

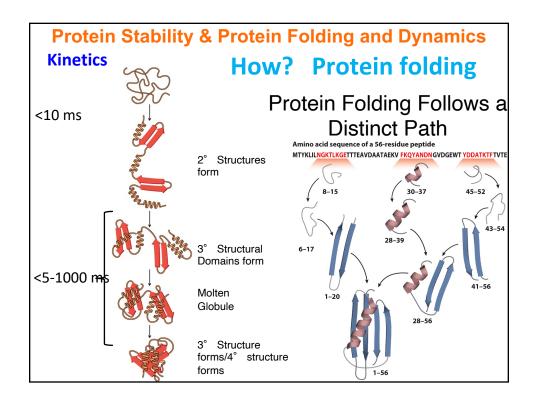
Protein Stability & Protein Folding and Dynamics

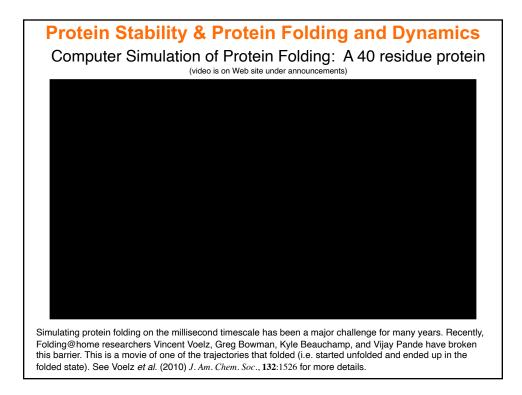
Primary structure determines Tertiary structure!

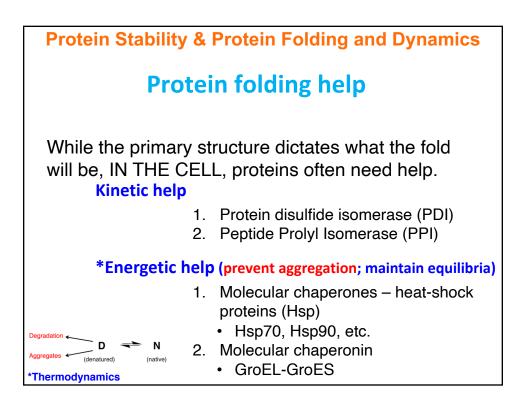
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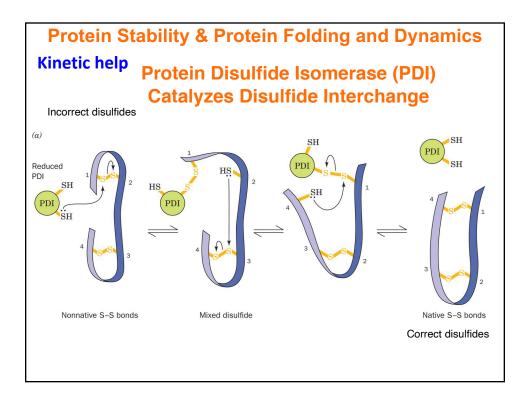
How Can Proteins Fold So Fast?

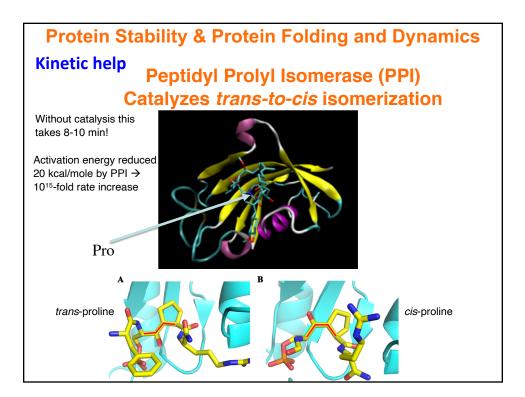
- Proteins fold to the lowest-energy state in the µsec– sec time scales. How can they find the right fold so fast?
- It is mathematically impossible for protein folding to occur by randomly trying every conformation until the lowest-energy one is found (Levinthal's paradox).
- Search for the minimum is therefore not random; there must be a PATHWAY toward the native structure, which is thermodynamically most favorable.

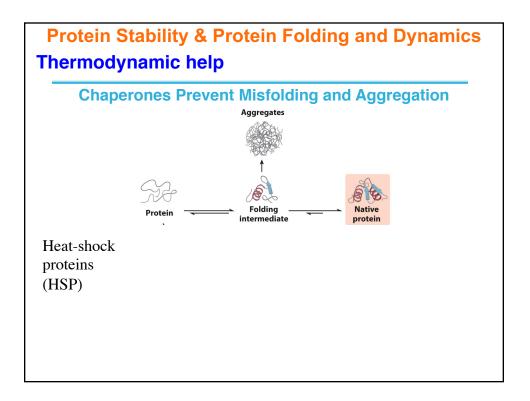


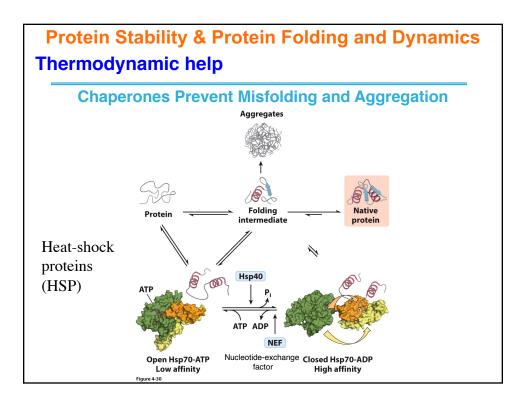


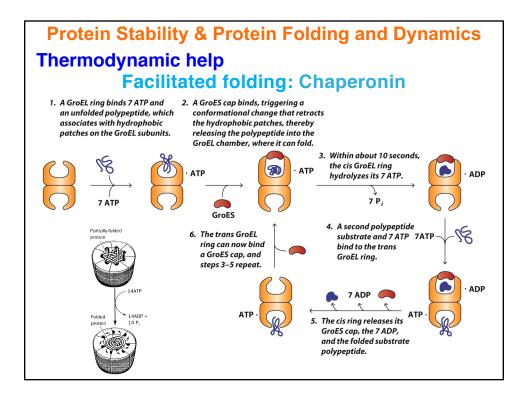


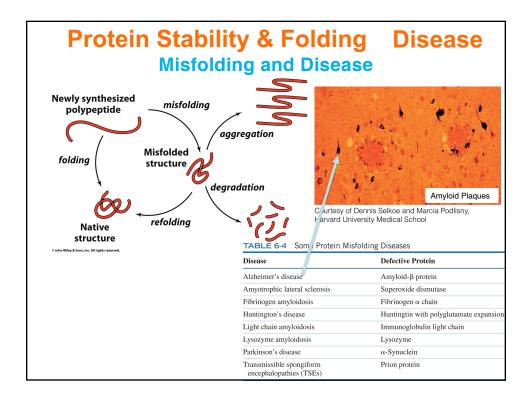


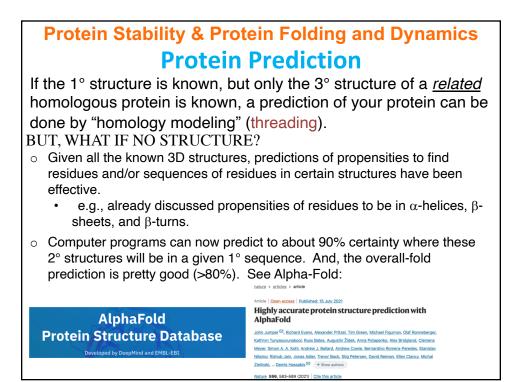












Protein Stability & Protein Folding and Dynamics Protein Stability

Key Concepts

• Protein stability depends primarily on hydrophobic effects and secondarily on electrostatic interactions.

- · A protein that has been denatured may undergo renaturation.
- Protein structures are flexible and dynamic; may include unfolded regions.

Key Concepts

Protein Folding

· Primary sequence dictates tertiary fold.

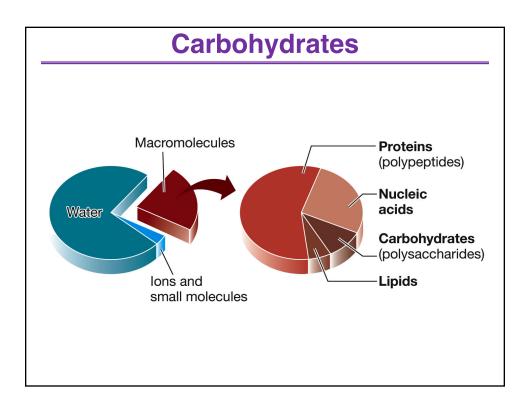
• A folding protein follows a pathway from high energy and high entropy to low energy and low entropy.

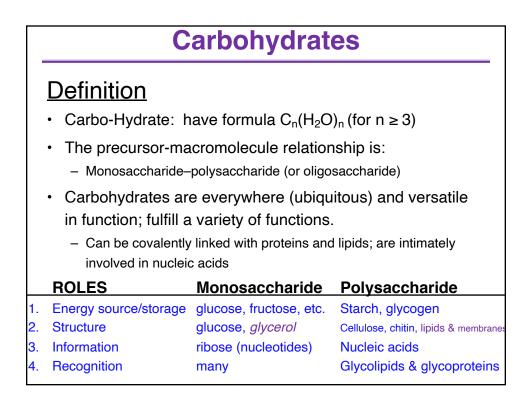
• Protein disulfide isomerase (PDI) catalyzes disulfide bond formation/exchange and Peptidyl Prolyl Isomerase (PPI) catalyzes *cis*-proline peptide bond formation.

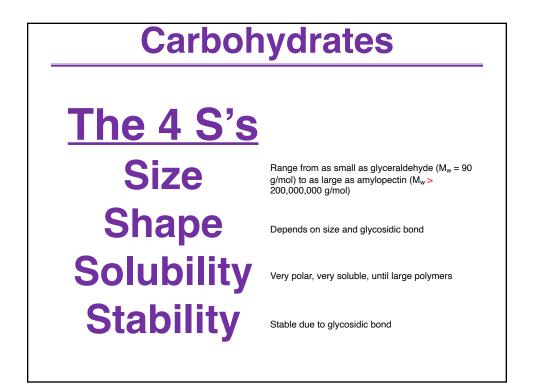
• A variety of molecular chaperones assist protein folding via an ATPdependent bind-and-release mechanism, including the Chaperonin "Anfinsen Chamber."

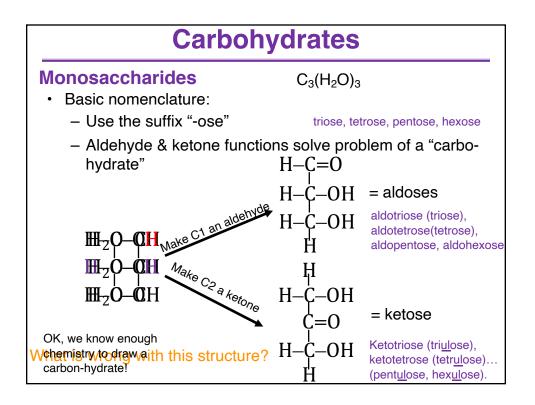
• Amyloid diseases result from protein misfolding, with many misfolded proteins forming fibrils with extensive β structure.

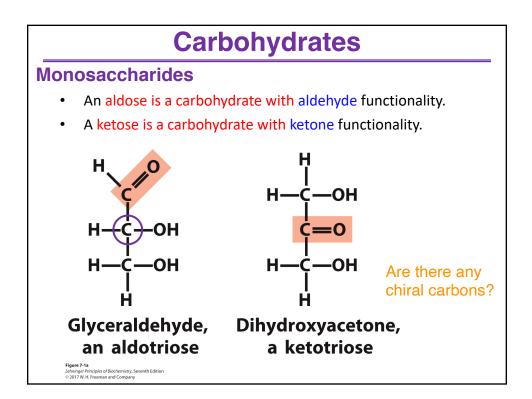


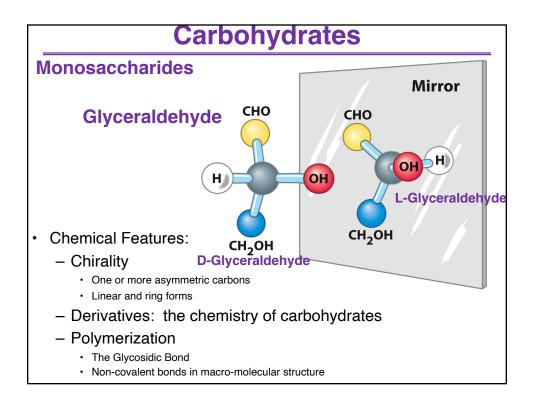


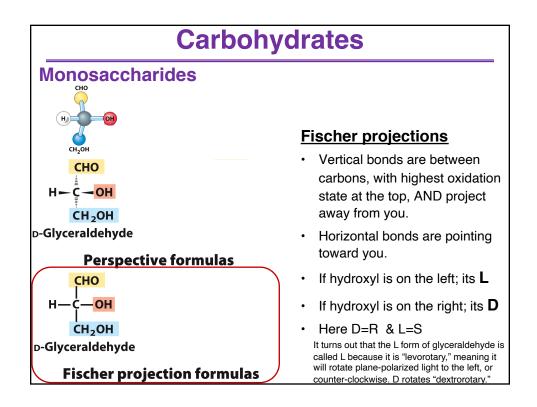


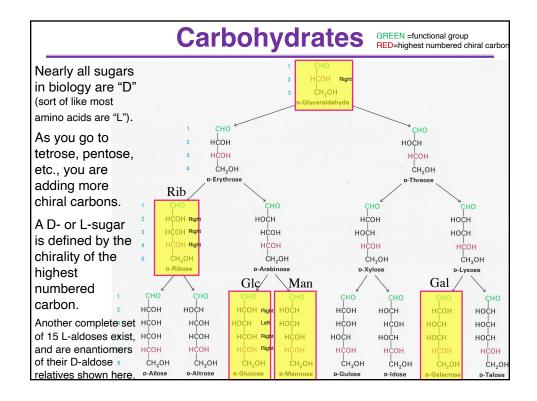


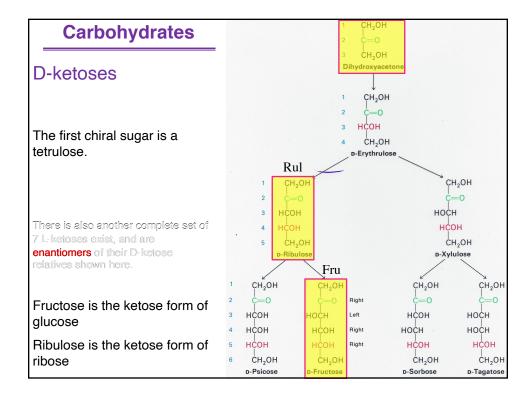


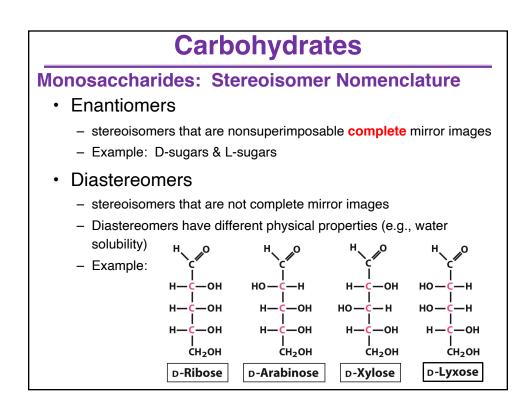


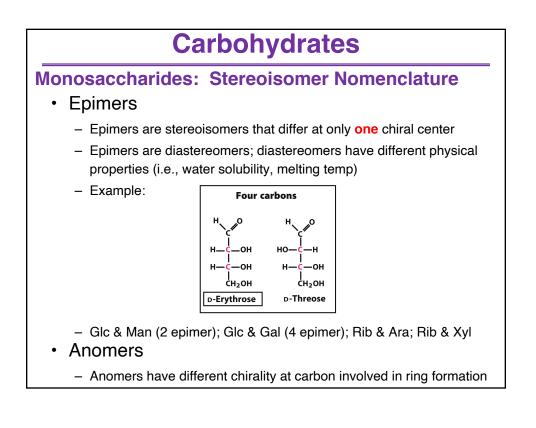


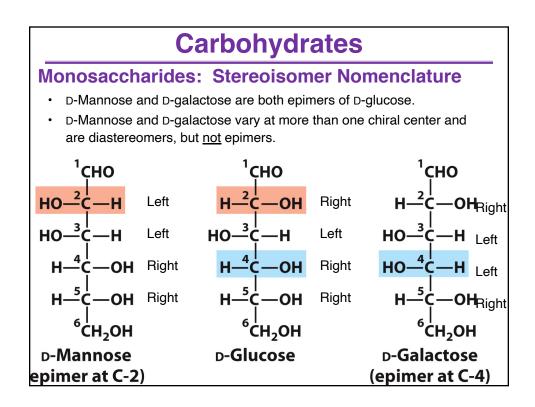


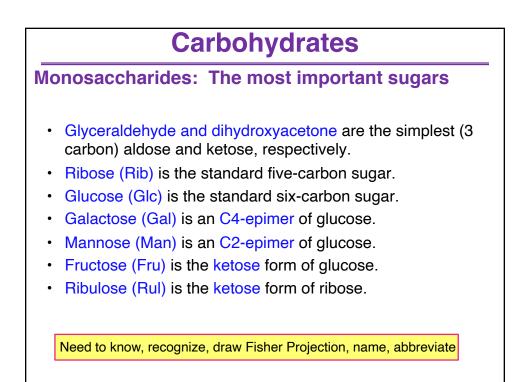


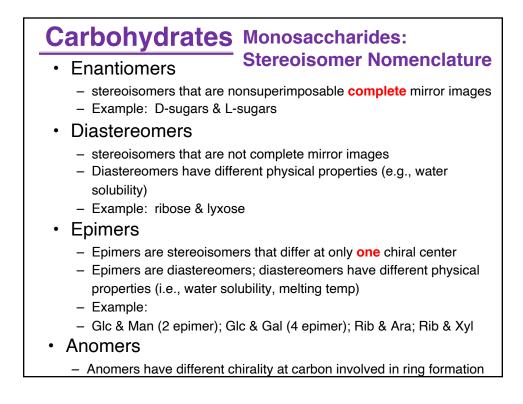


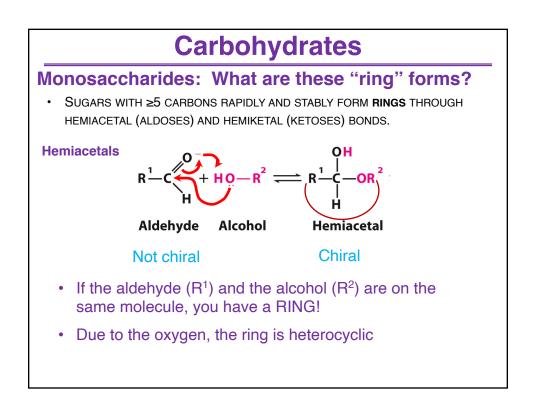


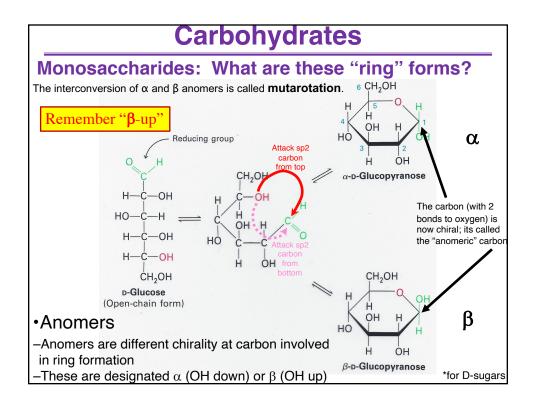


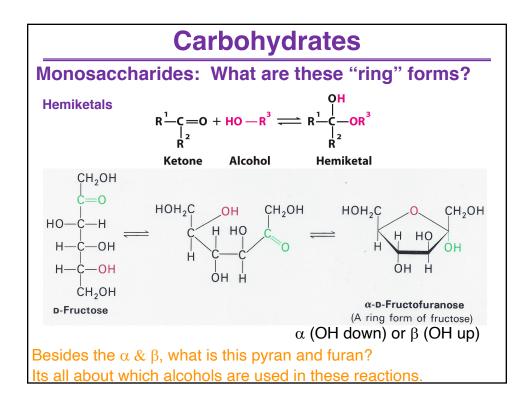


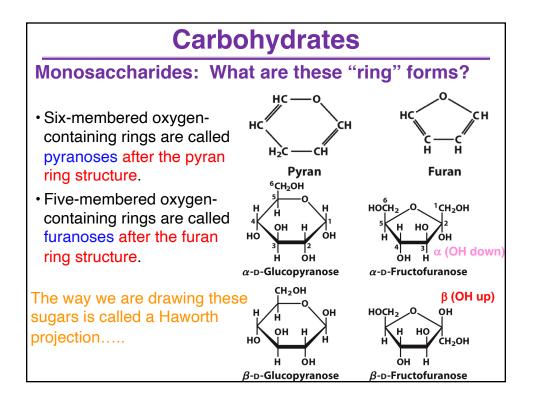


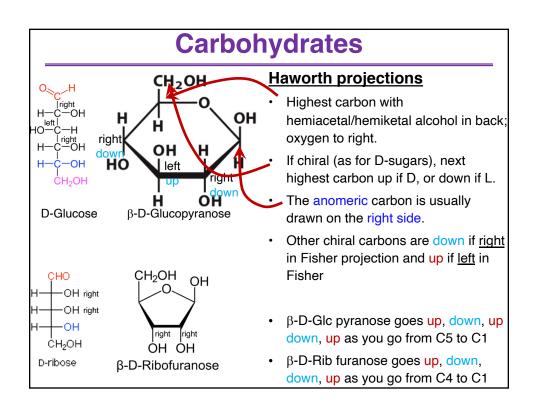


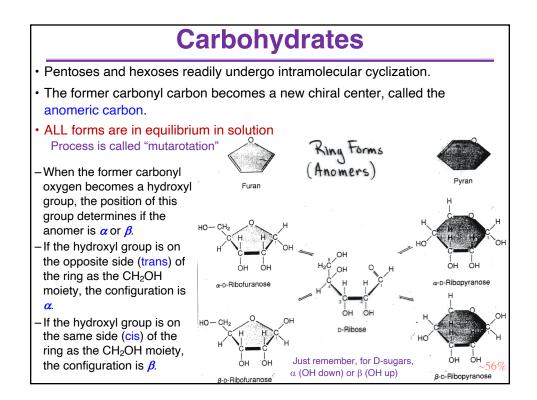












Carbohy	vdrates
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Relative amounts of tautomeric forms for some monosaccharide sugars at equilibrium in water at 40°C^a

Mono- saccharide	Relative Amount (%)					
	α-Pyranose	β-Pyranose	α-Furanose	β-Furanose	Total Furanos	
Ribose	20	56	6	18	24	
Lyxose -	71	29	ь	ь	<1	
Altrose	27	40	20	13	33	
Glucose	36	64	b	ь	<1	
Mannose	67	33	ь	b	<1	
Fructose	3	57	9	31	40	
^a In all cases, the of Angyal. The com	open-chain form position and co	is much less th nformation of s	an 1%. For dat sugars in solution	a on other suga on, Angew. Cho	rs, see S. m. 8:157	

