a protein is the overall conformation of the polypeptide chain, its three-dimensional structure. Secondary structures, which include the alpha (*a*) helix and the beta (*b*) sheet, are held together by hydrogen bonds. In contrast, the tertiary structure is pri-marily stabilized by hydrogen bonds between non-polar side chains of the amino acids and hydrogen bonds between polar side chains. (The quaternary structure describes the number and relative positions of the subunits in a multimeric protein.)

- 2. Despite the fact that folded proteins adopt conformations that are energetically favorable, the amount of time required for a particular protein to arrive at this conformation on its own can vary significantly. This is especially true if there are other "quasi-stable" conformations available to the polypeptide. Molecular chaperones function to protect an unfolded protein from participating in interactions that will take it off the "pathway" to its native, functional conformation. Chaperonins provide similar support to an unfolded protein. However, chaperonins can also use encapsulation and ATPase activity to give energetic "kicks" to misfolded proteins and get them back on the pathway toward their native folded state.
- 3. The active site of an enzyme is the region within which the substrate binds and is converted into product. The turnover number (k_{cat}) is the rate constant that can be used to calculate the rate at which a product is formed (*V*). The Michaelis constant