

Proteins		
Protein folding	not very efficient = about 30% of all newly synthesized polypeptides are misfolded and tagged	
ubiquitin liagase	ubiquitin tags misfolded proteins for the proteasome to breakdown	
Primary structure	<i>initial</i> folding of linear polypeptide is driven by hydrogen bond formation of polypeptide backbone to form alpha-helices and beta-sheets - to form the secondary structure	tertiary driven hydrophobic collapse

Enzymes		
Enzymes	often change shape when they bind their substrate(s).	NOT <i>always</i> protien
allosteric site	CAN be the same as an active site	ATP can be a substrate at active site or bind allostericly as inhibitor



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