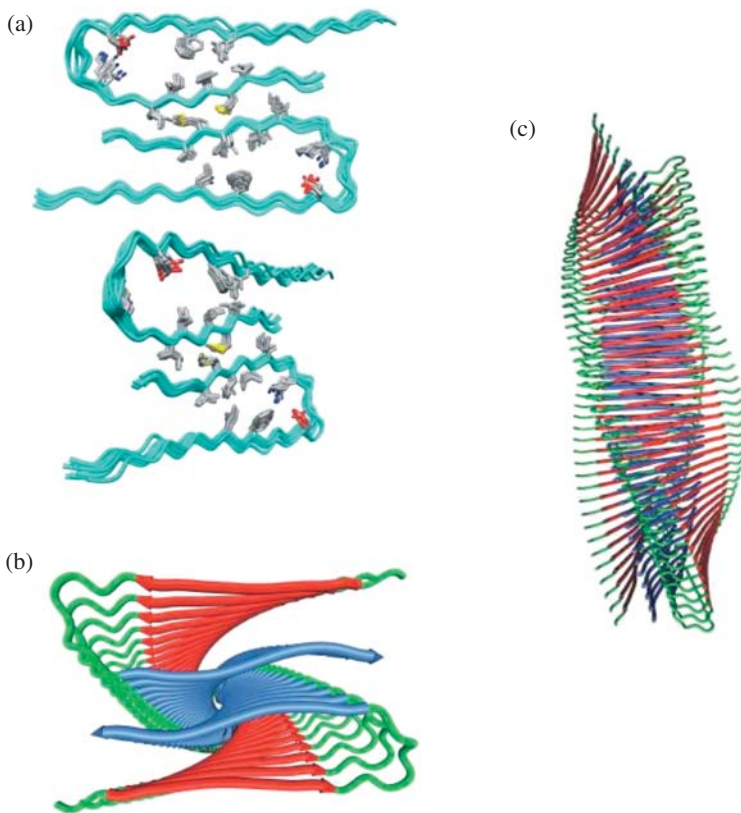
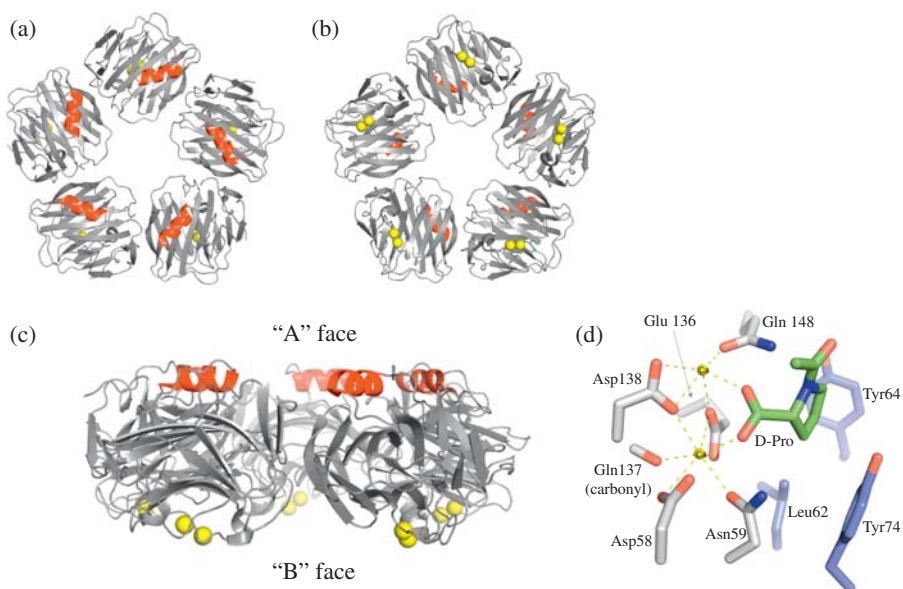


**FIGURE 26.1** Proposed structure of an TTR fiber based on deuterium exchange protection NMR and electron spin resonance data. Destabilization of strands C and D along with small modifications of the native fold expose edge strands A and B, leading to fiber formation and propagation. Loops between strands along with the N and C termini are exposed on the surface of the fiber, providing potential ligands for SAP. (From [28], with permission. Copyright © 2004 American Society for Biochemistry and Molecular Biology.)



**FIGURE 26.2** Proposed structure of Aβ(1–40) amyloid. (a) Aβ dimers interacting via hydrophobic residues 30 to 40. Dimers can be layered (b) with (c) illustrating how stacking can lead to fibril morphology. (Adapted from [33].)



**FIGURE 26.3** Three orientations of the SAP pentamer: (a) the five  $\alpha$ -helices on the A face of the protein, (b) the five double calcium binding sites on the B face of the protein with calcium atoms in yellow; and (c) side view of the pentamer (made from the coordinates 1SAC [40] and using the program PyMOL [61]); (d) calcium-binding site of SAP with the ligand D-proline. Residues making up the hydrophobic pocket are shown in blue, calcium coordinating residues in gray, and calcium atoms in yellow and the ligand green (prepared using PyMOL [61]).