

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.)

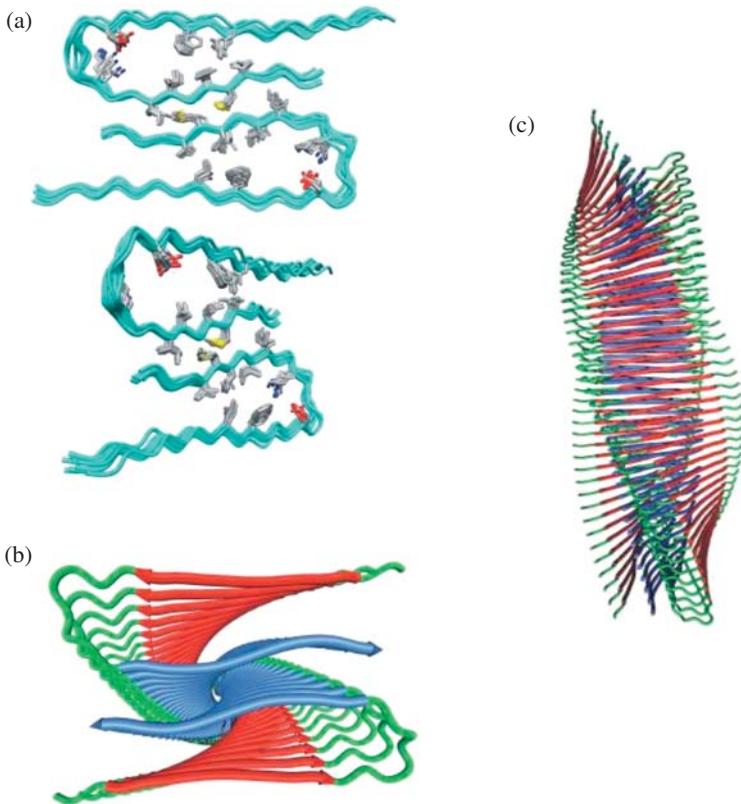


FIGURE 26.2 Proposed structure of Aβ(1-40) amyloid. (a) Aβ dimers interacting via hydrophobic residues 30 to 40. Dimers can be layered (b) with (c) illustrating how stacking can lead to fibril morphology. (Adapted from [33].)

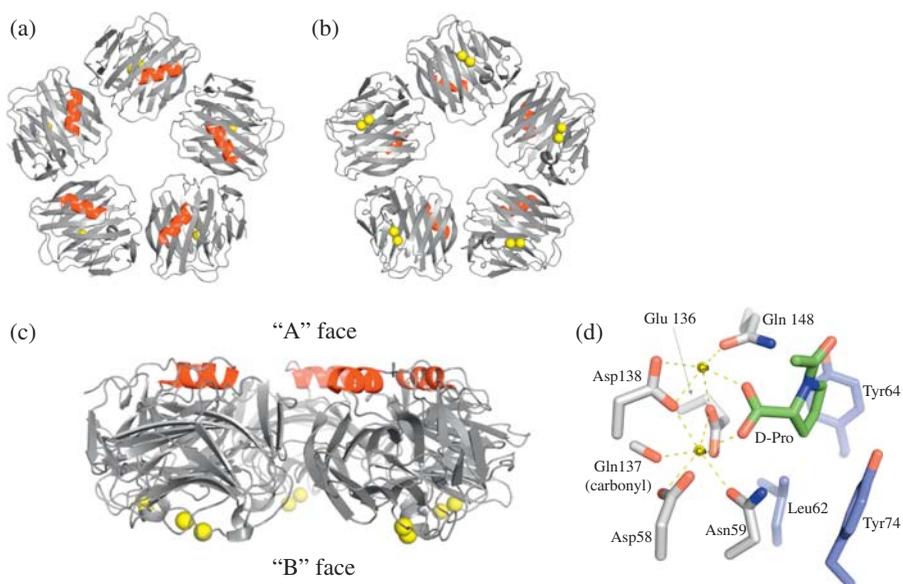


FIGURE 26.3 Three orientations of the SAP pentamer: (a) the five α -helices on the A face of the protein, (b) the five double calcium binding sites on the B face of the protein with calcium atoms in yellow; and (c) side view of the pentamer (made from the coordinates 1SAC [40] and using the program PyMOL [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]).