Cheatography

Bioc 201 Midterm 1 Review Cheat Sheet

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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 linear polypeptide chain -- amino acids linked together	*initial* 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 *always* protien
allosteric site	CAN be the *same* as an active site	ATP can be a substrate at active site or bind allostericly as inhibitor