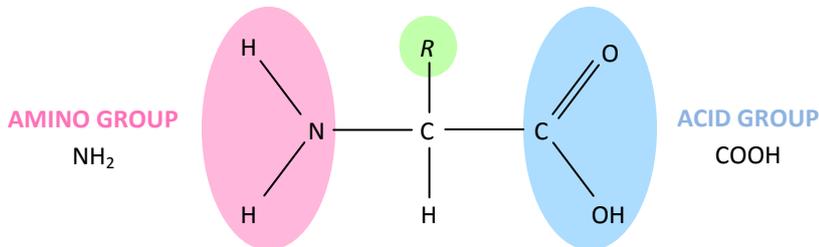


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# AMINO ACIDS AND PROTEINS

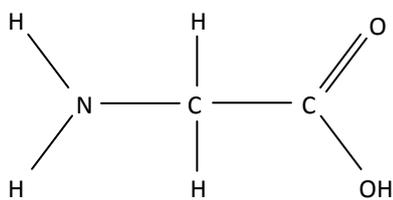
Proteins being made from amino acids

A **protein**, which is a **polymer**, is made up of many **amino acids** (which are individual **monomers**). Proteins are also made up of the elements carbon, oxygen and hydrogen, but unlike carbohydrates and lipids, also contain *nitrogen*. Some of them also contain the element *sulphur*. A protein is formed from many amino acids joined end-to-end.



The basic structure of an amino acid is shown. At one end of the molecule is an **amino group** (NH<sub>2</sub>), and a **carboxylic acid group** (COOH) is at the other end. They are separated by another carbon, which has one hydrogen bonded to it and also a **variable group** (R).

The *amino* (or amine) *group* is acidic, as it releases H<sup>+</sup> ions into solution. The *acid group* is basic (the opposite of acidic). The variable group, which is always written as R can be a wide range of different amino acids.

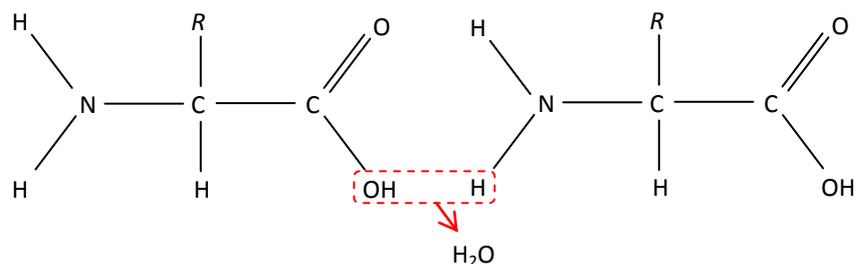


The diagram shows the structure of **glycine**. This is the simplest amino acid. The variable group R is another H atom. But there are 20 different amino acids which are naturally-occurring, and they all have different structures around the R group. There are other amino acids (in fact, thousands more) but these have all been manufactured artificially, and only those 20 occur naturally. Some R groups are very large – larger than the H<sub>2</sub>-N-C-C-OHO base of the structure.

Amino acids join together end-to-end to form a long chain, similarly to glucose molecules. The R groups that they contain do not affect how they bond: it is always in one long chain. A **condensation reaction** joins the molecules, whereby water is released in the process. The bond formed is a covalent bond (so it is quite stable and strong, simply heating it will not break the bond), called a **peptide bond**.

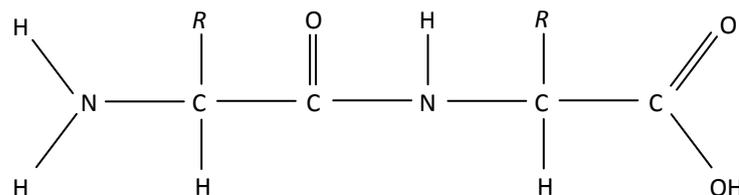
When you put two amino acids next to each other, it is immediately obvious how the reaction is going to take place: the OH (hydroxyl) group from the carbon of one molecule and the hydrogen atom from the nitrogen of the other molecule will supply the ingredients for the condensation reaction.

This new molecule which is produced (see below) is called a **dipeptide**. Of course the reaction is reversible using a **hydrolysis reaction** – this will break the peptide bond. This reaction will *use up* one water molecule (replaces) in order to form the OH and H groups once again.



This process of making and breaking peptide bonds is important in animals, for example in digestion, where it is important to break down **polypeptide** molecules into individual amino acids.

A *polypeptide* is a molecule which is made up of multiple amino acids, but might not necessarily be a protein...



**Peptide bond** - a bond formed between two amino acid molecules

**Polypeptide** - the name given to a larger structure consisting of multiple amino acids

A *polypeptide* is a chain of amino acids, but a *protein* is something made of amino acids which has a distinct biological function. A protein is made of *one or more* polypeptides (therefore, one polypeptide may be a protein, but not all polypeptides are proteins).

Examples of biological functions which make proteins include:

- ✓ structural uses (such as proteins of muscle or bone)
- ✓ membrane carriers and pores (used for movement of substances across a membrane)
- ✓ all **enzymes** are proteins
- ✓ many **hormones** are proteins

### PRIMARY STRUCTURE OF PROTEINS

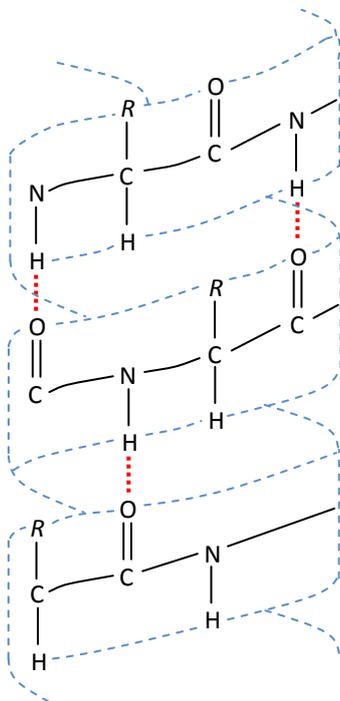
Proteins have different levels of complexity in their structure. They can be five amino acids long, or they can be hundreds of them long. Either way, they will have the amino  $\text{NH}_2$  group on one end of the chain and the carboxylic acid group on the other end.

The diagram below shows a chain of amino acids. Each box represents an individual amino acid, symbolised by three letters, for example, **glycine** (see the previous page) is one amino acid, where the *R* group is an H atom, and **cysteine** where the *R* group is an S atom.



The function of a protein is determined by its **primary structure**. The primary structure refers to the unique sequence of amino acids which make the polypeptide chain. For example, if a protein consists primarily of a sequence of amino acids with hydrophobic *R* groups, then it may be a protein found within a membrane (e.g. a transport protein).

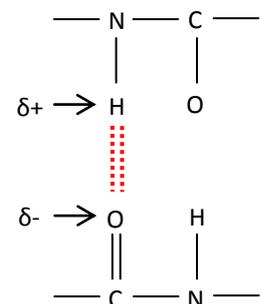
### SECONDARY STRUCTURE OF PROTEINS



The **secondary structure** of a protein refers to its formation of a 3D structure when a chain of amino acids coils, or folds. The most common secondary structure of proteins is the **alpha helix ( $\alpha$ -helix)** which forms when the chain *coils*. There are **hydrogen bonds** which hold the coils in place. These are not very strong bonds, but they keep the helix structure quite stable because there are so many of them.

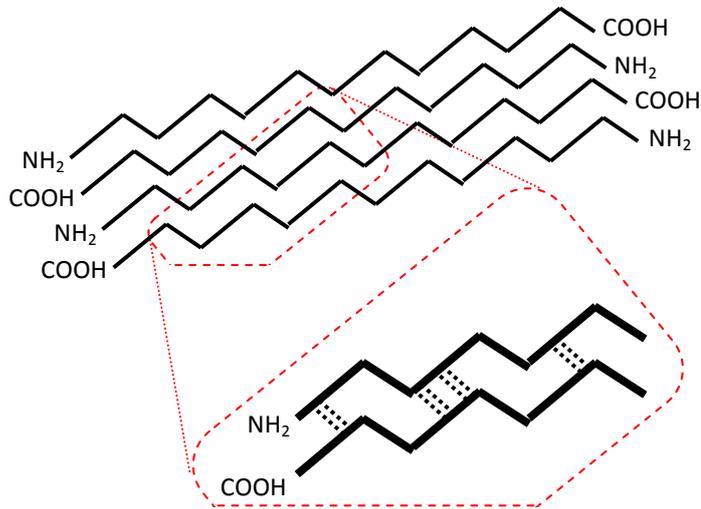
The helix shape and structure is shown to the left. The hydrogen bonds holding together the amino acids in the  $\alpha$ -helix occur are shown in this diagram below:

Hydrogen bonding can only take place between **polarised** substances (charged). This means it will happen between the hydrogen atom attached to the N of one amino acid and the oxygen atom of the secondary C of another amino acid, one of which will be positively charged, and the other negative. In this case, the hydrogen ion is positive (a positive charge is written as  $\delta+$ ) and the oxygen ion is negative ( $\delta-$ ).



This hydrogen bonding therefore takes place between the *polar groups of the peptide bonds*.

The alpha helix is not the only secondary structure that can be formed by proteins. There is a far less common structure, called the **beta pleated sheet**. A *pleat* is an angular fold within the polypeptide chain. A **beta pleat ( $\beta$ -pleat)** is the simple structure, formed by multiple polypeptides joining together side-by-side in a pleated chain (see the diagram on the following page). These pleats associate with each other and join together to form the beta pleated sheet (a series of beta pleats fixed together, resulting in a very thin but tall, almost 2D shape).



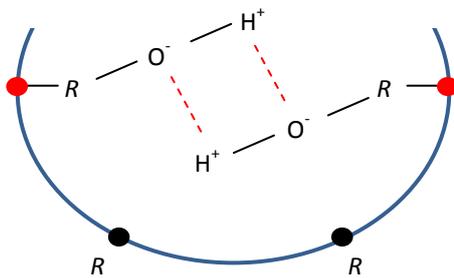
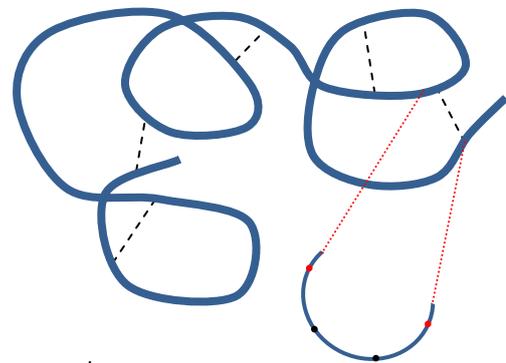
The polypeptide chains form a sheet and not a helix because they do not have the amino coding necessary, which is possessed by those amino acids that do form a helix.

Just like with the helices formed, a  $\beta$ -pleated sheet is held together by multiple hydrogen bonds.

### TERTIARY STRUCTURE OF PROTEINS

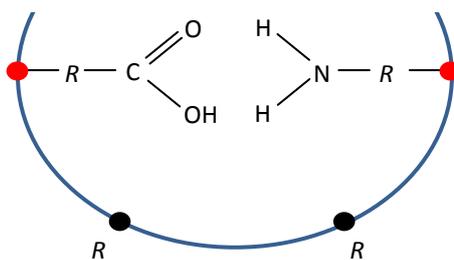
An  $\alpha$ -helix can wrap itself into a 3-dimensional complex shape. Polypeptides that do this form a **globular protein**. Their shape is maintained by bonding between the *R* groups of individual amino acids.

There are four different types of bonds that can be found between the *R* groups which maintain this globular **tertiary structure**...



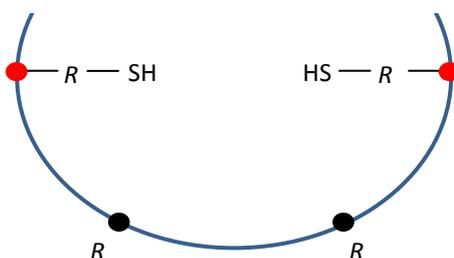
**A** – Hydrogen bonds between polar groups

Hydrogen bonds can form between oppositely charged ions in the groups which are polar, such as this hydroxyl group. Hydrogen bonds, as always, are very weak and easily broken; temperatures above approximately 40°C will cause a loss in their tertiary structure as the bonds become broken – this is called **denaturation**



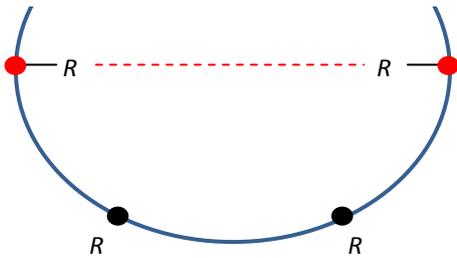
**B** – Ionic bonding of oppositely-charged *R* groups

When amino acids bond with each other, the COOH (carboxylic acid group) shown in the diagram no longer exists, as the OH is lost, but some amino acids have an extra acid group as their *R* group, like shown. The amino acid on the left is therefore an **acidic amino acid** and it *donates*  $H^+$  ions in solution, leaving an oxygen  $\delta^-$  and the nitrogen of the other amino acid (which is a **basic amino acid**) *accepts* the  $H^+$  ion. An **ionic bond** then forms between the  $O^-$  and the  $H^+$  ions



**C** – Disulphide bridges

When two cysteine amino acids are found near each other, they can form a very strong covalent bond called a **disulphide bridge** (or disulphide bond). They lose their hydrogen ions in an **oxidation** reaction, and the two sulphurs can then form the bond. This bond can be broken by reversing the reaction (i.e. in a **reduction** reaction)



**D – Hydrophobic, non-polar bonding**

Non-polar *R* groups are **hydrophobic** (i.e. hate water). Two amino acids close to each other with hydrophobic *R* groups will bond together, clustering to exclude water. The bond formed is a **hydrophobic bond** which is a very strong type of bond and hard to break.

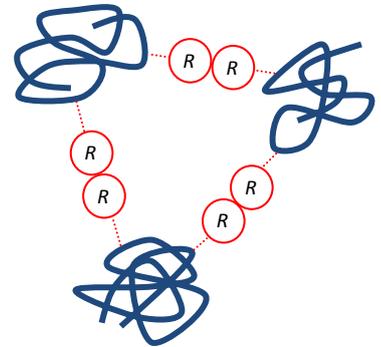
All globular proteins will roll up to form balls in 3D. But there are also **fibrous proteins**, which form fibres when they become three-dimensional. These are formed from regular and repetitive sequences of amino acids, and are usually insoluble in water, whereas globular proteins are most often soluble in water. An example of a fibrous protein is **keratin**. This is protein found in fingernails and hair. Fibrous proteins have only a primary and secondary structure, very few have this tertiary structure, as a fibre is a 2D shape. All globular proteins have a tertiary structure when in globular form, and also have a *quaternary structure*.

**QUATERNARY STRUCTURE OF PROTEINS**

A protein's **quaternary structure** (if they have one) refers to its state when it **polymerises** – i.e. when more than one globular protein joins together.

They bond together in exactly the same ways as the *R* groups join in the tertiary structure development: through ionic bonding, hydrogen bonding, hydrophobic bonding and forming disulphide bridges.

Examples of proteins which have a quaternary structure are **haemoglobin** and **antibodies**. You are required to know about *haemoglobin* and **collagen** for the exam.



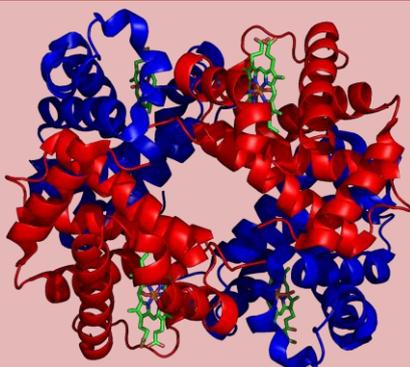
**COLLAGEN**



Collagen is a fibrous protein found in skin, bones, cartilage, tendons, teeth and the walls of blood vessels. It is an important **structural protein** found in most animals. Collagen consists of three polypeptide chains, each in the shape of a helix. The three helices wind around each other to form a *rope*. Almost every third amino acid in each chain is *glycine*. The small size of glycine allows the three strands to lie close together and form a tight coil. The strands are held together by *hydrogen bonds*. *R* groups of individual collagen molecules form bonds with other collagen molecules

These cross-links form **fibrils**. Many *microfibrils* bond together to form larger *macrofibrils*. These associate together to form much bigger bundles called **fibres**. Collagen, a fibrous protein, has a tremendous amount of **tensile strength**, i.e. can withstand a high pulling pressure

**HAEMOGLOBIN**



A haemoglobin molecule is made of four polypeptide chains. Each chain is wrapped around a group of atoms, called a **haem group** (see 2.8 Haemoglobin) which holds an **iron  $Fe^{2+}$  ion** in the centre, as shown in the diagram. Each iron ion is able to bond with two oxygen atoms (one oxygen molecule), so the haemoglobin molecule as a whole can carry up to eight oxygen atoms (or four molecules of oxygen)

The usual bonds are responsible for giving the haemoglobin molecule its quaternary structure: hydrogen bonds, hydrophobic bonds, ionic bonds and disulphide bridges. The molecule consists of two  $\alpha$ -chains and two  $\beta$ -chains