

	in cellulose so chitin forms linear sheets of strong fibres.	and the scales of fish.
--	--	-------------------------

Table 1.4.2: Some important polysaccharides and their roles.

EXTENSION

Structural differences between the glycosidic linkages in starch and cellulose affect an animal's ability to digest plant foods. Enzymes such as amylase break down starch but cannot break down cellulose polymers. Some animals, including cows and termites, digest cellulose by keeping special microorganisms in their digestive systems. These microorganisms produce cellulose-digesting enzymes. Humans and most animals do not make an enzyme capable of digesting cellulose, so cellulose fibres pass undigested through the body and are known as 'fibre' or roughage' ([Section 12.1](#)).

1.4.3 Ribose and deoxyribose

Pentose sugars are one component of the nucleotides which make up both DNA and RNA molecules. RNA contains the sugar ribose and DNA contains deoxyribose. The difference between the two molecules is the presence of hydroxyl ($-OH$) groups on the 2' carbon of the ribose. Ribose has an $-OH$ group and deoxyribose does not (Figure 1.4.9).

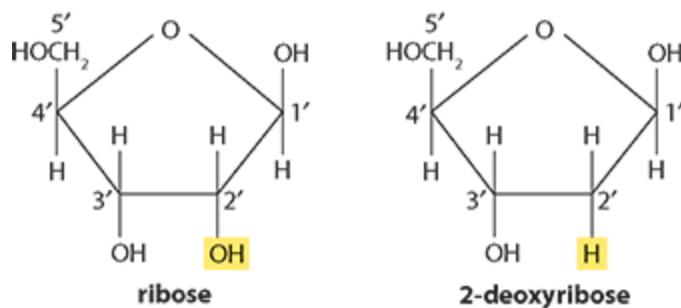


Figure 1.4.9: The structures of ribose and deoxyribose.

KEY POINT

You will notice that each of the numbered carbon atoms has a small dash next to it, for example 2' or 4'. The dashes are called primes. When spoken out loud they are called '2 prime' or '4 prime'. In DNA and RNA the ribose sugars are attached to other molecules that contain ring compounds. The primes help to distinguish from any numbers given to atoms in other rings.

Both DNA and RNA contain nucleotides which have the pentose sugars in a central position with a base attached to the 1' carbon and a phosphate group attached to the 5' carbon. The hydroxyl groups on the 3' and 5' positions enable the pentose groups to

link to one another via phosphodiester bonds between adjacent molecules.

You can read more about the detail of DNA and RNA structure in [Chapter 4](#).

TEST YOUR UNDERSTANDING

- 23** Compare the molecular arrangements of cellulose and amylose.

EXTENSION

Using molecular visualisation software

There are many websites that offer molecular visualisation software free of charge. One example is Jmol. Using this software you can look at 3D images of carbohydrates and see how they are assembled. Examine models of glucose and notice how the different atoms are shown. Compare models of unbranched amylose and branched amylopectin. Compare the linkages in unbranched and branched parts of each molecules.

Links

- How does excessive intake of carbohydrate lead to diabetes? ([Chapter 8](#))

1.5 Lipids

LEARNING OBJECTIVES

In this section you will:

- learn that lipids exist in different forms and have a range of properties
- learn how triglycerides are formed by condensation reactions between fatty acids and glycerol
- understand why non-polar lipids are hydrophobic
- learn that phospholipids contain a phosphate group and are amphipathic
- define fatty acids as saturated, monounsaturated or polyunsaturated
- recall that lipids are used as a long-term energy store
- learn that lipids release energy when they are oxidised
- understand that lipids are stored in adipose tissue
- recall that lipids insulate vital organs
- describe steroid hormones as non-polar molecules with a four ring structure and that they can enter cells via cell membranes.

GUIDING QUESTIONS

- How do the structures of different fatty acids and lipids affect their properties and functions?
- Why is it better to store energy as lipid rather than as other organic molecules?
- What are the benefits and risks of lipids in the human diet?

1.5.1 Structure and forms of lipids

Lipids are non-polar and hydrophobic molecules which are insoluble in water but do dissolve in organic solvents. Lipids include fats, waxes, oils, steroids and phospholipids. Fats and oils are part of a sub-group known as triglycerides. Those that are solid are generally referred to as fats, while those that are liquid are known as oils.

KEY POINT

lipids together with carbohydrates and proteins, are the main components of plant and animal cells. Two examples of lipids are triglycerides and cholesterol.

Different forms of lipid have a range of uses; some of these are shown in Table 1.5.1.

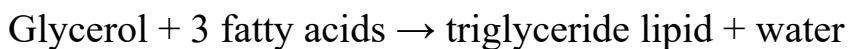
Lipid type	Some important uses
fats	<ul style="list-style-type: none">long-term energy reserve and concentrated source of energy for animalssupply essential fatty acids that the body cannot synthesise, and fat-soluble vitamins (A, D, E and K)constituent of cell membranes
oils	<ul style="list-style-type: none">energy reserve for plants found in seeds such as linseed and olives
waxes	<ul style="list-style-type: none">beeswax is used to construct honeycomblanolin is used to protect wool

	<ul style="list-style-type: none"> • plant waxes control evaporation from leaves
steroids	<ul style="list-style-type: none"> • form hormones and vitamins
phospholipids	<ul style="list-style-type: none"> • essential part of membranes and the nervous system

Table 1.5.1: Lipids and their uses in living organisms.

Triglycerides

Triglycerides are the most abundant group of lipids. They are formed by condensation reactions between three fatty acid molecules and one glyceride molecule. They are sometimes called neutral or true fats.



Fatty acids consist of long chains of carbon atoms with hydrogen atoms bound to them (Figure 1.5.1).

Lipids have no polar groups and so cannot dissolve in water, although they do dissolve in organic solvents such as chloroform and acetone. Lipids contain about twice as much energy per gram as carbohydrates and proteins (Table 1.5.2), but each type of storage molecule has its own advantages.

Molecule	Approximate energy content per gram/kJ
lipid	39
carbohydrate	17
protein	18

Table 1.5.2: Energy content of different molecules.

EXAM TIP

- Do not confuse the terms glyceride and glycerol.
- Glycerides are formed by the bonding between glycerol molecules and fatty acids.
- Glycerol is a molecule which has three hydroxyl functional groups ([Section 1.3](#)) which can be linked to three fatty acids to form triglycerides.

Fatty acids

There are many different fatty acids and they are all long carboxylic acid chains. At one end of the chain is a carboxyl group (-COOH) and at the other a methyl group (CH_3), and there are carbon atoms between them. The number of carbon atoms in a fatty acid is always an even number, most commonly 14–22, although shorter and longer chain fatty acids do exist. If the carbon chain is linked to the maximum number of H atoms with no double bonds we say that it is **saturated** because no more H atoms can be added. If the chain contains a double bond between two of the carbon atoms it is said to be **unsaturated** (Figure 1.5.2). A chain with just one double bond is **monounsaturated**, while one with two or more double bonds is said to be **polyunsaturated**. Polyunsaturated fatty acids tend to be liquids at 20°C and are mainly derived from plant sources. Examples are sunflower oil, corn oil and olive oil.

Unsaturated fatty acids occur as isomers and may be either a **cis** or a **trans** configuration. If the ‘spaces’ where additional hydrogen atoms could bond are both on the same side of the hydrocarbon chain, the fatty acid is known as a *cis* fatty acid.

The carbon chain of a *cis* fatty acid is slightly bent. If the spaces are on opposite sides, it is a *trans* fatty acid (Figure 1.5.3).

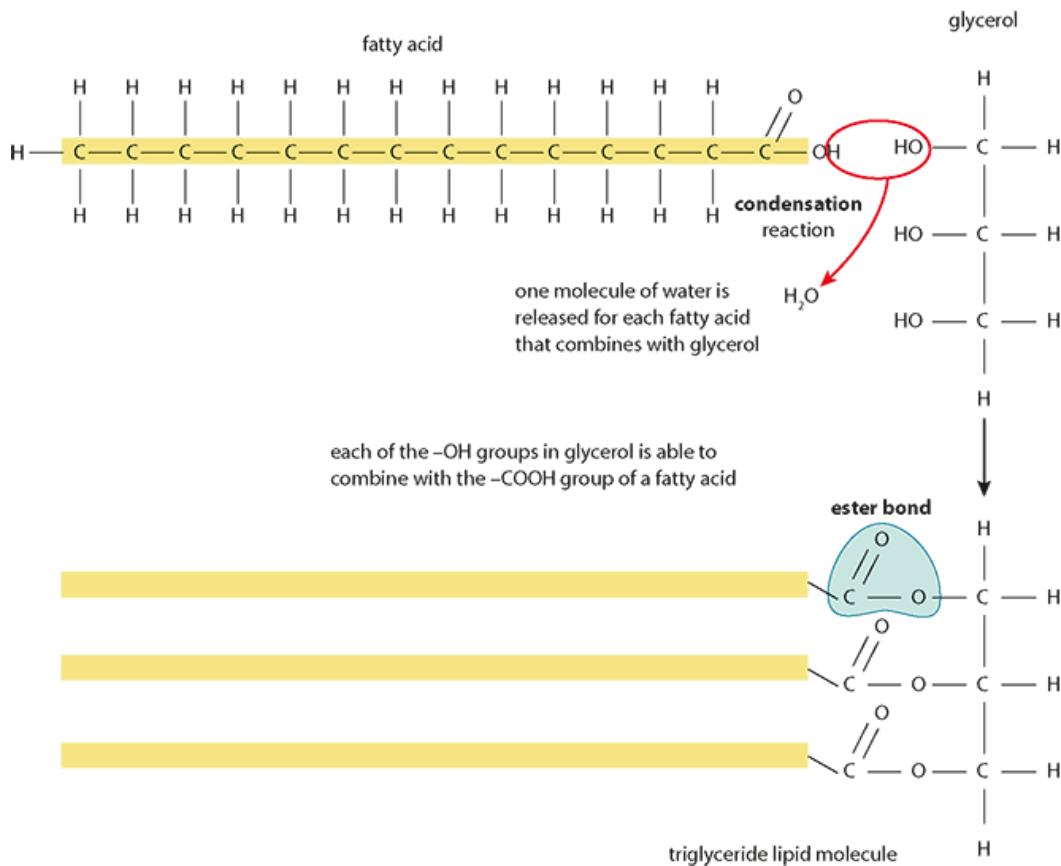
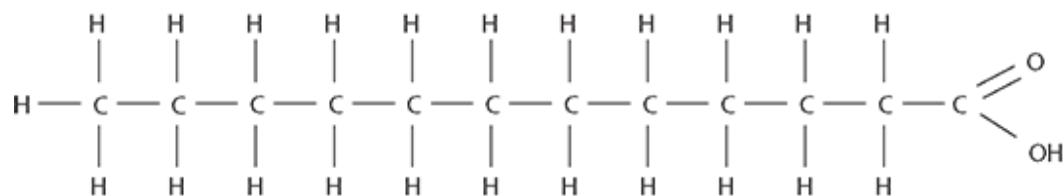
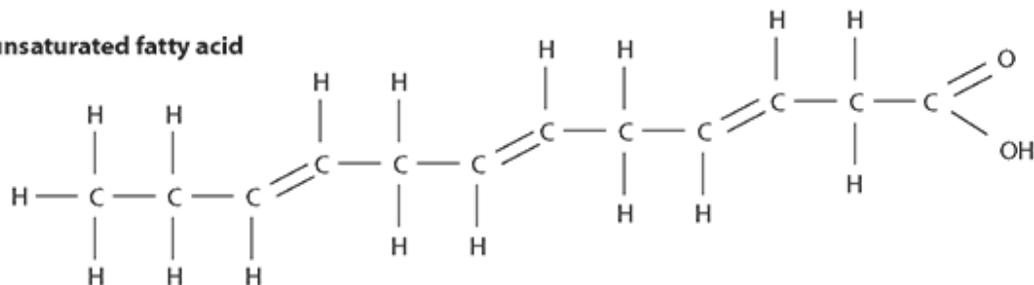


Figure 1.5.1: A triglyceride is formed by condensation reactions between three fatty acids and one glycerol molecule.

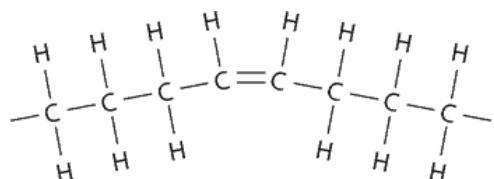
saturated fatty acid

every carbon atom in the hydrocarbon chain has the maximum number of hydrogen atoms bonded

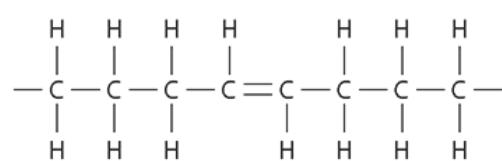
**unsaturated fatty acid**

this hydrocarbon chain includes three double bonds, which means the carbon atoms do not have the maximum number of hydrogen atoms bonded

Figure 1.5.2: Saturated and polyunsaturated fatty acids.



bent *cis* fatty acid – two hydrogen atoms are absent from the same side of the hydrocarbon chain



straight *trans* fatty acid – one hydrogen atom is absent from each side of the hydrocarbon chain

Figure 1.5.3: Structural diagrams of *cis* and *trans* fatty acids.

1.5.2 Saturated and unsaturated fatty acids and health

The relative amounts of different types of fatty acid in a person's diet can, in some cases, be correlated with health issues. Eating a diet that is high in saturated fatty acids is common in some western countries. In research, this type of diet is shown to have a positive correlation with an increased risk of coronary heart disease (CHD). A positive correlation between two measures is where, if one measure increases, so does the other. This does not mean that one causes the other, but it suggests a relationship (see Nature of Science, Correlation and cause).

Saturated fatty acids can be deposited inside the arteries, and if the deposits combine with cholesterol they may lead to atherosclerosis, a condition that reduces the diameter of the arteries and leads to high blood pressure ([Section 8.3](#)). Reliable evidence suggests that in countries where the diet is high in saturated fatty acids, and where many high-fat foods, animal products and processed foods are eaten, there is likely to be a high incidence of CHD. Since all fatty acids are high in energy, an excess of these foods in the diet can also lead to obesity, which places a further strain on the heart.

On the other hand, people who eat a Mediterranean-style diet, which is rich in unsaturated fatty acids from olive oil and fresh vegetables, tend to have a low incidence of CHD. These fats do not combine with cholesterol and so arteries tend to remain unblocked and healthy. One type of unsaturated *cis* fatty acid is the omega-3 group. These have a double bond at the third bond from the -CH₃ end of the molecule. Omega-3 fatty acids in our diet come from eating fish, such as salmon and pilchards,

walnuts and flax seed. Another group, the omega-6 fatty acids, have a double bond at the sixth position and come from vegetable oils. These two fatty acids are essential for human health and help with the absorption of vitamins and minerals.

THEORY OF KNOWLEDGE

Health issues: *trans* fats or saturated fats?

Trans fatty acids are produced when vegetable oils are hydrogenated (have hydrogen atoms added to their molecules). This changes their properties so they will spread more easily and last longer. *Trans* fatty acids are not often found in nature and have no known health benefits.

Hydrogenated fats are used in the manufacture of processed food, such as margarine, baked foods and coffee creamers, although many food manufacturers have reduced the amounts they use. *Trans* fats are metabolised in the liver and released as low-density lipoproteins (LDLs). Increased levels of LDLs in the blood is linked to an increased risk of cardiovascular disease.

Eating a diet that contains high levels of trans fats has been shown to lead to high cholesterol levels, which in turn can lead to CHD and strokes. But most people do not eat large amounts of trans fats. In Western Europe, for example, it has been estimated that most people eat only about half the maximum recommended level of these fats. Most health professionals advise that saturated fats are a greater risk to health because of their contribution to atherosclerosis.

To consider:

- 1 Do different scientists interpret evidence in the same way?

- 2** How can we make decisions about the relative harms and benefits of foods in our diet when there are conflicting views?

The evidence is not conclusive about which of the lipids are healthy and which are not. However, all health professionals recommend a balanced diet and recommend reducing the amount of processed food that is eaten.

1.5.3 Lipids and energy storage

Lipids are used to store energy. They are compact molecules and make an efficient long-term energy store. Lipids are high in energy; 1 gram of fat provides twice as much energy as the same mass of carbohydrate (Table 1.5.2). In addition to lipids that are part of the diet, any excess carbohydrate that a person eats is also converted into fats and stored in the body. All mammals store more of their energy reserves as fat than as glycogen. Stores are increased when food is abundant, or if a person eats more than they need for their activities. Fat is released from storage and used when energy is needed. Fatty acids are oxidised in the mitochondria, producing ATP for usable energy and releasing carbon dioxide and water.

A healthy diet is one in which energy intake matches energy used. If a person eats more than they need for their lifestyle, particularly if they do little or no exercise, they will gain weight as fat accumulates in their body. Fatty food contains a lot of energy and it can be easy to consume more kilojoules of energy than the body needs.

EXTENSION

Many small mammals such as hedgehogs, chipmunks, dormice and bats hibernate through the winter months. Their metabolism, heart rate and breathing slow down and their temperatures drop. To prepare for hibernation mammals feed in summer and autumn when food is abundant and they store fat which they use during their winter sleep. If they cannot store sufficient fat animals may die during hibernation, especially if the weather is very severe or they wake up too soon before fresh food is available in spring.

KEY POINT

mass is a measurement of the amount of matter an object contains but weight is a measurement of the pull of gravity on an object. Mass is measured in grams or kilograms whereas weight is measured in Newtons (N).

Non-scientists tend to use the word ‘weight’ when they are really talking about mass.

SCIENCE IN CONTEXT

Body mass index (BMI) is used as a way of assessing if a person’s body mass is healthy. It is calculated using the formula:

$$\text{BMI} = \frac{\text{weight (kg)}}{[\text{height (m)}]^2}$$

Table 1.5.3 shows the ranges of BMI values that are healthy and unhealthy in different groups of people.

BMI (non-Asian) kg/m ²	BMI (Asian) kg/m ²	Weight status
<18.5	<18.5	underweight
18.5–24.9	18.5–22.9	healthy
25.0–29.9	23.0–24.9	overweight
—	>25.0–29.9	pre-obese
>30.0	>30.0	obese

Table 1.5.3: World Health Organization health profiles for different BMI values.

Differences in BMI between individual adults of the same age and sex are usually due to body fat, although there are exceptions to this rule. BMI values will be overestimated for body builders and elite athletes whose bodies have a high proportion of muscle.

BMI values underestimate the amount of body fat for older people and for people with physical disabilities who may have muscle wasting. BMI is not accurate for people with eating disorders such as anorexia nervosa.

Despite these inaccuracies BMI values have been used as a quick and easy way to assess whether a person is carrying too much body fat. But it is important to remember that many other factors must also be taken into account before conclusions about a person's health can be made.

1.5.4 Phospholipids

Phospholipids are important molecules that are found in all cell membranes. A phospholipid molecule has two hydrophobic, fatty acid tails and a phosphate head which is hydrophilic.

Phospholipids can form bilayers because they are amphipathic molecules ([Section 2.1](#)). Lipid bilayers form when the hydrophobic tails in one layer align to face one another and leave the hydrophilic heads of both layers in contact with water.

Phospholipid membranes ([Figure 1.5.4](#)) form the outer layer of cells and are important in controlling what can enter and leave a cell. Molecules embedded in the membrane allow cells to communicate with other cells and parts of the body ([Section 5.2](#)).

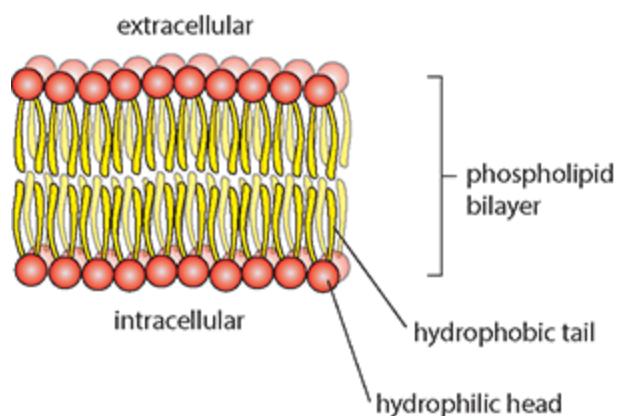


Figure 1.5.4: The phospholipid bilayer of a cell membrane.

Where is energy stored?

Digestion of lipids in our diet begins in the small intestine and releases fatty acids and glycerol that are absorbed across the intestinal membrane.

NATURE OF SCIENCE

Correlation and cause

As we study the occurrence of medical conditions that may be related to diet, it is important to distinguish between correlation and cause. A correlation between two variables, such as a high incidence of CHD and a high intake of saturated fatty acids, does not mean that CHD is caused by the fat intake.

Looking for correlation is one of the most common and useful statistical analysis techniques. Correlation describes the degree of relationship between two variables. For example, in the last 30 years, the number of people taking a holiday each year has increased. In the last 30 years, there has also been an increase in the number of hotels at holiday resorts. This data shows a **positive correlation**.

We could also consider annual deaths from influenza and the number of influenza vaccines given. In this case, there is a **negative correlation**. With these examples, we might feel safe to say that one set of data is linked to the other and that there is a **causal relationship** – because there are more tourists, more hotels have been built; greater use of the influenza vaccine has resulted in fewer deaths from influenza.

However, just because the data shows a trend it does not necessarily mean that there is a causal relationship. If we consider the number of people using mobile phones in the last 10 years against the area of Amazon rainforest cut down there would be a positive correlation. But this does not mean that the use of mobile phones has caused rainforest to be cut down – nor does it mean that a reduction in rainforest area results in more mobile phone use.

Observations without experiments can show a correlation but usually experiments must be used to provide evidence to show the cause of the correlation. To find evidence for correlation between diet and human health is difficult. It is not ethically possible to conduct experiments that restrict the diets of subjects to assess the affects on their health. So observational data or data from **epidemiological** studies is all we have to use. We must think about how the data is gathered and what other variables, such as lifestyle, genetics and family history, are important. There are difficulties in collecting objective data that accounts for all possible variables. It may never be possible to say that one type of diet or fatty acid is ‘good’ and another is ‘bad’, because individual subjects vary in so many different ways.

To consider:

- 1 Can you think of some other examples of two factors that are positively correlated but where one does not cause the other?
- 2 Why do you think it is very difficult to collect objective data about human diets and health?

TEST YOUR UNDERSTANDING

- 24 Name the type of reaction that produces a triglyceride.
- 25 Why are lipids an economical way for animals to store energy?
- 26 Distinguish between a saturated and unsaturated fatty acid.

- 27** Describe the difference between a *cis* and a *trans* fatty acid.
- 28** Calculate the BMI of a person who weighs 90 kg and is 1.6 m tall. What can you say about the health issues this person might face?

Once they have crossed the membrane, the molecules are recombined to form triglycerides that enter the lymphatic system via lacteals in the villi of the intestine. Digested lipids are either transported to the liver, or can be stored in the fat cells (adipocytes) that make up adipose (fat) tissue found throughout the body.

Adipose tissue is formed under the skin where it insulates the body from heat and cold, and around major organs, such as the kidneys and the heart, which it cushions and protects from damage.

Layers of adipose tissue are important insulators against cold environmental conditions for animals such as seals and whales which live on the ice and in freezing arctic waters. These animals are mammals and homeotherms so must maintain a constant body temperature.

KEY POINT

adipose tissue (body fat) formed of adipose cells containing stores of triglycerides found under the skin and around internal organs.

They all have thick layers of fat (blubber) to act as thermal insulation and protect them from the cold.

There are two types of adipose tissue: white adipose tissue which stores energy and brown tissue which generates heat. White tissue stores fat in large droplets whereas brown fat contains smaller droplets and has cells with large numbers of mitochondria.

The hormones leptin and estrogen as well as cytokines are also produced by adipose tissue.

1.5.5 Steroid hormones

Steroid hormones are produced by glands in the adrenal cortex, the testes and the ovaries. All steroid hormones are derived from cholesterol and have similar structures containing four fused rings (Figure 1.5.5).

Steroid hormones are non-polar molecules so they are able to pass through the phospholipid bilayers of cell membranes ([Section 6.2](#)). Once inside a cell, the hormones bind with special receptors which carry them to the nucleus of the cell where they influence transcription (Figure 1.5.6).

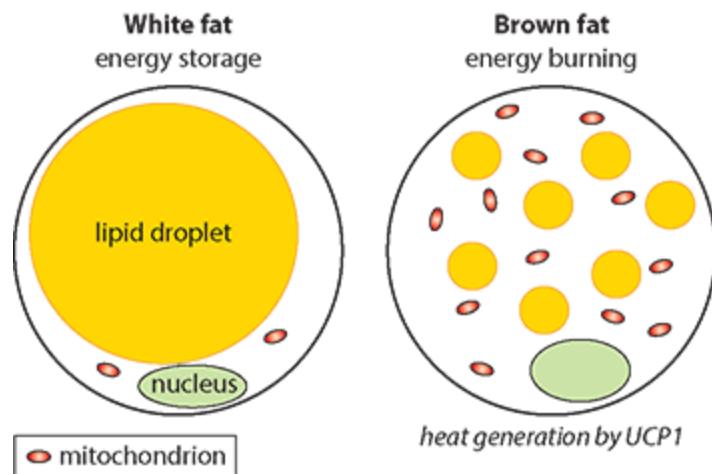


Figure 1.5.5: Comparison of white and brown adipose cells.

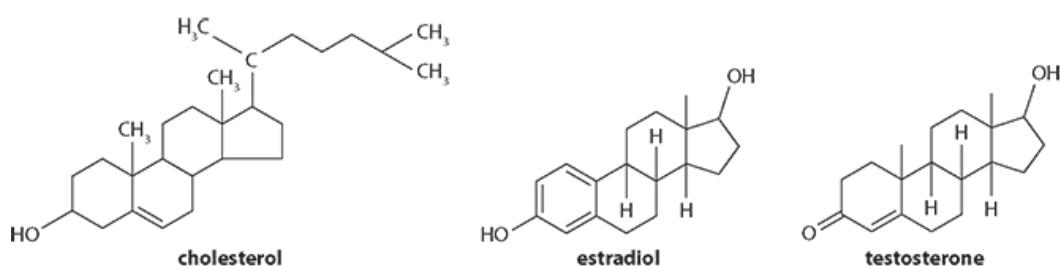


Figure 1.5.6: Structure of cholesterol and two important steroid hormones.

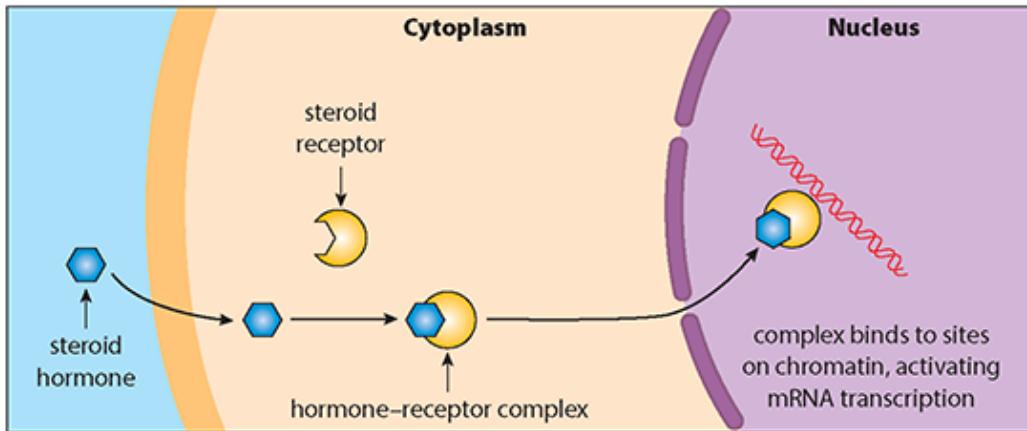


Figure 1.5.7: Steroid hormones enter cells and bind with special receptor molecules.

See Table 1.5.4 for a summary of the key properties of lipids.

energy content	lipids contain more energy per gram than carbohydrates, so lipid stores are lighter than carbohydrates storing an equivalent amount of energy.
density	lipids are less dense than water, so fat stores help large aquatic animals to float.
solubility	lipids are non-polar, insoluble molecules so they do not affect the movement of water in and out of cells by osmosis. Steroid hormones can pass through cell membranes.
insulation	lipids are also important in providing heat insulation. Fat stored under the skin reduces heat loss and is vital for animals such as seals, polar bears and whales, which live in cold conditions.

Table 1.5.4: The important properties of lipids that suit them to particular roles in living organisms.

TEST YOUR UNDERSTANDING

- 29** Name the type of reaction that releases energy from lipids.
- 30** State two roles for adipose tissue.
- 31** Outline the structure of a steroid hormone.
- 32** Why can steroid hormones pass through cell membranes?

Links

- How are the proportions of C, H and O different in carbohydrates and lipids? ([Chapter 1](#))
- How do the properties of phospholipids contribute to membrane structure and properties? ([Chapter 5](#))
- How do lipids influence temperature regulation in animals? ([Chapter 8](#))

1.6 Proteins

LEARNING OBJECTIVES

In this section you will:

- define the bond linking two amino acids as a peptide bond
- discover that only 20 of the 500 amino acids found in nature are used to build polypeptides
- learn that some amino acids cannot be synthesised in the body and must be obtained from food
- learn that amino acids can be linked in any sequence so living organisms can synthesise many different proteins
- discover that only complex proteins have quaternary structure
- learn how proteins are denatured by changes in pH or temperature

- learn how polar and non-polar amino acids influence the folding of tertiary structure
- learn how tertiary structure is held in place by disulfide bridges
- discover that conjugated proteins are formed as subunits are bound together, often involving a prosthetic group

- Recognise collagen as a non-conjugated protein and hemoglobin as a conjugated protein
- learn that a range of amino acids exist with properties that are determined by their R groups
- learn that there are four levels of structure in proteins: primary, secondary, tertiary and quaternary
- learn that proteins may have a fibrous or globular form

GUIDING QUESTIONS

- How do the components of a protein combine to form a functional protein?
- How is the function of a protein determined by its structural components?

1.6.1 Polypeptides

Polypeptides are built up from amino acid monomers during condensation reactions (Section 1.2 and Figure 1.6.6). Two amino acids are joined with a reaction between the amino (-NH₂) group of one amino acid and the carboxyl (-COOH) group of the other, forming a **peptide bond** and producing a dipeptide. If further condensation reactions occur, a series of amino acids can become joined to form a polypeptide. The covalent bonds linking the amino acids produce what is known as the **primary structure** of any protein that will be formed from the polypeptide.

In living cells, polypeptides are synthesised by ribosomes in the cytoplasm. Just 20 different amino acids are used to construct polypeptides. Nine of these amino acids, known as essential amino acids, have to be obtained from our food. The others, known as non-essential amino acids, can be made in the body. Polypeptides can consist of up to 400 amino acids and, because these can be linked together in any sequence, there is a huge range of possible polypeptides. Some amino acids may also be modified once the polypeptide has been incorporated into a protein molecule (Section 1.6.3) so that even more different structures can be formed.

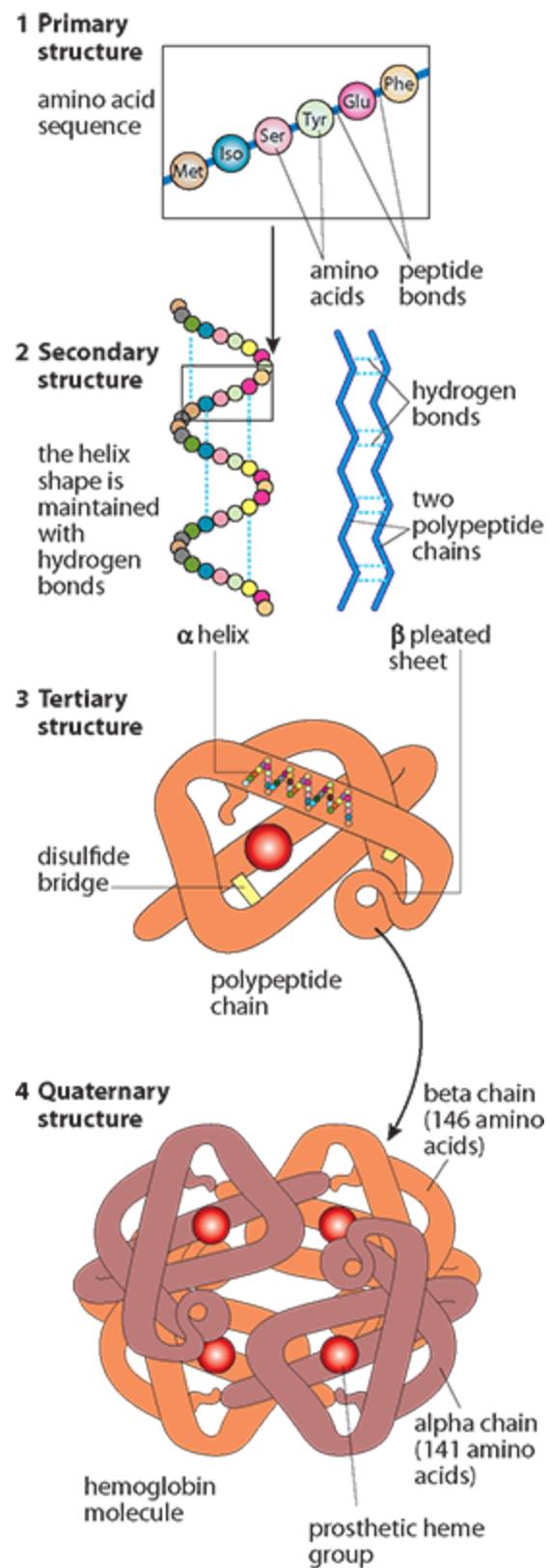


Figure 1.6.1: The structure of hemoglobin. Hydrogen bonds form between the amino acids in the polypeptide chain to form secondary structure and further folding can produce tertiary structure.

EXAM TIP

Make sure you can draw a molecular diagram to show how a peptide bond is formed between two amino acids. Remember that it is a condensation reaction, so water is produced.

The sequence of amino acids in a polypeptide is coded for by an organism's genes. Genes consist of a series of codons, each of which carries the specific code for one amino acid ([Chapter 4](#)). The sequence of codons in a gene is used as a template to direct the sequence in which the amino acids will be assembled.

1.6.2 Building a protein

Proteins are large, complex molecules, usually made up of hundreds of amino acid subunits. The way these subunits fit together is highly specific to each type of protein, and is vital to its function. Figure 1.6.1 illustrates the structure of the protein hemoglobin.

The first stage of protein production is the assembly of a sequence of amino acids to form the primary structure of a protein. A protein may either consist of one polypeptide or several linked together.

The basic chain of amino acids in a polypeptide folds and becomes a three-dimensional shape once it is complete. The shape, known as **secondary structure**, results from the formation of hydrogen bonds between different parts of the chain. The secondary structure forms as the polypeptide chain takes up a permanent folded or twisted shape. Some polypeptides coil to produce an α helix; others fold to form β pleated sheets. The most common shape is an α helix, held together by weak hydrogen bonds between the amino acids that lie in the turns of the structure. One section of a polypeptide may become an α helix while another takes up a β pleated form. The final shape will depend on the sequence of amino acids in the polypeptide.

KEY POINTS

peptide bond is a covalent bond between two amino acids.

polypeptide is a chain of amino acids formed by condensation reactions.

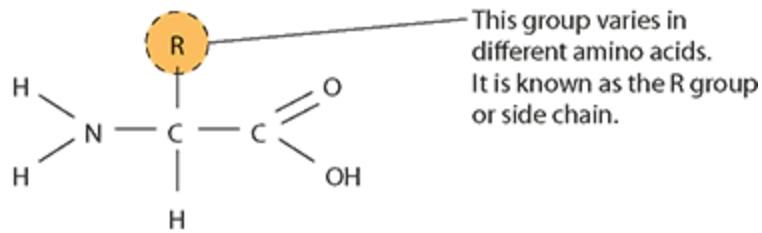
primary structure is the sequence of a polypeptide and number of amino acids in the molecule.

secondary structure is the three-dimensional form of sections of a protein. The two most common structural forms are α helices and β pleated sheets.

Living organisms synthesise many different proteins with many different functions (Table 1.6.1). Keratin, a structural protein found in hair, is an α helix. In other proteins, such as silk, polypeptides in parallel chains are linked to form flat, folded shapes known as β pleated sheets (Figure 1.6.1).

Further folding of polypeptide chains occurs in some proteins. This additional folding creates tertiary structure. Interactions occur between the R groups of the amino acids (Figure 1.6.2) and also within the polypeptide chain. The protein takes up a three-dimensional shape, which is held together by ionic bonds between particular R groups, as well as disulfide bridges (covalent bonds) between sulfur atoms of some R groups, and by weaker interactions between hydrophilic and hydrophobic side chains. Figure 1.6.3 shows the different types of bond involved in maintaining the tertiary structure of proteins. Tertiary structure is very important in enzymes (which are protein molecules) because the shape of an enzyme molecule gives it its unique properties and determines which substrates can fit into its active site ([Section 3.1](#)).

General structure of an amino acid



Structure of the simplest amino acid, glycine

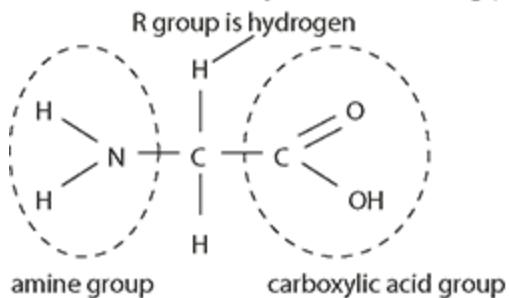


Figure 1.6.2: The general structure of an amino acid and the structure of glycine.

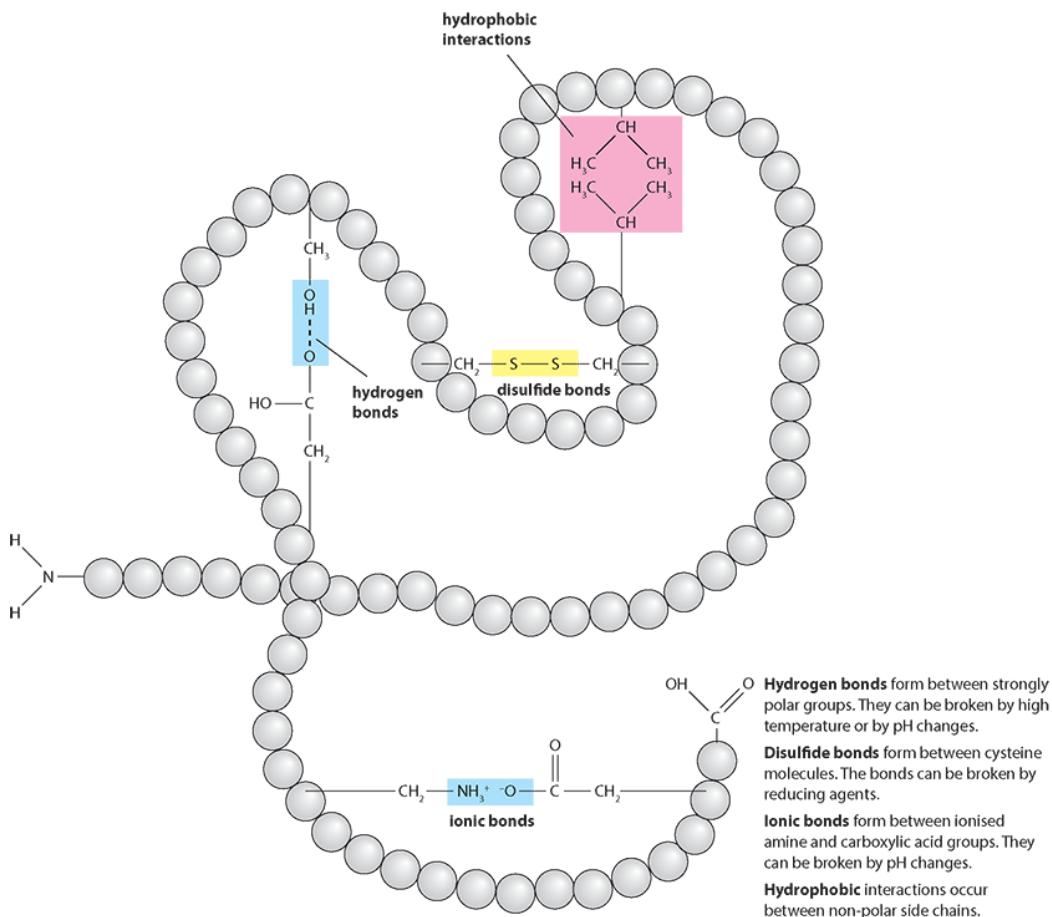


Figure 1.6.3: Types of bond that are important in protein structure.

Some proteins are composed of two or more polypeptides linked together and are said to have the final level of protein structure called quaternary structure. Quaternary structure links the polypeptide chains to form a single, large, complex protein. All the bonds that are important in the previous levels of structure hold the quaternary structure together. Examples of proteins that have quaternary structure are collagen Figure 1.6.4 (which has three polypeptide chains), hemoglobin (which has four), antibodies (which also have four) and myosin (which has six).

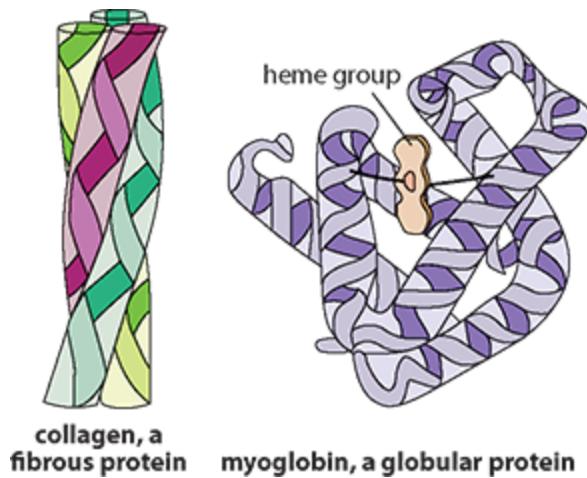


Figure 1.6.4: Structure of a fibrous and a globular protein.

TEST YOUR UNDERSTANDING

- 33** Draw the structure of a single amino acid. Use R to represent the chemically variable group.
- 34** Name the type of bond that links adjacent amino acids together.
- 35** Complete this sentence: Hydrogen bonds between amino acids cause a polypeptide to form a secondary structure and fold into either a or a
- 36** What type of proteins are enzymes?
- 37** Which of the following is not a property of a fibrous protein?
 - A** insoluble
 - B** parallel polypeptide chains
 - C** important in forming enzymes
 - D** tough but may be supple and stretchy

KEY POINT

quaternary structure of proteins made up from the association of several amino acid chains or subunits in a closely packed arrangement.

The pigment hemoglobin found in red blood cells has four subunits and the positioning of these subunits is very important for the role of hemoglobin in carrying oxygen ([Section 8.3](#)).

1.6.3 Fibrous and globular proteins

Protein molecules are categorised into two major groups by their shape:

- **Fibrous proteins** have structural roles in the body, they are long molecules and examples include collagen (Table 1.6.1) and keratin. Fibrous proteins are usually insoluble in water and, usually, have secondary structure with many α -helices with hydrogen bonds that give stability to the molecules.
- **Globular proteins** have a more complex rounded, three-dimensional shape and have either tertiary or quaternary structure. They have functional roles in the body. Most globular proteins are soluble in water. Globular proteins include enzymes, such as pepsin, and antibodies as well as two important respiratory proteins, myoglobin and hemoglobin.

Table 1.6.1 summarises the nature, shape and function of some important proteins.

Protein type	Shape	Function
insulin (globular hormone)	Active insulin has two polypeptide chains linked and held in place by disulfide bridges.	Produced by the pancreas, insulin stimulates the liver to take up glucose from the blood and store it as glycogen.

collagen (fibrous, structural)	Individual molecules are bound together by cross-linking covalent bonds. Collagen consists of three polypeptides wound around one another.	Present in connective tissue, builds muscle, tendons, ligaments giving them tensile strength, and gives elasticity to the skin of vertebrates.
immunoglobulin G (IgG) (globular)	Composed of two types of protein chain: two heavy chains and two light chains joined by disulfide bonds. This shape provides two antigen-binding sites so that antibody molecules can cross-link to antigens and hold them securely.	Infection control. Antibody produced by the immune system. Binds antigens from pathogens such as viruses, bacteria and fungi to fight infection.
DNA helicase (globular, enzyme)	Compact globular shape with a hexagonal arrangement of six identical subunits.	Separates double-stranded DNA to single strands allowing each strand to be copied during replication.

Table 1.6.1: The shape and functions of different proteins

1.6.4 Denaturation

Denaturation destroys the complex structure of a protein. Heat or the presence of strong acids or alkalis can all disturb the bonds between the different parts of a protein molecule and disrupt its structure. The primary structure of the protein will remain but secondary, tertiary and quaternary structures are usually lost. A denatured protein will have different properties from the original molecule. Enzymes are easily denatured by extremes of pH or temperature ([Section 3.1](#)) and lose the ability to function as catalysts. Some proteins lose their solubility or aggregate to form clumps as they denature and this can be observed during cooking. The heat used to cook meat denatures the proteins found in it so that its texture is changed. Egg becomes hardened as the proteins are denatured by heating.

1.6.5 Polar and non-polar amino acids

Amino acids are divided into two groups according to the chemical properties of their side chains or R groups (Figure 1.6.5). Polar and non-polar amino acids have different properties and their positions in a protein molecule affect the behaviour and function of the whole protein. The **tertiary structure** of proteins is influenced by the formation of disulfide bridges between these **R groups** (Figure 1.6.3).

Amino acids with non-polar side chains are hydrophobic. Those with polar side chains are hydrophilic. Non-polar amino acids are found in parts of proteins that are in hydrophobic areas, while polar amino acids are in areas that are exposed to an aqueous environment such as cytoplasm or blood plasma.

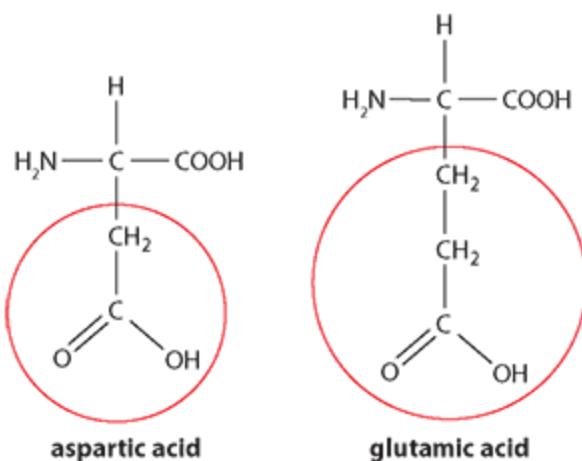


Figure 1.6.5: Aspartic acid and glutamic acid have side chains that are polar.

KEY POINTS

R group is a term used to abbreviate a group attached to a large biological molecule. Six of the 20 amino acids have

hydrocarbon R groups.

Tertiary structure is the three-dimensional structure of a protein due to interactions between the R groups of the amino acids.

Proteins are found in cell membranes and it is the polar hydrophilic amino acids that are found on the outer and inner surfaces where they are in contact with the aqueous environment, while the non-polar hydrophobic amino acids are embedded in the core of the membrane in contact with the hydrophobic tails of the phospholipid bilayer (Figure 1.6.6, see [Section 6.1](#)). This helps to hold the protein in place in the membrane. Some integral proteins act as channels, and the pore is lined with hydrophilic amino acids to enable polar substances to pass through.

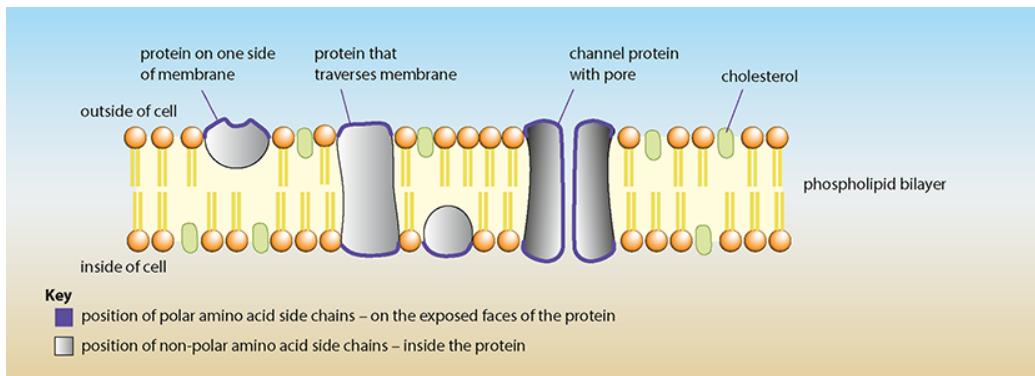


Figure 1.6.6: In membrane proteins, polar (hydrophilic) amino acids are found on the surfaces in contact with the aqueous environment, while non-polar (hydrophobic) amino acids are embedded inside the phospholipid bilayer.

Polar and non-polar amino acids are also important in enzymes, where they assist in the binding of substrates. An enzyme that acts on a polar substance (for example, amylase) has polar

amino acids in its active site, whereas lipases have non-polar amino acids in the active site. These amino acids help to form the temporary bonds between the enzyme and its substrate.

Polar amino acids on the surface of a protein increase its solubility while non-polar amino acids help a protein maintain its structure.

1.6.6 Prosthetic groups

Many proteins contain **prosthetic groups** and those that do are called **conjugated proteins**. Prosthetic groups are non-protein groups that are able to bind to different proteins or parts of them. We can see two examples of prosthetic groups in the respiratory pigments myoglobin (Figure 1.6.4) and hemoglobin which both contain a prosthetic heme group. Hemoglobin consists of four polypeptide chains, each one containing a heme group. The heme group (Figure 1.6.1) consists of a central Fe (iron) atom and a porphyrin ring. The prosthetic heme group is vital to the structure of hemoglobin because the shape of the whole protein is changed as oxygen binds to it. The iron group not only allows oxygen to bind but also holds the compact structure with four subunits in place and allows for progressively easier oxygenation as more oxygen molecules bind to the protein. Proteins with no prosthetic group are called **non-conjugated proteins**. Insulin (Fig 1.6.7) is an example of a non-conjugated protein.

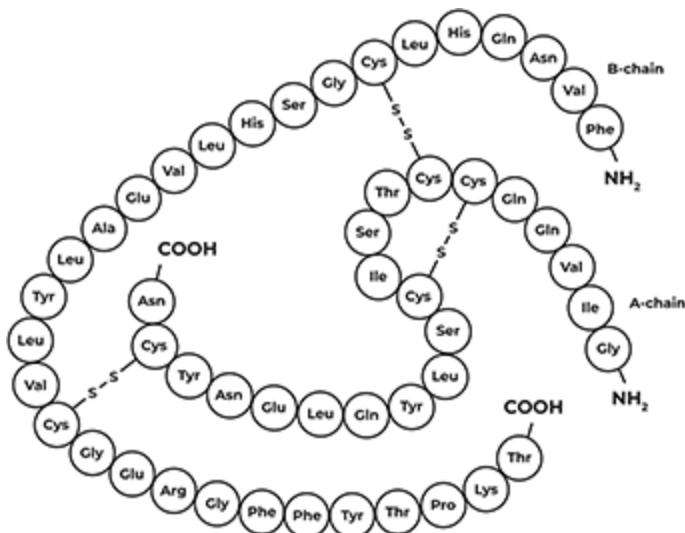


Figure 1.6.7: Insulin is a non conjugated protein

NATURE OF SCIENCE

Looking for trends and discrepancies: do all organisms use only 20 common amino acids in their proteins?

Humans can make 11 of the 20 amino acids we need to build proteins but we do not have the enzymes needed for the biosynthesis of the others. Plants, on the other hand, must be able to make all the amino acids they require.

Researchers have also investigated the trends in amino acid compositions of proteins found in species of the important kingdoms of Archaea, Bacteria and Eukaryotes. International databases ProteomicsDB and SWISS-PROT (which contain information about the structure and composition of proteins) can compare amino acid frequencies for 195 known proteomes and all recorded sequences of proteins. They discovered that the amino acid compositions of proteins do differ substantially for different kingdoms.

In addition to the variations in amino acids in proteins, some microorganisms and plants are able to make so called ‘non-standard’ amino acids by modifying standard amino acids. Some species are also able to synthesise many uncommon amino acids. For example, some microbes synthesise lanthionine, which is a modified version of the amino acid alanine. Many other proteins are modified after they have been produced. This ‘post-translational modification’ involves the addition of extra side groups to the amino acids in a protein.

Considering all the evidence, it seems that, although we can observe many similar proteins in different species, we cannot always say that the same amino acids are used in their

construction. The range of amino acids in proteins can vary considerably from species to species.

To consider:

- 1** What contribution have international databases made to our understanding of protein structure?
- 2** How can comparing proteomes and amino acids in different organisms help our understanding of evolutionary relationships?

As Table 1.6.1 shows, a wide range of proteins is found in different organisms and each protein has its own structural or biochemical function. Every individual organism has its own unique proteins, which are determined by its unique genome. The proteins found in an organism are known as its proteome, a term derived from a combination of the words ‘protein’ and ‘genome’.

KEY POINT

proteome the complete set of proteins expressed by a genome.

TEST YOUR UNDERSTANDING

- 38** Define a prosthetic group.
- 39** Outline the importance of hydrophilic amino acids in the tertiary structure of a protein.
- 40** State the difference between a conjugated and non-conjugated protein

Links

- How do proteins interact with phospholipid bilayers? ([Chapter 6](#))
- How does quaternary structure enable hemoglobin to collect oxygen? ([Chapter 8](#))
- How do protein hormones influence cell activity? ([Chapter 9](#))

1.7 Nucleic acids

LEARNING OBJECTIVES

In this section you will:

- recall that DNA is the genetic material of living organisms understand the components of a nucleotide
- learn that DNA and RNA are polymers of nucleotides with a sugar phosphate backbone
- understand that the bases in each nucleic acid form the basis of the genetic code
- recall the important differences between DNA and RNA
- understand the role of complementary base pairing in the replication and expression of genetic material
- understand that the genetic code is universal and diversity results from the enormous number of base sequences that are possible

- › learn how 5' to 3' linkages in the sugar phosphate backbone are significant for transcription and translation
- › learn that DNA is a double helix kept stable by purine to pyrimidine bonds
- › understand the structure of a nucleosome

- learn that Hershey and Chase provided evidence that DNA is the genetic material
- consider Chargaff's data on the ratio of pyrimidine to purine bases in many organisms.

GUIDING QUESTIONS

- How do the structures of nucleic acids enable them to store genetic information?
- How can molecular modelling permit predictions about a molecule's function?
- How does DNA fit into the small volume of the nucleus?

1.7.1 Structure of DNA and RNA

DNA (deoxyribonucleic acid) molecules make up the genetic material of living organisms. DNA is an extremely long molecule but, like proteins and carbohydrates, it is built up of many monomer subunits. The monomer subunits of DNA are called nucleotides. **RNA (ribonucleic acid)** is also built up of many nucleotides but these differ from DNA nucleotides in the type of pentose sugar they contain and the bases that are attached to them.

Each **nucleotide** consists of three parts – a pentose (five-carbon) sugar (deoxyribose or ribose), a phosphate group and a nitrogenous base (Figure 1.7.1). DNA contains four different bases: adenine, guanine, cytosine and thymine. These are usually known by their initial letters: A, G, C and T (Figure 1.7.2). RNA also contains four bases, but in an RNA molecule thymine is not present and is replaced by uracil (U).

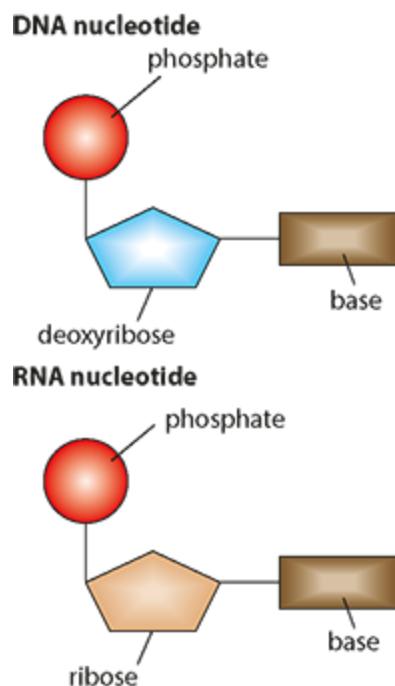


Figure 1.7.1: The general structure of DNA and RNA nucleotides.

To form a DNA molecule, nucleotide monomers are linked together. The phosphate group of one nucleotide links to the deoxyribose of the next molecule to form a chain of nucleotides, as shown in Figure 1.7.2. The sugar and phosphate groups are identical all the way along the chain and form the ‘backbone’ of the DNA molecule. The sequence of bases in the chain will vary and it is this sequence that forms the genetic code determining the characteristics of an organism.

Different organisms have DNA of different lengths and any base sequence is possible, this gives a DNA molecule a large capacity for storing genetic information.

The genetic code carried in the sequence of bases that make a DNA molecule is said to be **universal** because it is similar across all forms of life.

Two strands of nucleotides are linked by hydrogen bonds that form between the bases and this two-stranded structure makes up the double helix of a complete DNA molecule. Adenine always pairs with thymine and is bonded with two hydrogen bonds, while cytosine is paired with guanine by three hydrogen bonds. The arrangement is known as **complementary base pairing**. Notice that the two DNA chains run in opposite directions and are said to be **antiparallel**.

KEY POINTS

DNA (deoxyribonucleic acid) is the basic material of inheritance, contained in the nucleus in eukaryotes and the cytoplasm of prokaryotes; DNA consists of two strands of

nucleotide subunits containing the bases adenine, thymine, guanine and cytosine.

nucleotide is the basic chemical unit of a nucleic acid – an organic base combined with pentose sugar (either ribose or deoxyribose) and phosphate.

RNA (ribonucleic acid) a nucleic acid that contains the pentose sugar ribose and bases adenine, guanine, cytosine and uracil.

complementary base pairing is pairing of bases A–T and G–C in double-stranded DNA, and of A–U and C–G between DNA and RNA during transcription, and between tRNA and mRNA during translation.

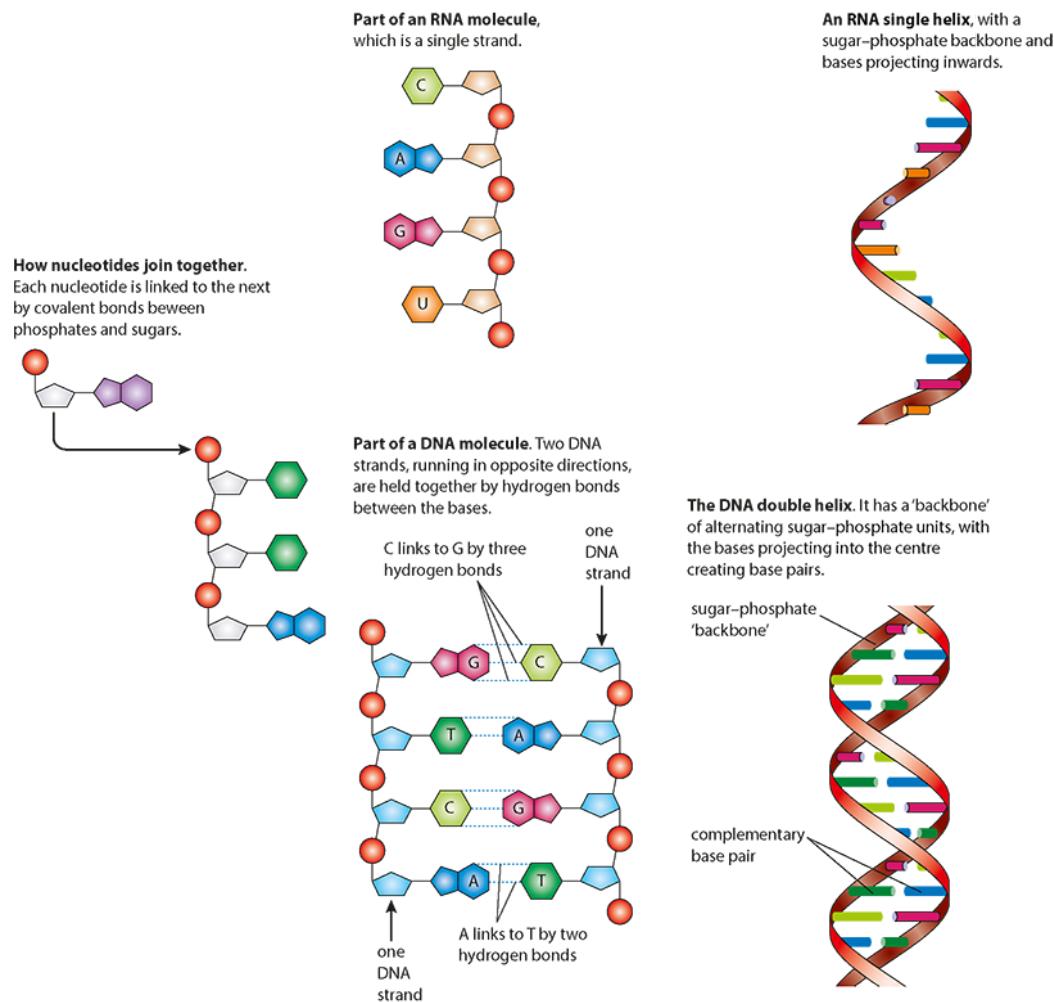


Figure 1.7.2: The structure of DNA and RNA.

KEY POINT

antiparallel means running in opposite direction; the two polynucleotide strands in a DNA molecule are antiparallel.

You can imagine the molecule rather like a rope ladder with the sugar phosphate backbone being the sides of the ladder and the rungs being formed by the hydrogen-bonded base pairs. To form the characteristic double helix of a DNA molecule, the ladder must be twisted to resemble a spiral staircase.

To form a molecule of RNA, nucleotide monomers are linked in a similar way to those of DNA. In the case of RNA the molecule remains single stranded and the bases it contains do not bond with bases in other RNA molecules.

Table 1.7.1 outlines the similarities and differences between the DNA and RNA molecules.

EXAM TIP

Make sure you can draw a simple diagram of DNA and RNA nucleotides using circles, pentagons and rectangles to represent the components.

Always draw DNA structure so that it shows two antiparallel strands and correctly paired bases. You will not be asked to show the helical shape. Try to think of a mnemonic that will help you remember the pairings of bases in DNA, for example Apple–Tart for adenine–thymine and Chocolate–Gateau for cytosine–guanine.

DNA	RNA
contains the five-carbon sugar deoxyribose	contains the five-carbon sugar ribose
contains the bases adenine, guanine, cytosine and thymine (A, G, C, T)	contains the bases adenine, guanine, cytosine and uracil (instead of thymine) (A, G, C, U)
a double-stranded molecule	a single-stranded molecule

Table 1.7.1: A comparison of the structures of DNA and RNA.

1.7.2 Complementary base pairing and DNA replication

DNA must replicate itself accurately when a cell divides, the genetic code it carries can be passed on to the daughter cells.

DNA replication copies DNA precisely so that new molecules are produced with exactly the same sequence of bases as the original strands.

As Figure 1.7.3 shows, this process does not occur in a haphazard manner. An enzyme called helicase unzips one region of the DNA molecule and nucleotides are added in a step-by-step process that links them to one another and to their complementary bases with hydrogen bonds in an area known as the replication fork. Details of the process are discussed in [Section 3.1](#).

The two new DNA strands that are produced are absolutely identical to the original strands. Complementary base pairing between the template strand and the new strand ensures that an accurate copy of the original DNA is made every time replication occurs. DNA replication is said to be **semi-conservative replication** because no DNA molecule is ever completely new. Every double helix contains one ‘original’ and one ‘new’ strand.

KEY POINT

DNA replication is the production of two new strands of DNA from one original molecule.

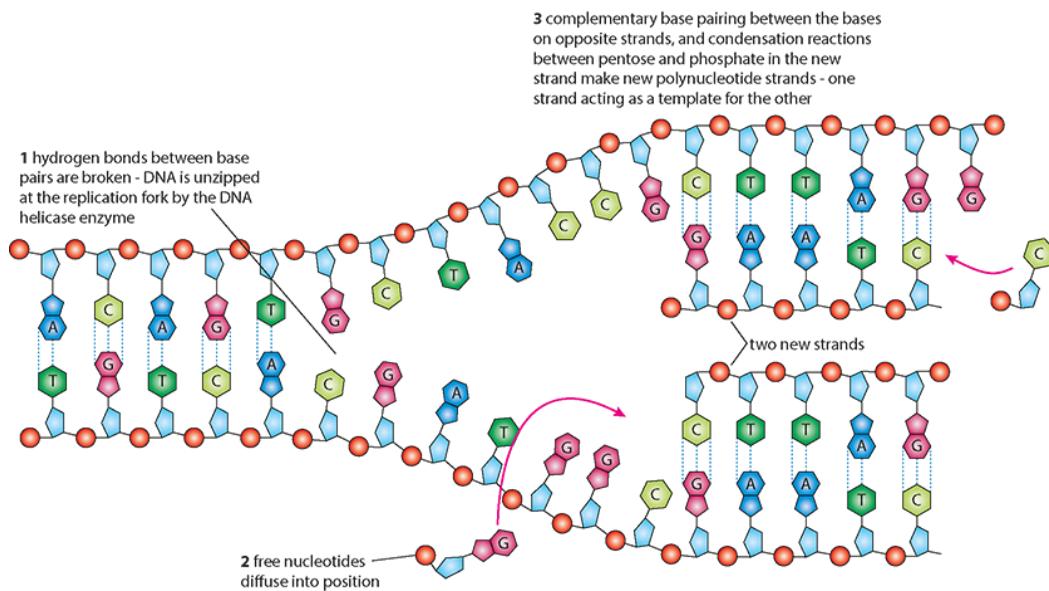


Figure 1.7.3: DNA replication.

KEY POINT

semi-conservative replication is when each of two partner strands of DNA in a double helix acts as a template for a new strand; after replication each double helix consists of one old and one new strand.

THEORY OF KNOWLEDGE

Collaboration versus competition

The story of the discovery of DNA's structure (see Nature of Science, Careful observation: the discovery of DNA) illustrates how important collaboration can be in scientific discovery. Cooperation and competition can both occur between research groups.

To consider:

- 1** Is keeping research discoveries secret ‘anti-scientific’?
Can it ever be justified?
- 2** How are shared and personal knowledge related in scientific research?

Complementary base pairing is also crucial to the process of gene expression. The genes carried in the DNA genetic code are eventually converted into the polypeptides and proteins that the cell needs. Complementary base pairing between DNA and RNA produces a single strand of messenger RNA (mRNA) in a process known as transcription ([Section 4.2](#)). This mRNA strand acts as a template for protein production in the cytoplasm.

1.7.3 DNA packaging in the nucleus

DNA is a very long molecule composed of many thousands of nucleotides. During DNA replication, DNA unwinds so it can be copied. At other times in the cell cycle ([Section 6.5](#)), DNA also unwinds so that its instructions can be used to make proteins. But as a cell prepares to divide, each DNA molecule is coiled into a compact chromosome so that it can be passed to new daughter cells.

KEY POINTS

chromosome in eukaryotes, a structure consisting of a long thread of DNA and protein that carries the genetic information of the cell; in bacteria, the DNA molecule that contains the genetic information of the cell.

histone is one of a group of basic proteins that form nucleosomes and act as scaffolding for DNA.

nucleosome refers to a part of a eukaryotic chromosome, made of DNA wrapped around histone molecules and held in place by another histone protein.

In eukaryotes, DNA is found in the nucleus surrounded by a nuclear membrane. Because the cell is very small, and because organisms have many DNA molecules per cell, each DNA molecule must be tightly packaged. This packaged form of the DNA is called a chromosome. DNA is coiled and then coiled again around a structure known as a **nucleosome** (see the Higher Level section on DNA structure and replication). A nucleosome consists of DNA associated with proteins known as histones. Histones have three key functions:

- packaging of DNA
- gene regulation
- supercoiling DNA during cell division.

Prokaryotes do not have **histone** proteins associated with their DNA. It remains free in the cytoplasm and is known as ‘naked’ DNA.

TEST YOUR UNDERSTANDING

- 41** State two differences between DNA and RNA.
- 42** Draw the structure of a DNA nucleotide.
- 43** Outline the importance of nucleosomes in the nuclei of eukaryotes.

1.7.4 DNA structure and replication

Nucleic acids are very large macromolecules composed of a backbone of sugar and phosphate molecules each with a nitrogenous base attached to the sugar. Here, the detailed structure of different nucleic acids is considered.

The 3'-5' linkage

A DNA nucleotide consists of the sugar deoxyribose to which are attached a phosphate group and a nitrogenous base. The carbons in the sugar are numbered from 1 to 5 in a clockwise direction starting after the oxygen at the apex (Figure 1.7.4).

- The base is attached to carbon 1.
- Carbon 2 has just a hydrogen attached instead of an OH group, this is the reason the sugar is called *deoxyribose*.
- Carbon 3 is where the next nucleotide attaches in one direction.
- Carbon 5 has a phosphate group attached to it, which is where the next nucleotide attaches in the other direction.

This means that each nucleotide is linked to those on either side of it through carbons 3 and 5. The linkages are called **3'-5' linkages**.

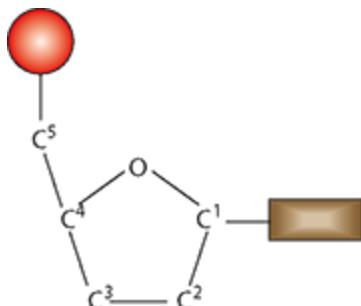


Figure 1.7.4: The structure of a nucleotide.

KEY POINT

3'-5' linkage bond between the 3' carbon atom of one sugar molecule and the 5' carbon atom of another; found in DNA and RNA molecules.

Antiparallel strands

Look back at Figure 1.7.2. This shows part of a DNA molecule in which two polynucleotide strands, running in opposite directions, are held together by hydrogen bonds between pairs of bases. Notice that the deoxyribose molecules are orientated in the opposite directions. Figure 1.7.5 also shows this: at one end of each DNA strand there is a free 3' carbon and at the other there is a free 5' carbon. (Ignore the fact that there is a phosphate group attached to this 5' carbon.) One strand runs in one direction whereas the other runs in the opposite direction. The strands are described as being antiparallel.

DNA bases and hydrogen bonding

The four DNA bases fall into two chemical groups called **pyrimidines** and **purines**. Cytosine and thymine are pyrimidines, and adenine and guanine are purines.

Cytosine pairs with guanine and thymine pairs with adenine, that is, a pyrimidine always pairs with a purine. This is because they are different sizes: pyrimidines are smaller than purines. The pairing of a pyrimidine with a purine ensures that the strands are always the same distance apart (Figure 1.7.5). Understanding that DNA strands are antiparallel and that hydrogen bonds

between the bases can be broken were crucial steps in working out how DNA is replicated.

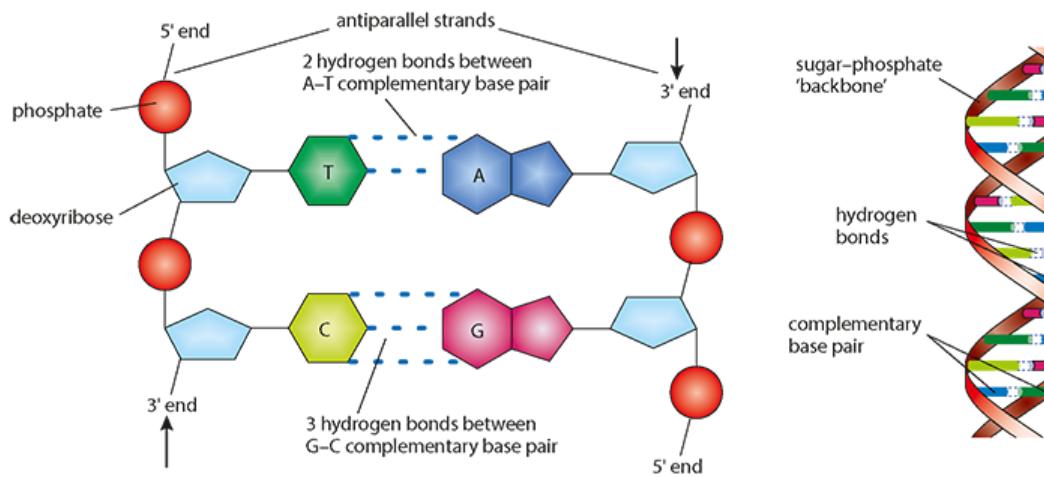


Figure 1.7.5: Hydrogen bonding between antiparallel strands of DNA.

NATURE OF SCIENCE

Careful observation: the discovery of DNA

James Watson and Frances Crick, together with Maurice Wilkins, were awarded the Nobel Prize for Physiology or Medicine in 1962 for their discovery of the structure of DNA (Figure 1.7.6). Watson and Crick put forward their theory for DNA structure in 1953. They based their ideas on the work of an American chemist, Erwin Chargaff, who calculated the proportions of the bases in DNA. Chargaff noticed that DNA varies from species to species and suggested that DNA was genetic material. He also observed that the bases in DNA appear in a 1 : 1 ratio; the number of guanine bases in DNA is equal to the number of cytosine bases, and the number of adenine bases is equal to the number of thymine bases. This suggested the base pair pattern of DNA, and helped Watson and Crick work out how the bases fitted into the double helix.

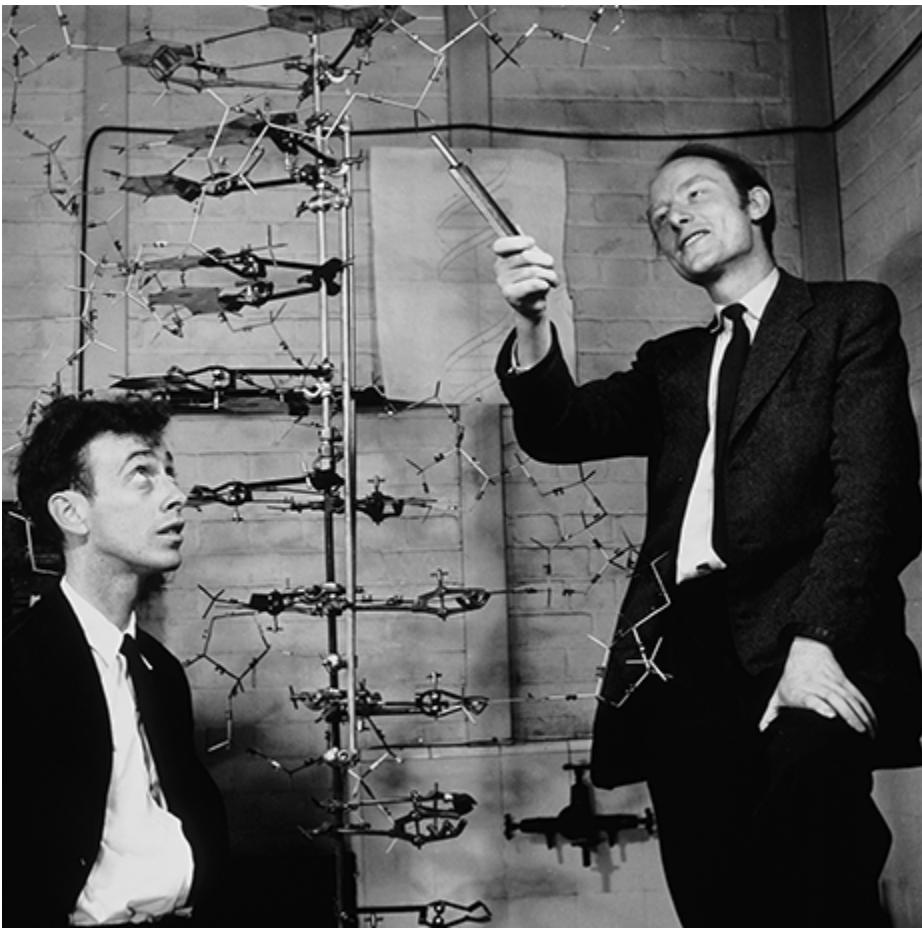


Figure 1.7.6: Watson and Crick built a 3D model to help formulate their proposal for the structure of DNA.

Watson and Crick suggested that DNA was composed of two parallel strands held together by pairs of bases, A pairing with T, and C with G. At the same time, in different laboratories, other researchers were trying to work out DNA's three-dimensional structure using X-ray diffraction. Rosalind Franklin (Figure 1.7.7) and Maurice Wilkins spent many hours trying to interpret photographs of diffraction patterns produced by DNA. From careful observation and calculation of the positions of certain markers on the X-ray photographs, Watson and Crick finally worked out that the two chains of DNA were wrapped into a double helix, linked at regular

intervals by the bases of the nucleotides. Furthermore, they were able to see from a model of DNA that there are 10 nucleotides per turn of the helix. It is important to remember that their achievement would not have been possible without the data, which were provided by the other scientists working on DNA structure at the time.



Figure 1.7.7: Rosalind Franklin was an expert in the field of X-ray crystallography. Her skill and careful observations enabled her to work out that the phosphate groups of DNA are found on the outside of the molecule. She died at the age of 37 before the Nobel Prize was awarded to Watson, Crick and Wilkins. Nobel prizes cannot be awarded posthumously.

To consider:

- 1** Inference, creativity and imagination are important in scientific discovery. Why was collaboration so important

in the discovery of the structure of DNA?

- 2 How important are awards and prizes for scientists who made new discoveries?

The accuracy of DNA replication

When Watson and Crick proposed their double-helix model for the structure of DNA in 1953, one of the most striking things they realised was that it immediately suggested a way that DNA could be replicated. If the two strands were unwound each one could provide a template for the synthesis of a new strand.

An essential feature of DNA is that it must be able to replicate itself accurately, so that when a cell divides, the genetic code it carries can be passed on to the daughter cells. In DNA replication, new molecules are produced with identical sequences of bases as the original strands (Figure 1.7.3). DNA replication takes place in the nucleus during interphase of the cell cycle when DNA is not tightly coiled ([Section 6.5](#)).

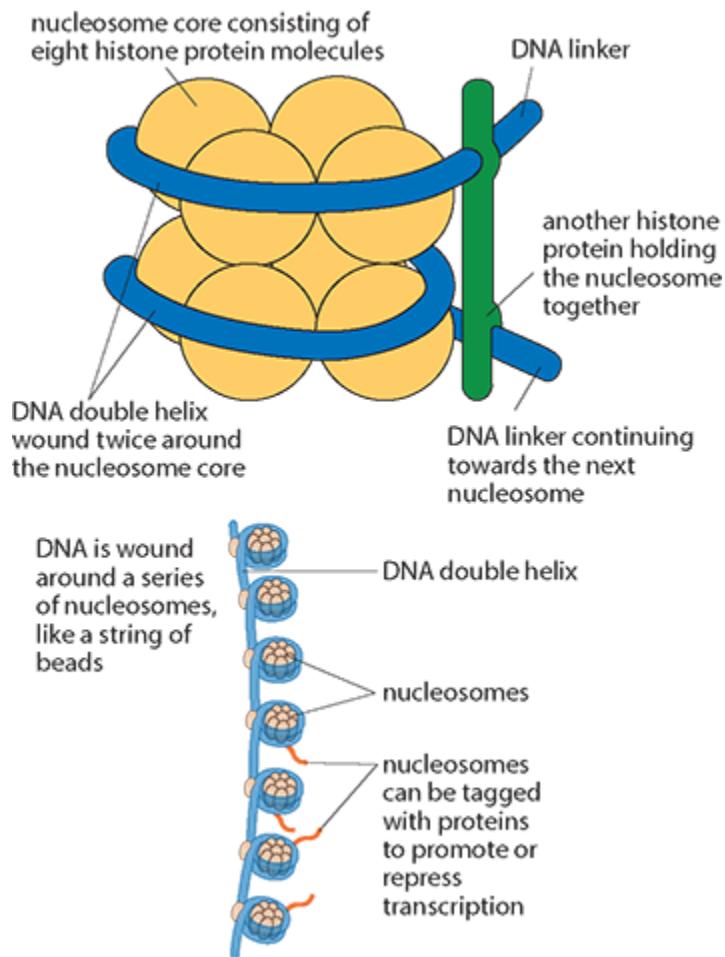


Figure 1.7.8: The structure of a nucleosome.

Nucleosomes

A eukaryotic chromosome is composed of a double strand of DNA combined with proteins. Some of these proteins, called histones, combine together in groups of eight to form a bead-like structure (Figure 1.7.8). The strand of DNA takes two turns around the first bead before continuing on to the next bead. It is held in place on the bead by a ninth histone. The group of nine histones with the DNA is called a nucleosome. The function of nucleosomes is to help supercoil the chromosomes during mitosis and meiosis and also to help regulate transcription.

(Section 4.4). Nucleosomes are linked together by a section of linker DNA.

1.7.5 The Hershey and Chase experiments

Hershey and Chase used bacteriophages (viruses that infect bacteria) to provide evidence that DNA is the genetic material.

Although DNA has been well known to science since the 19th century, it is surprising to think that it was not until the middle of the 20th century that scientists discovered its role as the genetic material. Until that time, most people believed that proteins were the molecules responsible for inheritance. Then, in 1952, Alfred Hershey (1908–1997) and Martha Chase (1927–2003) conducted a series of experiments with T2 phage (a type of bacteriophage), which confirmed that DNA was the genetic material. They were able to carry out these investigations thanks to two relatively new techniques: electron microscopy and radioactive labelling.

The structure of the T2 phage had recently been revealed using the electron microscope. The virus injects its DNA into the cell it infects, but leaves behind its protein coat. Hershey and Chase labelled the viral DNA with radioactive ^{32}P . Phosphorus is present in DNA but not in amino acids, so as they followed the transfer of the labelled material into the cytoplasm of the bacterium, Hershey and Chase knew that it was only DNA that was being transferred.

They then labelled viruses with ^{35}S (sulfur is present in amino acids but not in DNA). After these viruses had infected the bacterial cells, Hershey and Chase examined the discarded protein coats and found that they contained radioactive sulfur, but the bacterial cytoplasm did not. These results supported their hypothesis that DNA is the genetic material that infects the

bacteria, and protein (found in the protein coats) was not (Figure 1.7.9).

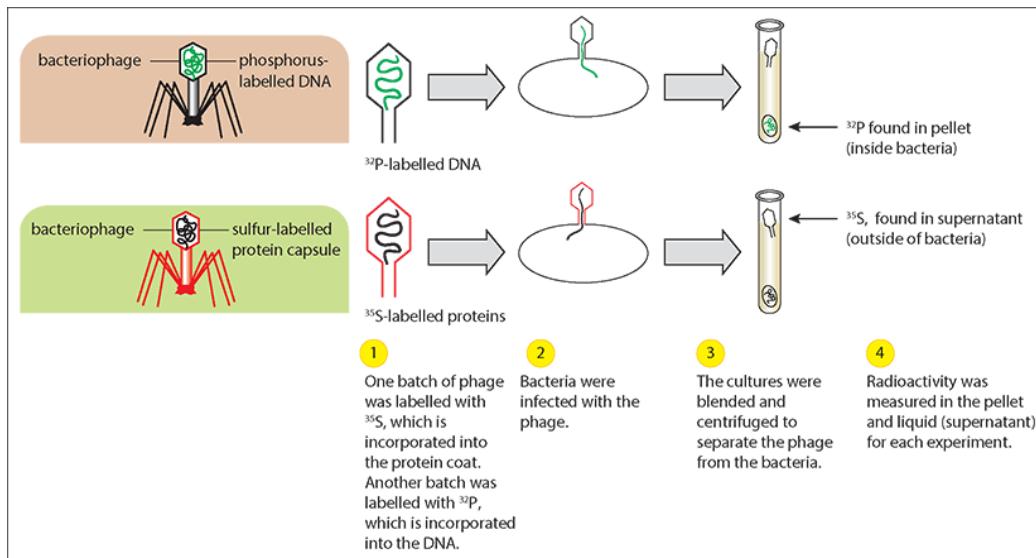


Figure 1.7.9: The Hershey and Chase experiment showed that the genetic material transferred to bacterial cells by infecting T2 phages is DNA, and not protein as previously believed.

EXAM TIP

Check your understanding of the Hershey and Chase experiment. Make sure you can interpret the results correctly. Try answering these questions.

- 1 What kind of virus was used in the experiment and why?
- 2 Why were two types of labelling used to identify the phages?
- 3 Why did Hershey and Chase conclude that DNA was the genetic material?

NATURE OF SCIENCE

Chargaff's rule

In the 1940s Austrian-born chemist Erwin Chargaff (1905 – 2002) discovered that in the double stranded DNA of any organism, the amount of guanine is equal to the amount of cytosine and that the amount of thymine is equal to the amount of adenine.

Chargaff's rule states that in any double stranded DNA molecule $A\% = T\%$ and $G\% = C\%$. Chargaff's work began with the hypothesis that if DNA from different species had different biological activities, there should also be differences in the chemistry of their DNA. With careful experimentation he was able to disprove the tetra nucleotide hypothesis that was current at the time, and which stated that DNA was formed of a large number of repeats of a GACT tetramer. His work was a good example of how a new hypothesis supported by experiments can falsify an earlier hypothesis.

This discovery was crucial in helping Watson and Crick as they worked out the structure of the DNA molecule.

To consider:

Why do scientific discoveries often depend on research that falsifies a widely held theory?

TEST YOUR UNDERSTANDING

- 44** Draw a nucleotide of DNA and label the carbon atoms 1 to 5.
- 45** State the evidence that Erwin Chargaff produced that assisted in the elucidation of the structure of DNA.

46 How many histone proteins are present in a nucleosome?

47 Why was the discovery of radioactive isotopes important in proving that DNA is the genetic material?

SELF-ASSESSMENT CHECKLIST

Think about the topics covered in this chapter. Which parts are you most confident with? Which topics require some extra practice?

I can...	Subsection	Needs more work	Nearly there	Confident to move on
define the terms organic and inorganic molecule	1.1.1			
define an organic molecule	1.1.1			
list the six most common elements in living things	1.1.2			
suggest uses for magnesium and calcium in living things	1.1.2			
list different functions for the element iron in plants and animals	1.1.3			
name an element that is toxic	1.1.4			

explain the terms polar, covalent and hydrogen bond in relation to water	1.2.1			
draw water molecules interacting with each other	1.2.1			
explain how water acts as a solvent for ionic and polar substances	1.2.2			
explain how water and plant sap transport dissolved molecules	1.2.2			
recognise that water is a metabolite and is used and produced during reactions	1.2.2			
define emergent properties	1.2.3			
explain how polarity gives water cohesive properties that support small	1.2.4			

organisms and allow water to travel in tubes				
explain how polarity give water adhesive properties and give an example of why these are important	1.2.4			
outline why a high specific heat capacity makes water temperature resistant to change	1.2.5			
describe how evaporation of water cools organisms	1.2.5			
explain why ice has a lower density than water and how ice helps aquatic organisms survive	1.2.5			
suggest how the transparency of water helps aquatic organisms survive	1.2.5			

outline some adaptations of organisms that live in aquatic habitats	1.2.6				
summarise a hypothesis to explain the origin of water on Earth	1.2.7				
suggest why scientists hunt for water when looking for extraterrestrial life	1.2.7				
outline how carbon atoms can form four covalent bonds to produce a variety of stable organic compounds	1.3.1				
state that carbohydrates, proteins, lipids and nucleic acids are organic compounds	1.3.2				
define a monomer and a polymer	1.3.3				

state what happens in a hydrolysis reaction	1.3.3				
state what happens during a condensation reaction	1.3.3				
identify carboxyl groups, amines and phosphate groups as functional groups found in organic molecules	1.3.4				
recognise how monosaccharide monomers are linked together by condensation reactions to form disaccharides and polysaccharides	1.4.1				
describe how carbohydrates have a range of different forms which give them their properties	1.4.1				
recognise that large	1.4.2				

carbohydrates are less soluble than small ones				
state glycogen and starch are compact structures that make them suitable storage molecules	1.4.2			
outline the structure of cellulose and how it is related to its structural function	1.4.2			
state that carbohydrates are short-term energy stores which are metabolised to release energy	1.4.2			
explain how alpha-d-glucose and beta-d-glucose are bonded together to produce amylose, amylopectin and cellulose (extension)	1.4.2			
	1.4.2			

list examples of branched polysaccharides and state their functions				
recall that pentose sugars are found in DNA and RNA molecules	1.4.2			
name different forms of lipid and give examples of their properties	1.5.1			
describe the arrangement of molecules in a triglyceride	1.5.1			
state why lipids are hydrophobic	1.5.1			
explain the terms saturated, unsaturated and polyunsaturated	1.5.2			
state why lipids are efficient in storing energy	1.5.3			
describe the importance of adipose tissue	1.5.4.			

name two steroid hormones and outline their roles in the body	1.5.5				
draw the structure of an amino acid	1.6.1				
explain the importance of R groups in amino acids and draw a peptide bond between two amino acids	1.6.1				
define a polypeptide	1.6.1				
outline the four levels of structure found in proteins	1.6.2				
describe how hydrogen bonds and ionic bonds are important in secondary and tertiary structure	1.6.2				
outline the differences between fibrous and globular proteins	1.6.3				
explain how	1.6.4				

denaturation alters protein structure				
explain the difference between polar and non-polar amino acids and how they influence protein folding	1.6.5			
define the terms prosthetic group and conjugated protein using hemoglobin as an example	1.6.6			
draw diagrams of DNA and RNA monomers	1.7.1			
name the bases found in DNA and RNA	1.7.1			
summarise the differences between DNA and RNA	1.7.1			
draw diagrams of DNA and RNA to show the sugar phosphate backbone	1.7.1			

draw a simple diagram of DNA to show the double helix and antiparallel strands	1.7.1			
explain complementary base pairing and why it is important in replication of DNA	1.7.2			
state that there is enormous diversity in the combinations of DNA bases	1.7.3			
label the 1–5 carbon atoms in a nucleotide and explain how they are linked in a sugar phosphate backbone	1.7.4			
outline the structure of nucleosomes and their importance in eukaryotes	1.7.4			
	1.7.5			

outline the Hershey and Chase experiment and its importance.

REFLECTION

Do you have any questions about water that need further investigation?

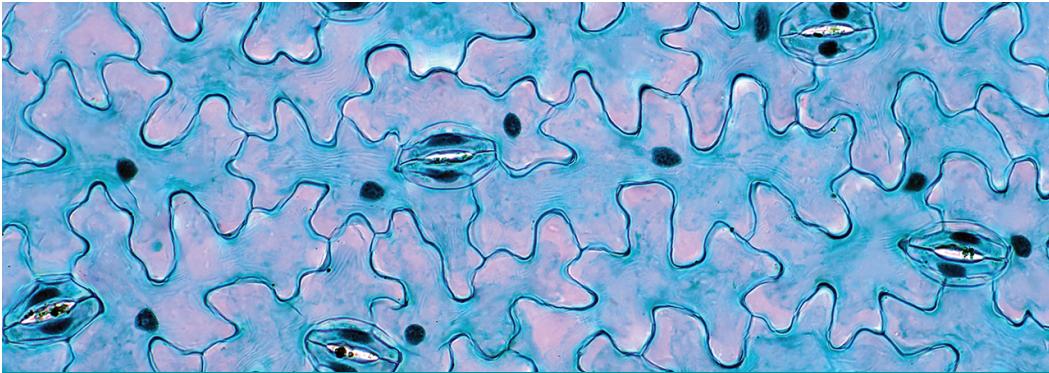
Thinking about the topics covered in the section, are there any areas that you have found particularly difficult?

What were the most challenging aspects of this topic? Why did you find them so?

If you were teaching this subject, what suggestions would you make to your students?

EXAM-STYLE QUESTIONS

You can find questions in the style of IB exams in the digital coursebook.



› Chapter 2

Metabolism, respiration and photosynthesis

C1.1, C1.2, C1.3

INTRODUCTION

Metabolic reactions are chemical processes that occur in all cells to keep them alive. Respiration and photosynthesis are two key metabolic pathways in ecosystems. Light energy from the Sun is trapped as chemical energy in photosynthesis and then the energy is transferred through food chains and released back to the environment as heat energy from respiration. The two pathways can be simply written as:



2.1 Enzymes and metabolism

LEARNING OBJECTIVES

In this section you will:

- learn that metabolic pathways are made up of chains and cycles of enzyme-catalysed reactions
- understand that metabolic processes can be anabolic or catabolic
- learn that enzymes are globular proteins that act as catalysts
- understand that enzymes have an area on their molecule, known as the active site, to which specific substrates bind
- learn that during enzyme-catalysed reactions molecules move about, and substrate molecules collide with the active sites on enzyme molecules
- discover how the rate of enzyme activity is influenced by temperature, pH and substrate concentration
- learn how enzyme molecules can be denatured

- understand how enzymes lower the activation energy of chemical reactions
- learn that enzyme inhibitors can be competitive or non-competitive

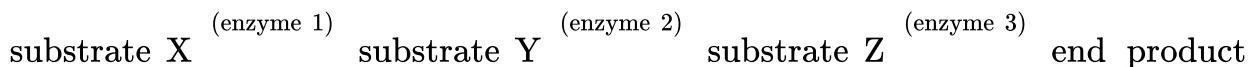
- understand how end-product inhibition can control metabolic pathways
- learn how co-enzymes and co-factors promote enzyme activity.

GUIDING QUESTIONS

- How are molecules transformed by metabolism?
- What is the role of enzymes in metabolic processes?
- What factors affect enzyme activity?

2.1.1 Metabolic pathways

Metabolic pathways consist of chains or cycles of reactions that are catalysed by enzymes. Metabolism includes all the chemical activities that keep organisms alive. Metabolic pathways may be very complex, but most consist of a series of steps, each controlled by an enzyme. Simple linear pathways involve the conversion of substrates to a final product:



KEY POINTS

anabolism refers to a series of metabolic pathways that build molecules from smaller subunits. These reactions require energy.

catabolism refers to a series of metabolic pathways that break down large molecules into smaller ones.

metabolism is the sum of the chemical reactions that occur within living organisms.

Each arrow represents the specific enzyme needed to catalyse the conversion of one substrate to the next. An example of a linear pathway is the breakdown of glucose in the glycolysis pathway ([Section 3.2](#), Respiration) and the digestion of starch to maltose and glucose in the digestive system:



Other metabolic pathways, such as photosynthesis or respiration, involve both chains of reactions and cycles of reactions. Two examples of cyclical pathways are the Krebs cycle in aerobic respiration and the Calvin cycle in photosynthesis ([Sections 3.2](#) and [3.3](#)). Both of these cycles have many enzyme-catalysed steps.

Some metabolic reactions, such as protein synthesis, take place inside cells and are said to be intracellular, while others, such as digestion, occur outside cells and are known as extracellular reactions.

There are two types of metabolic process: anabolic reactions which build new molecules and catabolic reactions which break down large molecules.

NATURE OF SCIENCE

How does scientific understanding change and develop over time?

What affects longevity: metabolic rate or size? In 1926 an American biologist, Raymond Pearl, proposed the *rate of living hypothesis*. It suggested that a key factor determining how long a species lives is the speed of their resting metabolism. His evidence came from his observations that bigger animals tend to live longer and have lower heart, breathing and metabolic rates. He proposed that longevity is inversely related to basal (resting) metabolic rate.

The rate of living hypothesis was a well accepted theory for nearly 50 years. But over time, other scientists have made observations that have cast doubt on it. For example, rats and bats have similar metabolic rates, but a bat lives several times longer than a rat. Modern statistical methods that correct for the effects of body size and species group do not support the theory. They show that metabolic rate does not correlate with longevity in either mammal or bird groups.

Another newer model to explore body size, metabolism and ageing looked at how these are linked within the same species. Some of the results support the original rate of living theory and others do not. Scientists allowed some animals to expend more energy than others which were kept inactive and found that the amount of energy used does affect lifespan within a species. But the results were confused by the discovery that in some species smaller individuals with higher rates of metabolism live longer than slower, larger members of the same species.

A *free radical theory* of ageing proposed in the twenty-first century provided a new way of linking metabolism to ageing. Oxygen free radicals are formed during cell respiration in mitochondria. They can damage cells and contribute to ageing. The free radical theory suggested that more or faster respiration could make organisms' lives shorter. But today, scientists believe that free radical damage from metabolism on its own cannot be the cause of ageing. The accumulation of other defects

and imperfections must also be important. It seems that free radical theory has served its purpose in our understanding of the ageing process. More investigations and newer theories are needed to advance our knowledge of how we grow old. Only recently, experimental tools, such as sequencing of DNA and profiling of proteomes and metabolites, have been developed and these may be used to begin assessing the many types of damage that cause cells and bodies to age.

To consider:

- 1 Scientific knowledge is provisional and theories must be modified in the light of new observations and evidence.
- 2 Which areas of biology do you think will be important in understanding the ageing process?
- 3 How has modern technology helped scientists gather data for new theories?

Two examples of anabolic reactions are protein synthesis, when amino acid monomers are linked by condensation reactions ([Section 1.6](#)), and photosynthesis ([Section 2.3](#)), which builds glucose molecules from carbon dioxide and water.

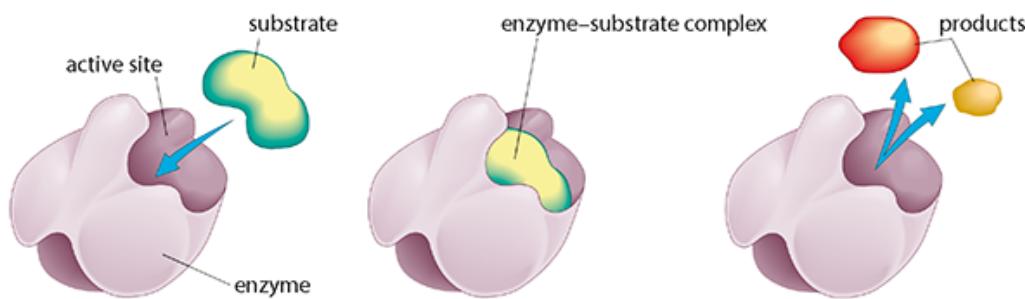
Catabolic reactions include the hydrolysis of large molecules, such as carbohydrates into glucose monomers during digestion, and respiration, which breaks down glucose to release energy.

2.1.2 Enzymes and active sites

An enzyme is a biological **catalyst**. Like all catalysts, enzymes speed up biochemical reactions, such as digestion and respiration, but they remain unchanged at the end of the process.

All enzymes are proteins with long polypeptide chains that are folded into three-dimensional shapes. The arrangement of these shapes is very precise and gives each enzyme the ability to catalyse one specific reaction. If the three-dimensional shape of an enzyme is destroyed or damaged, it can no longer function and is said to have undergone denaturation. Extremes of temperature, heavy metals and, in some cases, pH changes can cause permanent changes in an enzyme.

Some enzyme-controlled reactions, for example respiration and photosynthesis take place inside cells, others such as digestion take place in an extracellular space. Digestion in the gut is an example of extracellular enzyme activity.



a An enzyme has a cleft in its surface called the active site. The substrate molecule has a complementary shape.

b Random movement of enzyme and substrate brings the substrate into the active site. An enzyme–substrate complex is temporarily formed. The R groups of the amino acids in the active site interact with the substrate.

c The interaction of the substrate with the active site breaks the substrate apart. The two product molecules leave the active site, leaving the enzyme molecule unchanged and ready to bind with another substrate molecule.

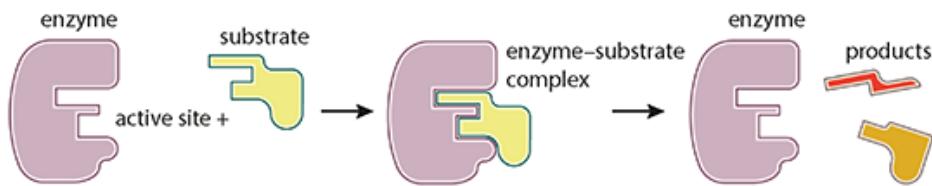


Figure 2.1.1: How an enzyme catalyses the breakdown of a substrate molecule into two product molecules.

KEY POINT

enzyme is a globular protein that functions as a biological catalyst of chemical reactions.

The three-dimensional shape of an enzyme is crucial to the way it works. In the structure of every enzyme is a specially shaped region known as an **active site** (Figure 2.1.1). It is here that the substrates and enzyme bind together. The substrates are the chemicals involved in the reaction catalysed by the enzyme. The shapes of the enzyme and substrate are complementary, so that they fit together perfectly like a key fits into a lock. The ‘lock-and-key hypothesis’ is a way of explaining how each enzyme can

be so specific. To unlock a door requires just one special key. To catalyse a reaction requires one special enzyme. Just as only one key fits perfectly into the lock, only one substrate fits perfectly into the active site of an enzyme.

Enzyme and substrate molecules move freely in solution and in most cases will eventually collide with one another. When a substrate molecule collides with the active site of an enzyme it will bind with it to form an enzyme–substrate complex. Once in place in an active site, substrates may be bonded together to form a new substance or they may be broken apart in processes such as digestion and respiration. For example, one type of enzyme bonds amino acids together to form a polypeptide, while very different enzymes are involved in digesting them.

Induced-fit model of enzyme action

In 1958, research published by Daniel Koshland (1920–2007) proposed a theory to explain how enzymes and substrates bind together. It is known as the **induced-fit model** of enzyme action. We know that substrates require a specific enzyme to catalyse their reactions and the model explains how only the correct substrate is able to bind to an enzyme.

KEY POINTS

active site is a region on the surface of an enzyme molecule where a substrate molecule binds and which catalyses a reaction involving the substrate.

induced-fit model is a model of enzyme action in which the shape of the active site alters when an enzyme binds to its substrate so that a reaction can take place.

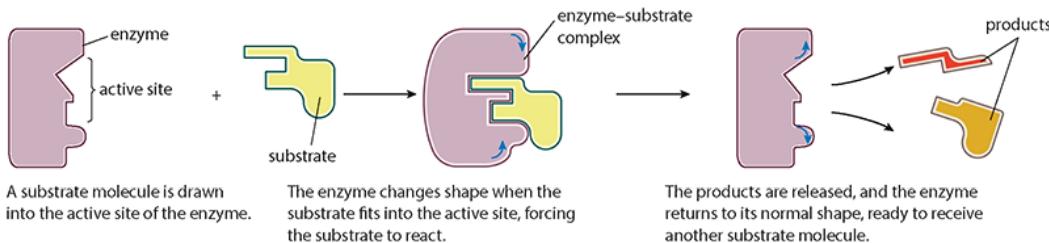


Figure 2.1.2: The induced-fit model of enzyme action.

As a specific substrate approaches an enzyme it induces the correct alignment of substrate and active site so that catalysis can take place. The specificity is a molecular recognition mechanism and it acts so that enzyme and substrate complement each other perfectly. Only the proper substrate is capable of inducing the proper alignment of the active site that will enable the enzyme to perform its catalytic function. The model also suggests that the active site continues to change until the substrate is completely bound to it.

Figure 2.1.2 shows how the substrate causes or induces a slight change in the shape of the active site so it can fit perfectly. As the enzyme changes shape, the substrate molecule is activated so that it can react and the resulting product or products are released. The enzyme is left to return to its normal shape, ready to receive another substrate molecule.

Factors affecting enzyme action

Enzymes work in many different places in living organisms and they require special conditions to work at their greatest, or optimum, efficiency. Temperature, pH and the concentration of the substrates involved all affect the rate at which enzymes operate and produce their products.

Temperature

Enzymes and their substrates usually meet as a result of random collisions between their molecules, which move freely in body fluids or cytoplasm. In the human body, most reactions proceed at their greatest rate at a temperature of about 37 °C and deviations from this optimum temperature affect the reaction rate, as the graph in Figure 2.1.3 shows.

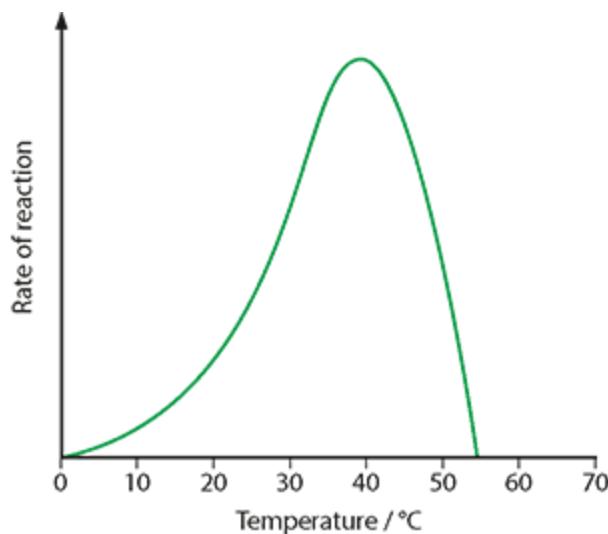


Figure 2.1.3: The effect of temperature on the rate of an enzyme-controlled reaction. An enzyme works most efficiently at its optimum temperature.

At less than 37 °C, molecules in solution move more slowly so the likelihood of collision between them is reduced. This slows down the production of products. At very low temperatures, enzymes hardly work at all and the rate of reaction is very low. As the temperature rises, molecular collisions are more frequent and energetic, and therefore the rate of the enzyme-controlled reaction increases.

As the temperature rises above the optimum, the enzyme and substrate molecules move faster, but atoms in the enzyme molecule itself also move more energetically, straining the bonds

holding it together. Eventually, these bonds may be stressed or broken to such an extent that the enzyme loses its three-dimensional shape and the active site can no longer receive substrate molecules. At these high temperatures, the structure is permanently destroyed: the enzyme is denatured and can no longer catalyse the reaction.

pH

pH is a measure of the relative numbers of H^+ and OH^- ions in a solution. A solution with a low pH value has many free H^+ ions and is acidic, whereas a high pH value indicates more OH^- ions and a basic solution. Pure water is neutral and has a pH value of 7, indicating that the number of OH^- and H^+ ions is equal.

Enzyme action is influenced by pH because the amino acids that make up an enzyme molecule contain many positive and negative regions, some of which are around the active site. An excess of H^+ ions in an acidic solution can lead to bonding between the H^+ ions and negative charges in the active site or other parts of the enzyme. These interactions can inhibit the matching process between the enzyme and its substrate, and slow down or even prevent enzyme activity. A similar effect occurs if a solution becomes too basic: the excess of negative ions upsets the enzyme in the same way. At extremes of pH, the enzyme may even lose its shape and be denatured. The changes are usually, though not always, permanent.

Not all enzymes have the same optimum pH. Proteases (protein-digesting enzymes) in the stomach have an optimum pH of 2 and work well in the acidic conditions there, but proteases in the small intestine have an optimum of pH 8. Most enzymes that work in the cytoplasm of body cells have an optimum pH of

about 7. The graph in Figure 2.1.4 shows how reaction rate varies with pH for this type of enzyme.

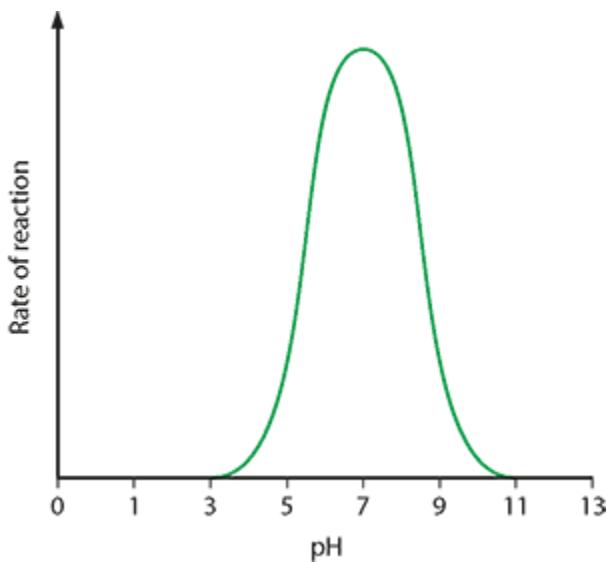


Figure 2.1.4: The effect of pH on the rate of an enzyme-controlled reaction. Changing pH affects the charges on the amino acid molecules in the enzyme. The shape of the enzyme and its active site changes, reducing the rate of reaction

Concentration of substrate

If there is a set concentration of enzyme present in a reaction mixture, and the concentration of substrate increases, the rate of production of the products will increase because of the greater chance of collisions between substrate and enzyme molecules. More collisions mean that the enzyme is able to process or ‘turn over’ more substrate molecules. But there is a limit to this increase in reaction rate. If the concentration of substrate increases too much, it will exceed the maximum rate at which the enzyme can work. When this happens, at any one moment all the active sites are occupied by substrate or product molecules, and so adding further substrate has no effect. The rate reaches its limit; you can see this as the plateau in the graph in Figure 2.1.5.

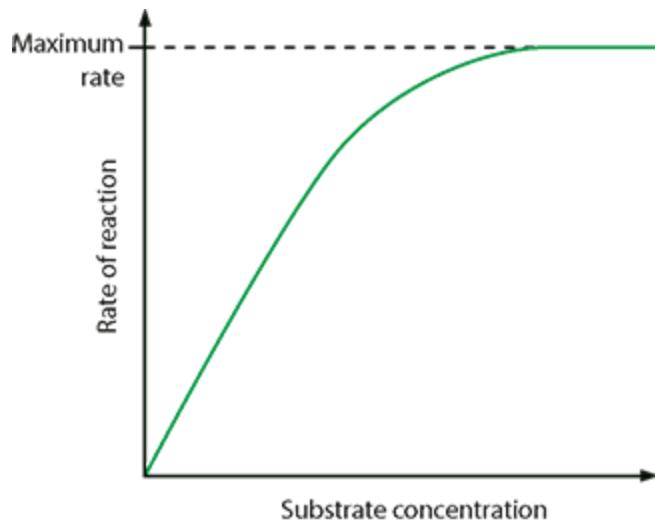


Figure 2.1.5: The effect of substrate concentration on the rate of an enzyme-catalysed reaction.

TEST YOUR UNDERSTANDING

- 1 Define the term metabolism.
- 2 Explain the difference between an anabolic and a catabolic reaction.
- 3 Complete this sentence:
Enzymes are proteins that act as in metabolic reactions.
- 4 Describe why temperature tends to speed up the rate of enzyme activity using the terms ‘molecular motion’ and ‘collision’.
- 5 Why does increasing the substrate concentration in a enzyme-controlled reaction produce a graph that levels off after a certain concentration is reached?

2.1.3 Activation energy

Enzymes work by lowering the **activation energy** of the substrate or substrates. For a metabolic reaction to occur, the substrate has to reach an unstable, high-energy ‘transition state’ where the chemical bonds are destabilised, and this requires an input of energy, which is called the activation energy. When the substrate reaches this transition stage, it can then immediately form the product. Enzymes can make reactions occur more quickly because they reduce the activation energy of reactions they catalyse to bring about a chemical change (Figure 2.1.6).

KEY POINT

enzymes do not change the quantity of product that is formed, only the rate at which the product is formed.

Metabolic reactions that occur in living organisms have to occur at the body temperature of the organism, which is never high enough to bring substrates to their transition state. The active site of an enzyme is very important because it can lower the amount of energy needed to reach a transition state, so the reaction can occur at the temperature of the organism.

Key

1 = activation energy without catalyst

2 = activation energy with catalyst

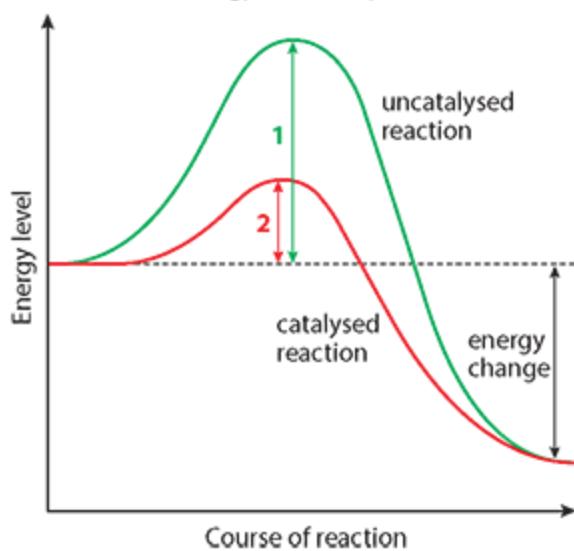


Figure 2.1.6: Graph to show activation energy for an exothermic reaction with and without a catalyst.

2.1.4 Competitive and non-competitive inhibition

Enzyme inhibitors are substances that reduce or prevent an enzyme's activity. Some inhibitors are competitive and others non-competitive.

KEY POINT

enzymes can be affected by the presence of other molecules that temporarily bind to them, either at the active site or at an allosteric site, a region on the surface of an enzyme to which an allosteric, effector molecule binds.

Inhibition by a molecule whose structure is similar to that of the substrate molecule that normally binds to the active site is an example of **competitive inhibition**. Competitive inhibitors compete with the substrate to occupy the active site of the enzyme, and prevent the substrate molecules from binding (Figure 2.1.7, left-hand side). These inhibitors are not affected by the enzyme and do not form products. The rate of reaction of the enzyme is lower because substrate molecules cannot enter the active site of the enzyme molecules that are blocked by an inhibitor. At low concentrations of substrate, competitive inhibitors have a more significant effect than at higher concentrations, when the substrate can outcompete the inhibitor (Figure 2.1.8). A competitive inhibitor occupies the active site temporarily, so the inhibition is reversible.

Permanent binding of an inhibitor to the active site or to another part of an enzyme is known as **non-competitive inhibition**. Inhibitors may bind at part of the enzyme molecule where they

partly block access of the substrate to the active site, or they may cause a change in the shape of the enzyme so that the substrate cannot enter the active site (Figure 2.1.7, right-hand side). Increasing the concentration of substrate in the presence of a non-competitive inhibitor does not overcome inhibition (Figure 2.1.8).

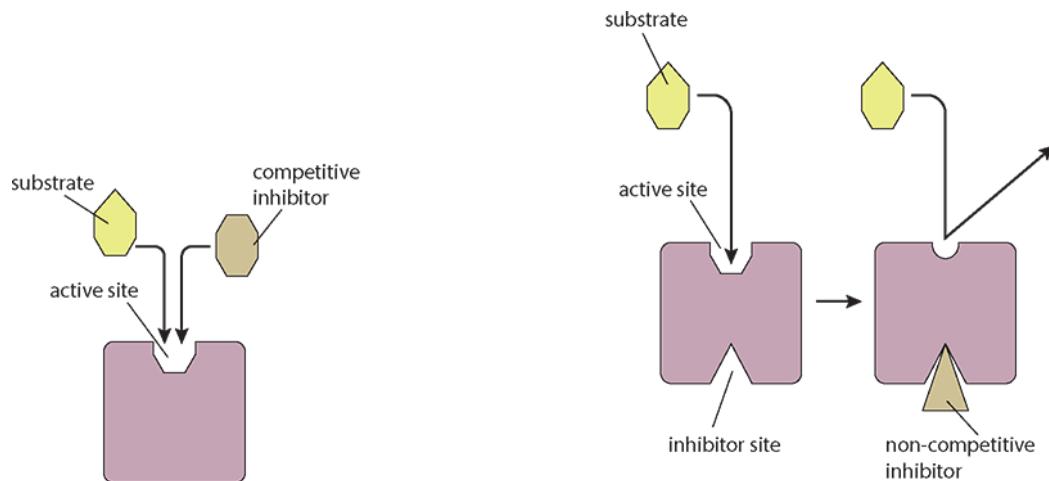


Figure 2.1.7: (Left) Competitive inhibition and (right) non-competitive inhibition.

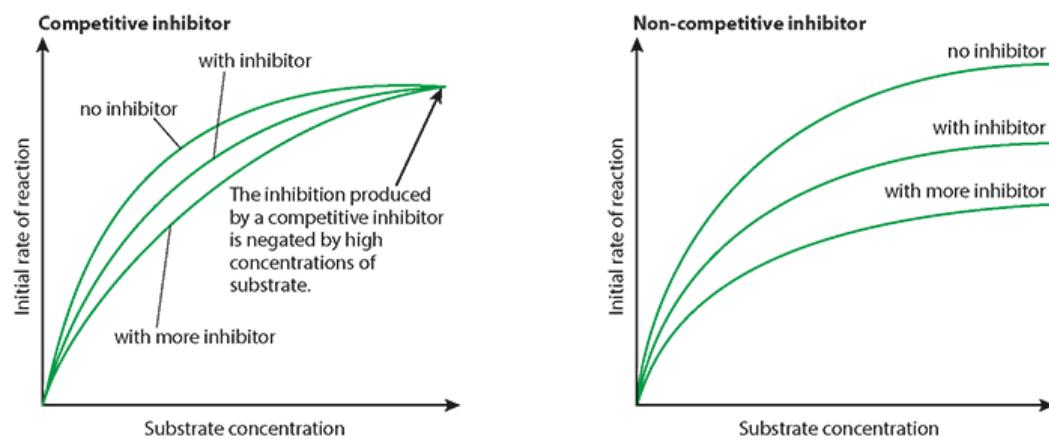


Figure 2.1.8: Graphs to show the effects of competitive and non-competitive inhibitors on reaction rate, as substrate concentration increases.