Protein Folding

Sem-2

Dr. Swapna Mukherjee

Department of Microbiology

Insertion into ER &Protein folding

- *single-pass transmembrane proteins* have their hydrophilic N-terminal segment on the exoplasmic face and their hydrophilic C-terminal segment on the cytosolic face; other single-pass proteins have the reverse orientation.
- *multi- pass transmembrane proteins* have membrane-spanning α-helical segments

- Typically, **protein translocation** into the ER involves cleavable amino terminal signal peptides in precursor proteins and sophisticated transport machinery.

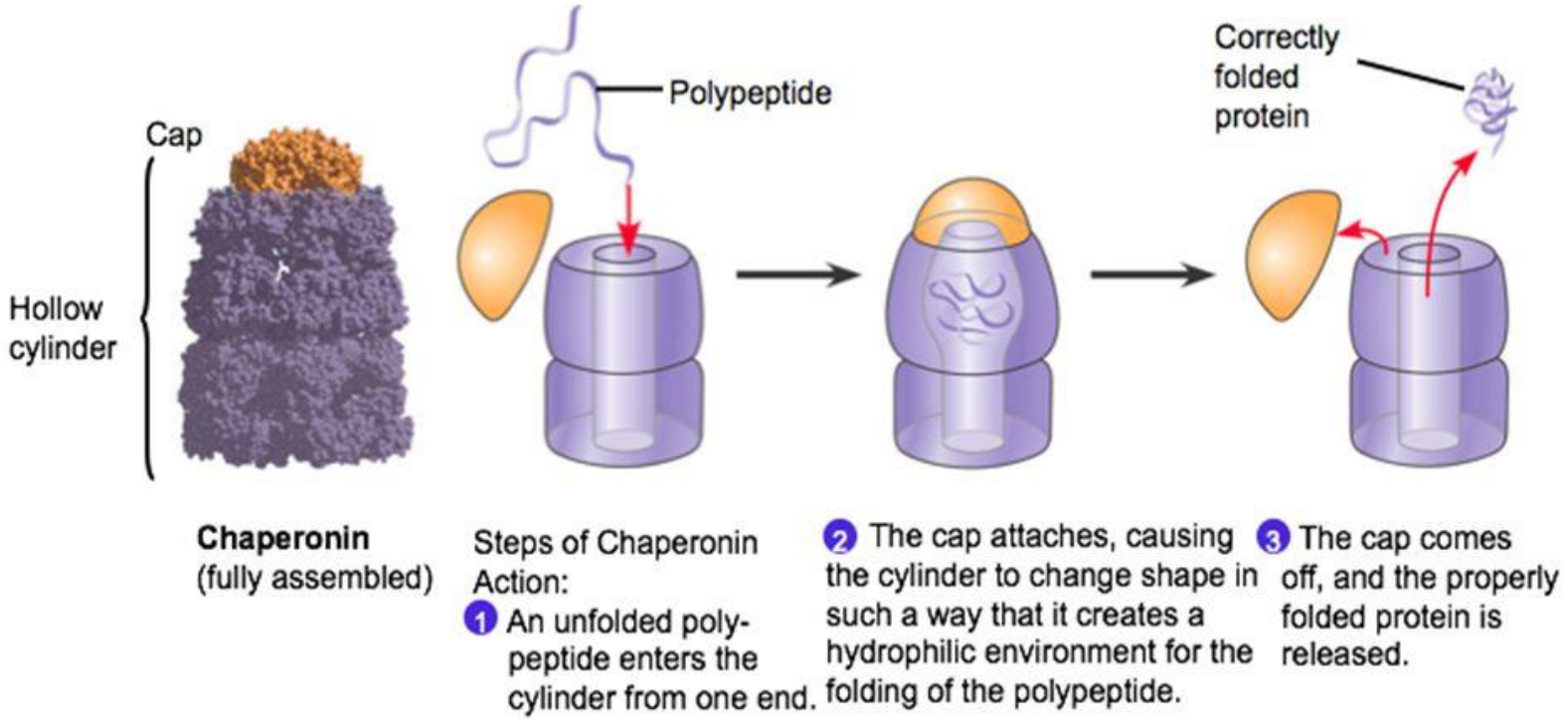
- The signal peptides for ER targeting are 15 to 30 amino acid residues in length

- They have a tripartite organization, comprised of a core of hydrophobic residues flanked by a positively charged amino terminal and a polar, but uncharged carboxy terminal region

- **GroEL** belongs to the chaperonin family of molecular chaperones, and is found in a large number of bacteria.
- **GroEL** is a dual-ringed tetradecamer, consisting of seven subunits each.
- **GroEL** requires the lid-like cochaperonin protein complex **GroES**.
- In eukaryotes, proteins **Hsp60** and **Hsp10** are structurally and functionally nearly identical to GroEL and GroES, respectively

Chaperonins

– Are protein molecules that assist in the proper folding of other proteins



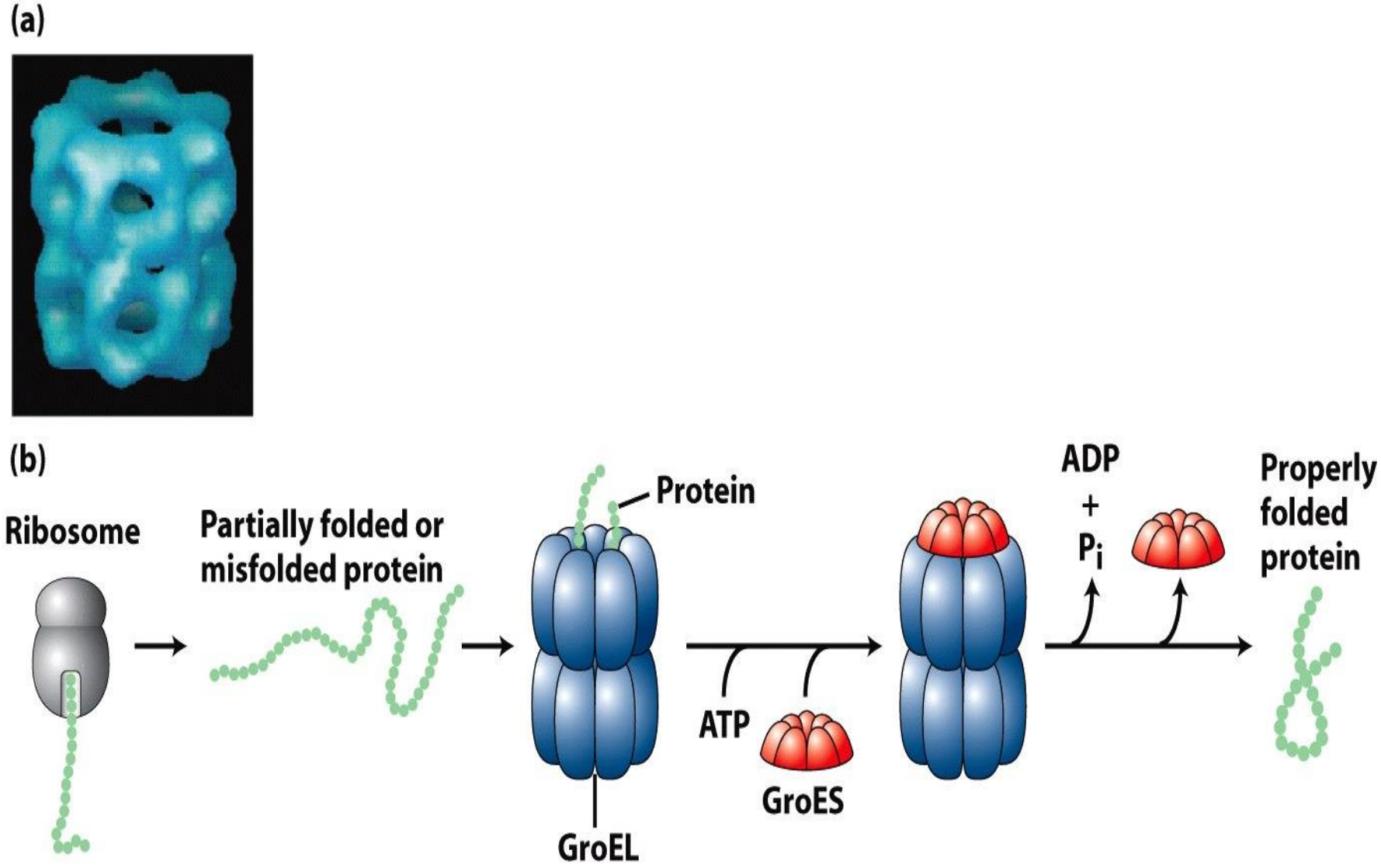


Figure 3-17
Molecular Cell Biology, Sixth Edition