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The big picture

Have you ever wondered how scientists develop new medications to treat disease? What exactly do they target and why? Due to their central role in biological processes, proteins have become prime targets for therapy and are at the heart of many scientific breakthroughs. Scientists and researchers have recognised that by understanding the structure, function and interactions of proteins, they can unlock vital insights into diseases and develop targeted treatments.

Proteins can act as messengers, transmitting signals between cells, thereby influencing cellular processes. In the context of cancer, proteins are of particular interest because they can promote metastasis, which is the spread of cancer cells, through interactions with other molecules.

One example of a protein that is involved in cancer metastasis is latent TGF-beta binding protein 3 (LTBP3), found in the extracellular matrix of cells including cancer cells. While the exact mechanism of how LTBP3 functions is still under study, recent findings have shown that inhibiting LTBP3 from binding to other signalling molecules prevents the spread of cancer cells (**Figure 1**). When researchers targeted this protein, they were able to prevent cancer cells from entering blood vessels, thus preventing them from spreading to other parts of the body.

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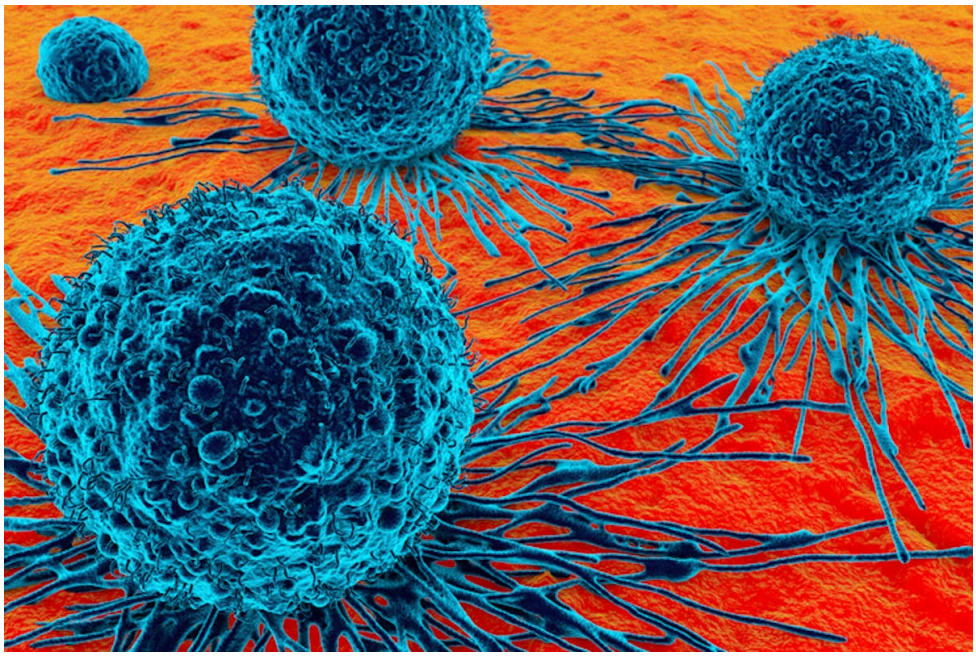


Figure 1. Cancer cells forming new blood vessels.

Credit: ROGER HARRIS/SCIENCE PHOTO LIBRARY, Getty Images

To target these proteins, researchers require extensive knowledge of their structure and function. How can the structure of a protein be so essential to a protein's function? How can a protein's environment affect its structure and function? How can understanding the complexity of the structure of proteins such as LTBP3 be the key to developing novel medicines to treat diseases?

In this subtopic, you will learn about the structure and function of proteins, gaining knowledge that serves as a basis for understanding the critical roles of proteins.

Prior learning

Before you study this subtopic make sure that you understand the following:

- Condensation and hydrolysis reactions (see section B1.1.1—3 (/study/app/bio/sid-422-cid-755105/book/chemical-bonding-andpolymerisation-id-44681/)).

B1. Form and function: Molecules / B1.2 Proteins

Fundamentals of amino acids

Student view

Overview (/study/ap 422-cid-755105/o

B1.2.1: Generalised structure of an amino acid B1.2.2: Condensation reactions of amino acids

B1.2.3: Dietary requirements for amino acids

Learning outcomes

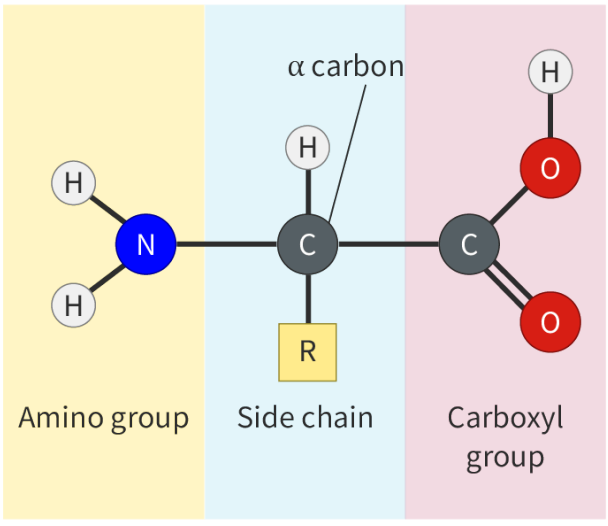
By the end of this section you should be able to:

- Draw a diagram of a generalised amino acid showing the alpha carbon atom with amine group, carboxyl group, R-group and hydrogen attached.
- Write the word equation for condensation reactions between amino acids to form dipeptides.
- Draw a generalised dipeptide after modelling the reaction with molecular models.
- Explain the difference between essential and non-essential amino acids.

Proteins are complex macromolecules composed of one or more chains of amino acids. They play essential roles in many biological processes, including structural support, catalysis and signalling pathways. Understanding the structure of amino acids and how they join together is essential for understanding the significance of protein structure and function.

Generalised structure of an amino acid

Amino acids are the monomers that are used to make proteins. There are 20 unique amino acids but each has the general structure shown in **Figure 1**.



Student view

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Figure 1. General structure of an amino acid.

More information for figure 1

The diagram illustrates the general structure of an amino acid, divided into three vertical sections:

1. **Amino Group Section (Yellow):**
2. On the left, there is an amino group with a nitrogen (N) atom bonded to two hydrogen (H) atoms. This section is labeled "Amino group."

3. **Central Section (Blue):**

4. In the middle, the central carbon (C), known as the alpha carbon, is bonded to one hydrogen atom at the top and an R group at the bottom, indicating a side chain. This section is labeled "Side chain."

5. **Carboxyl Group Section (Pink):**

6. On the right, there's a carboxyl group with a carbon (C) atom double-bonded to one oxygen (O) atom and single-bonded to another oxygen atom, which in turn is bonded to a hydrogen atom. This section is labeled "Carboxyl group."

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The central carbon is known as the alpha (α) carbon and it is covalently bonded to four different chemical groups:

- a carboxyl group (−COOH)
- an amino group ($-NH_2$)
- a hydrogen atom (−H)
- a unique organic side chain called the R-group.

Each of the 20 amino acids has a different R-group. R-groups can be non-polar or polar, linear or in ringed form, providing each amino acid with distinct chemical and physical properties.

Student view

Overview (/study/ap 422-cid-755105/o

Condensation reactions forming dipeptides and longer chains of amino acids

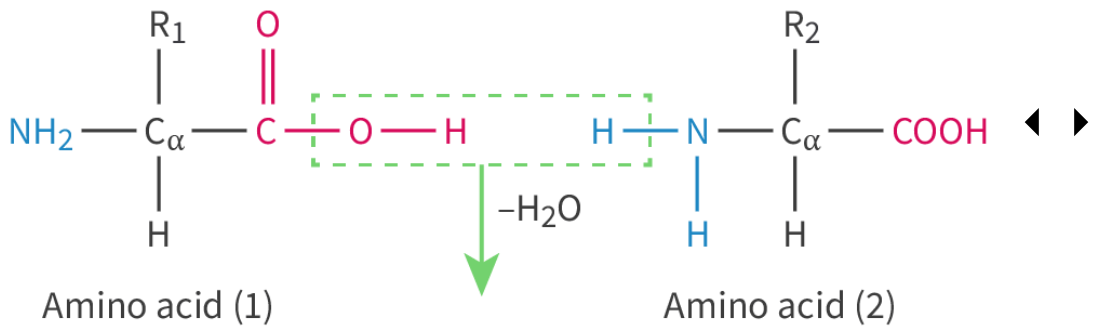
Amino acids join together through a condensation reaction (**Interactive 1**). A peptide bond is formed when the carboxyl group (–COOH) of one amino acid reacts with the amino group ($–NH_2$) of another amino acid to form a dipeptide. A molecule of water (H_2O) is released as a byproduct. The peptide bond formed is a type of covalent bond and, therefore, is very stable.

Concept

Word equation:

amino acid + amino acid → dipeptide + 1 water molecule

Use the slider in **Interactive 1** to reveal the products of the condensation reaction.



Interactive 1. Condensation Reaction Between Two Amino Acids.

More information for interactive 1

An interactive chemical reaction illustrates the condensation reaction between two amino acids. Users can move a slider to observe how these reactants interact to form a peptide bond.

Amino acid 1 is positioned on the left, and amino acid 2 is on the right.

Amino acid 1 features a central carbon atom labeled Cα, which is single-bonded to an R1 group at the top, an NH2 group on the left, an H atom at the bottom, and a second carbon atom on the right. This second carbon atom is double-bonded to an O atom at the top and single-bonded to another O atom on the right, which is

Student view

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further bonded to an H atom, forming a carboxyl group (COOH).

Amino acid 2 features a central carbon atom labeled C_α, which is single-bonded to an R_2 group at the top, an N atom on the left, an H atom at the bottom, and a COOH group on the right. The N atom is further bonded to an H atom on the left and another H atom at the bottom, forming an amino group (NH_2).

During the condensation reaction, the OH group from the carboxyl end of amino acid 1 and an H atom from the NH_2 group of amino acid 2 are eliminated to form H_2O.

Then, the remaining portions of the two amino acids bond together via a peptide bond formed between the second C in amino acid 2 and the N in amino acid 2. This results in the formation of a dipeptide, featuring the CONH linkage. In the product, the left end with the NH_2 group is labeled N-terminus, and the right end with the COOH group is labeled C-terminus.

This interactivity helps users understand how a peptide bond is formed between two amino acids.

The N-terminal (amino-terminal) end of the dipeptide refers to the free amino group that is not involved in the peptide bond, while the C-terminal (carboxyl-terminal) end refers to the unbound carboxyl group. More amino acids can be added to the dipeptide through the formation of a new peptide bond between an incoming amino acid and the C-terminal (carboxyl terminal) of the dipeptide. This process can be repeated multiple times to form longer chains of amino acids, called polypeptides. Every time an amino acid joins the growing polypeptide strand and a new peptide bond is formed, another water molecule is released. Subtopic D1.2 (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43547/) covers the formation of polypeptides.

Dietary requirements for amino acids

Amino acids can be classified as either essential or non-essential. Essential amino acids are the amino acids that your body cannot produce and therefore you must obtain them from the food that you eat. Essential amino acids are necessary for proper growth, maintenance and repair of the body's tissues and organs. Non-essential amino acids can be produced by the body from other amino acids or by the breakdown of proteins. Non-essential amino acids, although not required in the diet, still have important functions in the body. It is important to consume a balanced diet that includes the appropriate combination of protein sources to ensure the body's needs are met.

Student view

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Vegan diets can provide all the essential amino acids necessary for a healthy diet through plant-based protein sources such as beans, lentils, nuts, seeds and tofu (**Figure 2**). However, if following a vegan diet, it is necessary to ensure that adequate amounts of these protein sources are consumed for optimal health.

Figure 2. Plant-based proteins are excellent sources of essential amino acids.

Credit: fcafotodigital, Getty Images

Creativity, activity, service

Strand: Activity
Learning outcome: Demonstrate the skills and recognise the benefits of working collaboratively

Promote awareness of alternative diets by organising a culinary competition or food festival. This event should focus on highlighting the nutritional richness and diversity of plant-based protein sources, such as quinoa, lentils, chia seeds and tofu.

Participants can be encouraged to use their cooking skills and creativity to prepare innovative and delicious plant-based dishes that meet essential nutritional requirements and cater to different preferences. The event could also include interactive sessions that educate attendees on the nutritional value of plant-based diets and the environmental and ethical benefits of reducing meat consumption.

Student view

Try the activity below to model condensation reactions.

Overview (/study/ap 422-cid-755105/o

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Social skills — Working collaboratively to reach a common goal
- **Time required to complete activity:** 45 minutes
- **Activity type:** Pair activity

Building molecular models

Molecular modelling is a useful tool to visually understand the 3D structure of molecules. To better understand how amino acids join together through condensation reactions, you can use molecular modelling to model this reaction.

Materials

- Molecular modelling kit (such as a Molymod or K'NEX set) or sticks and marshmallows (different colours) if no kit is available.

Instructions

1. Start by selecting the amino acids you want to build. Some common ones include alanine, glycine and leucine.
2. If you are using a molecular modelling kit, select the appropriate building blocks for each amino acid. If you are using sticks and marshmallows, assign each colour of marshmallow to a different atom type, such as carbon, nitrogen and oxygen.
3. Begin building each amino acid by connecting the atoms together according to the correct bond angles and lengths. For example, alanine has a central carbon atom bonded to a hydrogen atom, a methyl group (CH_3), an amine group (NH_2) and a carboxyl group (COOH) (**Figure 3**).
4. Continue building the amino acids until you have all the ones you want to connect.
5. To form a peptide bond, remove the hydrogen atom from the amine group of one amino acid and the hydroxyl (OH) group from the carboxyl group of another amino acid.
6. Connect the two amino acids with a peptide bond, which is a covalent bond between the carbon atom of the carboxyl group and the nitrogen

Student view

Overview (/study/ap 422-cid-755105/o

atom of the amine group. This forms a dipeptide.

7. Repeat this process to add more amino acids and form a longer polypeptide chain.
8. When you are finished, examine your molecular models to see the different shapes and structures of the amino acids and the overall polypeptide chain. Share your model with your teacher and class.

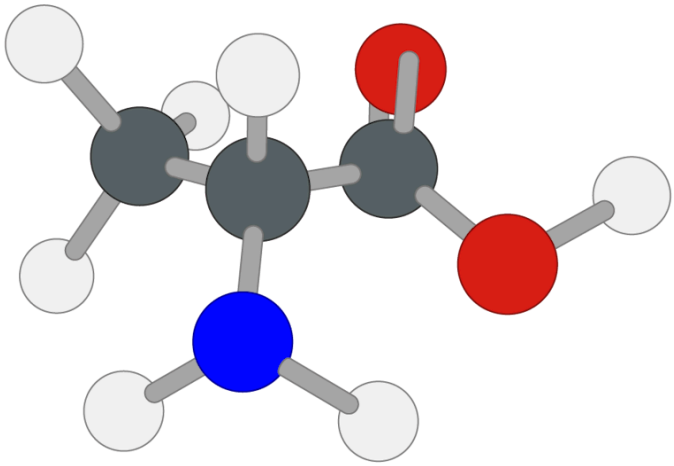

Figure 3. Model of alanine.

5 section questions

B1. Form and function: Molecules / B1.2 Proteins

Protein structure

B1.2.4: Infinite variety of possible peptide chains B1.2.5: Effect of pH and temperature on protein structure

Learning outcomes

By the end of this section you should be able to:

- Recognise that there are 20 amino acids coded for in the genetic code.
- Name examples of polypeptides and know their function.
- Describe the effect of extreme pH and temperature on protein structure ('denaturation').

Student view

Overview (/study/ap 422-cid-755105/o

To understand the relationship between amino acid sequences and the diversity in form and function of proteins, you must first explore the universality of the genetic code.

Infinite variety of possible peptide chains

The genetic code is a set of rules that specifies how information stored in DNA is translated into the sequence of amino acids that make up proteins. It serves as a universal language for all living organisms and provides the instructions for protein synthesis. The genetic code provides the instructions for the synthesis of proteins through the processes of transcription and translation, which is explored in detail in subtopic D1.2 (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43547/). During transcription, DNA is transcribed into mRNA, and during translation, the mRNA is translated into a sequence of amino acids.

The genetic code is composed of codons, which are groups of three nucleotides that specify the type of amino acid or stop signal required. There are 64 different codons in total, but only 20 amino acids, so the genetic code is said to be degenerate. This means that some amino acids are coded for by multiple codons, which allows for the possibility of silent mutations. Silent mutations are where a change in the DNA sequence does not result in a change in the amino acid sequence of the protein.

The infinite variety of possible peptide chains arises from the ability to combine the 20 different amino acids in any sequence. This allows for creation of an almost limitless number of unique proteins with different structures and functions. The genetic code, combined with the ability to generate diverse combinations of amino acids, is what makes the complexity and diversity of life possible.

Based on the three letters that are a present in a codon, a codon table (**Figure 1**) can be used to deduce which amino acid the codon codes for. For example, if the codon is **GCU**, you will use the table to see where the first letter is G, the second letter is C and the third letter is U. In this case, you will find that GCU codes for the amino acid alanine.

Student view

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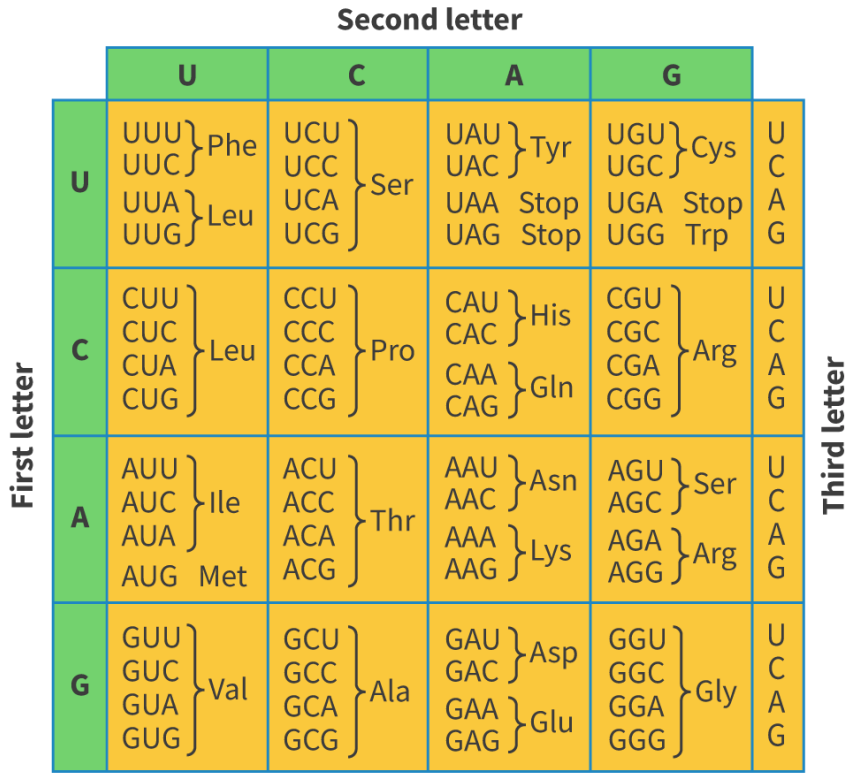


Figure 1. A codon table.

More information for figure 1

The image is a genetic codon table used to determine which amino acids correspond to specific codon sequences of RNA. The table is structured into rows and columns. Each row is labeled with a letter on the left side, representing the first letter of the codon, while each column is headed by another letter at the top, representing the second letter. The last column on the right provides possibilities for the third letter. Inside the grid, combinations of three-letter codons are matched to their respective amino acids. For instance, under the 'G' row for the first letter, 'C' column for the second letter, and 'U' in the third letter's column, the codon GCU corresponds to the amino acid alanine (Ala). Each codon group is bracketed with arrows pointing to their respective amino acids. The chart is color-coded for better distinction but does not rely on color for understanding.

[Generated by AI]

Examples of polypeptides

A polypeptide is a chain of amino acids that is linked together by peptide bonds, whereas a protein is a complex, three-dimensional structure that is made up of one or more polypeptide chains. The three-dimensional structure of proteins is discussed in section B1.2.1–3 (/study/app/bio/sid-422-cid-755105/book/fundamentals-of-amino-acids-

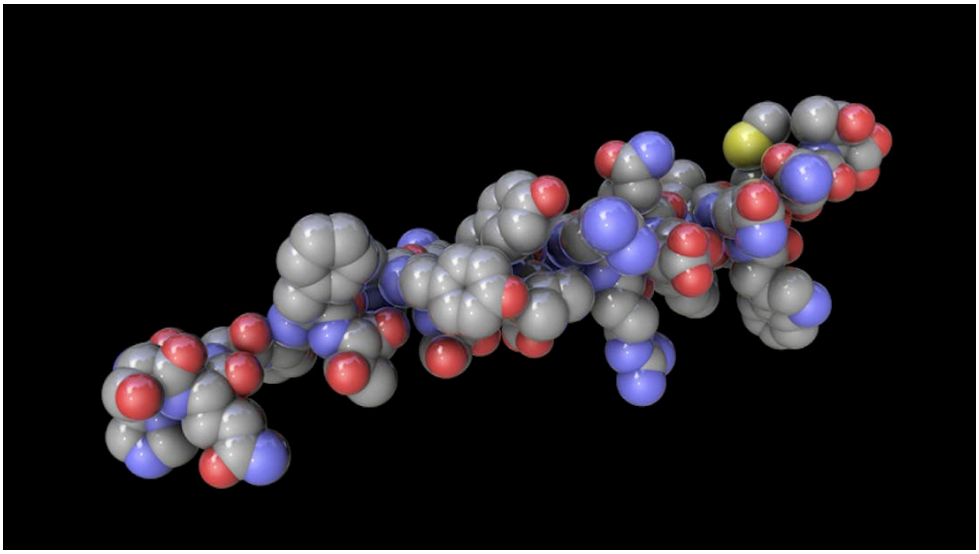
Student view

Overview (/study/ap 422-cid-755105/o

id-45486/). Proteins can be composed of one or more polypeptide chains. In a protein composed of only one polypeptide chain, the amino acids will interact with each other, folding the chain into a functional protein. In proteins composed of more than one polypeptide, the polypeptide chains can additionally interact with each other, contributing to the overall structure of the protein.

Single-chain polypeptides serve crucial functions as both enzymes and hormones. These molecules possess a specific primary structure, which refers to the linear sequence of amino acids that make up the protein. Here are examples of polypeptides:

- **Lysozyme** is an enzyme that is composed of 129 amino acids and is present in tears and saliva. It has antimicrobial properties, disrupting the cell walls of certain bacteria thereby providing a defence mechanism against microbial infections.
- **Alpha-neurotoxins** represent a group of polypeptides that are present in snake venom which specifically target and disrupt the nervous system. These polypeptides range from 60 to 75 amino acids in length and can bind to and inhibit specific receptors, inducing neurotoxic effects, paralysis and possibly death.
- **Glucagon** is a hormone composed of 29 amino acid residues (**Figure 2**). This hormone is crucial for regulating blood sugar levels. Glucagon is secreted from the pancreas when glucose levels in the blood are low, stimulating the liver to release stored glucose into the bloodstream, thereby raising blood sugar levels.
- **Myoglobin** is an oxygen-binding protein, mainly found in muscle tissues, which is composed of 153 amino acid residues. It facilitates the storage and release of oxygen to muscle fibres, particularly during periods of low oxygen availability, such as strenuous physical activity.



Student view

Overview (/study/ap 422- cid- 755105/o

Figure 2. Glucagon structure.

Credit: KATERYNA KON/SCIENCE PHOTO LIBRARY, Getty Images

More information for figure 2

The image depicts the 3D molecular structure of glucagon, a protein. The representation uses a ball-and-stick model where different colored spheres represent various atoms within the glucagon molecule. The structure appears intricate, indicating the complex arrangement of atoms that define the protein's configuration. The spheres are color-coded to usually denote different elements, though specific colors cannot be addressed without further information.

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Effect of pH and temperature on protein structure

The structure of proteins is vital for their biological function and any changes to their structure can result in a loss of activity. Denaturation is a process in which the structure of a protein is altered causing it to lose function, usually permanently. Two factors that can cause denaturation of proteins are pH and temperature.

All proteins have a specific range of temperature and pH for their optimal activity. As all enzymes are proteins, it is essential for them to be exposed to their ideal conditions to maintain efficiency. Extreme changes in pH can affect protein solubility and shape by altering the protein’s charge. This can lead to irreversible changes in protein structure, causing inactivity. For example, the enzyme pepsin requires an acidic environment to function, while an alkaline environment will render it inactive.

Temperature is another critical factor that can cause protein denaturation. High temperatures can break the weak hydrogen bonds holding the protein structure together, causing the protein to unfold and lose function. Most human proteins function optimally at body temperature (~37 °C). Some organisms that live in extreme high-temperature environments have proteins that can only function at higher temperatures. Low temperatures can also affect protein structure, but to a lesser extent than high temperatures.

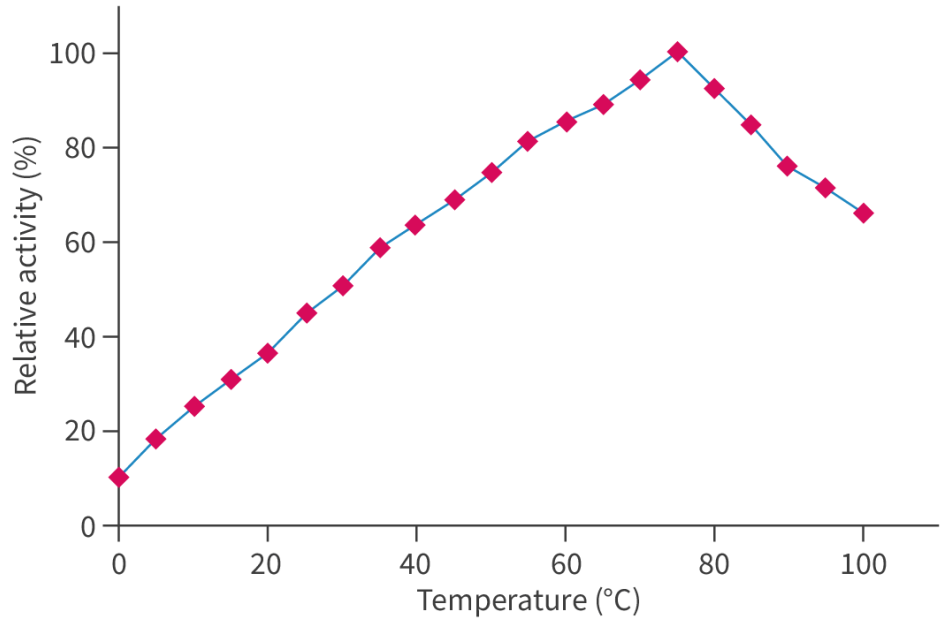
Student view

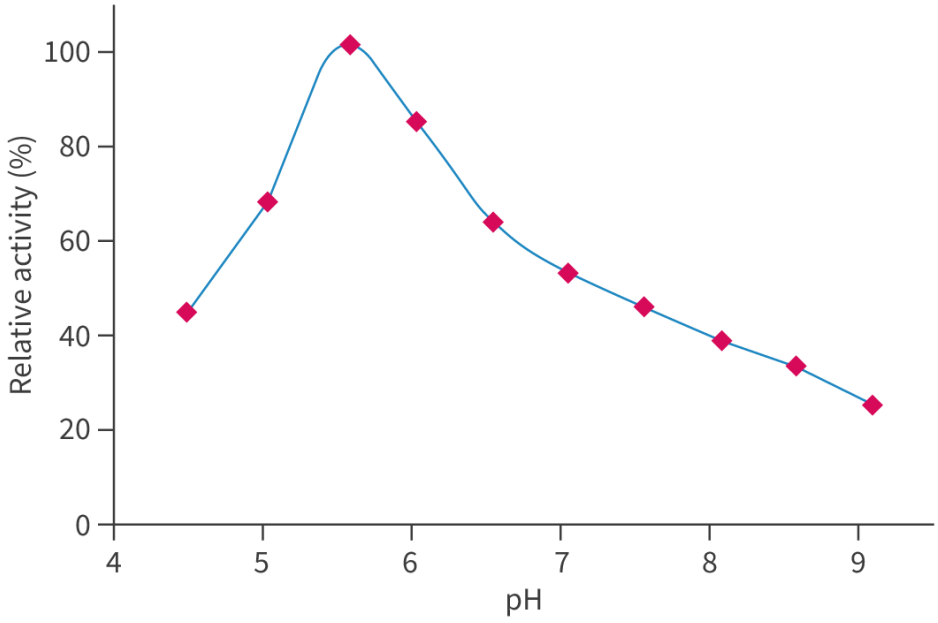
Overview (/study/ap 422-cid-755105/o

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Reflecting at all stages of the assessment and learning cycle
- **Time required to complete activity:** 30 minutes
- **Activity type:** Individual and group activity

Alpha-amylase (α-amylase) is an enzyme that has the ability to break down starch to maltose through hydrolysis. Experiments were performed to test the impact of different pH levels and different temperatures on the relative activity of soybean α-amylase. The data are depicted in **Figure 3**.





Student view

Overview (/study/ap 422-cid-755105/o

Figure 3. Graphs showing enzyme activity and temperature and effect of pH on the relative activity of soybean α-amylase.

More information for figure 3

The image consists of two line graphs. The first graph displays the relationship between temperature (in °C) on the X-axis and the relative activity (in %) of the soybean α-amylase on the Y-axis. The data points form a line that shows an initial increase from 0°C, peaking at around 70°C with a relative activity of 100%, and then declining beyond 70°C.

The second graph illustrates the effect of pH on relative activity. The X-axis represents pH values ranging from 4 to 9, while the Y-axis shows the relative activity (in %). The graph peaks at a pH of around 6, where the enzyme exhibits its highest activity at approximately 100%. After the peak, the activity decreases as the pH moves toward 9.

[Generated by AI]

Use the graphs in **Figure 3** to answer the following questions:

1. Determine the optimum pH and temperature for soybean α-amylase activity.
2. Suggest **two changes** that can be observed in the reaction vessel that could be used to indicate α-amylase activity.
3. Outline **two conditions** that must be kept constant in both experiments to ensure accurate results.

Once you have attempted to answer the questions individually, compare your answers with members of your group and discuss.

Section Student... (0/0) 5 section questions Feedback Print (/study/app/bio/sid-422-cid-755105/book/fundamentals-of-amino-acids-id-45486/print/) Assign

B1. Form and function: Molecules / B1.2 Proteins

Primary, secondary, and tertiary structure of proteins (HL)

B1.2.6: Chemical diversity in the R-groups of amino acids (HL)

B1.2.7: Impact of primary structure on the conformation of proteins (HL)

B1.2.8: Pleating and coiling of secondary structure of proteins (HL) B1.2.9: Tertiary structure of proteins (HL)

B1.2.10: Effect of polar and non-polar amino acids on tertiary structure (HL)

Student view

Overview (/study/ap 422-cid-755105/o

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Recall that the properties of R-groups as either hydrophobic or hydrophilic (polar or charged; acidic or basic) determine the properties of assembled polypeptides.
- Describe that the sequence of amino acids and the precise position of each amino acid within a structure determines the three-dimensional shape of proteins.
- Explain that the secondary structure of a protein depends on hydrogen bonding in regular positions to stabilise alpha helices and beta-pleated sheets while the tertiary structure of a protein depends on hydrogen bonds, ionic bonds, disulfide covalent bonds and hydrophobic interactions.

As described in section B1.2.1–3 (/study/app/bio/sid-422-cid-755105/book/fundamentals-of-amino-acids-id-45486/), proteins have remarkable ability to perform a wide variety of functions in living organisms, ranging from catalysing chemical reactions to providing structural support. The secret to the versatility of proteins lies in the ability of proteins to adopt a vast array of three-dimensional shapes. In this section, you will explore how the shape of a protein is a consequence of its sequence of amino acids and the interactions between them.

It is possible to view the 3-D structure of proteins using a tool called AlphaFold Protein Structure Database (https://alphafold.com/about). It is an artificial intelligence system that is able to computationally predict protein structures.

Student view

Overview (/study/ap 422-cid-755105/o

Chemical diversity in the R-groups of amino acids as a basis for the immense diversity in protein form and function

Amino acids are linked together by ribosomes to make polypeptides (see subtopic D1.2 (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43547/)). In section B1.2.1–3 (/study/app/bio/sid-422-cid-755105/book/fundamentals-of-amino-acids-id-45486/), you learned about the general features of amino acids. While amine groups and carboxyl groups are used to link amino acids together, the R-group is what gives each amino acid its unique characteristics. The R-groups of the amino acids present in a polypeptide determine the properties of the assembled polypeptides.

R-groups can be hydrophobic or hydrophilic. Hydrophobic R-groups are non-polar and tend to repel water molecules. Hydrophilic R-groups are polar or charged, acidic or basic, and tend to attract water molecules. Polar R-groups contain partial charges that interact with water molecules, while charged R groups can be either positively charged (basic) or negatively charged (acidic).

There are four levels of protein structure:

- primary structure
- secondary structure
- tertiary structure
- quaternary structure.

Primary structure of proteins

The primary structure of a protein refers to the specific sequence of amino acids that are joined together to form a polypeptide chain (**Figure 1**). The unique sequence of amino acids determines how the polypeptide chain will fold, ultimately leading to the three-dimensional structure of the protein. This means that the precise position of each amino acid within the protein structure is critical in determining its shape. Change in the sequence of amino acids may result in significant changes to the protein's structure and function. (See subtopic D1.3 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43250/) to learn more about mutations.)

Student view

Overview (/study/ap 422- cid- 755105/o

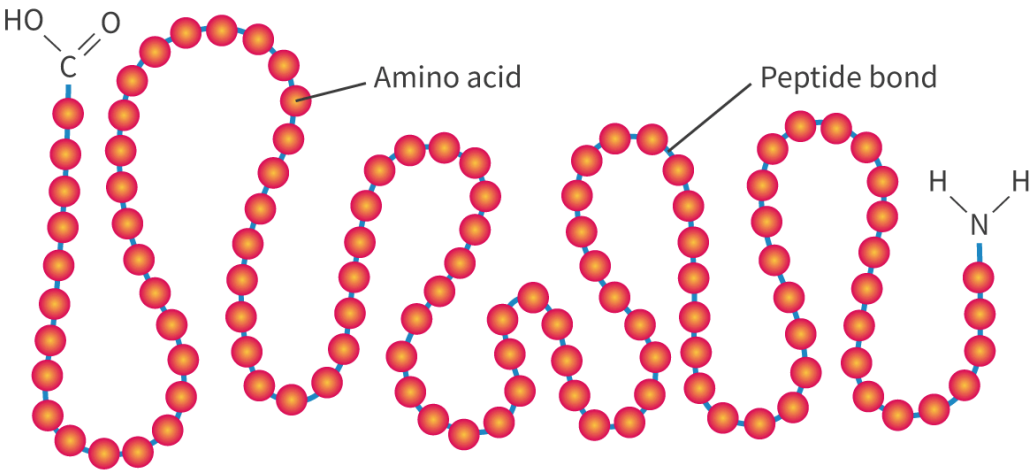


Figure 1. Primary structure of a protein.

More information for figure 1

The image is a diagram illustrating the primary structure of a protein with a sequence of amino acids connected in a linear chain. Each amino acid is represented by a colored sphere. The diagram highlights "amino acid" and "peptide bond" with labeled lines pointing to specific points in the chain. The chain begins with a carboxyl group (labeled HO and C=O) and ends with an amino group (labeled H and N). The entire sequence of amino acids forms a single continuous chain which is shown in a zigzag pattern to denote the polypeptide chain's linear structure.

[Generated by AI]

Secondary structure of proteins: pleating and coiling

The secondary structure of a protein refers to the local folding patterns that occur within the polypeptide chain, and two common types of secondary structures are alpha helices and beta-pleated sheets (**Interactive 1**).

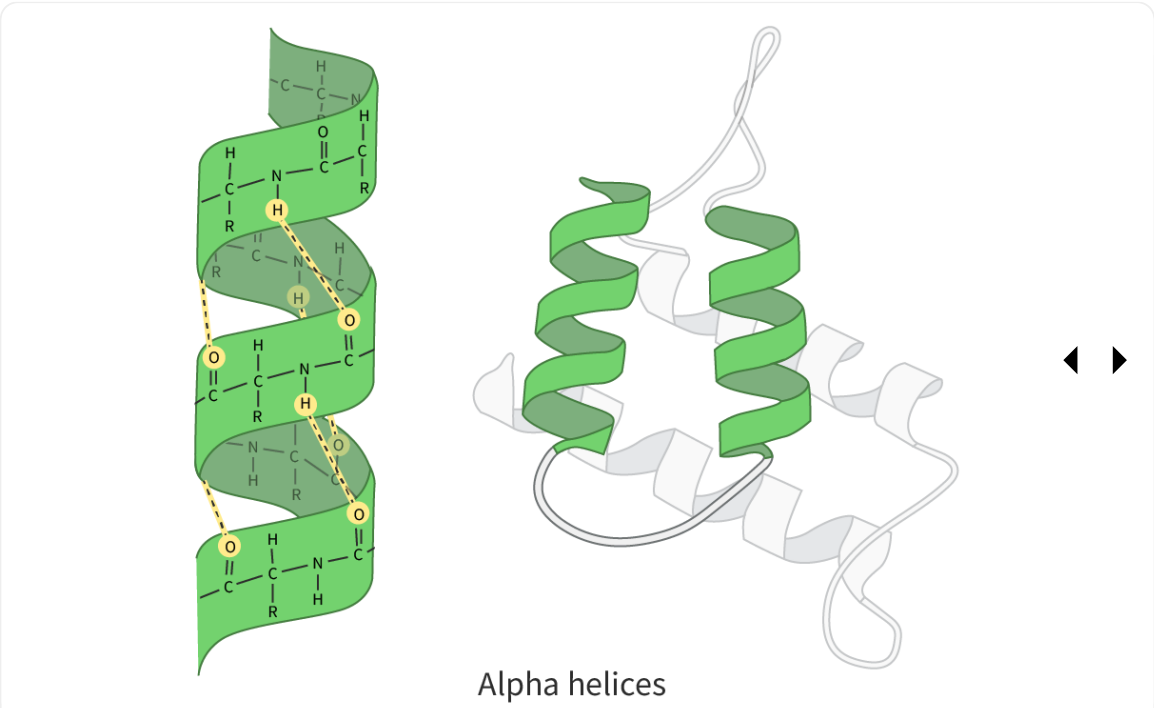
The formation of alpha helices and beta-pleated sheets is facilitated by the ability of the polypeptide chain to fold into coils and pleats, respectively. This is achieved through hydrogen bonding between the carboxyl group of one amino acid and the amino group of another amino acid in a different part of the polypeptide chain. These hydrogen bonds occur in regular positions and help to stabilise and aid in the formation of the secondary structure. Although a hydrogen bond on its own is considered to be a weak form of bonding, collectively, hydrogen bonds are strong enough to hold the conformation of the protein.

Student view

Overview (/study/ap 422-cid-755105/o

In an alpha helix, the hydrogen bond forms between the amine hydrogen of one amino acid and the carboxyl oxygen of another amino acid that is four residues away in the sequence. This repeated pattern of hydrogen bonding allows the polypeptide chain to coil and form the characteristic helical structure.

In contrast, beta-pleated sheets form when sections of the polypeptide chain run parallel to each other, and hydrogen bonds form between adjacent strands. These hydrogen bonds create a pleated sheet-like structure, with the individual strands forming the flat surface of the sheet (**Interactive 1**).



Interactive 1. Alpha Helices and Beta-Pleated Sheets: Two Types of Protein Secondary Structure.

More information for interactive 1

This interactive slider showcases the two main types of secondary structures found in proteins: alpha helices and beta-pleated sheets. At first, the interactive shows the image of alpha helices with a slider handle located on the right-hand side. The user can drag the slider from the right towards the left to reveal another image representing beta pleated sheets. The user can again drag the slider from left to right, or from right to left to transition between the images. This allows students to visually transition between the two structures by dragging a slider handle across the image.

Read below to learn about the secondary structure of protein in each image:

Alpha Helices:
On the left side of the slider is the alpha helix structure, with the label “Alpha helices” at the bottom. It features a green coiled ribbon-like structure that represents a segment of a polypeptide chain. Molecular structures with atoms are shown on this alpha helix structure labelled by standard

Student view

Overview (/study/ap 422-cid-755105/o

chemical notation (e.g., H for hydrogen, O for oxygen, N for nitrogen, and C for carbon). Yellow dotted lines illustrate hydrogen bonds connecting the amino hydrogen of one amino acid to the carbonyl oxygen of another amino acid four positions down the chain. These hydrogen bonds allow the protein to twist into a spiral shape. On the right of this structure, the alpha helix is depicted as a green coil embedded in a more complex white and grey protein chain.

Beta-Pleated Sheets:
Sliding from the right to the left, show beta-pleated sheets, with the same label at the bottom. Sliding the image from the right side displays beta-pleated sheets, shown in purple. This structure includes zigzag polypeptide chains positioned side by side, and connected at the top forming a sheet-like appearance. Molecular structures with atoms are shown on this beta-pleated sheet labelled by standard chemical notation (e.g., H for hydrogen, O for oxygen, N for nitrogen, and C for carbon). The chemical structure again highlights hydrogen bonding between adjacent strands using yellow dotted lines. The hydrogen bonds are formed between the amino hydrogen of one strand and the carbonyl oxygen of another strand. The strands run parallel or antiparallel to each other, and the pleated shape results from the folding pattern. On the right, beta sheets are shown as wide, flat arrows, some pointing upwards, while some pointing downwards, embedded within a folded protein structure in light grey.

This interactive demonstrates secondary structure in proteins and explains how amino acid chains fold into specific shapes due to hydrogen bonding. It emphasises the folding that occurs after a protein is formed and how this folding is stabilised by multiple hydrogen bonds. The comparison between the coiled alpha helices and the folded beta sheets assists viewers in understanding how proteins take on complex, stable shapes that are essential for their biological functions.

Overall, the ability of polypeptide chains to form pleats and coils through hydrogen bonding plays a crucial role in determining the secondary structure of a protein. This, in turn, affects the protein's overall three-dimensional shape and its ability to perform its specific biological functions.

Tertiary structure of proteins

Tertiary structure is the further folding of the polypeptide. It is dependent on the interaction between R-groups, which may include the formation of hydrogen bonds, ionic bonds, disulfide covalent bonds and hydrophobic interactions (**Interactive 2**). These interactions stabilise the structure of the protein. The tertiary structure gives rise to the overall three-dimensional shape of the protein. You will learn more about these different interactions below.

Student view

Hydrogen bonds

Hydrogen bonding between polar R-groups in the tertiary structure of a protein plays a crucial role in stabilising its three-dimensional shape by holding distant regions of the polypeptide chain together. This stabilising effect is critical for maintaining the protein's functional integrity and any slight deviations from the correct structure can impair the activity of the protein significantly.

Ionic bonds

Ionic bonding is a type of chemical bond that forms between oppositely charged ions. In proteins, the R-group can undergo binding or dissociation of hydrogen ions, resulting in a positively or negatively charged state, respectively. These charged R-groups can then interact with oppositely charged atoms in other molecules, forming ionic bonds. These ionic bonds can further contribute to the overall stability and function of the protein.

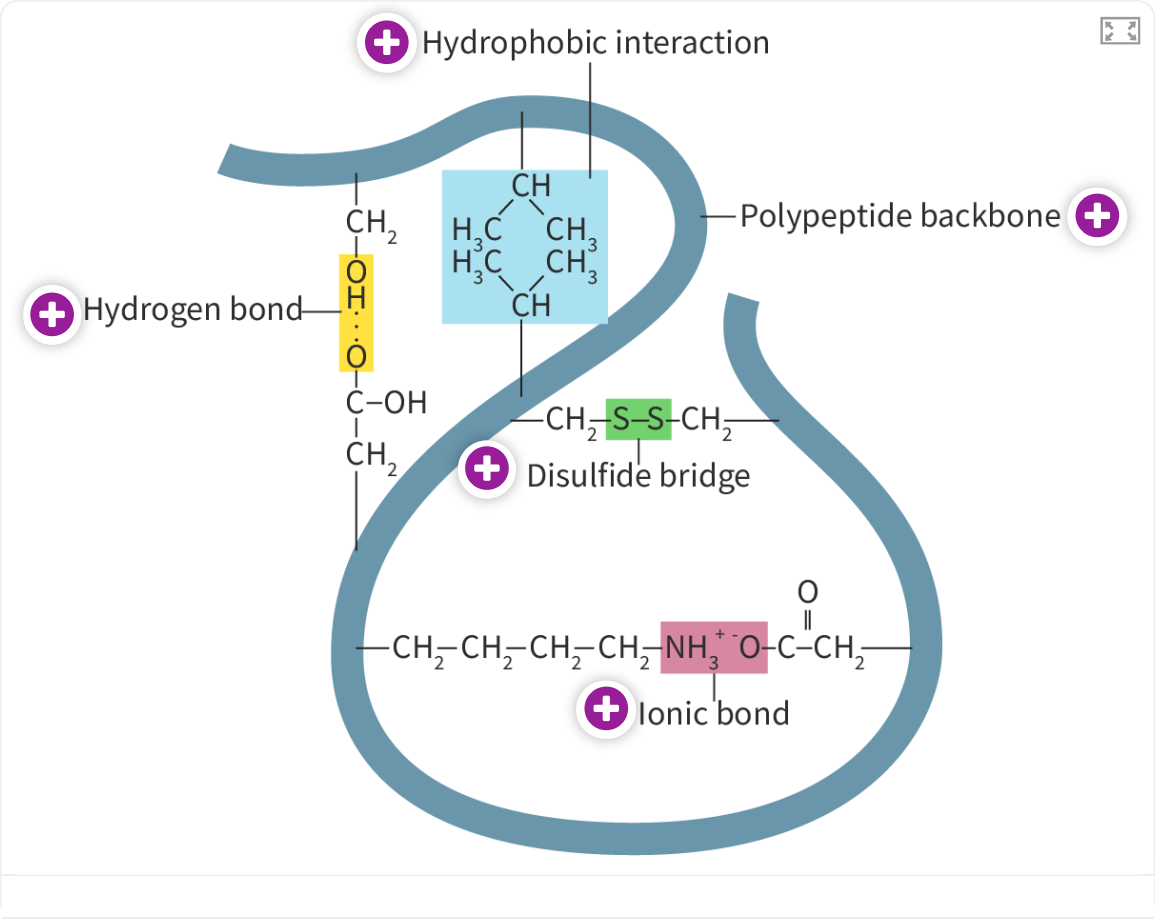
Disulfide covalent bonds

Disulfide covalent bonds form between pairs of cysteine amino acid residues, which contain sulfur atoms. These bonds are critical for stabilising the tertiary and quaternary structures of proteins by forming covalent bonds that help to maintain the protein's overall three-dimensional shape, contributing to its stability and function.

Hydrophobic interactions

Hydrophobic interactions occur between non-polar amino acids. This occurs as water is a polar molecule and forms hydrogen bonds with polar amino acids. As the non-polar amino acids are unable to interact with water, they tend to clump together into hydrophobic clusters in the interior of the protein, to minimise contact with the surrounding water molecules. These hydrophobic interactions stabilise the protein's tertiary structure and quaternary structures.

Overview (/study/ap 422-cid-755105/o



Interactive 2. The Tertiary Structure of a Protein Is Stabilised by Different Interactions.

More information for interactive 2

The interactive diagram illustrates a portion of a protein's tertiary structure, focusing on different types of intermolecular interactions that help stabilise the protein's 3D shape. The protein's polypeptide backbone is represented by a thick, blue ribbon-like line that loops around in a loose figure-eight shape.

There are five key interactions with labels, each marked by a purple plus (+) sign representing interactive hotspots. These hotspots can be clicked in the interactive to reveal more detailed explanations. The hotspots are named as hotspot 1, hotspot 2, hotspot 3, hotspot 4 and hotspot 5

Read below to learn about each interaction, its label, and the detailed description in the hotspot:

Hotspot: 1

Hydrophobic interaction: This hotspot is located at the top center and highlights the hydrophobic interaction, where a group of nonpolar hydrocarbon side chains (CH_3 and CH groups) are clustered together in a blue-shaded box. These interactions occur because hydrophobic groups tend to avoid water, tucking themselves into the interior of the protein and contributing to its compact, folded structure.

Clicking on hotspot 1 reveals the text "The tendency of non-polar molecules to aggregate and repel water molecules."

Hotspot 2:

Polypeptide backbone: This hotspot is located at the top right corner and it represents the entire polypeptide backbone in the image. The blue looped ribbon in the image represents the polypeptide chain, the main structure of the protein made of repeating units of amino acids.

Clicking on hotspot 2 reveals the text "A chain of amino acids that is linked together by peptide

Student view

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bonds."

Hotspot 3:

Hydrogen bond: This hotspot is located at the left side of the interactive and it represents the hydrogen bond. A yellow box highlights a bond between a hydrogen atom (H) attached to an oxygen (—OH) group and another oxygen atom from a nearby group. This weak bond stabilises protein structure and is labelled as a hydrogen bond.

Clicking on hotspot 3 reveals the text "A type of weak chemical bond that occurs between a partially positively charged hydrogen atom and a partially negatively charged atom, such as oxygen."

Hotspot 4:

Disulfide bridge: Hotspot 4 is located in the middle of the image and represents the disulfide bridge in the tertiary structure of the protein. Near this hotspot, a green-colored box highlights an S—S bond between two sulfur atoms (each from a $—CH_2—S$ group). This is a covalent bond formed between cysteine residues and is called a disulfide bridge—a strong stabilising interaction.

Clicking on hotspot 4 reveals the text "Covalent bonds that form between pairs of cysteine amino acid residues, which contain sulfur atoms."

Hotspot 5:

Ionic bond: Hotspot 5 is located at the bottom of the image and represents the ionic bonds. A pink shaded area shows an NH_3^+ group (positively charged) interacting with a COO^- group (negatively charged). This electrostatic attraction is labelled as an ionic bond and it helps to anchor distant parts of the polypeptide chain together.

Clicking on hotspot 5 reveals the text "A type of chemical bond that forms between oppositely charged ions."

This interactive diagram helps learners explore the key forces that stabilise a protein's tertiary structure such as hydrophobic interactions, hydrogen bonding, disulfide bridges, and ionic bonds alongside the polypeptide backbone. This promotes a deeper understanding of protein folding and structure-function relationships in biochemistry.

Effect of polar and non-polar amino acids on tertiary structure of proteins

As you have seen in the previous section, polar and non-polar amino acids affect the tertiary structure of proteins. Hydrophilic polar amino acids orient to the outside towards the aqueous environment, whereas hydrophobic non-polar amino acids are protected in the core, minimising unfavourable interactions between hydrophobic side chains and water molecules.

The resulting compact, folded conformation exposes hydrophilic surfaces to the solvent and buries hydrophobic residues in the protein's interior, thereby contributing to protein stability and function. Myoglobin, a protein found in muscle tissue that binds and stores oxygen, and haemoglobin, a protein responsible for transporting oxygen throughout the body, are both examples of globular proteins with hydrophobic cores. There is more detail on globular

Student view

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proteins and the structure of these proteins in section B1.2.11–12 (/study/app/bio/sid-422-cid-755105/book/quaternary-structure-of-proteins-and-form-id-44446/).

Integral proteins also have regions with hydrophobic amino acids, helping them to embed in membranes (see subtopic B2.1 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43205/)). Rhodopsin, a protein found in the cell membrane of retinal cells responsible for absorbing light, is an example of an integral membrane protein that has hydrophobic regions (**Figure 2**).

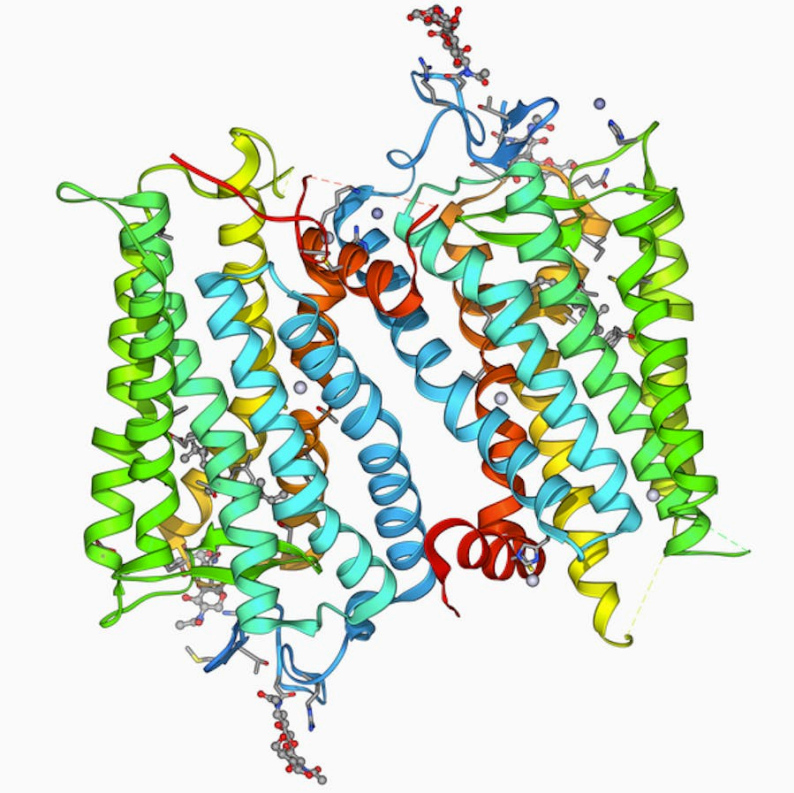

Figure 2. 3D structure of rhodopsin, a protein embedded in the cell membrane of retinal cells.

Credit: LAGUNA DESIGN, Getty Images

More information for figure 2.3

The image depicts the 3D structure of the rhodopsin protein, an integral membrane protein found in retinal cells. The structure is represented as a series of colorful helices, indicating different polypeptide chains or regions within the protein. The helices are intertwined, suggesting the protein's complex folding and its ability to embed within the cell membrane. The use of different colors helps to distinguish various sections of the protein, possibly representing functional or structural domains. There are also small molecular representations around the helices, indicating interactions with other molecules or membrane components.

[Generated by AI]

Student view

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Theory of Knowledge

Limitations of scientific models in understanding proteins

Scientists use various models to study proteins, such as computer simulations and protein engineering. While computer simulations can be used to look at the overall shape of the protein, protein engineering is a process that involves designing, modifying or creating new proteins with specific properties. This field has grown tremendously in recent years and has led to the development of new drugs, industrial enzymes and other biotechnological applications.

Although there are many advantages to protein engineering, it also presents several challenges and limitations. It is important to note that engineered proteins may not always perform as expected in real-life settings. Proteins may be affected by factors such as pH, temperature and concentration, which can impact their stability, activity and specificity. As a result, the behaviour of an engineered protein in a laboratory setting may not accurately reflect its performance in a complex biological system.

Another challenge is that the function of a protein often depends on its interactions with other molecules, such as other proteins, nucleic acids or small molecules. These interactions can be difficult to predict and may vary depending on the specific conditions in which the protein is studied.

As these models are based on simplifications and assumptions that may not accurately reflect the complexity of real-life proteins, scientists must carefully take into account the complexity of real-life proteins when interpreting research findings. The limitations of scientific models should always be considered when making conclusions.

Use the simulation in the following activity to change the composition of a polypeptide and see how this affects the folding of the polypeptide strand in different environments.

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Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:** Research skills — Using search engines and libraries effectively
- **Time required to complete activity:** 20 minutes
- **Activity type:** Individual activity

This activity aims to explore the role of hydrophobic and hydrophilic interactions in protein folding.

Follow the link to LabXchange Protein Folding (https://www.labxchange.org/library/items/lb:LabXchange:a664fc10:lx_simu simulation.

In this simulation you can generate a random polypeptide strand or choose a polypeptide strand with more hydrophobic or hydrophilic amino acids. You can then watch how the polypeptide will fold in an aqueous environment. You can also change the solvent to oil to see how the conformation of the polypeptide may change.

Instructions

1. Click 'Start simulation'.
2. Choose solvent to either be water or oil.
3. Use bottom tabs to choose the type of protein you would like to see folded. Press the play arrow (bottom centre) to activate folding.
4. Repeat for different solvents and for different types of protein.

Questions

- What effect does changing the solvent have on the polypeptide?
- What happens to a mostly hydrophilic polypeptide chain when it is added to oil?
- What happens to the hydrophobic polypeptide chain when it is added to water?

Student view

5 section questions

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B1. Form and function: Molecules / B1.2 Proteins

Quaternary structure of proteins and form and function in globular and fibrous proteins (HL)

B1.2.11: Quaternary structure of proteins (HL) B1.2.12: Form and function in globular and fibrous proteins (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Explain the difference between conjugated (example: haemoglobin) and non-conjugated proteins (example: insulin).
- Describe the difference in shape between globular and fibrous proteins and understand that their shapes make them suitable for specific functions.
- Explain the form and function of insulin and collagen.

The function of a protein arises from its unique structure. Proteins can have different levels of protein structure, including primary, secondary, tertiary and sometimes quaternary structures, depending on the number and types of interactions between the amino acid residues within the protein chain. In this section, you will learn about the quaternary structure of some proteins. You will then explore the form and function of globular and fibrous proteins.

Quaternary structure

The quaternary structure of a protein refers to the arrangement and interaction of two or more polypeptide chains to form a functional protein. An example of a protein that has quaternary structure is haemoglobin, which consists of four individual polypeptide chains: two of which are designated ‘α-chains’ and two which are designated ‘β-chains’ (**Figure 1**). Haemoglobin is considered to be a

Student view

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conjugated protein as it is associated with a non-protein component called haem. Haem is a complex molecule with iron in its centre. It is responsible for binding to oxygen in the lungs and facilitates the transport of oxygen throughout the body.

The four subunits of haemoglobin are held together by non-covalent bonds, and the interactions between the subunits allow haemoglobin to undergo conformational changes necessary for its oxygen-carrying function. The quaternary structure of haemoglobin is essential for its biological function and highlights the complexity and importance of protein structure in biological systems.

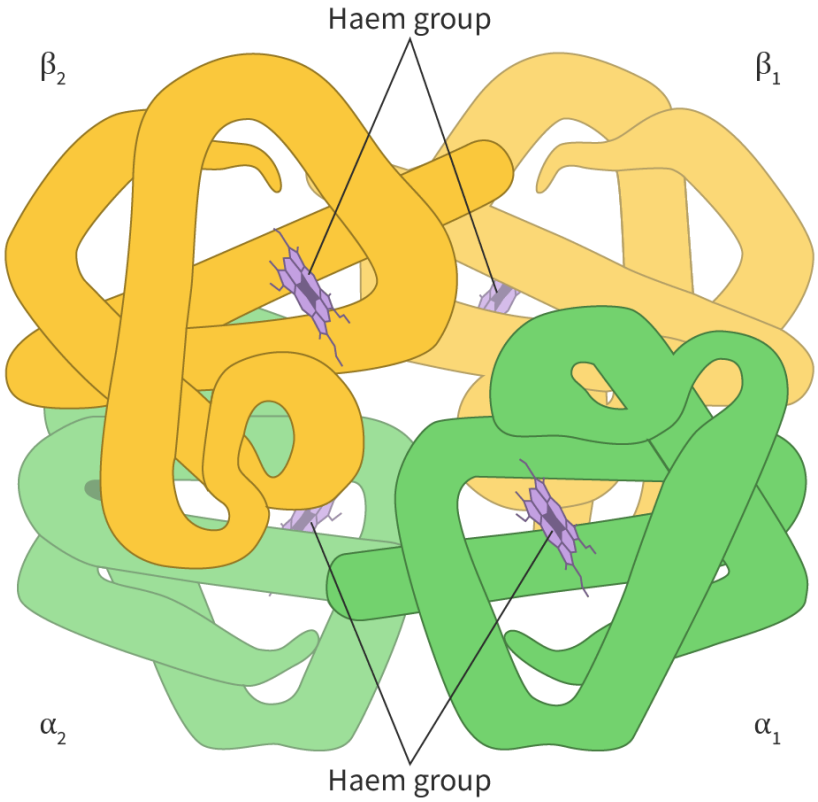

Figure 1. Haemoglobin.

More information for figure 1

The image shows a diagram of the haemoglobin protein structure. Haemoglobin is depicted with four intertwined subunits labeled as α1, α2 in green, and β1, β2 in yellow. Each subunit is drawn in a ribbon-like style, showcasing how they are intertwined and held together. The subunits encircle and connect with distinct haem groups, which are critical for oxygen binding, marked within each subunit. The haem groups are illustrated as purple planar structures attached to the inner surface of the subunits via small lines. This diagram emphasizes the spatial arrangement and interaction between the subunits and the haem groups, which contributes to its function in oxygen transport.

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Conjugated and non-conjugated proteins

While all proteins consist of at least one polypeptide chain, some proteins consist of two or more polypeptide chains. Others may include one or more non-polypeptide components as well.

Proteins that consist only of polypeptide subunits are called non-conjugated proteins. For example, collagen, which is composed of three polypeptide subunits, and insulin, which is composed of two polypeptide subunits, are both examples of non-conjugated proteins. Insulin and collagen will be covered in more detail below.

While some proteins may be non-conjugated, others may be conjugated. Conjugated proteins have non-protein components such as metal ions or carbohydrates in addition to having polypeptide subunits. These non-protein components have the ability to increase a protein's diversity and functionality. For example, non-protein components play a crucial role in many enzymes, helping them perform their catalytic functions.

Another more specific example of how non-protein components impact protein function is the protein haemoglobin. As mentioned, haemoglobin is composed of four polypeptide chains and contains haem. Haem, which contains iron at its centre, is the non-protein component of haemoglobin. Haem is essential to the function of haemoglobin as it is responsible for the binding of oxygen, allowing haemoglobin to transport oxygen throughout the body.

Globular and fibrous proteins

The structure of a protein determines its function as it allows the protein to interact with other molecules and its environment. Differences in shape, solubility and function are due to differences in the amino acid composition and the way the polypeptide chains are folded and arranged.

After a polypeptide chain is synthesised, it undergoes a process called protein folding in which it adopts a specific three-dimensional shape that is critical for its proper function. The folding process is influenced by various chemical and physical forces, such as hydrogen bonding, ionic bonding and hydrophobic

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interactions, and is determined by the sequence of amino acids in the protein as well as the cellular environment in which it is synthesised. Once proteins take their final form, they can be classified as either globular or fibrous.

Globular proteins

Globular proteins are complex proteins that are usually spherical in shape with irregular folds. They are soluble in water and play important roles as enzymes (see subtopic C1.1 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43208/)), transporters and regulators. Insulin is an example of a globular protein that consists of two polypeptide chains: the α-chain and β-chain (**Figure 2**). They are arranged in a specific three-dimensional shape that is held together by hydrogen bonds, hydrophobic interactions and disulfide bonds.

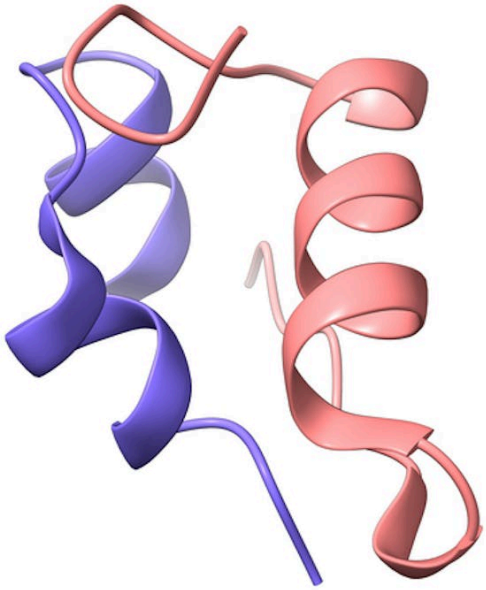

Figure 2. 3D image of insulin.

Credit: vdvornyk, Getty Images

Insulin is a hormone that regulates the amount of glucose in the blood. It is produced by the pancreas and released into the bloodstream in response to high blood sugar levels. Insulin binds to specific receptors on cells, allowing glucose to enter the cells and be used for energy or stored for later use.

The overall structure of insulin is compact and globular with a hydrophilic exterior and a hydrophobic interior. The hydrophilic exterior allows insulin to interact with water and other hydrophilic molecules in the blood. This is

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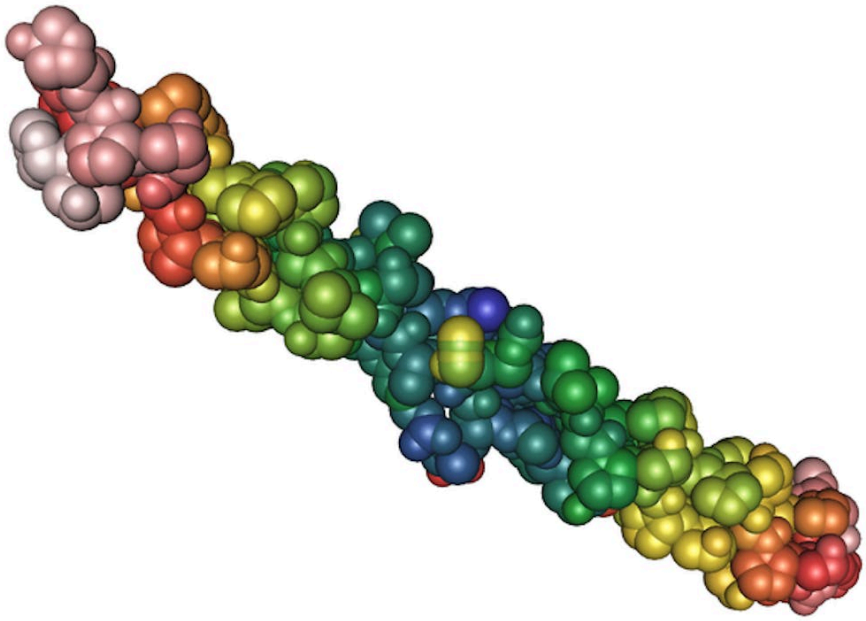
important because insulin needs to travel through the bloodstream to reach its target tissues, and bind to its receptors. The hydrophobic interior of the insulin protein helps to stabilise the shape of the protein, allowing it to maintain its globular shape, which is essential for the insulin to bind to its receptor.

Fibrous proteins

Fibrous proteins are simpler than globular proteins in structure and have a long, narrow shape. They are usually composed of repeating structures that are designed for strength and stability and are insoluble in water. Fibrous proteins provide structural support and stability to cells and tissues such as skin, tendons, and bone.

An example of a fibrous protein is collagen – the most abundant protein in the body, forming the main component of connective tissue in animals, including skin, bone and cartilage. It is made up of three polypeptide chains that are twisted together in a triple helix structure (**Figure 3**). Each chain is rich in the amino acid glycine, and it contains many proline and hydroxyproline residues. These residues allow the chains to twist together into a tight helix that is held together by hydrogen bonds and van der Waals forces. The triple helix structure of collagen is long and thin, giving collagen fibres their characteristic elongated fibrous shape. The fibres are very strong and flexible, resisting forces without breaking. This provides structural support to tissues, helping them to maintain their shape and integrity.



Student view

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Figure 3. 3D image of collagen.

Source: "1BKV Collagen triple helix (https://commons.wikimedia.org/wiki/File:1bkv_collagen_02.png)" by Nevit Dilmen is licensed under CC BY-SA 3.0 (https://creativecommons.org/licenses/by-sa/3.0/deed.en)

More information for figure 3.3

The image depicts a 3D molecular model of collagen, highlighting the triple helix structure. The model is composed of three intertwined chains, with each segment represented by different colored spheres. These spheres likely indicate the positions of atoms or groups of atoms, emphasizing the spatial arrangement of the helix. The structure is elongated and fibrous, characteristic of collagen, providing a visual example of the protein's complex structure, which is integral to its function as a major component of connective tissues such as skin, bone, and cartilage.

[Generated by AI]

Aspect: Observations

Technology has revolutionised the field of biology by providing the means to observe structures that are beyond the capabilities of our unaided senses. One remarkable example is cryogenic electron microscopy (cryo-EM), a groundbreaking technique that utilises an electron beam to capture highly detailed images of specimens that have been frozen to extremely low temperatures. Cryo-EM has enabled the imaging of individual protein molecules and their interactions with other molecules, providing unprecedented insights into their intricate structures and the dynamic nature of molecular interactions within living organisms.

By pushing the boundaries of scientific exploration, cryo-EM exemplifies the progressive nature of scientific inquiry and highlights the role of technology in expanding our understanding of the natural world. This breakthrough has not only deepened our comprehension of the fundamental mechanisms underlying life but has also opened new avenues for discovery and application, allowing researchers to investigate the subtle intricacies of protein structures, unravel complex molecular pathways, and gain valuable insights into the molecular basis of diseases. By bridging the gap between what is

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visible and what is invisible, cryo-EM has revolutionised biology and has played a critical role in the ever-evolving nature of scientific exploration.

Try this research activity to learn more about proteins.

Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:**
  - Research skills — Using search engines and libraries effectively
  - Social skills — Working collaboratively to reach a common goal
- **Time required to complete activity:** 90 minutes
- **Activity type:** Group activity

Your task

You will work in small groups for this activity. Your group will be given the name of a fibrous or globular protein of which to research the structure and function. In your group, prepare a poster about the protein and present it to the class.

Possible globular proteins to research:

- enzymes (e.g. catalase, lipase, amylase, protease, DNA polymerase, RNA polymerase)
- transport proteins (e.g. ferritin, albumin)
- regulatory proteins (e.g. glucagon, growth hormone, calcitonin)
- antibodies (e.g. immunoglobulin G, immunoglobulin A, immunoglobulin E, monoclonal antibodies)
- structural proteins with a globular domain (e.g. actin, tubulin, fibrinogen).

Possible fibrous proteins to research:

- elastin
- fibroin
- myosin

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- titin
- laminin.

5 section questions

Summary and key terms

- Each of the 20 amino acids consists of an alpha carbon atom attached to an amine group, carboxyl group, H atom and an R-group. Each of the 20 amino acids has a unique R-group, providing it with its unique structure.
- Amino acids join together to make a protein through condensation reactions. When amino acids join together, peptide bonds are formed.
- Essential amino acids are amino acids that your body cannot synthesise while non-essential amino acids can be produced by the body from other amino acids or by the breakdown of protein.
- There are 20 amino acids coded for in the genetic code and the genetic code serves as a universal language for all living organisms and provides the instructions for protein synthesis.
- Extreme pH and temperature can cause the denaturation of a protein as it causes the breaking of bonds, causing the protein to lose its 3D conformation.

Higher level (HL)

- The properties of R-groups can be either hydrophobic or hydrophilic (polar or charged; acidic or basic) and these R-groups determine the properties of assembled polypeptides including a protein's three-dimensional shape.
- The primary structure of a protein refers to the specific sequence of amino acids that are joined together to form a polypeptide chain while the secondary structure of a protein refers to the local folding patterns that occur within the polypeptide chain. Two common types of secondary structures are alpha helices and beta-pleated sheets.
- Tertiary structure is the folding of the polypeptide into its three-dimensional shape. It is dependent on the interaction between R-groups, which may include

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the formation of hydrogen bonds, ionic bonds, disulfide covalent bonds and hydrophobic interactions. These interactions stabilise the structure of the protein.

- Quaternary structure refers to the arrangement and interaction of two or more individual polypeptide chains (subunits) to form a functional protein.
- Globular proteins are soluble complex proteins, usually spherical in shape with irregular folds, which play important roles as enzymes, transporters and regulators (e.g. insulin). Fibrous proteins are insoluble simpler proteins that have a long, narrow shape. Fibrous proteins provide structural support and stability to cells and tissues such as skin, tendons and bone (e.g. collagen).

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Key terms

Review these key terms. Do you know them all? Fill in as many gaps as you can using the terms in this list.

1. A polypeptide is composed of amino acids that are joined together through .
2. The of an amino acid gives it its unique characteristics.
3. The is a set of rules that specifies how information stored in DNA is translated into the sequence of amino acids that make up proteins.
4. Extreme temperature can cause proteins to undergo .
5. A is a chain of amino acids that is linked together by peptide bonds, while a is a complex, three-dimensional structure that is made up of one or more polypeptide chains.
6. [HL] The of a protein refers to the specific sequence of amino acids that are joined together to form a polypeptide chain.
7. [HL] covalent bonds are bonds that form between pairs of cysteine amino acid residues, which contain sulfur atoms.
8. [HL] refers to the arrangement and interaction of two or more individual polypeptide chains to form a functional protein.
9. [HL] Alpha helices and beta-pleated sheets contribute to the of a protein.
10. [HL] proteins play an important role in structural support.

Quaternary structure | primary structure | Disulfide | secondary structure | genetic code | peptide bonds | Fibrous | denaturation | protein | R-group | polypeptide

Section Student: (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/primary-secondary-tertiary-structure-proteins-id-45488/print/) Assign

Check

Student view

Checklist

What you should know

After studying this subtopic you should be able to:

- Draw a diagram of a generalised amino acid showing the alpha carbon atom with amine group, carboxyl group, R-group and hydrogen attached.
- Write the word equation for condensation reactions between amino acids to form dipeptides.
- Draw a generalised dipeptide after modelling the reaction with molecular models.
- Explain the difference between essential and non-essential amino acids.
- Recognise that there are 20 amino acids coded for in the genetic code.
- Name examples of polypeptides and know their function.
- Describe the effect of extreme pH and temperature on protein structure ('denaturation').
- Describe that the sequence of amino acids and the precise position of each amino acid within a structure determines the three-dimensional shape of proteins.

Higher level (HL)

- Explain the difference between conjugated (example: haemoglobin) and non-conjugated proteins (example: insulin).
- Explain that the secondary structure of a protein depends on hydrogen bonding in regular positions to stabilise alpha helices and beta-pleated sheets while the tertiary structure of a protein depends on hydrogen bonds, ionic bonds, disulfide covalent bonds and hydrophobic interactions.
- Describe the difference in shape between globular and fibrous proteins and understand that their shapes make them suitable for specific functions.

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- Explain the form and function of insulin and collagen.
- Recall that the properties of R-groups as either hydrophobic or hydrophilic (polar or charged; acidic or basic) determine the properties of assembled polypeptides.

Investigation

- **IB learner profile attribute:** Thinkers
- **Approaches to learning:** Thinking skills – Experimenting with new strategies for learning
- **Time required to complete activity:** 60 minutes
- **Activity type:** Individual activity

Your task

SDS-PAGE is a valuable technique that scientists use to separate proteins based on their molecular weight, making it a useful tool for studying the diversity of proteins. Researchers can use SDS-PAGE to identify and quantify different proteins within a sample and to understand the relationship between amino acid sequence and protein structure.

To learn more about SDS-PAGE, watch **Video 1**.

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Video 1. SDS-PAGE explained - Protein Separation Technique

More information for video 1

1

00:00:00,300 --> 00:00:03,737

narrator: SDS-page is a gel

electrophoresis technique

2

00:00:03,804 --> 00:00:06,306

used for protein separation.

3

00:00:06,740 --> 00:00:10,577

After treatment, with SDS,

the proteins of a sample

4

00:00:10,644 --> 00:00:14,648

can be separated due

to differences in their molecular weight.

5

00:00:15,649 --> 00:00:20,220

A sample containing a variety

of different proteins can be analyzed.

6

00:00:20,821 --> 00:00:25,325

SDS-page is short for sodium

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Dodecyl Sulfate,

7

00:00:25,492 --> 00:00:28,629

PolyAcrylamide Gel Electrophoresis.

8

00:00:28,962 --> 00:00:32,833

The proteins in the sample

have distinct charges

9

00:00:32,900 --> 00:00:36,570

based on the composition

of amino acid side chains.

10

00:00:37,004 --> 00:00:39,540

Proteins are folded in various shapes

11

00:00:39,606 --> 00:00:44,011

due to the polarity

of the side chains and the non-covalent

12

00:00:44,144 --> 00:00:46,013

or covalent interactions.

13

00:00:46,647 --> 00:00:50,851

Upon treatment with SDS,

which is an anionic detergent,

14

00:00:51,018 --> 00:00:52,920

the proteins are denatured.

15

00:00:52,986 --> 00:00:55,522

The disruption of non-covalent bonds

16

00:00:55,822 --> 00:00:58,458

leads to the unfolding of the proteins.

17

00:00:58,659 --> 00:01:04,331

Section Student (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/quaternary-structure-of-proteins-and-form-id-44446/print/) Assign

Student view

Overview (/study/ap 422-cid-755105/o

SDS molecules will bind to the amino acid

residues covering the proteins.

18

00:01:04,831 --> 00:01:07,434

Since SDS is negatively charged,

19

00:01:07,501 --> 00:01:11,038

all proteins possess

a similar mass-to-charge ratio now

20

00:01:11,171 --> 00:01:14,842

as well, and this is the intention of SDS.

21

00:01:14,942 --> 00:01:17,344

Make the protein similar in charge

22

00:01:17,578 --> 00:01:20,914

to separate them solely

on their molecular weight,

23

00:01:21,315 --> 00:01:25,986

but before that, proteins might be

also treated additionally,

24

00:01:26,153 --> 00:01:28,555

with beta Mercaptoethanol.

25

00:01:28,722 --> 00:01:33,060

This substance is intended

to resolve the di sulfide bonds,

26

00:01:33,126 --> 00:01:35,796

which cannot be denatured by SDS.

27

00:01:36,230 --> 00:01:40,267

Better beta Mercaptoethanol

reduces the di sulfide bonds.

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28

00:01:40,501 --> 00:01:42,836

The protein sample was treated

29

00:01:42,903 --> 00:01:46,640

with those molecules resulting

in unfolded proteins,

30

00:01:46,707 --> 00:01:50,344

all having nearly

the equal mass-to-charge ratio.

31

00:01:51,144 --> 00:01:55,449

To separate the proteins

inside the sample, a gel is needed.

32

00:01:55,716 --> 00:02:00,287

This polyacrylamide gel

can be divided into two layers.

33

00:02:00,554 --> 00:02:07,261

On top is the stacking gel with a low pH

to concentrate all proteins in one band.

34

00:02:07,728 --> 00:02:11,632

Below is the resolving

or separating gel,

35

00:02:11,698 --> 00:02:16,303

which allows for protein separation

according to their molecular weight.

36

00:02:16,470 --> 00:02:19,306

The gel is inserted into a chamber

37

00:02:19,640 --> 00:02:23,243

and everything will be

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filled up with buffer solution.

38

00:02:23,810 --> 00:02:27,648

The protein samples are then

pipetted into the wells,

39

00:02:27,714 --> 00:02:31,818

and the electrodes

are connected to the power supply.

40

00:02:32,119 --> 00:02:34,488

When the electric voltage is applied,

41

00:02:34,588 --> 00:02:36,456

the negatively charged proteins

42

00:02:36,523 --> 00:02:41,962

will run through the path

of the gel from the cathode to the anode.

43

00:02:43,030 --> 00:02:45,232

In a heterogeneous protein sample,

44

00:02:45,599 --> 00:02:49,870

the proteins will travel

through the gel with different velocity.

45

00:02:50,003 --> 00:02:52,439

Large proteins run more slowly,

46

00:02:52,706 --> 00:02:54,508

whereas small proteins

47

00:02:54,575 --> 00:02:57,444

will run faster

in the separating gel.

48

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00:02:57,744 --> 00:03:01,849

This separation

works because of the gel structure.

49

00:03:02,316 --> 00:03:05,419

The gel is built up

like a net or a sheet.

50

00:03:05,652 --> 00:03:08,589

Small particles can easily pass.

51

00:03:08,655 --> 00:03:10,424

Large ones take more time.

52

00:03:10,924 --> 00:03:15,028

In fact, we cannot see this

illustrated separation directly.

53

00:03:15,662 --> 00:03:18,966

After running the gel,

it has to be stained first.

54

00:03:19,566 --> 00:03:22,503

Therefore, one can use Coomassie blue,

55

00:03:22,569 --> 00:03:24,671

a dye

to visualize proteins.

56

00:03:24,938 --> 00:03:29,243

After Coomassie staining,

the different protein bands are revealed.

57

00:03:29,309 --> 00:03:33,881

Traditionally, the first well might be

used for marker proteins.

58

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00:03:33,947 --> 00:03:38,652

This mixture contains proteins

where the size is already known.

59

00:03:38,952 --> 00:03:43,524

The marker can be used as a reference then

to determine the molecular weight

60

00:03:43,690 --> 00:03:45,826

of the proteins in the sample.

61

00:03:46,660 --> 00:03:48,529

When we want to identify

62

00:03:48,662 --> 00:03:52,299

or confirm the presence

of a specific protein,

63

00:03:52,366 --> 00:03:55,068

the gel is used

for Western Blot analysis,

64

00:03:55,135 --> 00:03:57,938

a technique based on antibody detection.

65

00:03:58,305 --> 00:03:59,706

That's it for today.

66

00:03:59,773 --> 00:04:00,807

Thanks for watching!

67

00:04:00,941 --> 00:04:04,778

And make sure to subscribe

for more scientific content.

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Your task: By performing this simulation, you will gain appreciation for the intricate details and diligence that experiments need to be successful.

- Follow the link to Lab Xchange Running A Protein Gel (https://www.labxchange.org/library/items/lb:LabXchange:227cccb5:lx_simulation:1) simulation and choose level 1.
- Then click 'Start simulation'. Follow the steps provided in the simulation, being sure to read and understand the sections labelled *context*, *materials* and *predictions* before beginning the protocol. In the *materials* section, you can click on any of the materials to gain more information about each of the items.
- Complete the protocol. It has six main steps:

1. Collecting the cells.
2. Adding the sample buffer.
3. Denaturing the proteins.
4. Centrifuging the samples.
5. Loading the gel.
6. Conducting protein electrophoresis.

Follow the detailed steps presented in the simulation to complete each part.

- Once the protocol is complete, make sure to go through your results and answer the questions present in the results tab.
- Then complete the reflection tab which includes the following questions:

1. How are restriction enzymes and Cas9 similar?
2. How are restriction enzymes and Cas9 different?

International Mindedness

Sharing new techniques and scientific procedures with the global community is a fundamental responsibility of scientists, as it ensures that scientific progress is made through open sharing and collaboration.

The western blot technique was first described in a research paper published in 1979 by George Stark and his colleagues in *Analytical Biochemistry* journal. This technique was developed to detect specific proteins in complex biological samples like tissue extracts and cell lysates.

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Since its discovery, the western blot technique has been widely used by researchers worldwide for various applications. The technique has been used to study protein expression and function in various organisms. It has also been used in clinical research to identify specific disease markers, including cancer-associated proteins.

It is an ethical obligation to promote the common good by making scientific knowledge and expertise widely accessible. When scientists share their findings and knowledge, they can help advance science and technology, leading to significant improvements for society as a whole.

B1. Form and function: Molecules / B1.2 Proteins

Reflection

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/reflection-id-46872/print/) Assign

Teacher instructions

The goal of this section is to encourage students to reflect on their learning and conceptual understanding of the subject at the end of this subtopic. It asks them to go back to the guiding questions posed at the start of the subtopic and assess how confident they now are in answering them. What have they learned, and what outstanding questions do they have? Are they able to see the bigger picture and the connections between the different topics?

Students can submit their reflections to you by clicking on 'Submit'. You will then see their answers in the 'Insights' part of the Kognity platform.

Reflection

Now that you've completed this subtopic, let's come back to the guiding question introduced in The big picture (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43531/).

- What is the relationship between amino acid sequence and the diversity in form and function of proteins?
- How are protein molecules affected by their chemical and physical environments?

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With these questions in mind, take a moment to reflect on your learning so far and type your reflections into the space provided.

You can use the following questions to guide you:

- What main points have you learned from this subtopic?
- Is anything unclear? What questions do you still have?
- How confident do you feel in answering the guiding questions?
- What connections do you see between this subtopic and other parts of the course?

⚠ Once you submit your response, you won't be able to edit it.

0/2000

Submit

Rate subtopic B1.2 Proteins

Help us improve the content and user experience.

☆ ☆ ☆ ☆ ☆

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