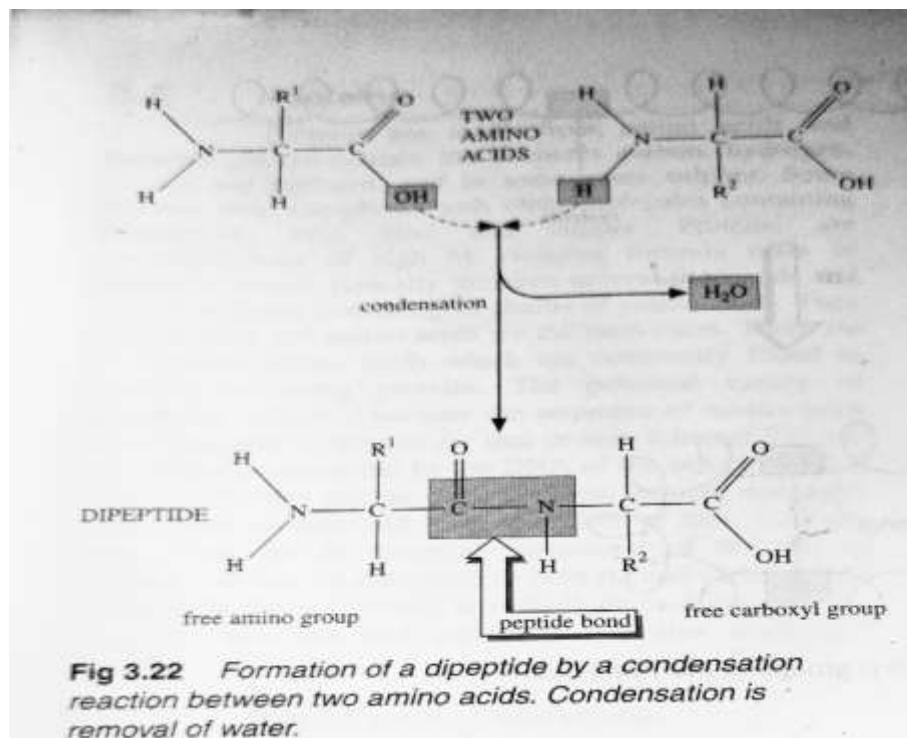


Bonds Used in Protein Structure

Amino acids combine to form proteins. They are joined together by a type of bond known as peptide bond. Once these bonds have been formed, however the protein typically folds into a particular shape as a result of other types of bonds, namely ionic bonds, disulphide bonds, hydrogen bonds, and hydrophobic interactions.

Peptide Bond

This is formed when a water molecule is eliminated during a reaction between the amino group of one amino acid and carboxyl group of another. The process of elimination of water is known as condensation and the bond formed is a covalent bond called peptide bond. The compound formed is called dipeptide. It possesses a free amino group at one end, and of a free carboxyl group at the other end. This enables further combination between the dipeptide and other amino acids. If many amino acids are joined together in this way, a polypeptide is formed. See figure 3.22



Ionic Bond

Acidic and basic R groups exist in an ionized (charge) state at certain pHs. Acidic R groups are negatively charged and basic R groups are positively charged. They can therefore be attracted to each other, forming ionic bonds. In an aqueous environment this bond is much weaker than covalent bond and can be broken by changing the pH of the medium. This helps to explain the disruptive effect that changes in pH can have on protein structure. For example, adding acid to milk makes it curdle because the ionic bond in casein (milk protein) are broken and the protein ceases to be soluble.

Disulphide Bond

The amino acid cysteine contains a sulphydryl group, $-SH$, in its R group. If two molecules of cysteine line up alongside each other, neighbouring sulphydryl groups can be oxidized and form a disulphide bond. Disulphide bonds may be formed between different chains of amino acids or between different parts of same chain. In the later case the disulphide bonds make the molecule fold into a particular shape. They are strong and not easily broken.

Hydrogen Bond

When hydrogen is part of an OH or NH group it becomes slightly positively charged (electropositive). This is because the electrons that are shared, and which are negatively charged, are attracted more toward the O or N atoms. The hydrogen may then be attracted towards a neighbouring electronegative oxygen or nitrogen atom, such as the O of a $C=O$ group or the N of an NH group. $C=O$ and NH groups occur along the length of polypeptide chains, and they can interact to produce regular shapes such as the alpha helix. The hydrogen bond is weak, but as its occurrence is frequent, the total effect makes a considerable contribution towards molecular stability.

Hydrophobic Interactions

Some R groups are non-polar and therefore hydrophobic, such as those on the amino acid tyrosine and valine. If a polypeptide chain contains a number of these groups and is in an aqueous environment, the chain will tend to fold so that the maximum number of hydrophobic groups comes into close contact and exclude water. This is how many globular protein fold up. The hydrophobic groups tend to point inward toward the center of the roughly spherical molecule while the hydrophilic groups face outward into the

aqueous environment, making the protein soluble. In the same way membrane protein can have hydrophobic regions inside the membrane alongside the hydrophobic tails of the phospholipids, while the hydrophilic region face outward alongside hydrophilic phosphate heads of the phospholipids.