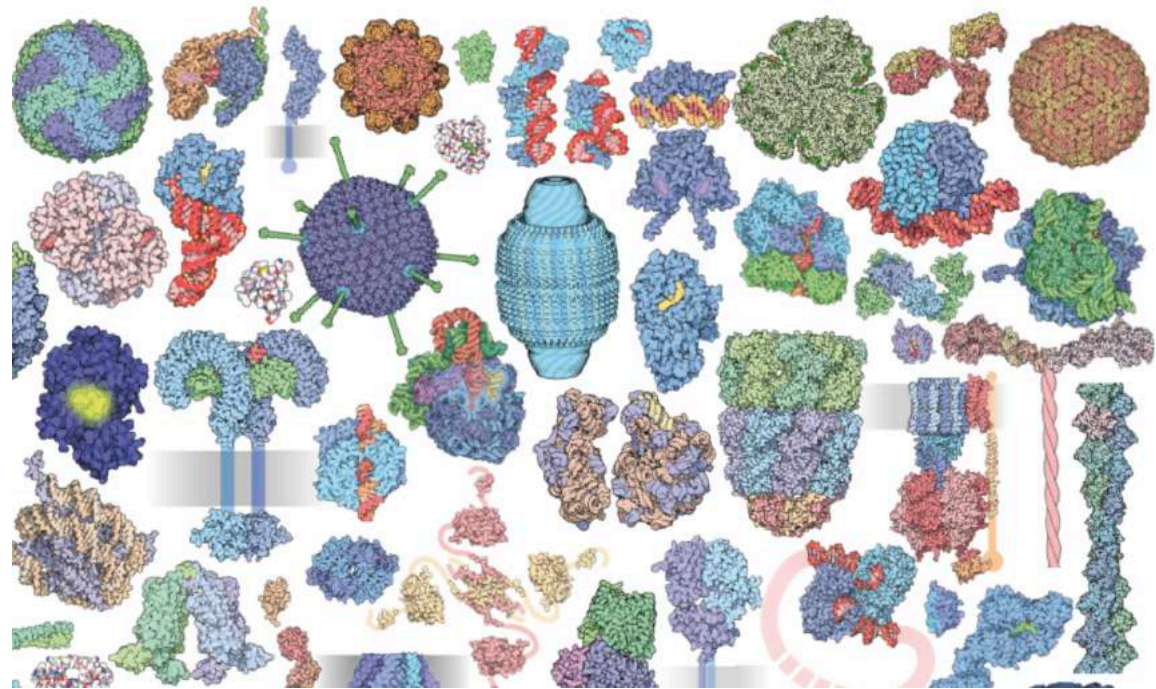
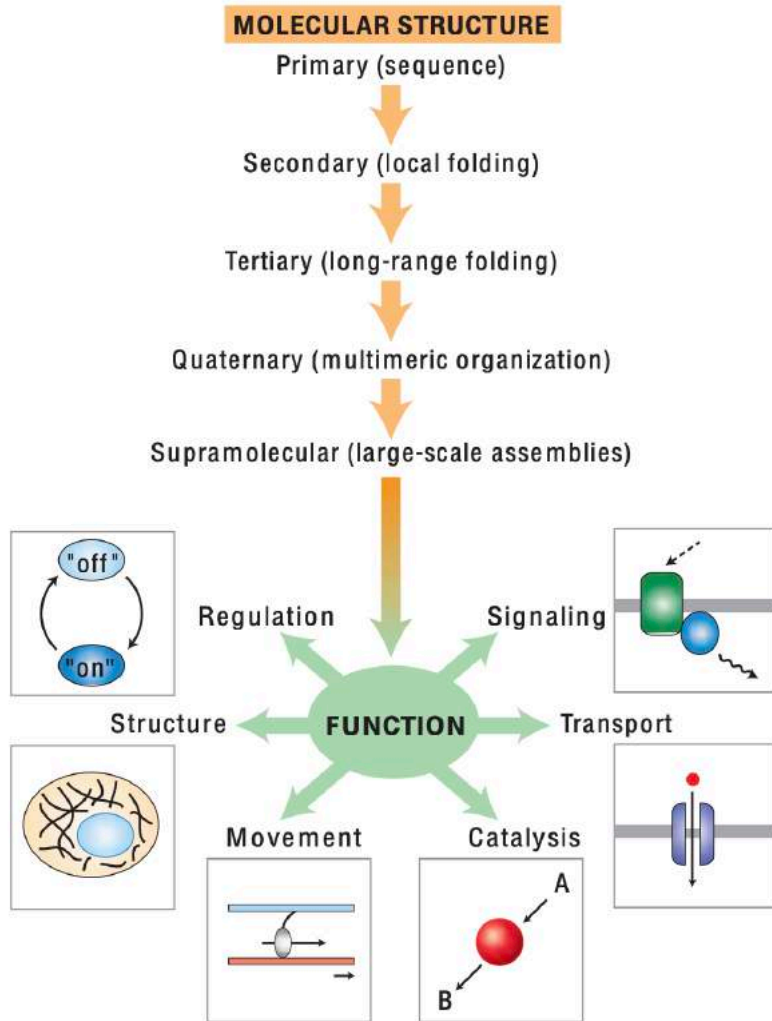


Recap

The four levels of protein hierarchy:

- **Primary structure:** The linear sequence of amino acids linked together by peptide bonds
- **Secondary structure:** Localized spatial arrangement of the polypeptide chain
- **Tertiary structure:** Complete three-dimensional structure of a polypeptide chain
- **Quarternary structure:** Some individual polypeptides with their own tertiary structures can associate into a quaternary structure defining a multi-chain complex.

Protein structure and function are correlated

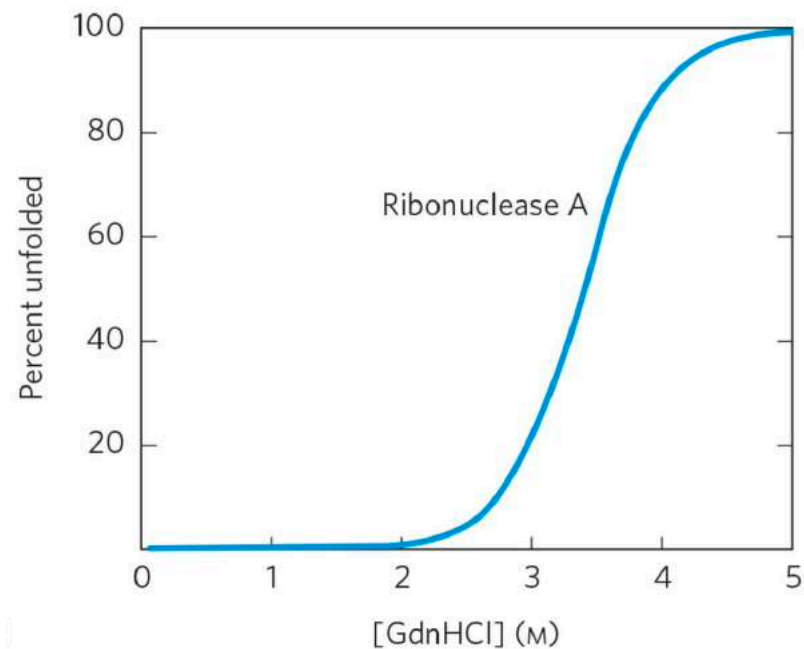
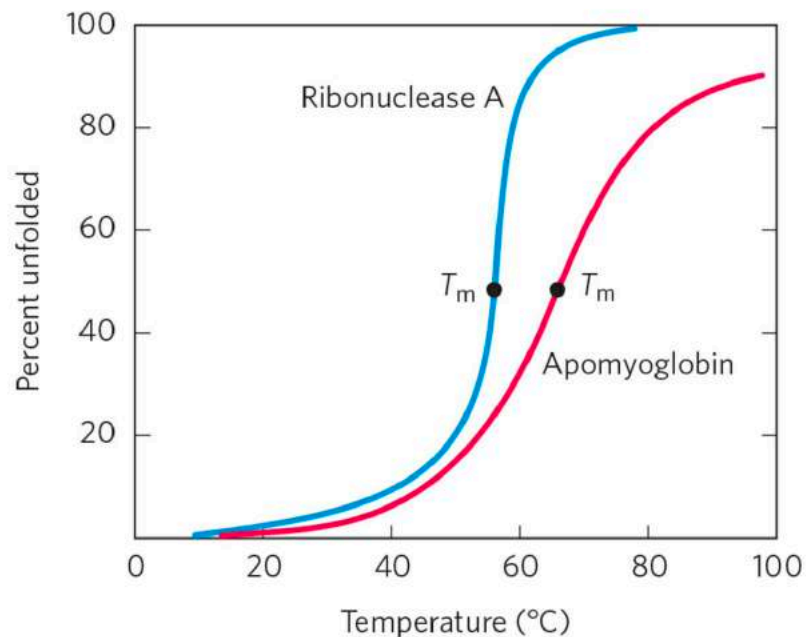


Diverse macromolecular assemblies can be made from the diverse protein structures created from the same 20 amino acids

Protein denaturation

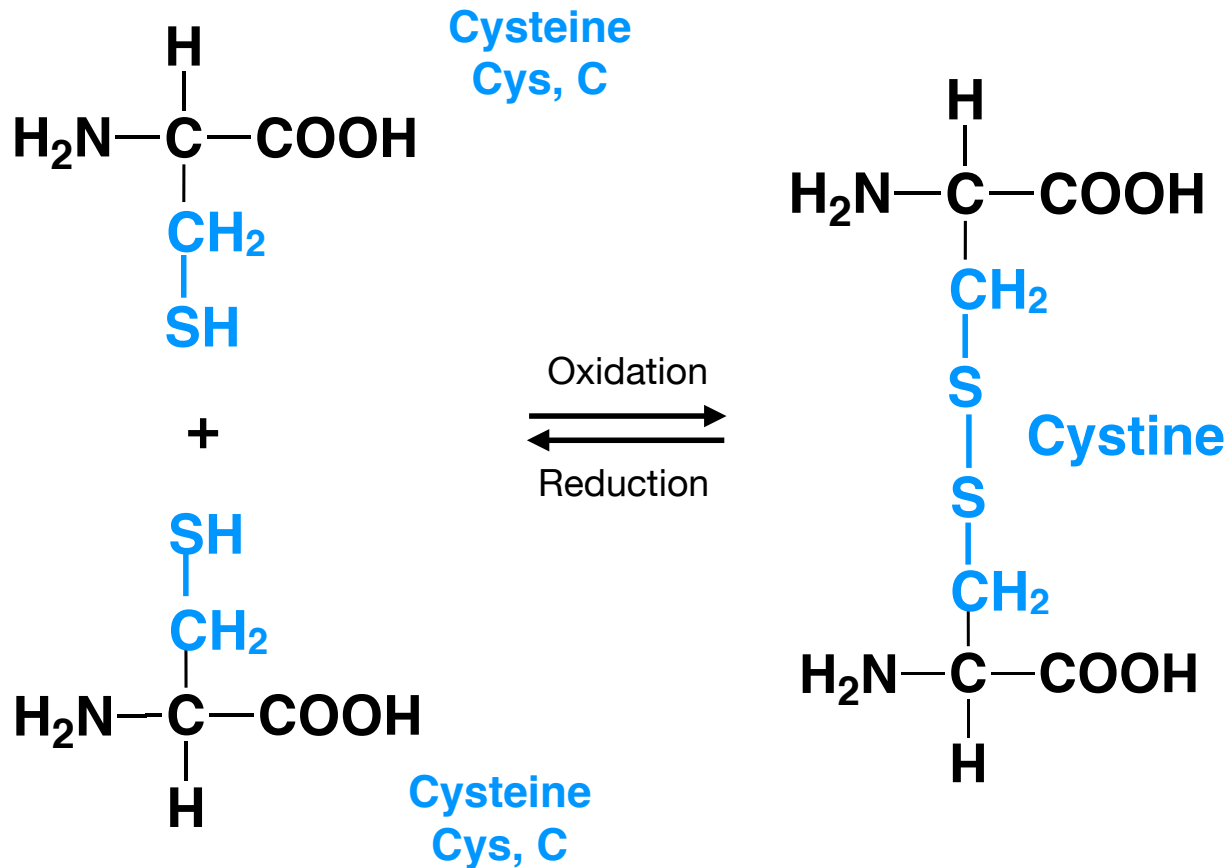
Loss of structure causes loss of function in proteins

Certain globular proteins can be denatured (lose their native conformation) by heat, extremes of pH, or denaturing reagents



Cystine: recap

Disulfide bonds



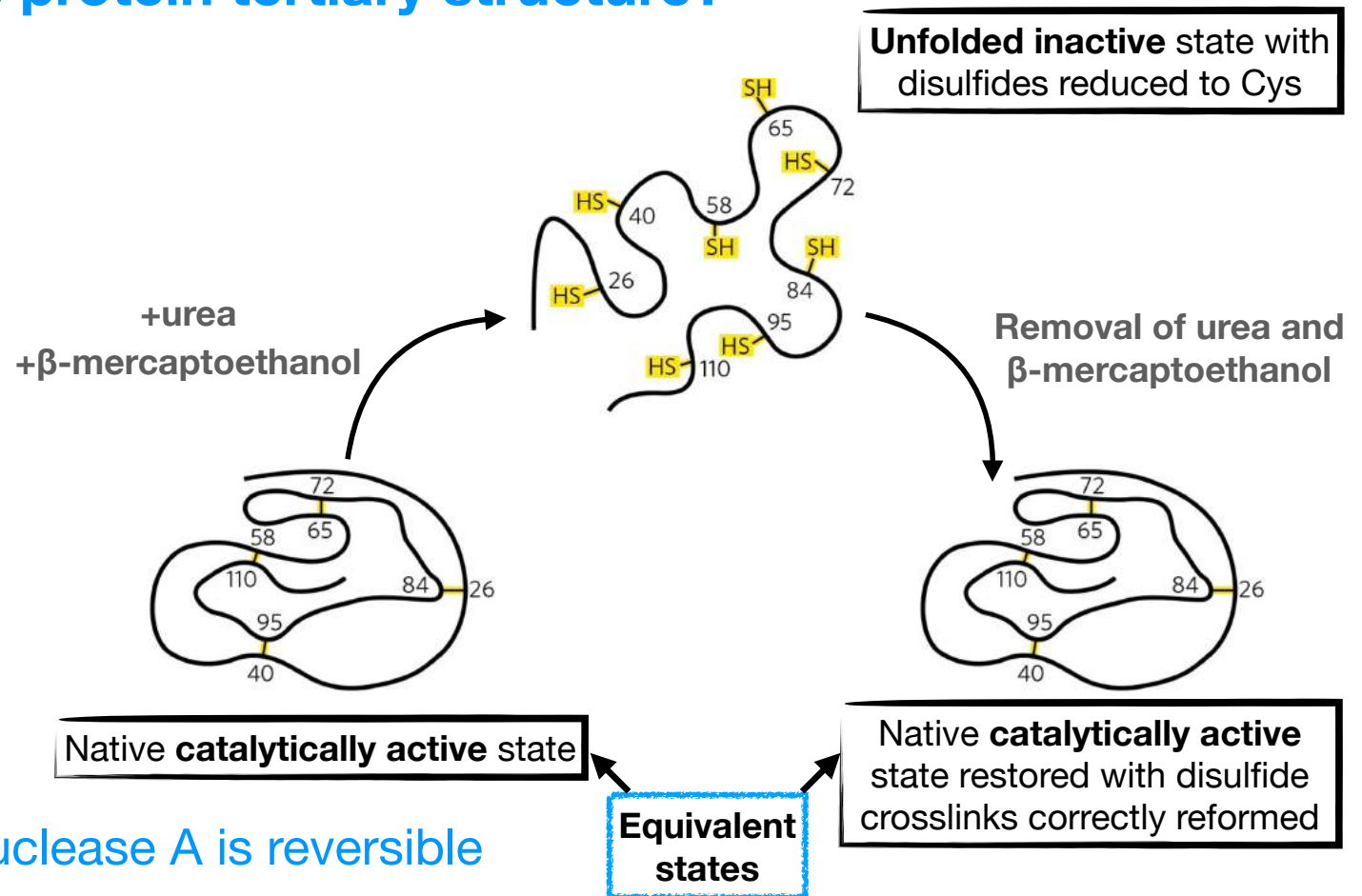
- **Disulfide bridges** (or S-S linkages/bonds) can form between two side chain cysteines and result in a **cystine**.
- S-S bonds are important for the **structural integrity** of peptides and proteins and influence protein structure at the secondary and tertiary levels.
- Can be intermolecular and intramolecular.

Protein renaturation experiments

What determines protein tertiary structure?



Christian Anfinsen performed these experiments in the 1950s



Denaturation of ribonuclease A is reversible

Anfinsen's dogma

Primary amino acid sequence determines tertiary structure

- Anfinsen and other scientists showed that denaturation of some proteins is reversible and the tertiary structure of a globular protein is determined by its amino acid sequence.
- Certain globular proteins denatured by heat, extremes of pH, or denaturing reagents will regain their native structure and their biological activity if returned to conditions in which the native conformation is stable. This process is called **renaturation**.
- Anfinsen's dogma is also known as the **thermodynamic hypothesis states that: "the native conformation is determined by the totality of interatomic interactions and hence by the amino acid sequence, in a given environment"**

Even though all proteins have the potential to fold into their native structure, many require some assistance