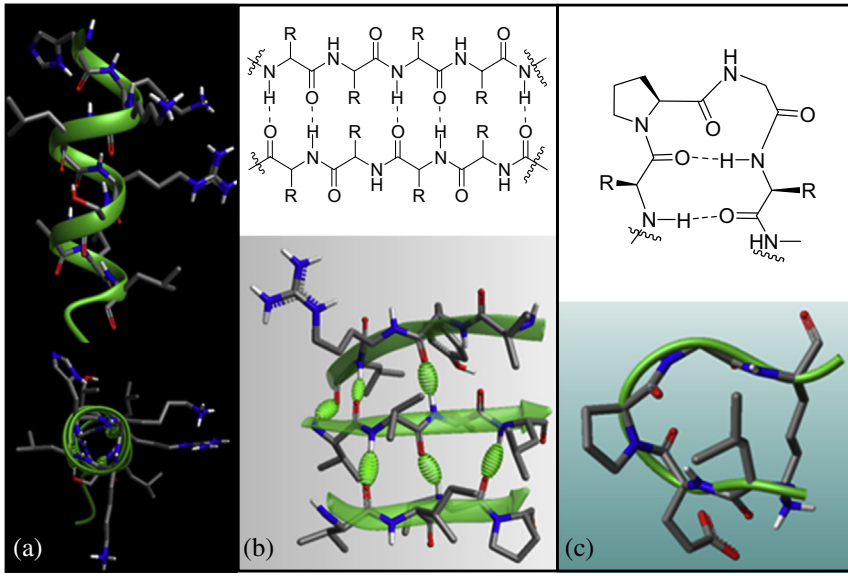

FIGURE 3.9 (a) The α-helix is a common structural motif in proteins that is formed by hydrogen-bonding interactions between the amide units in the backbone of a peptide chain. There are 3.6 amino acid residues per turn, and each complete turn is 5.4 Å in length. The side chains protrude from the barrel shape formed by the rotation of the peptide chain as seen in the two views provided. (b) β-Sheets are formed from extended peptide chains connected by a series of hydrogen bonds between the backbone amide moieties of each chain. The peptide chains can be either parallel or antiparallel to each other. (c) β-Turns occur when four to five amino acids in a peptide chain form a 180° turn. They are stabilized by hydrogen bonding and are often found between β-sheets.

defines its three-dimensional shape, and therefore its function. The major drug targets, enzymes, GPCRs, ion channels, and membrane transport proteins (transporters) are all protein structures created by the aforementioned forces. While there are certainly additional available drug targets, such as protein/protein interactions, DNA, and RNA, the pharmaceutical industry has focused most of its energy, sometimes unknowingly, on these classes of targets. As such, an exploration of each class is warranted.

ENZYMES

In simplest terms, enzymes are protein catalysts employed by nature to facilitate the chemical transformations required to sustain life. The concept of enzymes was first proposed by Wilhelm Kühne in 1877, but it was not until many years later that it would be recognized that enzymes are a kind of protein. Jack bean urease, the enzyme responsible for converting urea into ammonia and carbon dioxide, was crystallized by James B. Sumner in 1926 and was the first enzyme to be recognized as a