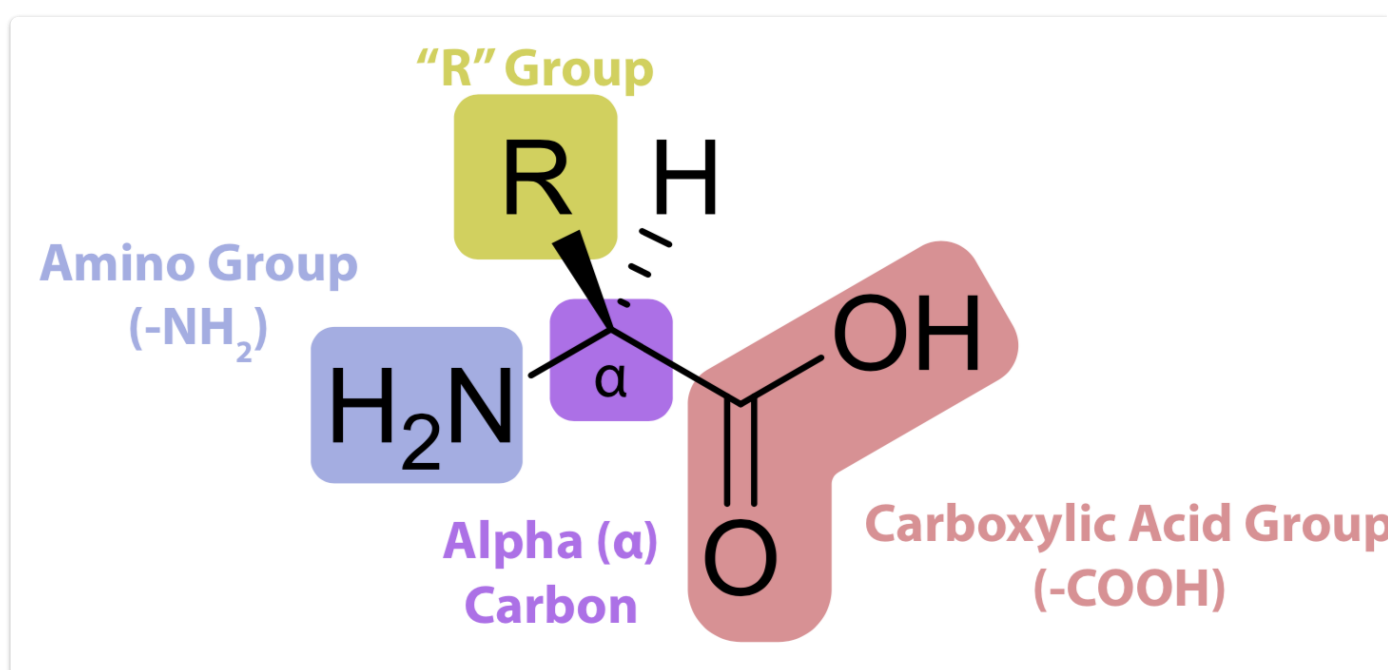


Amino Acids

Amino Acids

#Chemistry

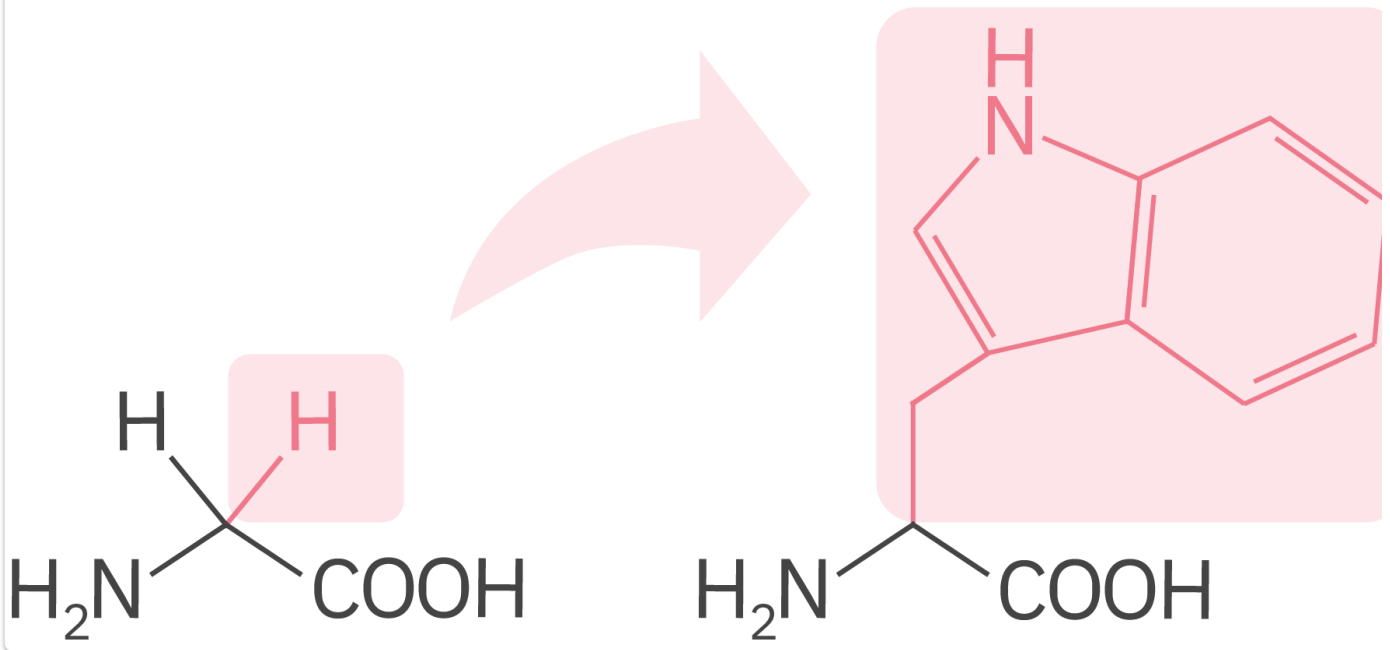
An amino acid is a carbon compound with both an amine group (-NH_2) and a carboxyl group (-COOH). Both of these groups are **attached to the same carbon**, which we call the central carbon atom. It has two more groups attached: a **hydrogen atom** (H) and a **variable amino acid side chain** (when unspecified, we use R). This is the general structure.



The side chain (or R group) is what makes each amino acid unique. In the amino acid glycine, the side chain is a humble hydrogen atom, but there are many different kinds of side chains, such as the aromatic carbon structure in the amino acid tryptophan:

Glycine

Tryptophan



Properties of Amino Acids

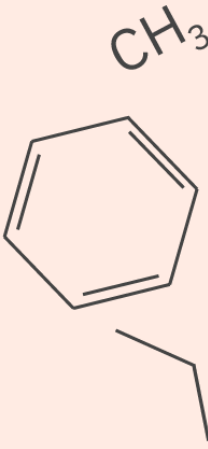
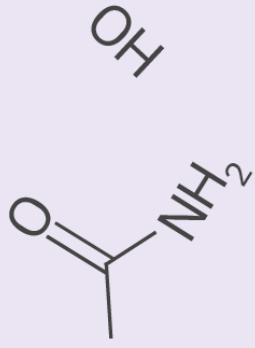
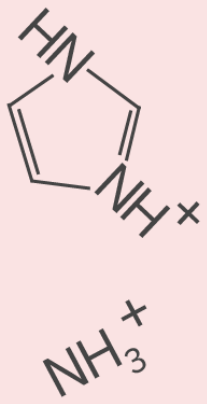
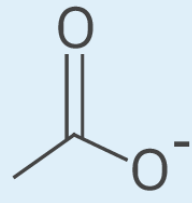
Non-polar amino acids have non-polar side chains, typically alkyl groups.

Polar amino acids contain polar groups such as $-OH$ or $-CONH_2$.

Positively-charged amino acids typically contain additional $-NH_2$ groups.

In solution, the $-NH_2$ group accepts a proton, becoming a $-NH_3^+$ group. As a result, it is also basic.

Negatively-charged amino acids typically contain additional $-COOH$ groups.

			
Non-polar	Polar	Positive	Negative

Amino Acid Reactions

Amino acids react together in a condensation reaction to form a **peptide**.

In a condensation reaction, the carboxyl group $-COOH$, of one amino acid reacts with the amino group $-NH_2$ of the other amino acid. This produces a **peptide (or amide)** link between the carbon atom of the carboxyl group and the nitrogen atom of the amino group.

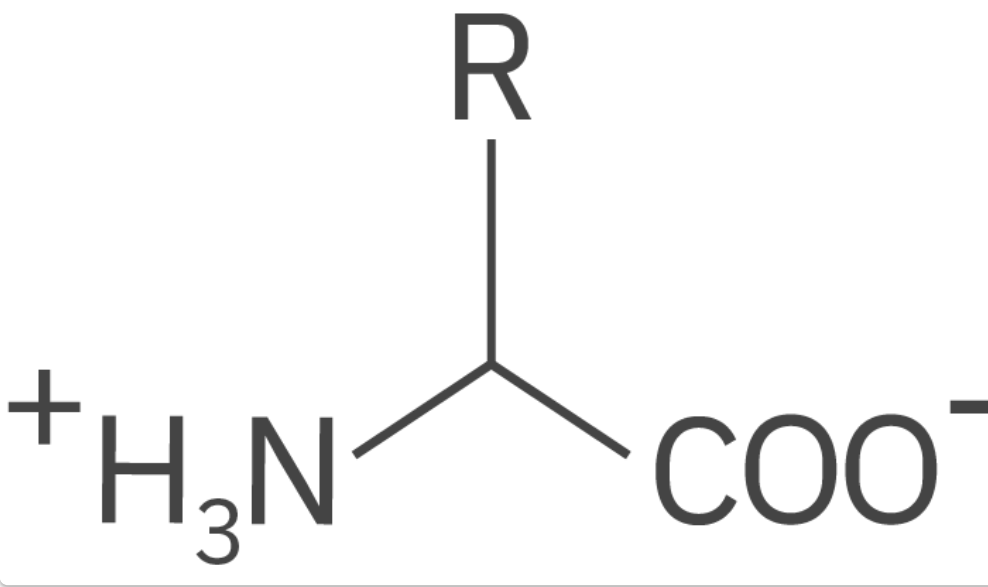
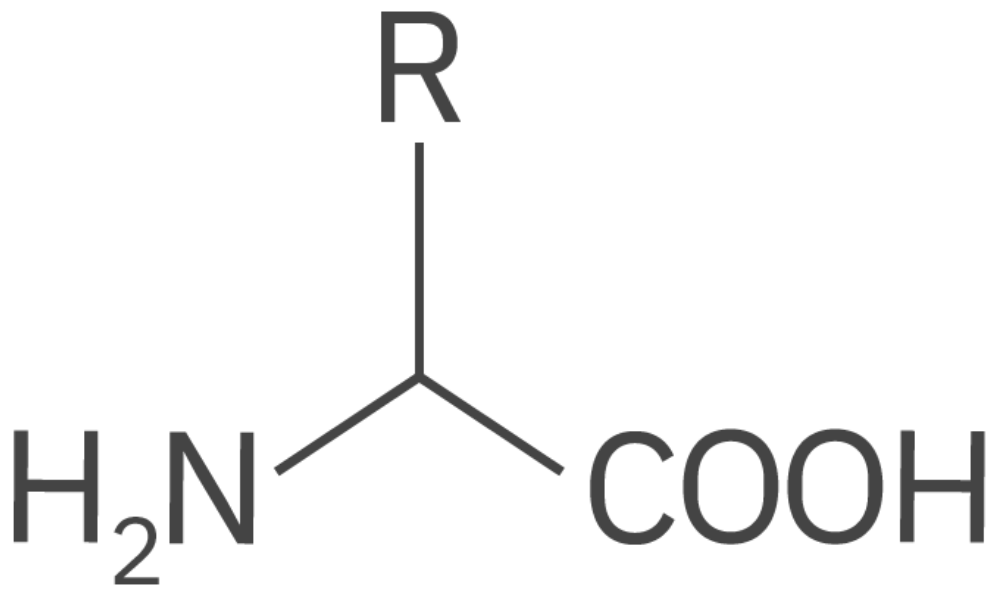
The reason we call this a condensation reaction is because another molecule is squeezed out of the reaction: water. It is formed from the hydroxy group of the carboxyl group and a hydrogen atom from the amino group.

Zwitterions

Amino acids also share common properties, their ability to form zwitterions.

We are more likely to see the zwitterion in solutions with a **moderate-to-neutral** pH.

A zwitterion comes about when the weakly acidic $-COOH$ group of the amino acid donates its proton to the weakly basic $-NH_2$ group. On the surface, this subtle change has no effect: both molecules still have a **net neutral charge**.

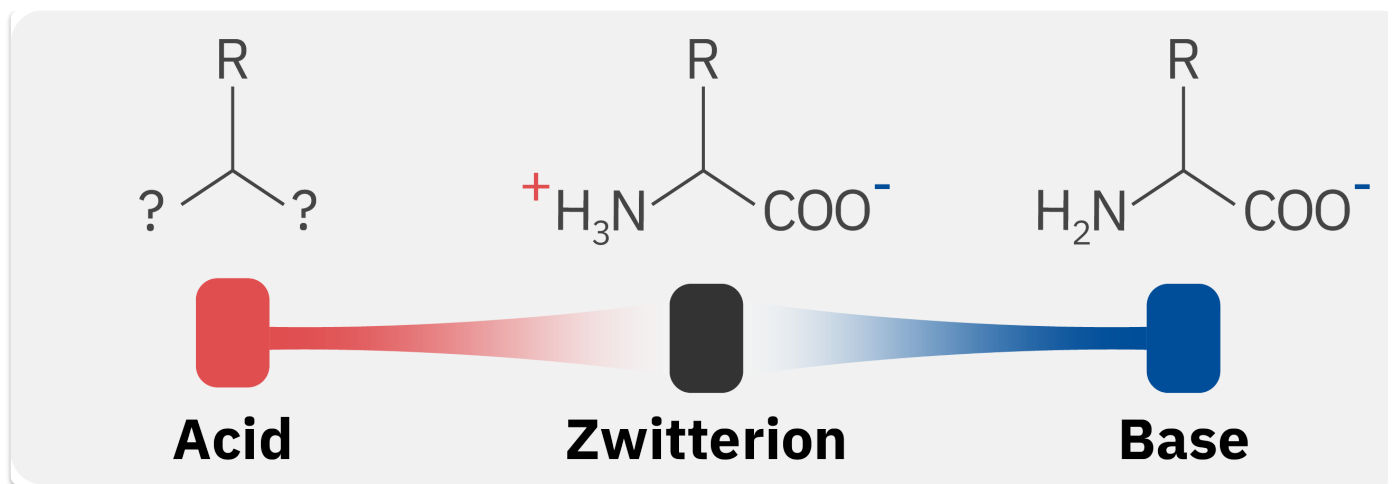


However, as the diagram above shows, the regular amino acid (on the left) has a **uniform distribution** of neutral charge; in the zwitterion, $-\text{NH}_3^+$ is **slightly positive** and the $-\text{COO}^-$ group is **slightly negative**. This is what defines a zwitterion: it is a molecule with **separate** positively and negatively charged groups.

As the pH swings one way or another, the amino acid **changes its form** accordingly.

****Amino acids may act as an acid or a base depending on the pH of the solution.****

When the solution is **acidic**, there is an **excess of protons** (H^+). This means that both the amino and the carboxyl group **pick up protons**, existing as $-\text{NH}_3^+$ and $-\text{COOH}$ respectively. Altogether, the amino acid has a **net positive charge**, and is in acid form (cationic form).



Isoelectric Point

****The isoelectric point (pI) is the pH where the amino acid is at a net neutral charge, i.e. where the zwitterionic form is most dominant.****

Anything below the isoelectric point is acidic for the amino acid (will pick up an extra hydrogen).

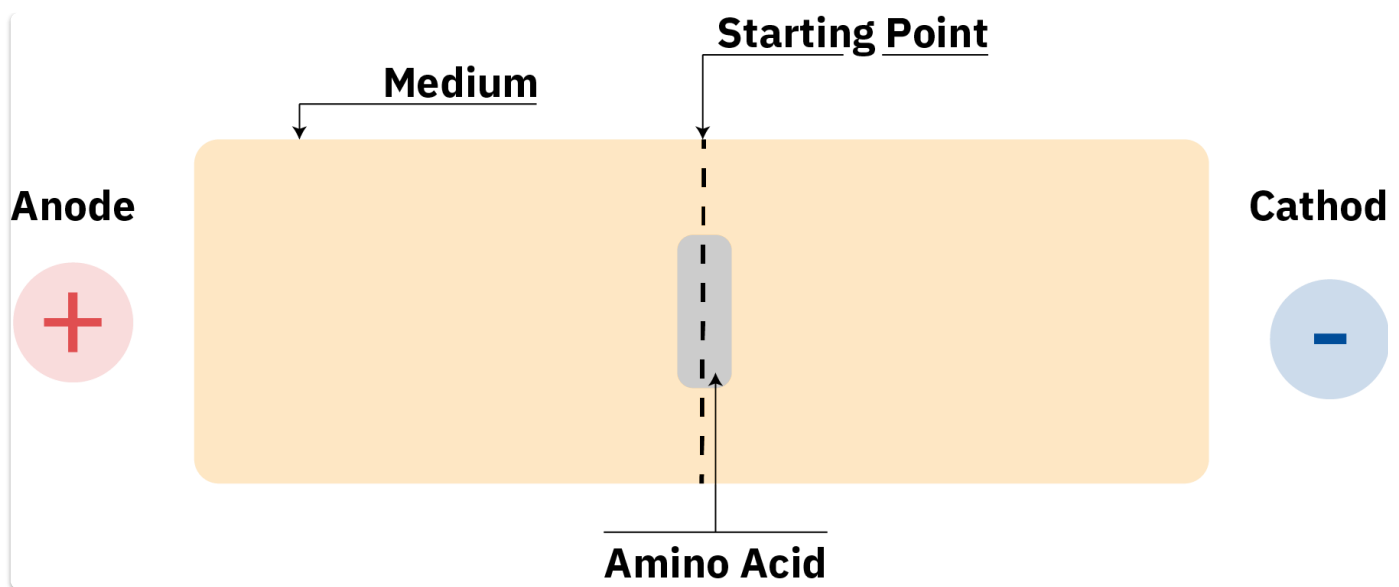
Any pH higher than the isoelectric point, the amino acid will give up a H^+ in an acidic solution.

****We can make use of the isoelectric point in electrophoresis.****

Electrophoresis is a procedure that **separates molecules** based on their movement under the influence of an **electric field**. To perform this procedure, scientists insert a solution of **mixed molecules** in the middle of a **medium** (typically a gel). They buffer the pH of the medium to a **set value**, and then apply an electric field.

When the pH is **more acidic** than the pI, the amino acid becomes positively charged, so it **moves to the cathode**.

When the pH is **more basic** than the pI, the amino acid becomes negatively charged, so it **moves to the anode**.



AMINO ACIDS					POLAR				
NON-POLAR									
Glycine	Alanine	Valine	Cysteine	Phenylalanine	Serine	Threonine	Tyrosine	Asparagine	Glutamine
					POSITIVE			NEGATIVE	
Leucine	Isoleucine	Methionine	Tryptophan	Proline	Lysine	Arginine	Histidine	Aspartic Acid	Glutamic Acid

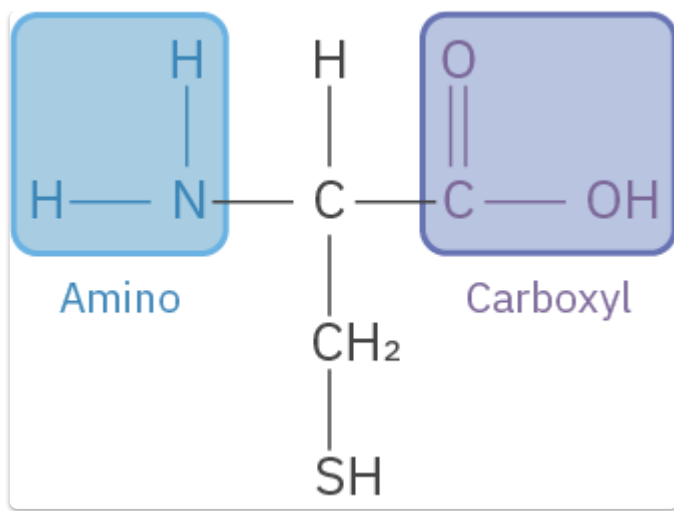
Primary and Secondary Structure of Proteins

The **most simple** form of a protein is the **primary structure**. This level of organisation involves the **number, type and sequence of amino acids**.

The amino acids within the primary structure are **covalently bonded** together to **form a polypeptide chain**; you can think of this chain almost like different coloured marbles threaded onto a string.

****Polypeptide chains have two distinct ends:****

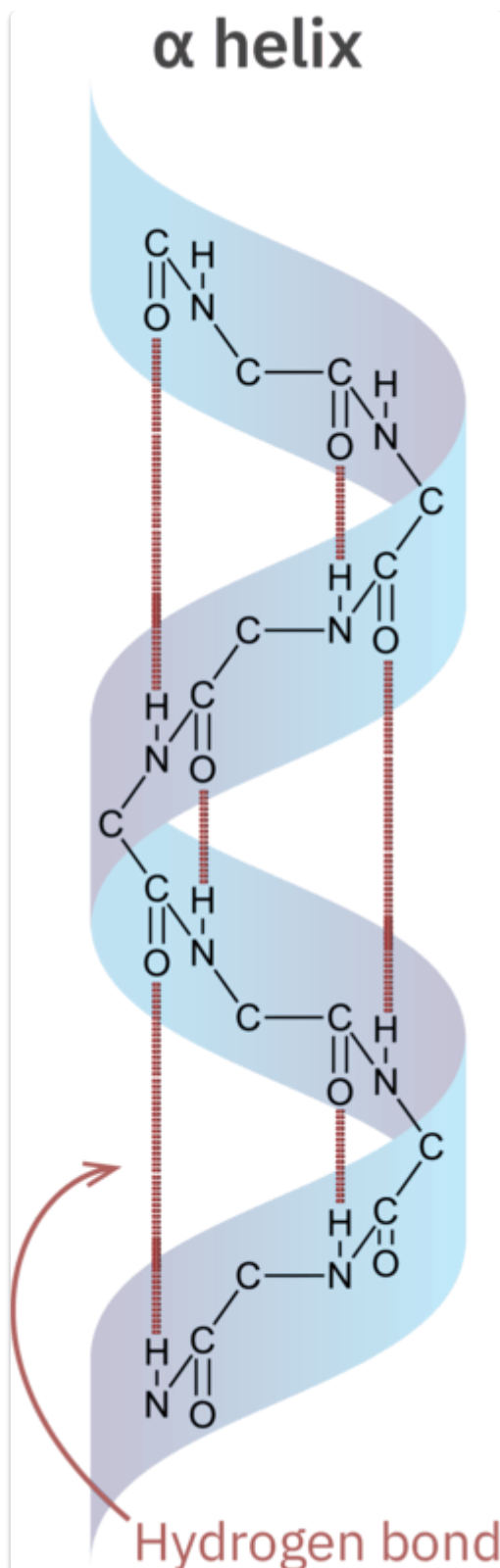
If we look at the **amino acid cysteine**, shown in the image to the right, we can see that this molecule has **different functional groups** on either end. On the left-hand side of the molecule is an **amino group** $-NH_2$ also known as an amine group, while on the right-hand side of the molecule is a **carboxyl group** $-COOH$



A peptide link joins amino acids together to create polypeptide chains. However, despite the length of the polypeptide chain, one end of the chain will have an **amino acid with an exposed amino group** which is called the **N-terminal amino acid**. Likewise, the other end of the chain will have an **amino acid with an exposed carboxyl group** which is called the **C-terminal amino acid**.

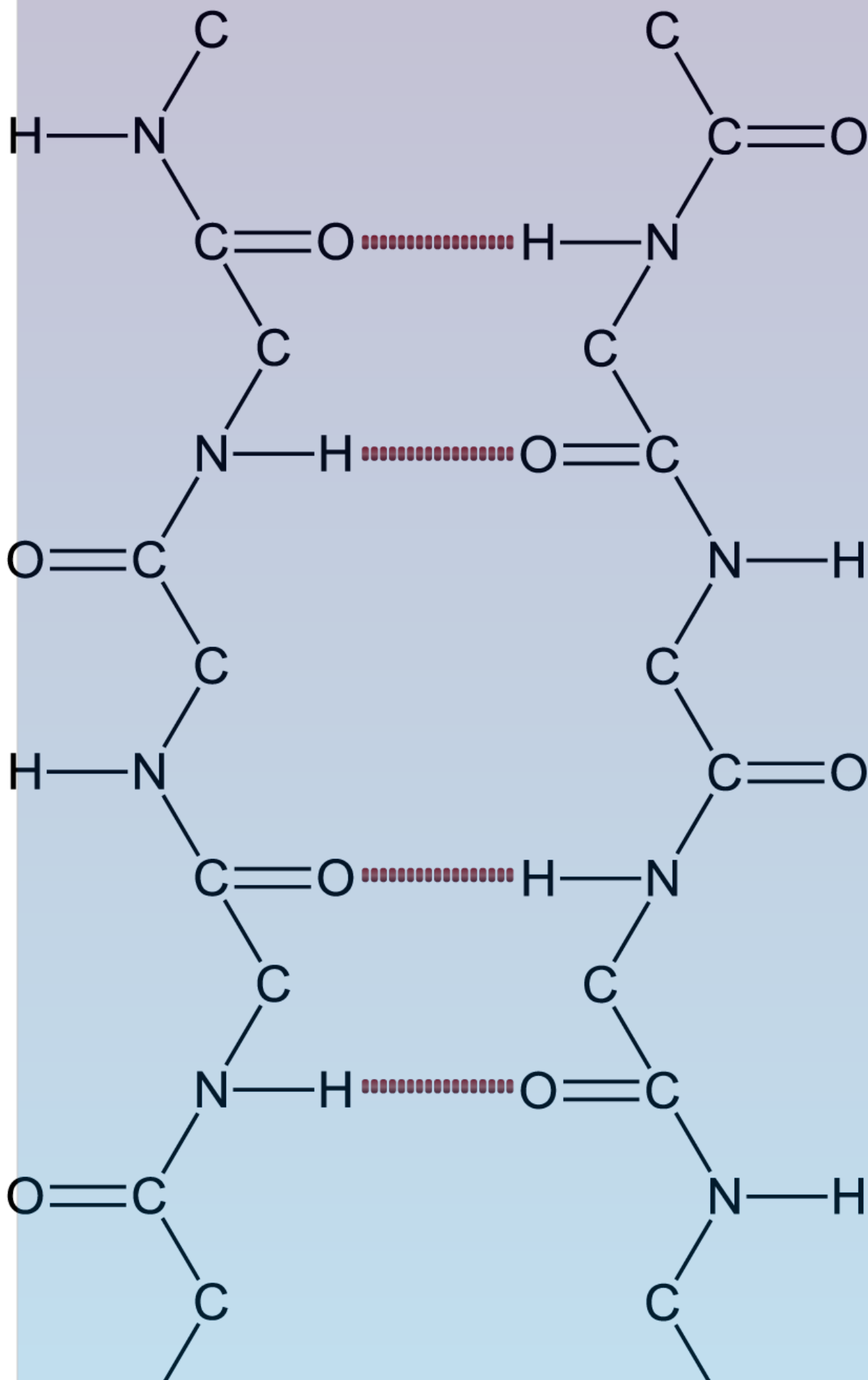
When **drawing** the primary protein structure, the polypeptide chain is **always written** with the **N-terminal** amino acid to the **left**, and the **C-terminal** amino acid to the **right**.

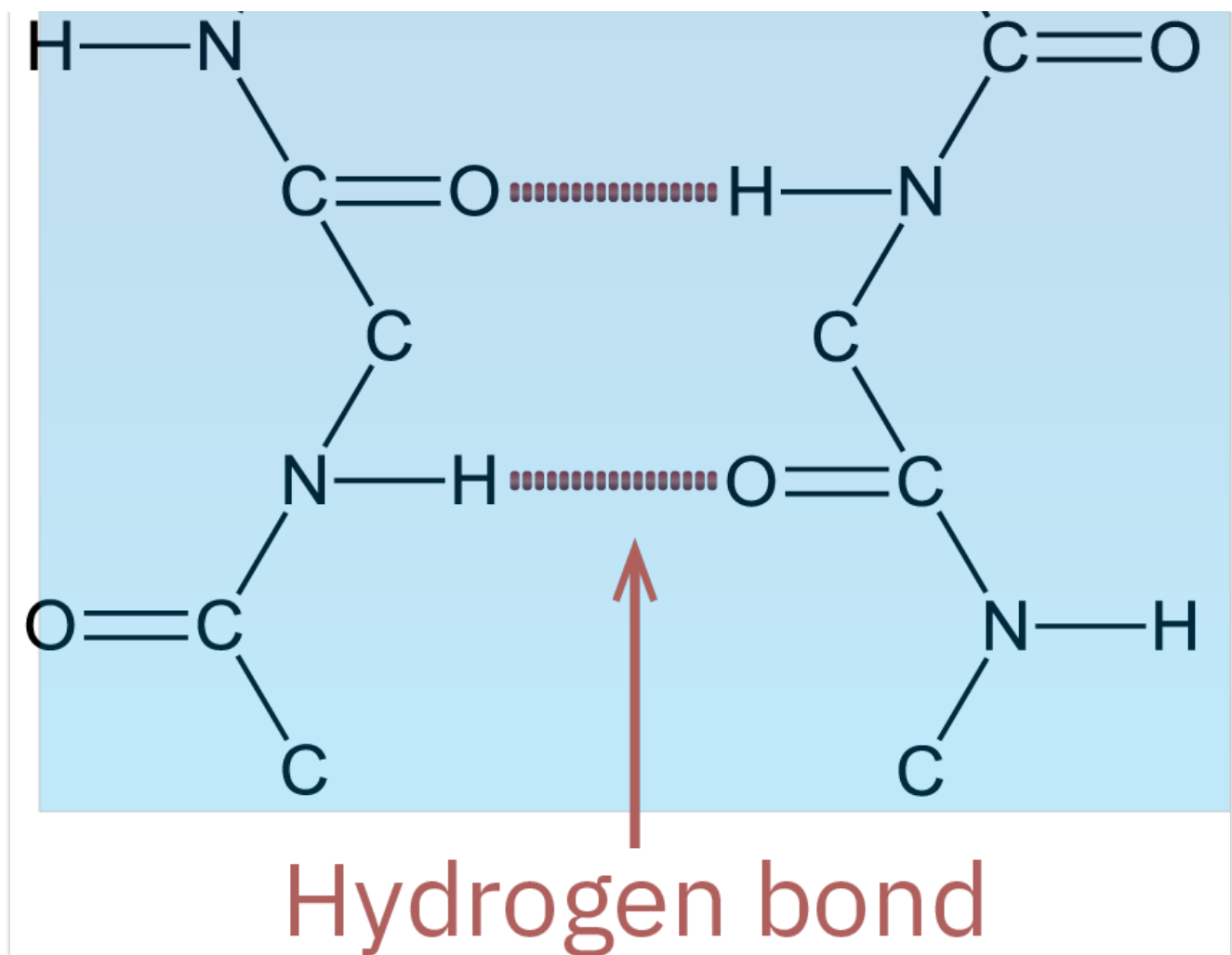
****Hydrogen bonds can form between peptide links due to the polar nature of the $-\text{NH}$ group and the $-\text{CO}$ of another amino acid.** The **side chains**, or **RRR groups**, poke outwards from the coil and are **able to rotate**. This is an important feature for the next level of protein structure.



Instead of hydrogen bonds forming in a way that produces a coil, β -pleated sheets are formed **between peptide links** on **neighbouring sections of polypeptide chains**. In the image to the right, you can see that the backbone of a polypeptide chain has a recurring pattern in the atoms, $-N - C - C - N - C - C-$. Amino acids with **smaller side chains** are able to **line up much more accurately** to form β -pleated sheets than those with larger side chains. This more accurate alignment means that **they stabilise the protein structure**.

β -pleated sheet

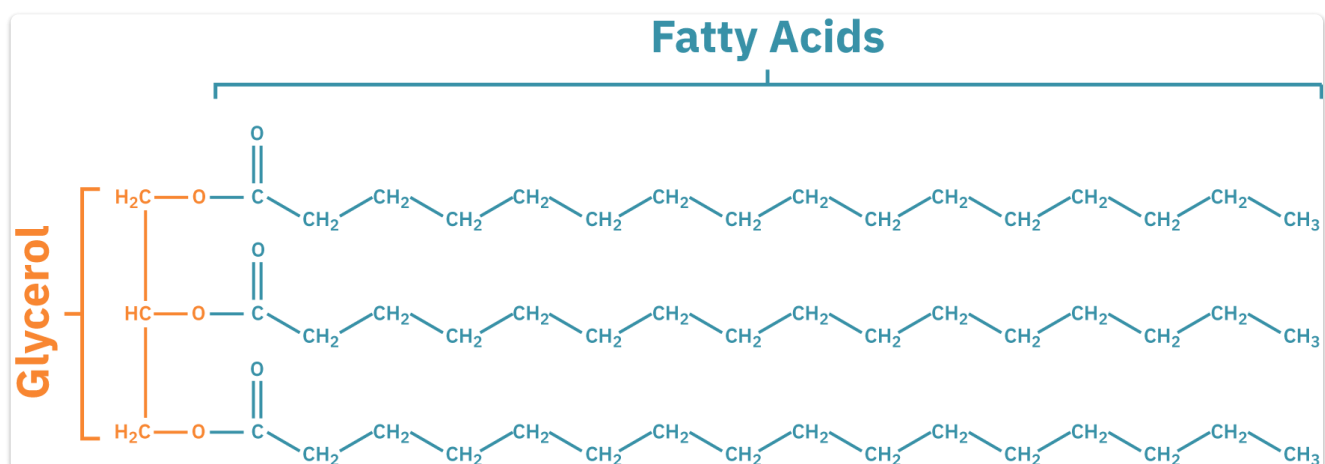




Lipids

At its most basic, a triglyceride is made up of one alcohol and three fatty acids.

The alcohol in question is **glycerol**, a three-carbon molecule with three hydroxy groups attached $-OH$. The three fatty acids are all carboxylic acid alternatives, containing the carboxyl group $-COOH$ and a long carbon chain.

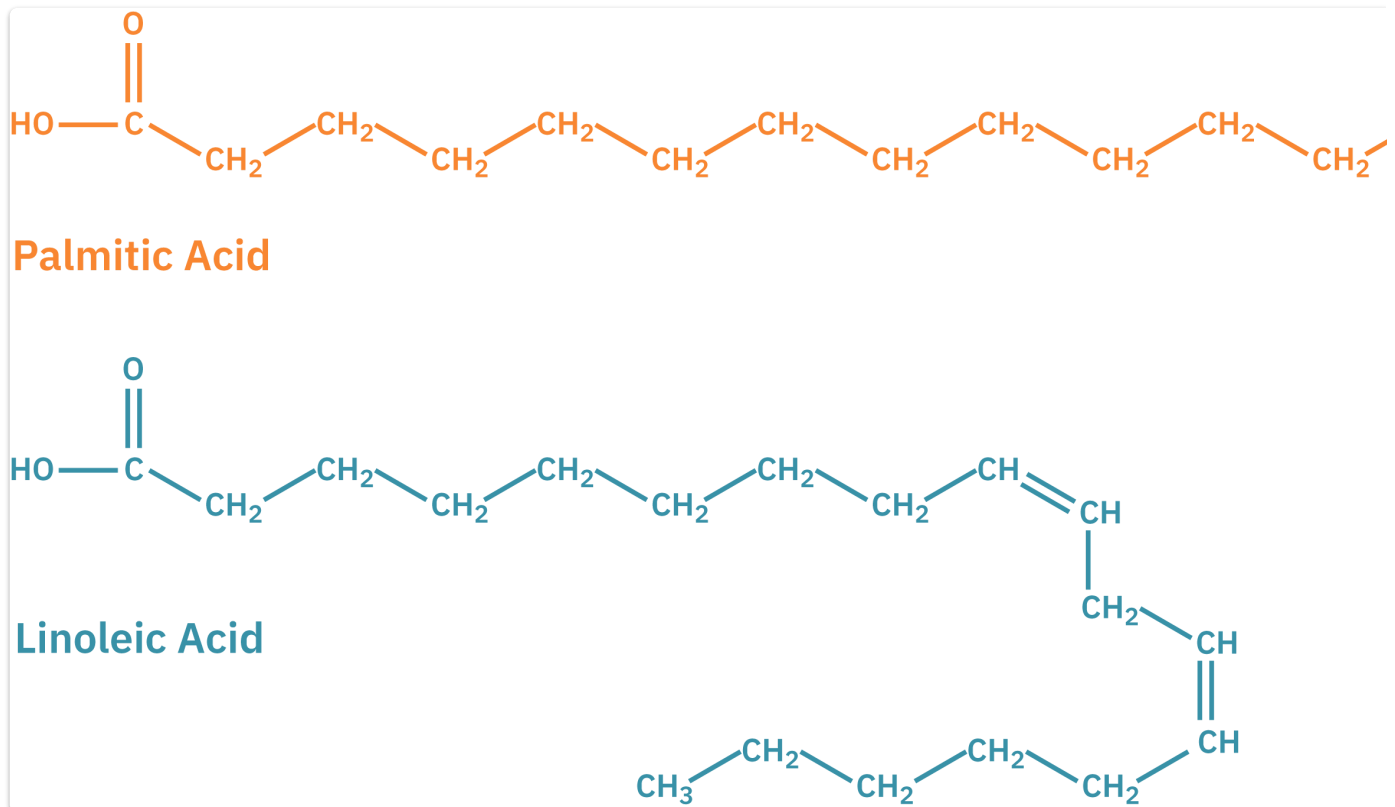


The fatty acids of triglycerides need not always be identical. When they are, naming the triglyceride is easy. For example, **linolein** is a triglyceride **only containing linoleic acid**. When

they aren't, we simply call the molecule a triglyceride.

****We classify triglycerides based on whether their fatty acids are saturated or unsaturated.****

A fatty acid is saturated when it contains single Carbon bonds. A fatty acid is unsaturated when it contains double or even triple carbon bonds. Saturated fatty acids are typically **linear and tightly packed**, whereas unsaturated fatty acids are **kinked and do not pack as easily**. Saturation affects a triglyceride's **physical properties**.



Notice how linear the chains of palmitic acid (saturated) are compared to linoleic acid (unsaturated).