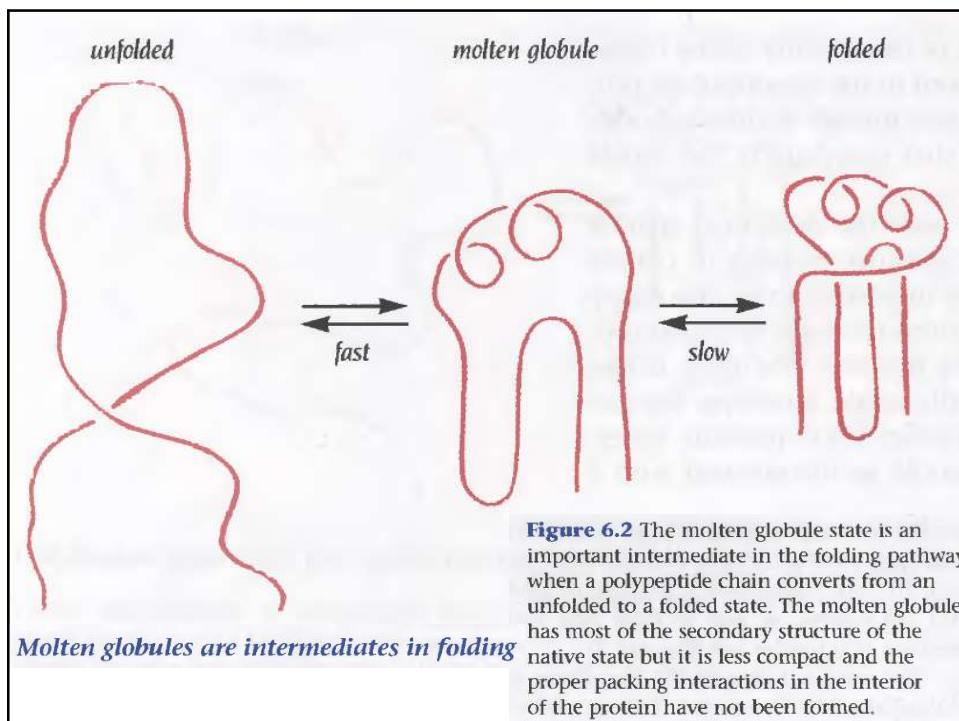
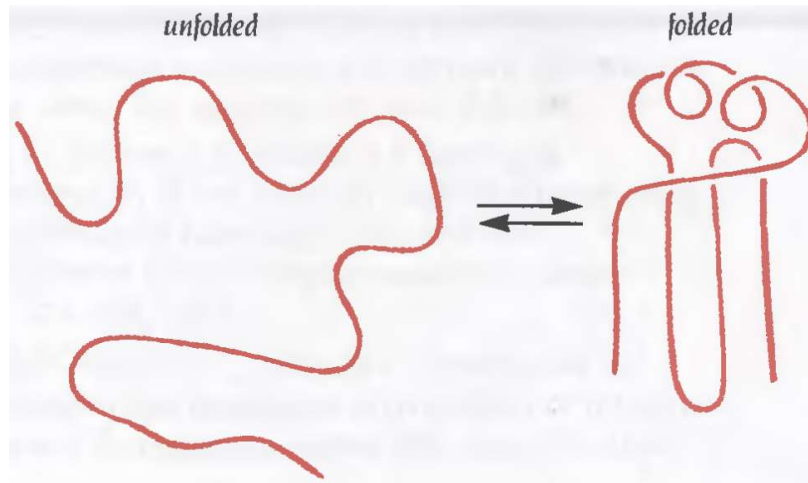
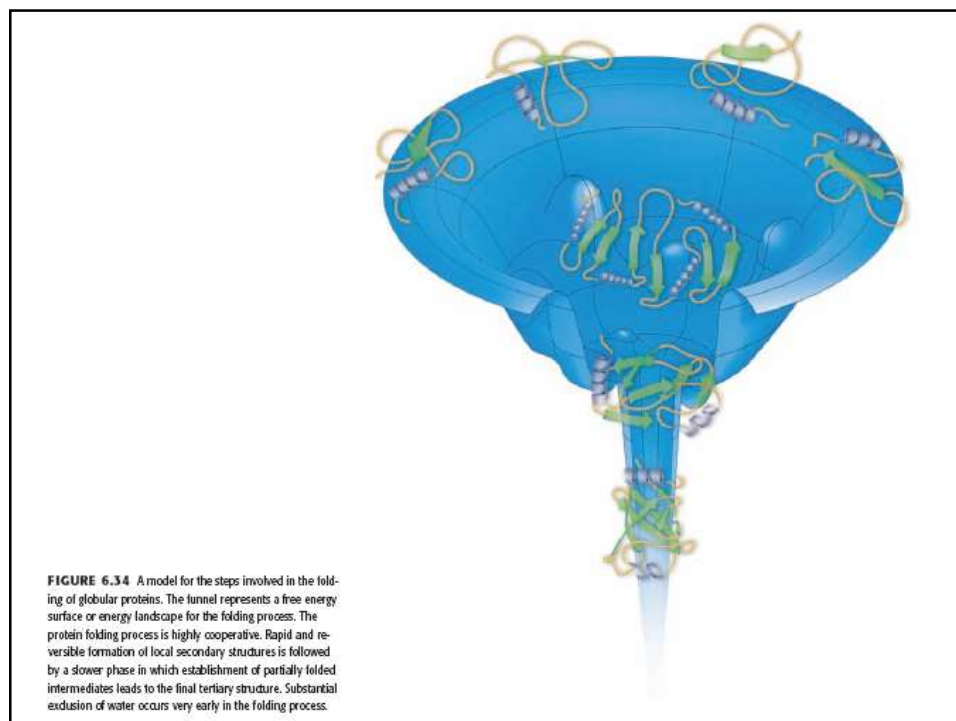
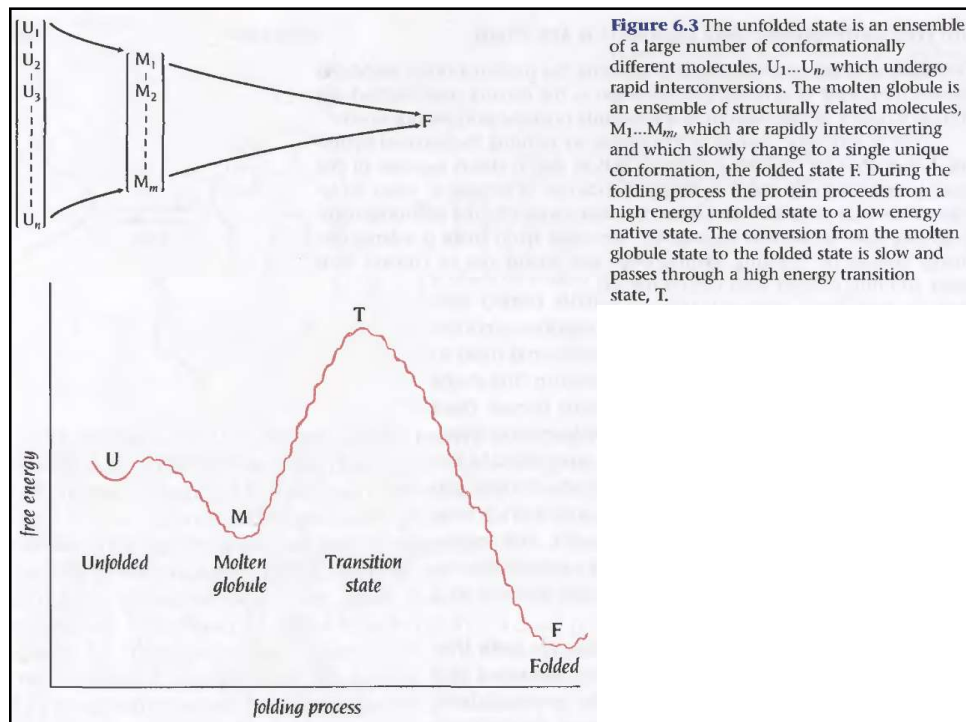


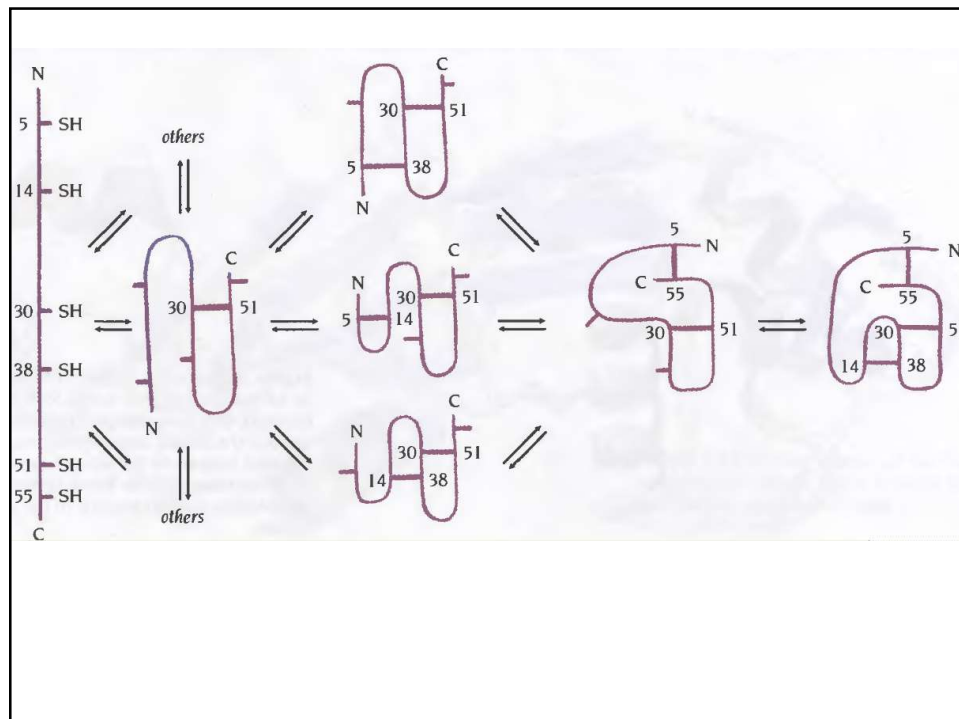
Folding and Flexibility

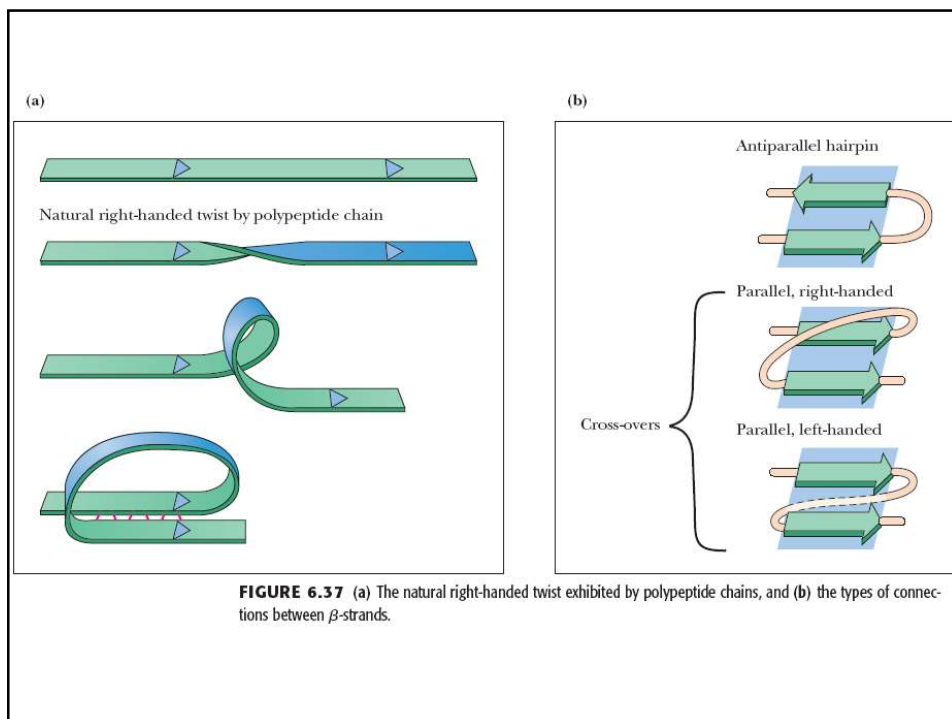
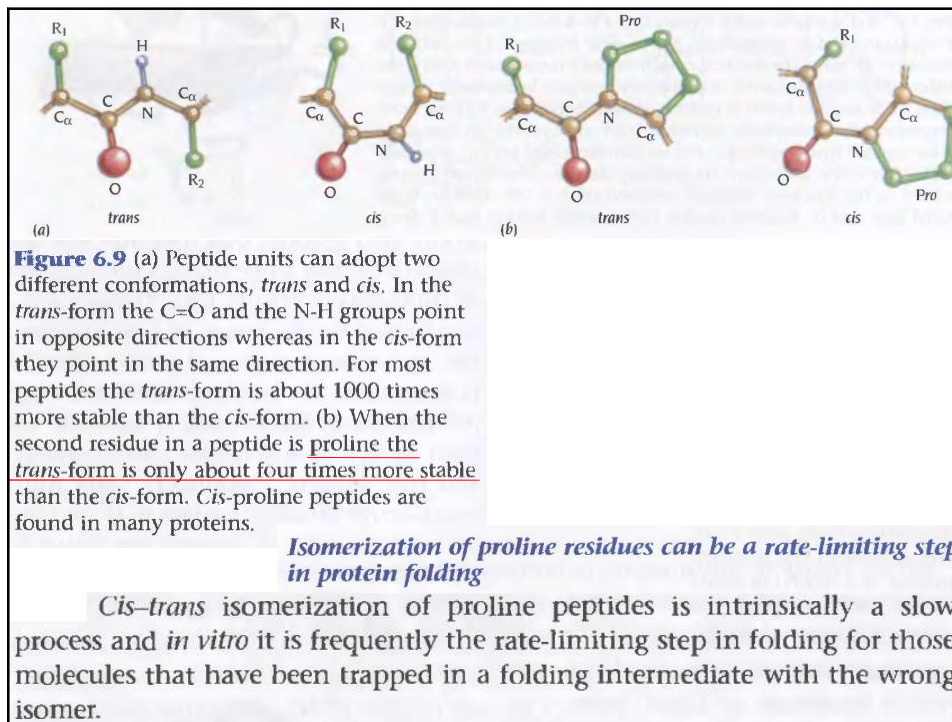




Many proteins can fold spontaneously *in vitro*, although some appear to fold more slowly/less accurately than they do *in vivo*. Although the primary sequence ultimately dictates tertiary structure, several obstacles to correct folding exist, including:

- aggregation of partially folded intermediates via intermolecular hydrophobic interactions;
- isomerization of proline residues;
- formation of disulfide linkages between incorrect pairs of cysteine residues.





Some Proteins Are Intrinsically Unstructured

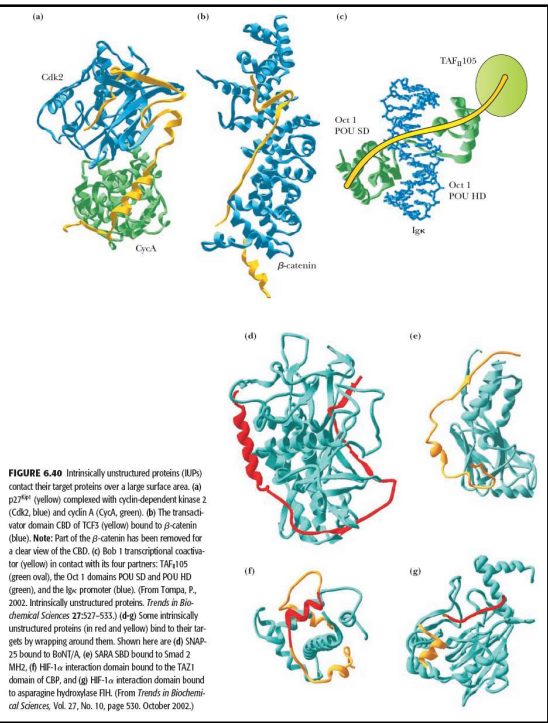


TABLE 6.3 Aggregation Symmetries of Globular Proteins	
Protein	Number of Subunits
Alcohol dehydrogenase	2
Malate dehydrogenase	2
Superoxide dismutase	2
Triose phosphate isomerase	2
Glycogen phosphorylase	2
Aldolase	3
Bacteriochlorophyll protein	3
Concanavalin A	4
Glyceraldehyde-3-phosphate dehydrogenase	4
Immunoglobulin	4
Lactate dehydrogenase	4
Prealbumin	4
Pyruvate kinase	4
Phosphoglycerate mutase	4
Hemoglobin	2 + 2
Insulin	6
Aspartate transcarbamoylase	6 + 6
Glutamine synthetase	12
TMV protein disc	17
Apo ferritin	24
Coat of tomato bushy stunt virus	180

