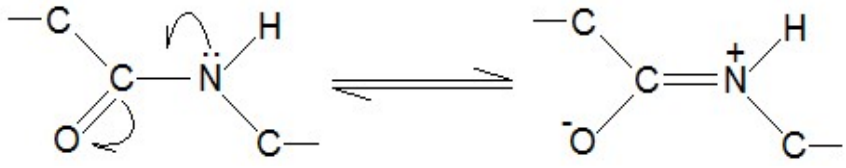
1. **Fibrous proteins** are stringy, tough, and usually insoluble in water. They function primarily as structural parts of the organism. Examples of fibrous proteins are α-keratin in hooves and fingernails, and collagen in tendons.
2. **Globular proteins** are somewhat water-soluble (forming colloids in water), unlike the fibrous proteins. They are folded into roughly spherical shapes. They usually function as enzymes, hormones, or transport proteins.

Types of Chemical Bonds in Proteins:

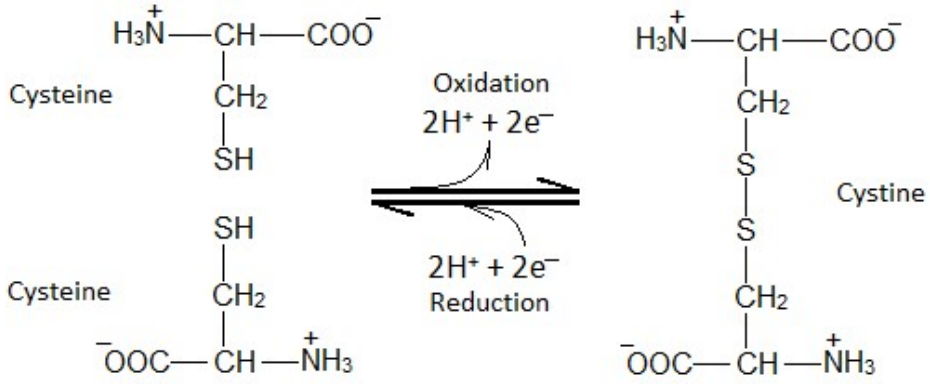
First: Two types of covalent bonds that include.

1. **Peptide bonds:** A peptide bond is a chemical bond formed between two molecules when the carboxyl group of one amino acid reacts with the amino group of another amino acid, releasing a molecule of water (H_2O). Examination of the geometry of the protein backbone reveals that the peptide bond is essentially rigid and planar. Thus for a pair of amino acids linked by a peptide bond, six atoms lie in the same plane: the α-carbon and CO group of the first amino acid and the NH group and α-carbon atom of the second amino acid. The peptide bond has considerable double-bond character due to a resonance structure (as shown in the figure below), which prevents rotation about this bond and thus constrains the conformation of the peptide backbone. The double bond character is also expressed in the length of the bond between CO and the NH groups. The C-N distance in a peptide bond is typically 1.32 Å, which is between the values expected for a C-N single bond (1.49 Å) and a C=N double bond (1.27 Å).



2. **Disulfide bonds:** Second kind of covalent bonds is possible between any cysteine residues present. Cysteine residues can form disulfide bridges (also called disulfide linkages) which can join two chains or link a single chain into a ring. Mild oxidation joins two molecules of a thiol into a disulfide, forming a disulfide linkage between the

two thiol molecules. This reaction is reversible, and a mild reduction cleaves the disulfide. Similarly, two cysteine sulfhydryl groups are oxidized to give a disulfide linked pair of amino acids. This disulfide-linked dimer of cysteine is called cystine.

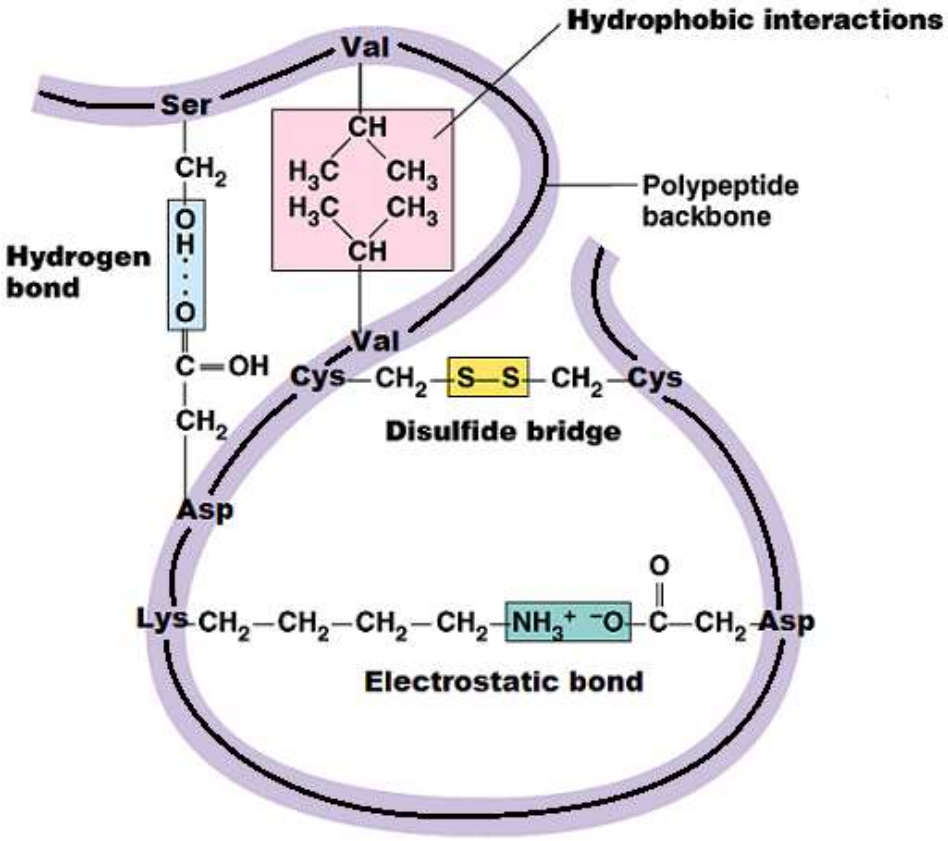


Second: Non-covalent bonds, which usually include.

1. **Hydrogen bonds:** Linus Pauling first suggested that H bonds (between water and the protein and within the protein itself) would play a dominant role in protein folding and stability. Hydrogen bonds form between the oxygen of the C=O of each peptide bond in the strand and the hydrogen of the N-H group of the peptide bond four amino acids below it in the helix. The hydrogen bonding in a *ß-sheet* is between strands (inter-strand) rather than within strands (intra-strand). The carbonyl oxygens in one strand hydrogen bond with the amino hydrogens of the adjacent strand. The hydrogen bonds make the secondary structure of protein especially stable.
2. **Electrostatic Forces:** Electrostatic forces are mainly of charge-charge and charge-dipole interactions. Typical charge-charge interactions that favor protein folding are those between oppositely charged R-groups such as Lysine or Arginine and Glutamic acid or Aspartic acid. A substantial component of the energy involved in protein folding is charge-dipole interactions. This refers to the interaction of ionized R-groups of amino acids with the dipole of the water molecule.
3. **Hydrophobic interactions:** The hydrophobic interactions of non-polar side chains are believed to contribute significantly to the stabilizing of the structures in proteins. This interaction is really just an application of the solubility rule that "likes dissolve likes".

The non-polar groups mutually repel water and other polar groups and results in a net attraction of the non-polar groups for each other. Hydrocarbon alkyl groups on Ala, Val, Leu, and Ile interact in this way. In addition, aromatic ring on Phe can "stack" together. In many cases this results in the non-polar side chains of amino acids being on the inside of a globular protein, while the outside of the proteins contains mainly polar groups.

The following figure shows the types of chemical bonds that play important roles in stabilizing protein structure.



Levels of structure in proteins:

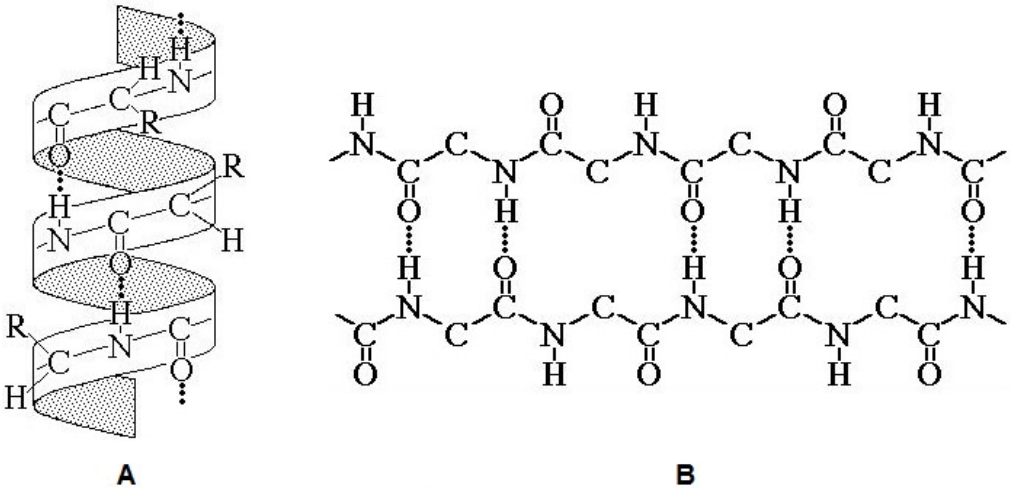
Structural features of proteins are usually described at four levels of complexity:

Primary structure: The primary protein structure refers to the unique sequence of amino acids and the location of disulfide bonds. The amino acids when linked by peptide bonds are referred to as residues. Short chains of amino acid residues are often called (oligo-) peptides. Simply, the

primary structure of a protein is what is encoded in the DNA. Thus, all the properties of the protein are determined, directly or indirectly, by the primary structure.

Secondary structure: Protein structures are also classified by their secondary structure. Secondary structure refers to regular, local structure of the protein backbone, stabilized by intramolecular and sometimes intermolecular hydrogen bonding of amide groups.

There are two common types of secondary structure. The most prevalent is the alpha helix. The alpha helix (α has a right-handed spiral conformation, in which every backbone N-H group donates a hydrogen bond to the backbone C=O group of the amino acid four residues before it in the sequence. The other common type of secondary structure is the beta strand. A Beta strand (β strand) is a stretch of polypeptide chain, typically 3 to 10 amino acids long, with its backbone in an almost fully extended conformation. Two or more parallel or antiparallel adjacent polypeptide chains of beta strand stabilized by hydrogen bonds form a beta sheet. For example, the proteins in silk have a beta-sheet structure. Those local structures are stabilized by hydrogen bonds and connected by tight turns and loose, flexible loops.



A B

A- The peptide chain curls into a helix so that each peptide carbonyl group is hydrogen-bonded to N¬H hydrogen on the next turn of the helix. Side chains are symbolized by green atoms in the space-filling structure.

B- The pleated sheet arrangement. Each peptide carbonyl group is hydrogen bonded to N¬H hydrogen on an adjacent peptide chain.

Tertiary structure: The spatial arrangement of secondary structure elements results in the formation of the tertiary structure or fold of a protein. The tertiary structure is held together by

non-covalent interactions (hydrogen bonding, ionic interactions, van der Waals forces, and hydrophobic packing), disulphide bonds and metal ion coordination.

An example of the tertiary structure is a single-domain globular protein. Globular proteins are sphere-like proteins that are more or less soluble in aqueous solutions (the other two protein classes are membrane and fibrous proteins).

Quaternary structure: Some proteins form assemblies (units) with other molecules, this is called the quaternary structure. Two examples are haemoglobin which is an assembly of four globular proteins and the actin microfilament, composed of many thousands actin molecules.

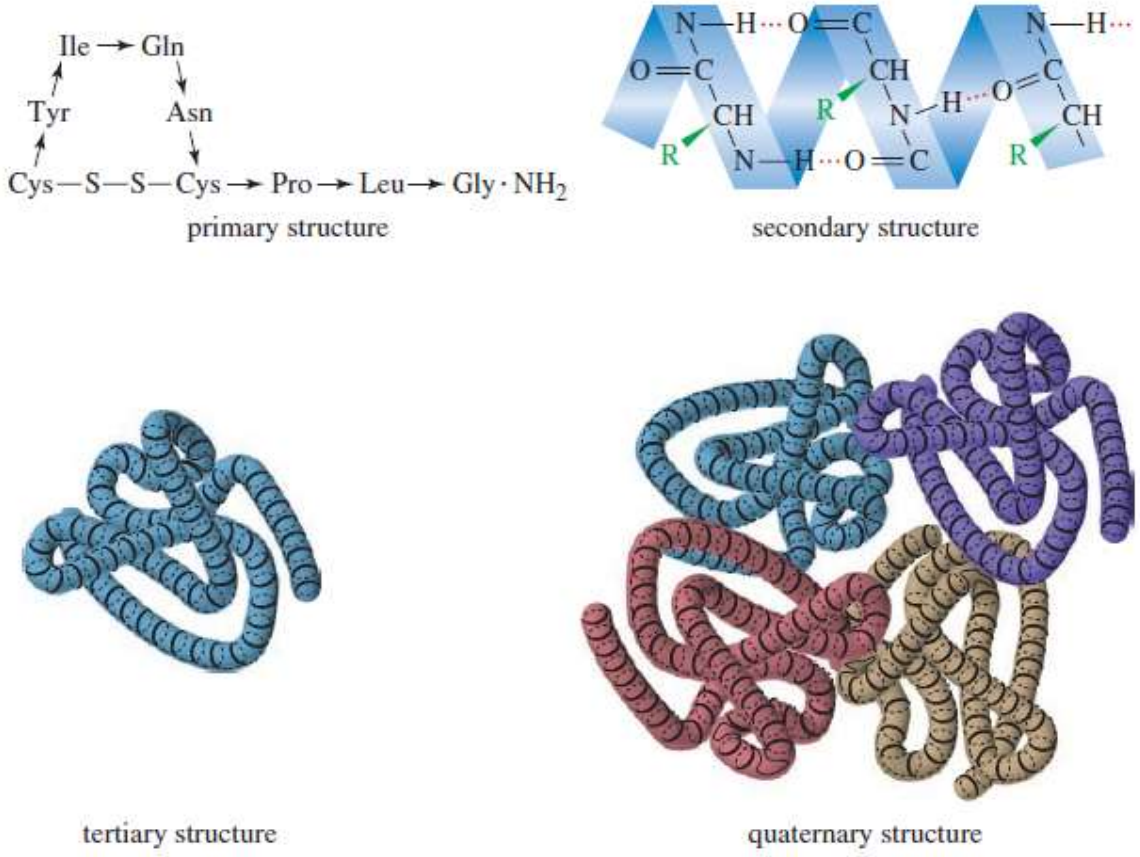


Figure 1: A schematic comparison of the levels of protein structure. Primary structure is the covalently bonded structure, including the amino acid sequence and any disulfide bridges. Secondary structure refers to the areas of helix, pleated sheet, or random coil. Tertiary structure refers to the overall conformation of the molecule. Quaternary structure refers to the association of two or more peptide chains in the active protein.