Bonds Stabilizing Protein Structure

Amino acid residue :
The part left over after losing a hydrogen atom from its amino group and the hydroxyl moiety from its carboxyl group.

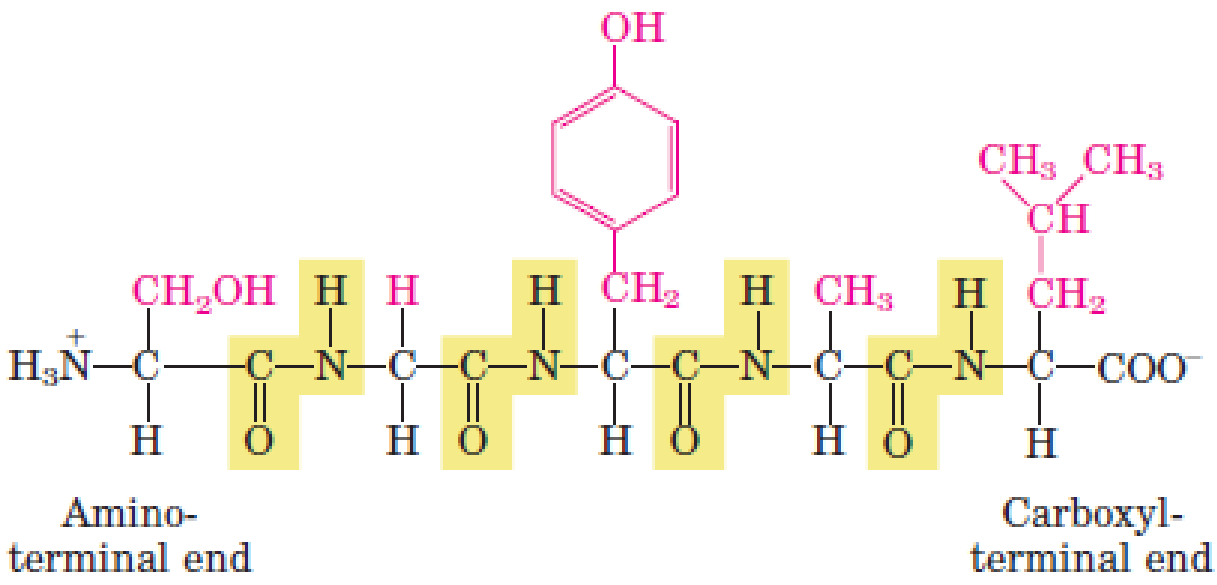


FIGURE 3–14 The pentapeptide serylglycyltyrosylalanylleucine, or Ser–Gly–Tyr–Ala–Leu. Peptides are named beginning with the amino-terminal residue, which by convention is placed at the left. The peptide bonds are shaded in yellow; the R groups are in red.

Peptides:

1.Dipeptide

2.Tri peptide

3.Tetra peptide

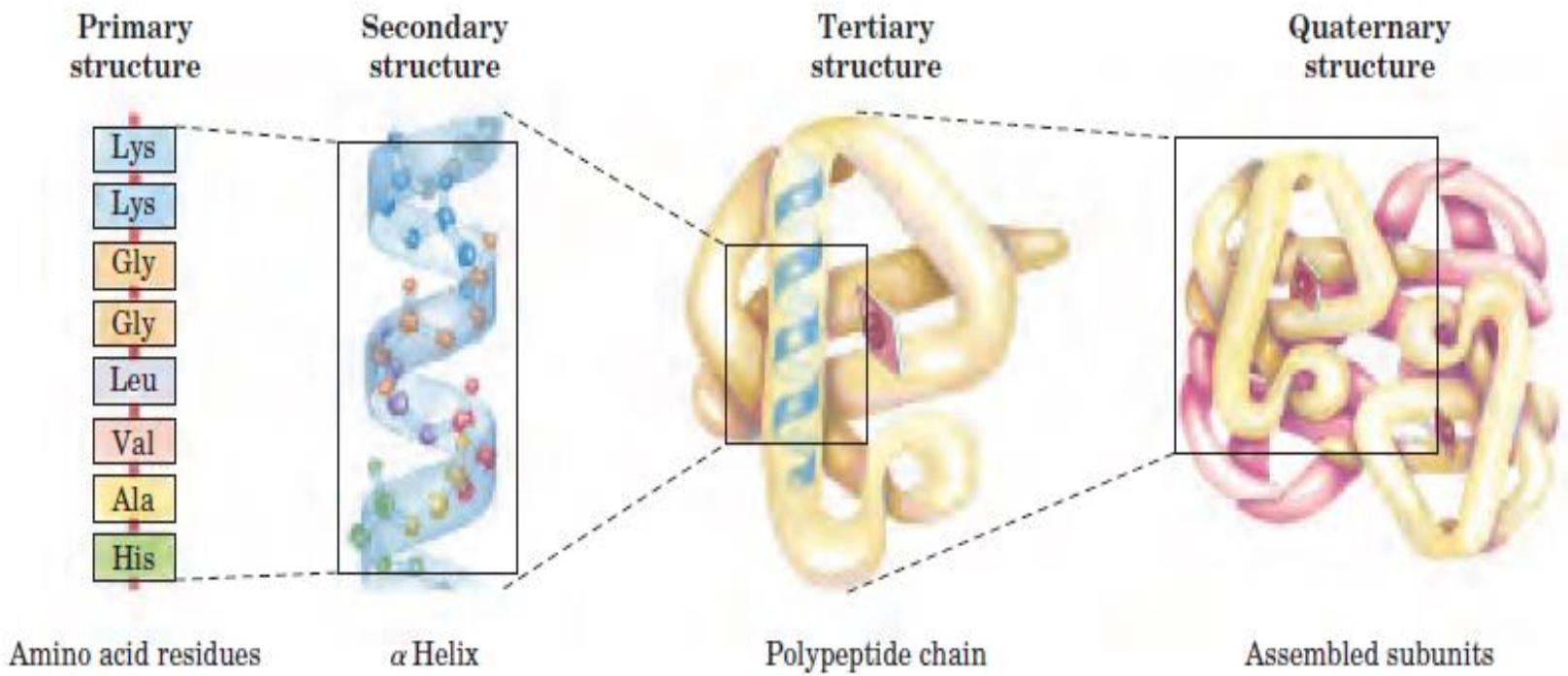
4.Penta peptide

5.Oligo peptide

6.Poly peptide

There Are Several Levels of Protein Structure

1. Primary structure
2. Secondary structure
3. Tertiary structure
4. Quaternary structure



- **Protein conformation**: The spatial arrangement of atoms in a protein.
- **Thermodynamically the most stable**, having the lowest Gibbs free energy.
- **Native proteins**: Proteins existing in any of their functional, folded conformations.
- **Stability:** The tendency to maintain a native conformation.
- **Unfolded state:** High degree of **conformational entropy** along with hydrogen-bonding interactions in the polypeptide chain with solvent.

Bonds Stabilizing the Protein Structure

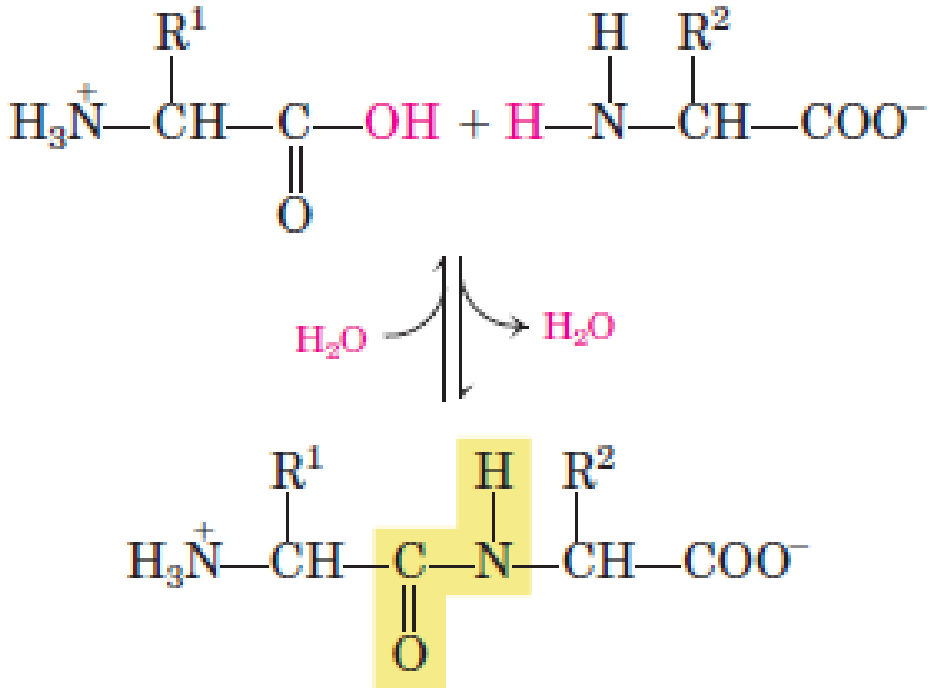
1. Covalent **Bonds**

2. Non-covalent **Bonds**

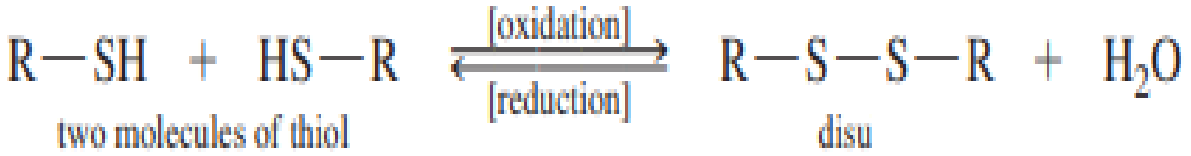
Covalent Bonds

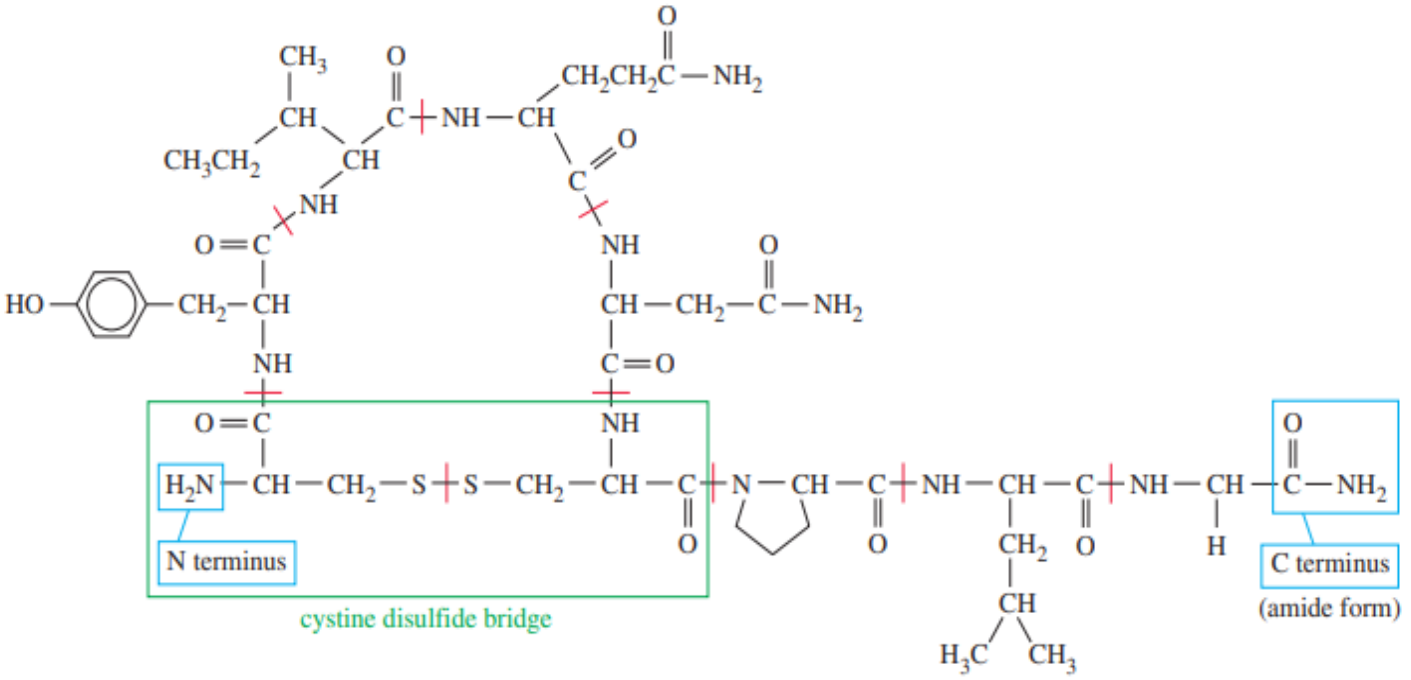
- **Peptide Bond:**

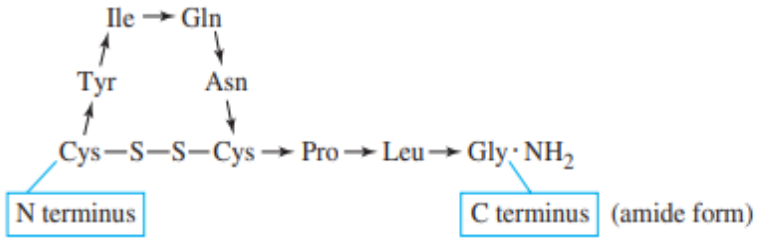
  A covalent bond formed by removal of the elements of water (dehydration) from the α-carboxyl group of one amino acid and the α–amino group of another.



Disulfide linkage: Cysteine residues can form disulfide bridges (also called disulfide linkages) which can join two chains or link a single chain into a ring.







Non-Covalent Bonds

1. Hydrophobic bond or interactions
2. Van Der Waals interactions
3. Electrostatic or ionic bond or salt bond or salt bridge
4. Hydrogen Bond

1. Hydrophobic Interactions

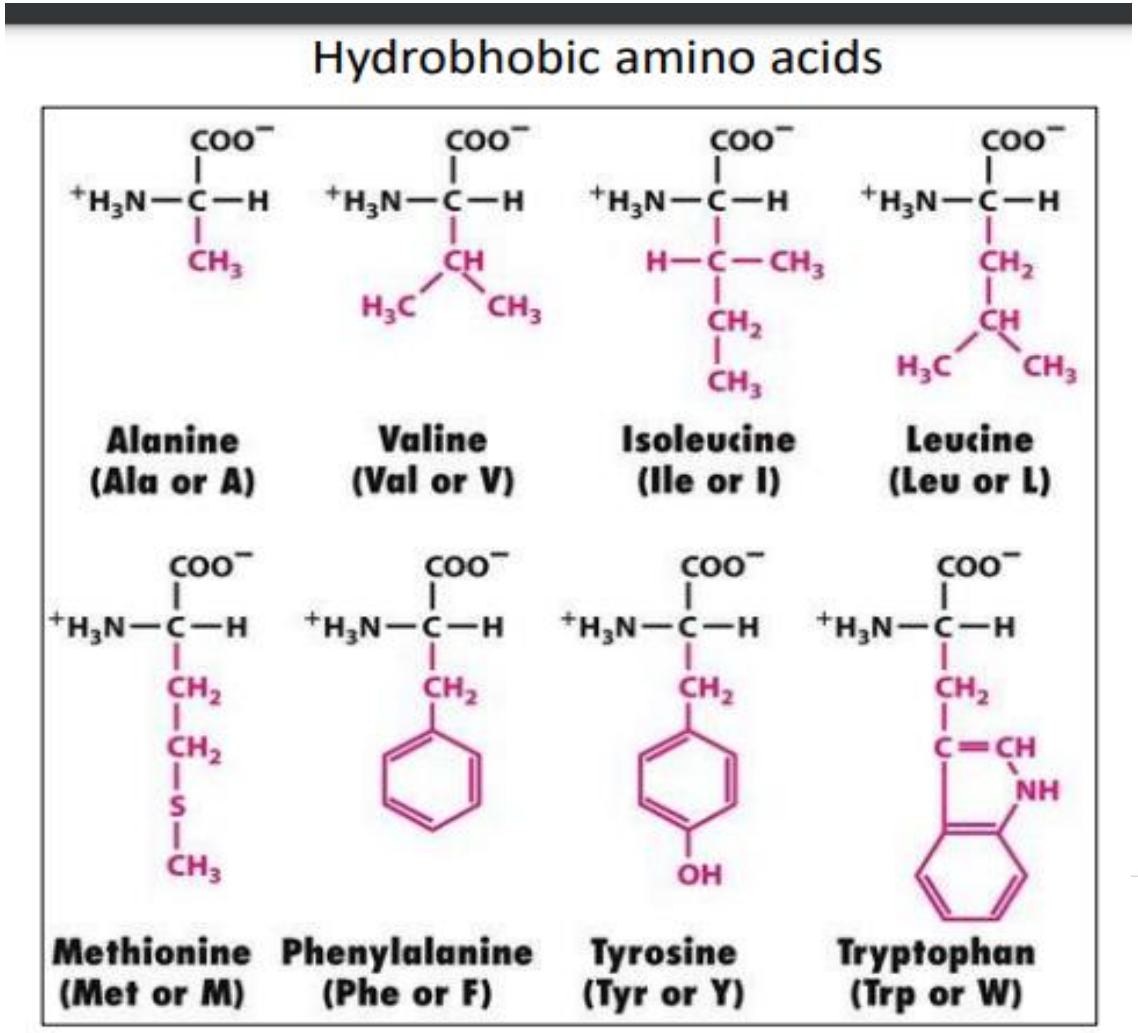
Hydrophobic bonds are a major force driving proper protein folding. Some amino acids have side-chains which repel water, or are hydrophobic.

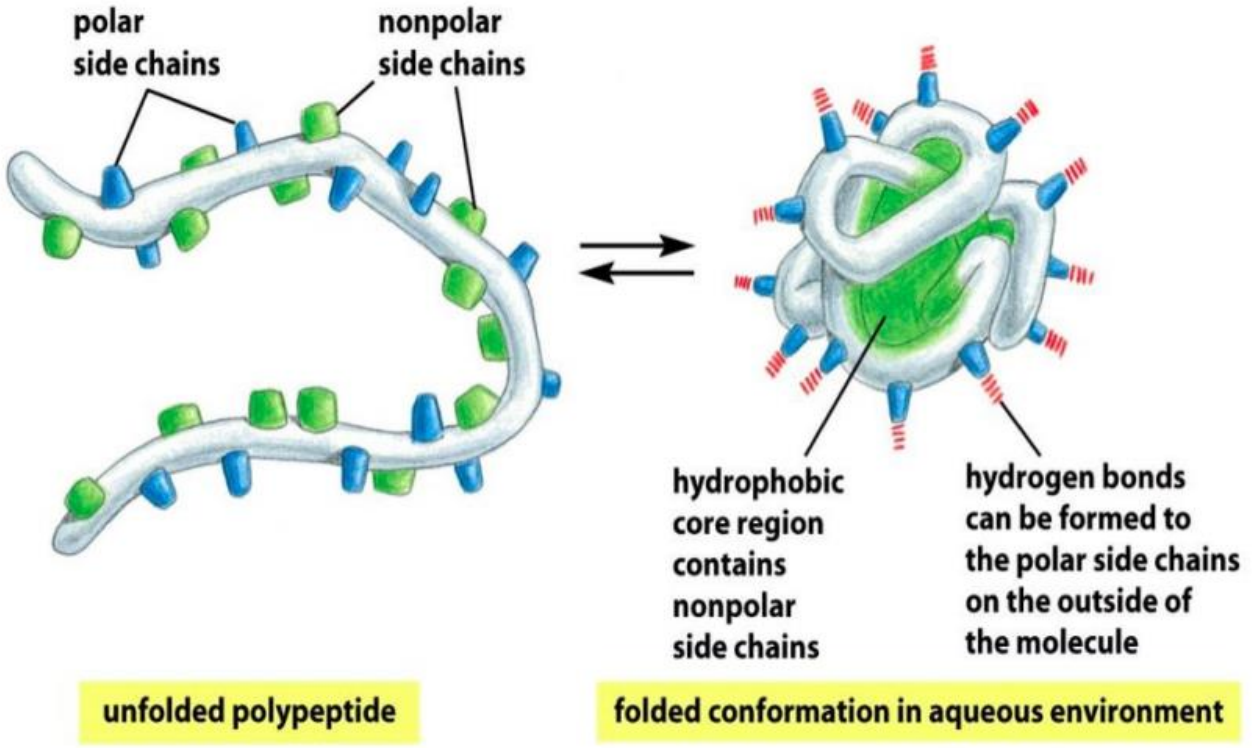
The hydrophobic nature of the amino acids enables them to interact with one another by what is called hydrophobic “interactions”.

The aggregation of nonpolar side chains in the interior of a protein is favored by the increase in entropy of the water molecules that would otherwise form ordered “cages” around the hydrophobic groups.

Hydrophobic interactions forms an interior, hydrophobic protein core, where most hydrophobic side chains can closely associate and are shielded from interactions with solvent H_2O's.

1. Hydrophobic interaction





2. Van Der interaction

In 3-dimensional structure of proteins , the formation of Van der Waals forces depends on the shape of the side-chain; if the atoms within the side-chains of neighboring amino acids fit well, then Van der Waals force is formed.

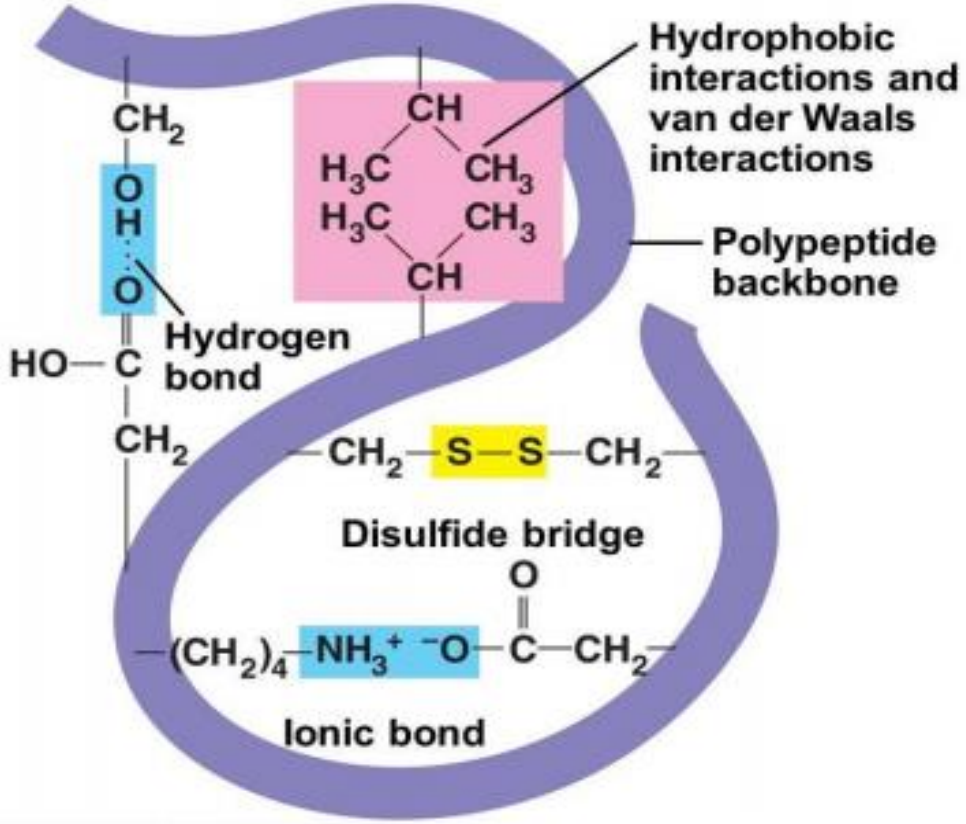


Figure 5: Van der Waals interaction between side chains of amino acids

Van der Waals forces can play important roles in protein-protein recognition when complementary shapes are involved. This is the case in antibody-antigen recognition, where a "lock and key" fit of the two molecules yields extensive Van der Waals attractions.

3. Ionic Bonds- Salt Bridges

Salt bridges in proteins are bonds between oppositely charged residues that are sufficiently close to each other to experience electrostatic attraction.

Ionic bonds are formed as amino acids bearing opposite electrical charges are juxtaposed in the hydrophobic core of proteins.

An ionic or salt bridge can be formed between the carboxylate ion of an acidic residues such as aspartic acid or glutamic acid and an ammonium ion of the basic residue such as lysine, arginine or histidine

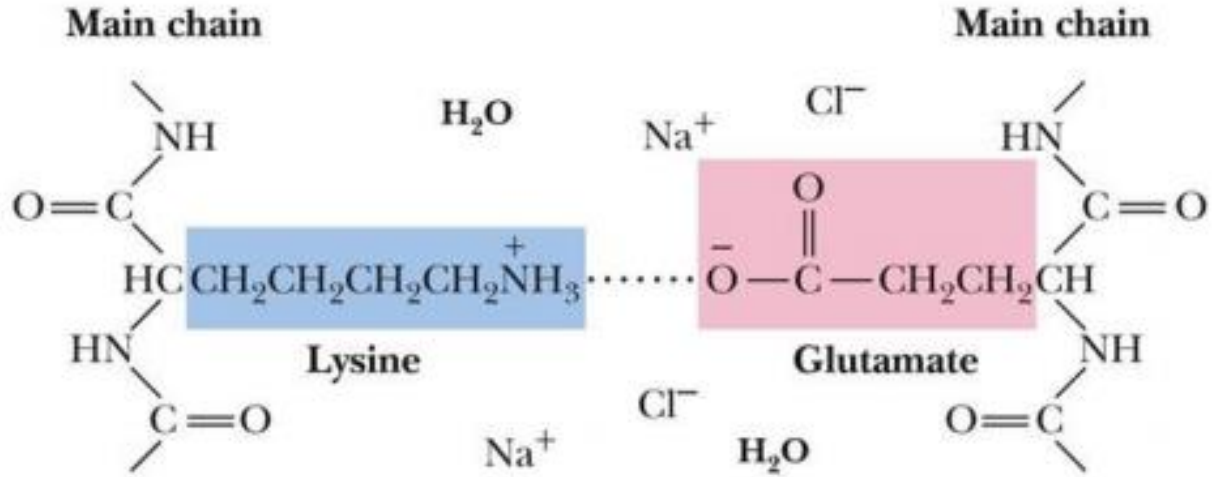


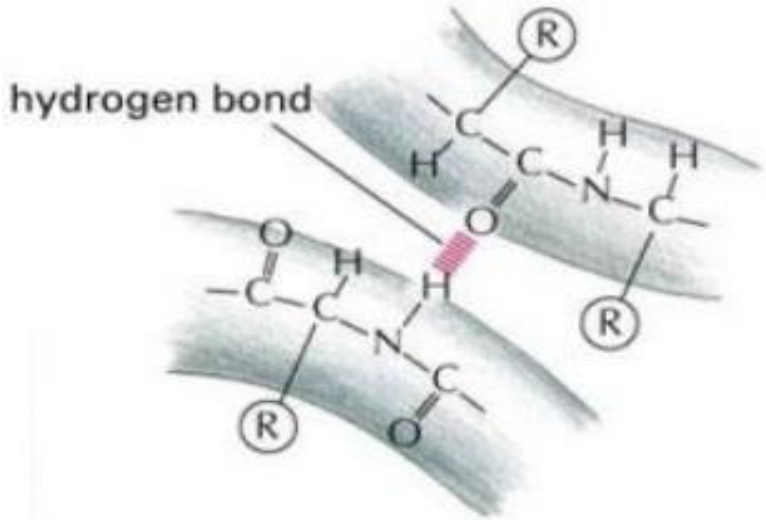
Figure 6: Salt bridge between side chains of amino acids

4. Hydrogen bond:

The correct 3-dimensional structure of a protein is often dependent on an intricate network of H-bonds. These can occur between a variety of atoms, involving:

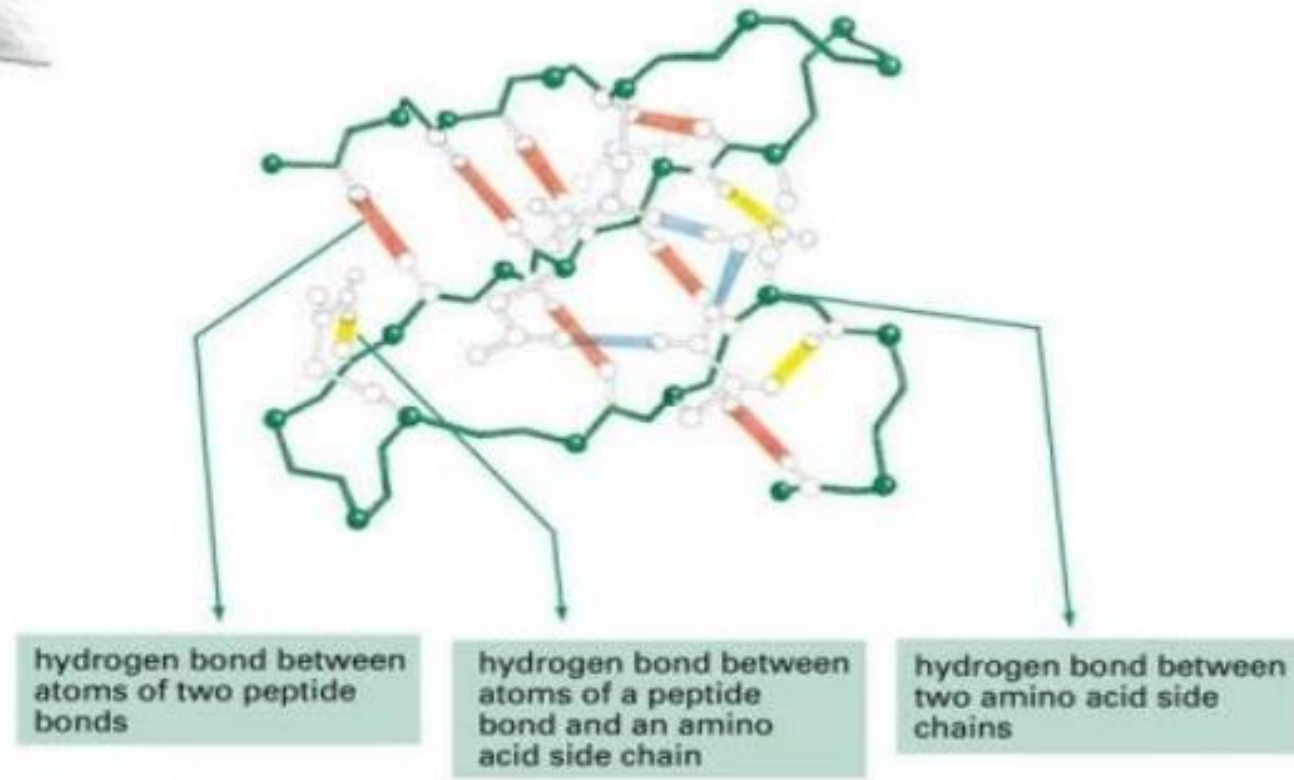
- atoms on two different amino acid sidechains
- atoms on amino acid sidechains and water molecules at the protein surface
- atoms on amino acid sidechains and protein backbone atoms
- backbone atoms and water molecules at the protein surface
- backbone atoms on two different amino acids

Polar groups exposed on the surface of proteins often have water as their hydrogen bonding partner. Polar groups within the core region usually form hydrogen bonds with other groups within the protein.



Proteins maximise hydrogen bonding.

Most bonds are between residues that are close in sequence.



- H-bonds form between 1) atoms involved in the peptide bond; 2) peptide bond atoms and R groups; 3) R groups

Summary: Stabilising forces in protein structure