Introdution

What do Biologists do ?

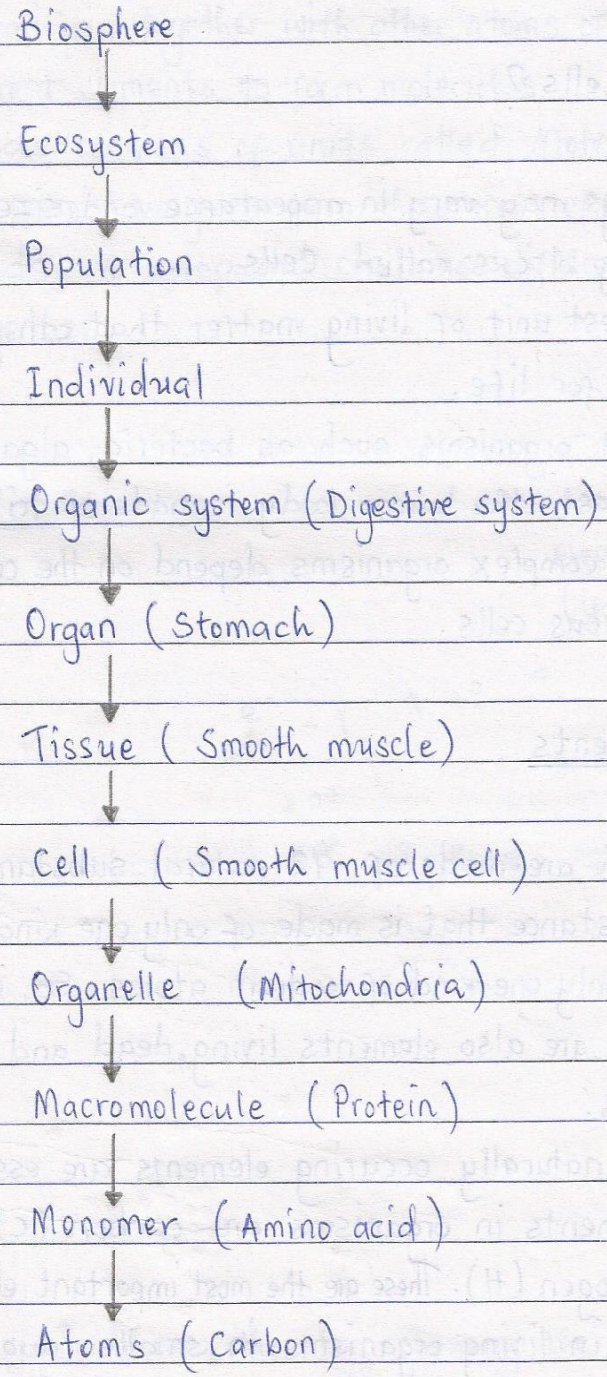


Figure 1 : Levels of biological organisation from atoms, the smallest components of living things, to the biosphere, the entire living planet.

Biologists study every aspect of life at every level of its organisation; from the atom that actually make up the molecules to the biosphere or ecosystem that make up the biosphere.

Why do we study Cells?

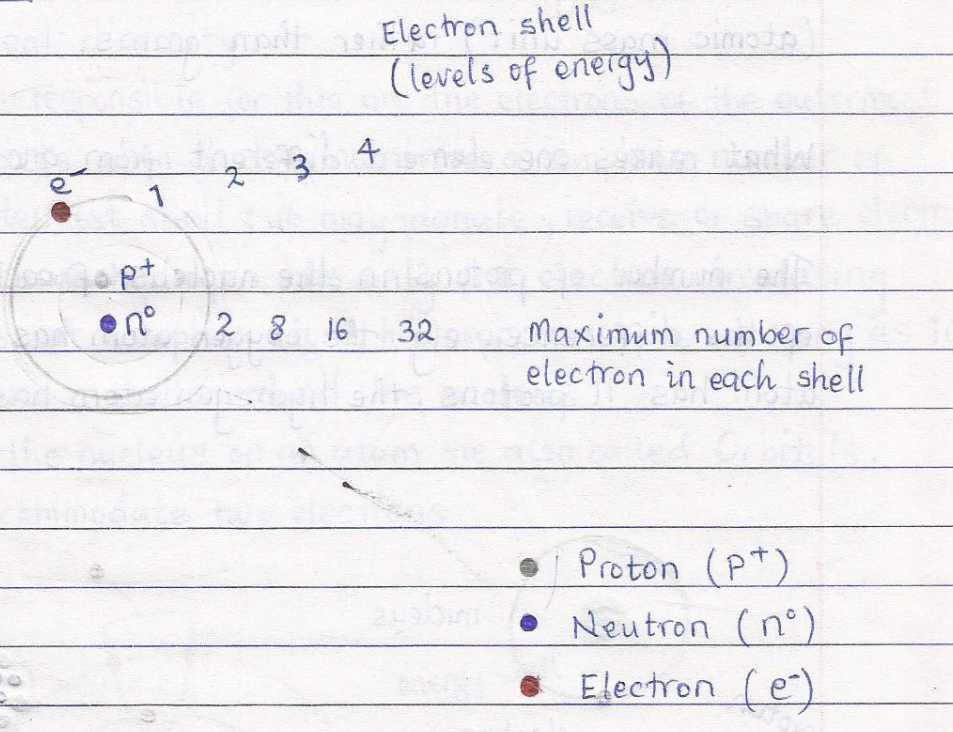
Although living things may vary in appearance and size, all are composed of the basic building blocks called Cells.
The Cell is the simplest unit of living matter that can carry on all the activities necessary for life.
Some of the simplest organisms such as bacteria, algae consist of a single cell. In contrast, the human body is made of trillions of cells. The live processes of such complex organisms depend on the coordinated activities of the various cells.

Atoms and Elements

All parts of the earth are made of 92 natural substances called Elements
An element is a substance that is made of only one kind of Atom, e.g Sodium is made of only one kind of sodium atoms. So, it is an element. Carbon and mercury are also elements living, dead and none-living things are made of elements.
Only 21 of the 92 naturally occuring elements are essential for life. The most common elements in organisms are carbon (C), nitrogen (N), oxygen (O) and hydrogen (H). These are the most important elements to life. Other elements occur in living organisms in smaller quantities; these include phosphorus (P), potassium (K), sodium (Na), sulphur (S), iron (Fe), magnesium (Mg) and chlorine (Cl), even calcium (Ca).

Each element is made up of atoms.
The atom is the smallest sub-division of elements that retain the characteristic chemical properties of that element.
Atoms can join together with other atoms of the same element or with atoms of different elements to form molecules.
Compounds consists of units called Molecules. Atoms can combine in many different ways to form thousands of different substances called compounds. A compound contains different atoms of elements that join together.

Atomic Structure



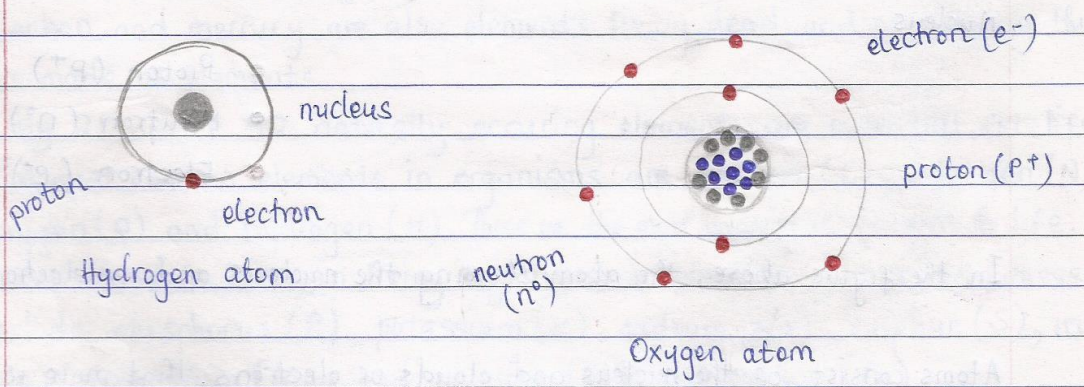
In the figure above, the atom showing the nucleus and 4-electron shells.

Atoms consist of the nucleus and clouds of electrons that move round the nucleus. At the centre of an atom is the nucleus. The nucleus contains two types of particles – protons (+) which have a positive charge and neutrons (n°) which are negatively charged.

Around the nucleus are one or more shells filled with electrons (e^-). Electrons are tiny particles which are negatively charged, in fact with a single (-) charge.
Because atoms contain equal numbers of protons and electrons, these particles cancel each other and therefore the atom remains neutral, neither positively nor negatively charged.
The number of protons in the nucleus gives the atomic number of the atom. However, the weight of the atom is given by the sum of the number of protons and neutrons.
These sub-atomic particles differ also in terms of their mass. Electrons are so small that their mass is negligable, but each proton and neutron has more weight than the electron. Their mass is measured in a.m.u (atomic mass unit) rather than grams.

What makes one element different from another?

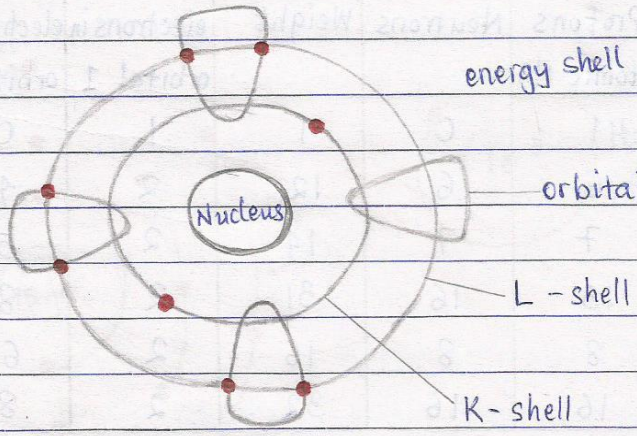
The number of protons in the nucleus of each of an atom is the cause of the difference, e.g the oxygen atom has 8 protons, the sodium atom has 11 protons, the hydrogen atom has 1 proton and so on.



The number of protons in the nucleus of an atom is called the atomic number. Therefore, the atomic numbers of H, O and Na are 1, 8, 11, respectively. It therefore follows that each element has its own unique atomic number.

The atomic weight of an atom of an element is the sum of the number of protons and neutrons in the atomic nucleus.
The electrons are shown to be in shells around the nucleus. These shells represent the different energy levels of the electrons, not their physical position.
The first energy level can hold only two electrons and is filled first. The second energy level can hold only eight electrons and is filled next. The third and subsequent ~~hold~~ levels of energy hold increased numbers of electrons, each containing more than the preceding levels.

The biochemistry of life depends upon the ability of the atoms to react and combine with one another to produce a wide range of molecules required for biological diversity.
The atomic particles responsible for this are the electrons of the outermost shell. An atom reacts when it does not have a complete number of electrons in its outermost shell; it may donate, receive or share electrons.
A simple atom such as hydrogen has only one electron circulating around the nucleus. A complex atom, however, can have as many as 106 electrons in the various shells around the nucleus.
The shells around the nucleus of an atom are also called Orbitals.
One orbital can accommodate two electrons.

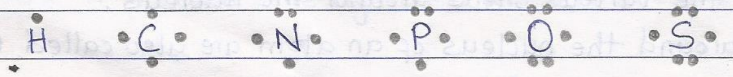


The first shell around the nucleus is called the K-shell while the second shell is called the L-shell.
Each shell may contain one or more orbitals within which electrons may be located.
Every atom of an element has the same number of orbiting electrons which is almost equal to the number of positively charged protons in the nucleus.

For example, Oxygen is an element with the atomic number of 8 and the atomic weight of 16. Its nucleus contains 8 protons and 8 neutrons. There are 8 circulating electrons outside the nucleus. Two of these electrons are contained in the one spherical orbital of the first K-shell. The second L-shell which can accommodate as many as 8 electrons. In the case of Oxyge one of the four (4) orbitals of the second (2^{nd}) shell is not occupied by a pair of electrons.
The third shell called the M-shell may contain from 4 to 9 orbitals. In all, there are as many as 7 shells (K-Q) that may be present around the nucleus of successfully more complex atoms.

- The capacity of an energy level is determined from the formula $2n^2$.

Six different common atoms are important in the structure of most molecules in living systems.

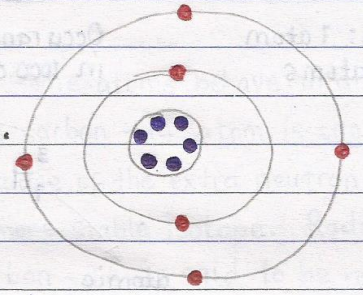


Atom	N^{o} of Protons Atomic N^{o}	N^{o} of Neutrons	Atomic Weight	N^{o} of electrons in orbital 1	N^{o} of electrons in orbital 2	N^{o} of electrons in orbital 3	N^{o} of chemical bonds
Hydrogen	1	0	1	1	0	0	1
Carbon	6	6	12	2	4	0	4
Nitrogen	7	7	14	2	5	0	3
Phosphorus	15	16	31	2	8	5	5
Oxygen	8	8	16	2	6	0	2
Sulphur	16	16	32	2	8	6	2

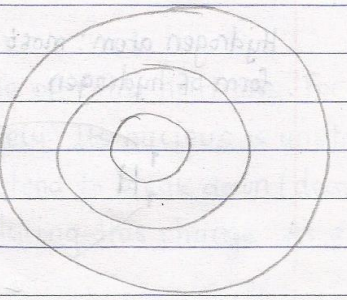
- The 'n' in the formular $2n^2$ is an integer that designates each energy level and is referred to as the Principal Quantum number.

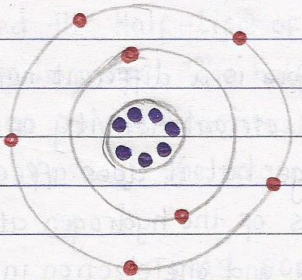
For the first energy level, n = 1; for the second energy level, n = 2; and so forth.

- The energy level closest to the nucleus of an atom is the weakest and lowest in energy. Each successive level out from the nucleus is higher in energy and has a progressive higher capacity to hold electrons.

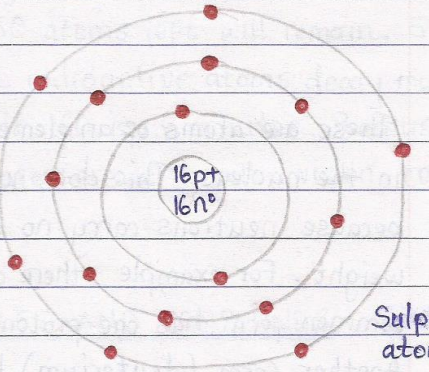


Carbon atom

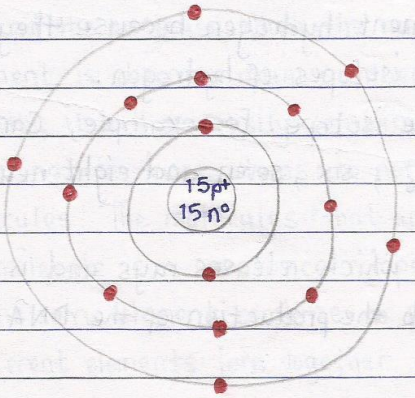




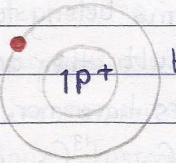
Nitrogen atom



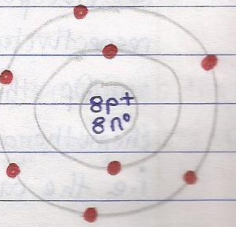
Sulphur atom



Phosphorus atom

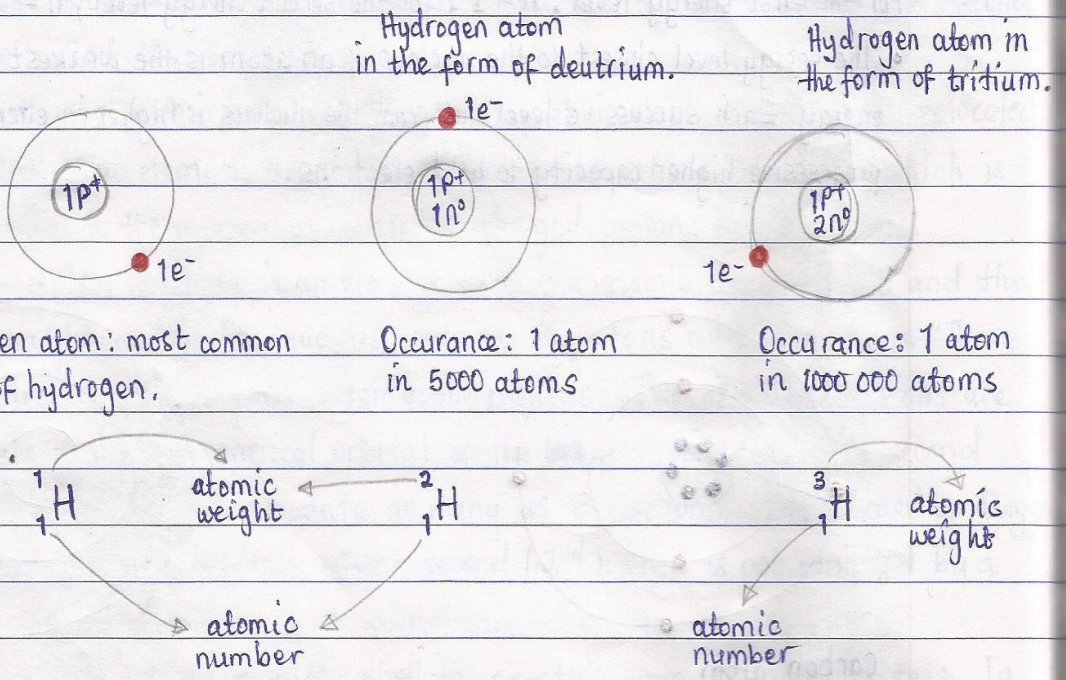


Hydrogen atom



Oxygen atom

ISOTOPES



These are atoms of an element in which there is a different number of neutrons in the nucleus. This does not affect the electrical activity of these atoms because neutrons carry no electrical charge, but it does affect their atomic weight. For example there are three forms of the hydrogen atom. The most common form has one proton in the nucleus and one electron in the outershell. Another form (deuterium) has one proton and one neutron in the nucleus. The third form (tritium) has one proton and two neutrons in the nucleus. All the three forms belong to the element hydrogen because they all have one proton. As a result, they are called isotopes of hydrogen.

Most elements have more than one isotope. For example, Carbon has three (3) isotopes $^{12}C_6$, $^{13}C_6$ and $^{14}C_6$, six, seven and eight neutrons respectively.

Of other isotopes is Cobalt 60 which releases rays and is used in chemotherapy because its rays disturb the production of the DNA of cancer cells i.e the cancer cells die.

Isotopes are atoms of the same element with the same number of protons but different number of neutrons. For example, Carbon has three isotopes: carbon - 12, carbon - 13 and carbon - 14. Chlorine has two isotopes: Chlorine-35 and Chlorine - 37.

RADIOACTIVITY

Some atoms behave in an unusual way because of extra neutrons. For example the carbon - 14 atom is one that behaves strangely. Its nucleus is unstable because of the extra neutrons in the nucleus and tend to break down (decay) to a more stable isotope. Radiation is given out during this change. As a result, carbon - 14 is said to be radioactive.

Carbon - 14 atoms decay very slowly. Suppose you start with 100 atoms of C-14. After 5000 years (in fact 5700 years) there will be half of them left. After another 5700 years, half of the 50 atoms left will remain. 5700 years is called the Half-Life of C-14. Some radioactive atoms decay much faster than carbon - 14. The half-life of cobalt - 60 is 5 minutes. Because radiation from radioactive isotopes can interfere with cell division, cobalt - 60 isotope is used in the treatment of cancer.

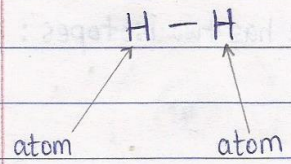
ATOMS FORM MOLECULES AND COMPOUNDS

It is known that the atoms of each element have a specific number of electrons around the nucleus. When the number of electrons in the outermost shell of an element is the maximum number, the element is described as unreactive. As a result, it will not easily combine with other elements.

In nature, most atoms do not exist alone. Instead, they combine to form molecules. The molecules that are formed exist on their own.

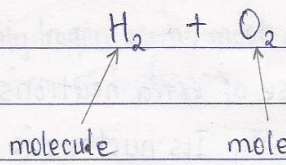
A molecule is a substance comprised of two or more atoms; sometimes two atoms of the same element combine to form a molecule but more typically atoms of different elements join together.

The molecules that contain atoms of different elements are called Compounds.



H_2

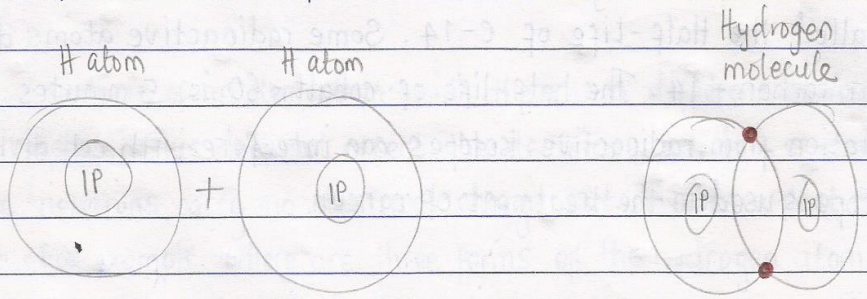
molecule



H_2O

compound

When two atoms of hydrogen combine, the molecule of hydrogen is formed. Atoms of different elements can combine to form chemical compounds as well. For example, when hydrogen and oxygen react, a chemical compound consisting of two atoms of hydrogen and one of oxygen. The molecule of water is the smallest of unit of the compound water.

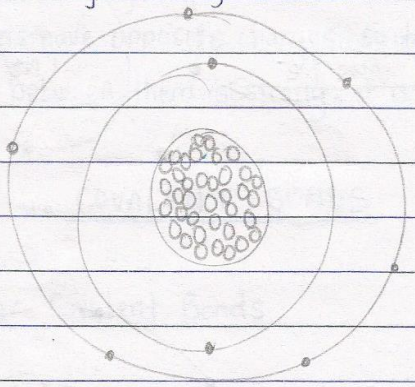


Hydrogenation

The characterists of compounds are always very different from those of the elements that comprise them. For example, what happens when you join the element (Na) Sodium, the silvery metal that explodes when it comes in contact with water, with the element chlorine, a deadly yellow gas which was used to kill troops in World War One (WW1), the result is a crystalline solid called Sodium Chloride (NaCl) which is table salt.

THE ENERGY WITHIN THE ATOM

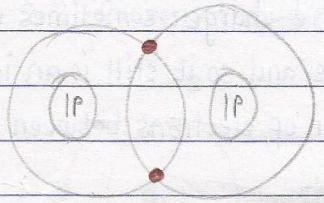
All atoms possess energy because electrons are attracted to the positively charged nucleus. You may ask why electrons are not pulled into the nucleus.



It uses energy to overcome attractive forces and keep electrons moving around the nucleus. Electrons have energy of position, which is called Potential Energy (P.E). Electrons also have energy due to their motion or Kinetic Energy (K.E).

CHEMICAL BONDS

Atoms in the molecules are held together by chemical bonds.

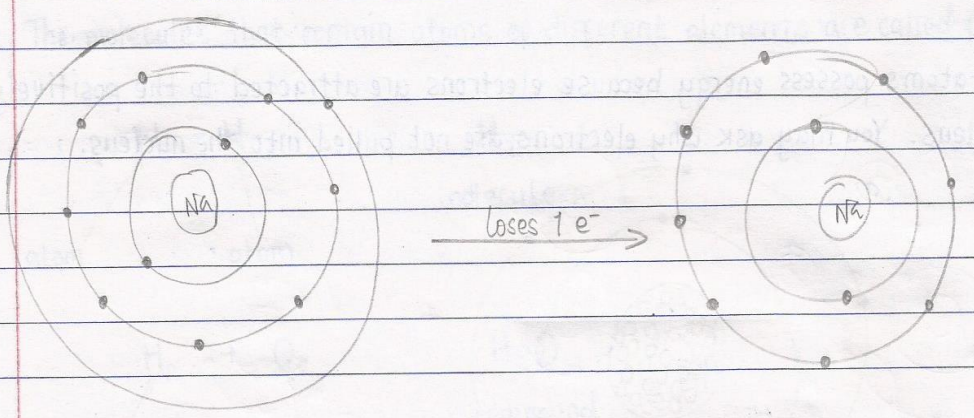


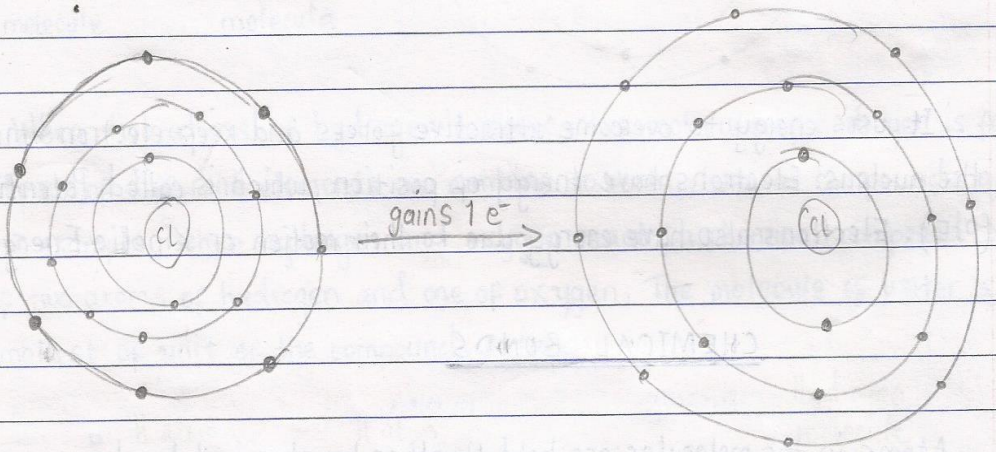
molecule of hydrogen

Atoms come together and overlap using energy to form bonds. However, energy is also needed to break the bonds.

The making and breaking of these chemical bonds involves energy. These chemical bonds come in three types : ionic, covalent and the weaker hydrogen bond. Isolated atoms are usually unstable because their outer electron shell is not full. They, therefore, form chemical bonds with other atoms so that their outer shells are filled and they reach a stable state.

IONIC BONDS





In ionic bonding, electrons are transferred between atoms to form ions.
An ion is an atom that carries an electric charge; sometimes it may be a group of atoms that carries an electric charge and so it still is an ion.
Electric charges result from the transfer of electrons between atoms, either by losing or gaining electrons.

Losing electrons (e^-)
The sodium atom (Na) is a good example: it just has one electron in its outer shell. It can combine obtain a full outershell by losing this electron to another atom. The result is a sodium ion.

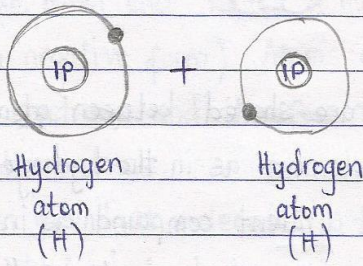
Gaining electrons (e^-)
The chlorine atom (Cl) has seven electrons in its outershell. It can reach the full shell by accepting just one electron from another atom; it then becomes a chloride ion.

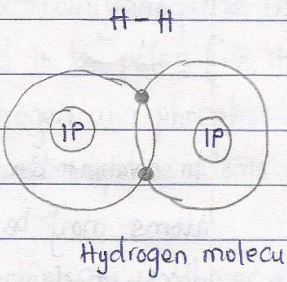
An ionic bond is formed when an atom of sodium transfers its outershell electron to an atom of chloride. Having given up an electron, sodium becomes positively-charged, and having received an electron, chlorine becomes negatively-charged. The two ions have opposite charges, so they attract each other. The force of attraction between them is strong, it is called an Ionic bond.

COVALENT BONDS

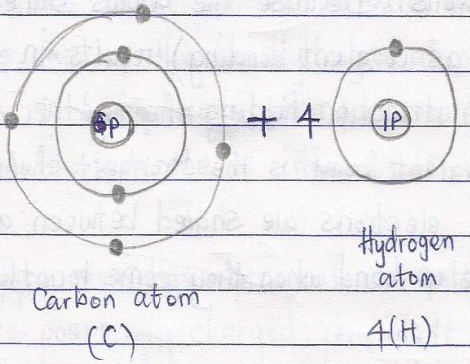
1. Non-Polar Covalent Bonds

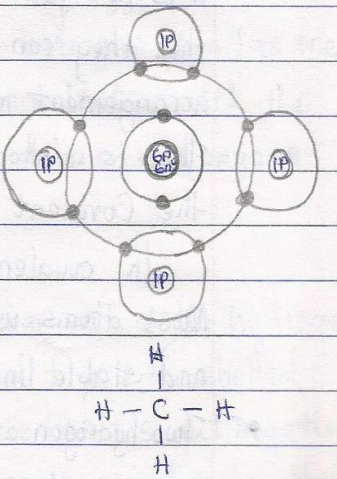
Example: Hydrogen





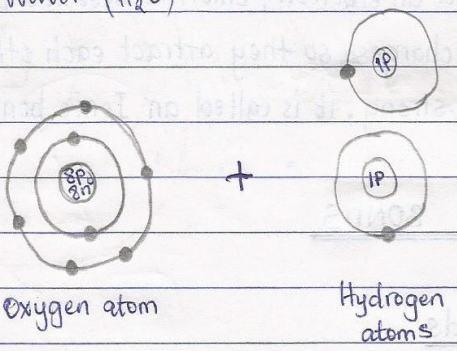
Example 2: Carbon + Hydrogen (non-polar)

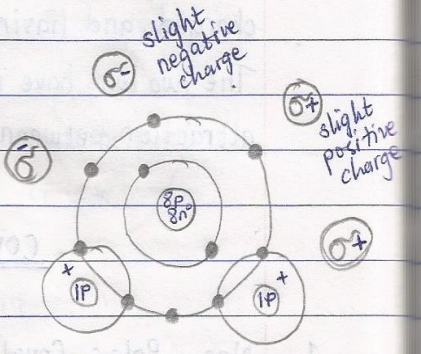




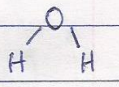
2. Polar Covalent Bonds

Example : Water (H_2O)





Polar molecule



In covalent bonding, electrons are shared between atoms to form a molecule. The atoms may be of the same element as in the hydrogen molecule (H_2) or of different elements forming a covalent compound as in the methane molecule (CH_4).

The hydrogen atom has only one electron; its shell can hold two electrons, so it is not full. When two H atoms get close enough, their shells overlap and then they can share electrons. Because the atoms share electrons, (this arrangement referred to as covalent bonding) results in filled outermost shell. There is a strong force of attraction holding them together. This force is called the Covalent Bond. Covalent bond is the strongest chemical bond.

In covalent bonding electrons are shared between atoms to form molecules. Most atoms use this type of bond when they come together. It forms a strong and stable link between them.

- Two hydrogen atoms alone have one electron in a 1s orbital

There are two types of covalent bonds namely: Non-polar and Polar covalent bonds.

Non-polar covalent bonds

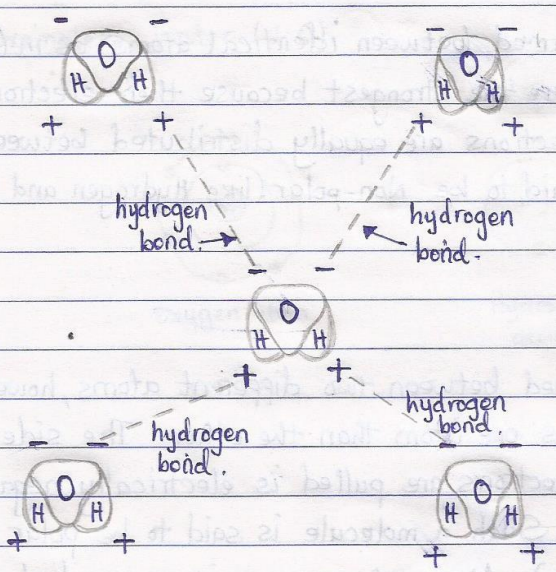
Covalent bonds that are formed between identical atoms as in (O_2) oxygen gas and hydrogen gas (H_2) are the strongest because their electrons are equally shared. Since the electrons are equally distributed between the two atoms, these molecules are said to be Non-polar (like Hydrogen and Methane).

Polar covalent bonds

When covalent bonds are formed between two different atoms, however the electrons may be pulled towards one atom than the other. The side of the molecule towards which the electrons are pulled is electrically negative in comparison to the other end. Such a molecule is said to be polar (i.e it has a positive and a negative form). Atoms of oxygen, nitrogen and phosphorus strongly attract electrons and therefore are called Electronegative atoms when they bond with other atoms.
Water is the most abundant molecule in the body and therefore it serves as the solvent in the body's chemical reactions catalyzed mainly by enzymes. A molecule of water consists of two hydrogen atoms and one oxygen atom. Each oxygen atoms has six electrons in its outer shell and each hydrogen atom has one electron. So each of the two hydrogen atoms shares an electron with the oxygen atom. Each hydrogen atom forms a covalent bond with the oxygen forming a stable molecule of water (H_2O).

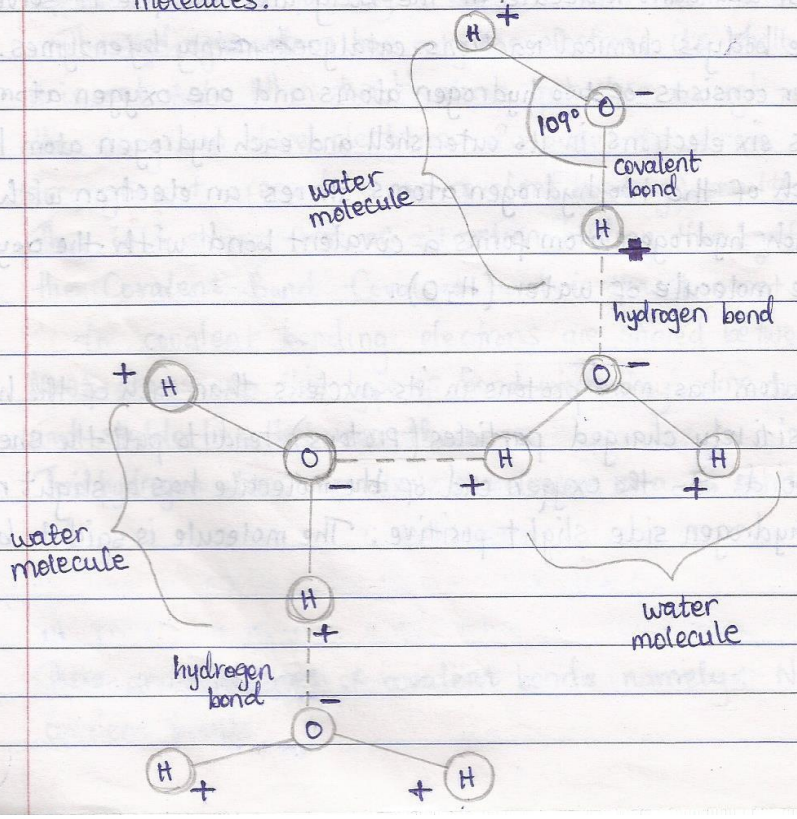
But the oxygen atom has more protons in its nucleus than each of the hydrogen atoms. These positively charged particles (protons) tend to pull the shelled electrons in the bond. So the oxygen end of the molecule has a slight negative charge and the hydrogen side slight positive. The molecule is said to be polar.

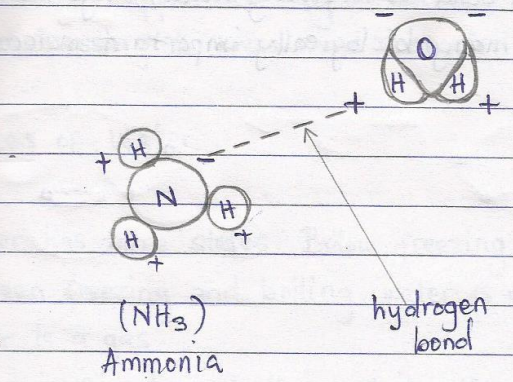
3. Hydrogen Bond (the weakest bond)



The hydrogen bond is the weakest bond of all covalent bonds. However when water molecules are so many (ie millions or trillions of H_2O molecules), the bonds become stronger because of the reinforcements of other bonds.

NOTE: The hydrogen atom bond cannot be formed between more than four water molecules.





Water (H_2O)

(NH_3)
Ammonia

hydrogen bond

* The covalent bond in the water (H_2O) molecule in the diagrams is illustrated with a solid line to show that it is a strong bond.

$O^- - - - H^+$

$N^- - - - H^+$

Hydrogen bonds are weak bonds that result from the attraction of a +vely charged hydrogen atom in a polar molecule to a -vely charged atom.
Frequently oxygen or nitrogen in another polar molecule.
Oxygen and nitrogen attract electrons within a molecule and, therefore, they often have a slightly negative charge. Note that hydrogen bonds form between molecules such as water molecules or within DNA whereas covalent bonds occur between atoms that make up these molecules. Hydrogen bonds are important in biological systems. Living organisms are composed of many molecules that contain Hydrogen atoms bonded with O or N atoms thereby creating the possibility for many hydrogen bonds.
In contrast to ~~by~~ covalent bonds, but like ionic bonds in an aqueous environment, hydrogen bonds are constantly being formed and broken at room temperature because the the energy produced by the movement of water is enough to break the bonds.

When two water molecules are in close contact, they are opposing charges attracting each other. This forms the hydrogen bonds. Therefore, the attraction is between a partially positively charged hydrogen atom in a molecule and some negatively charged oxygen atom in a molecule. This attraction called a hydrogen bond is weaker than that which occurs in either ionic or covalent bonds. And for this reason, it is illustrated by a dash or dotted line rather than a solid line.

Hydrogen bonds are very important in determining the properties of water and of large molecules. Although each bond is relatively weak, large numbers of H bonds act to maintain the shape of many biologically important molecules.

WATER

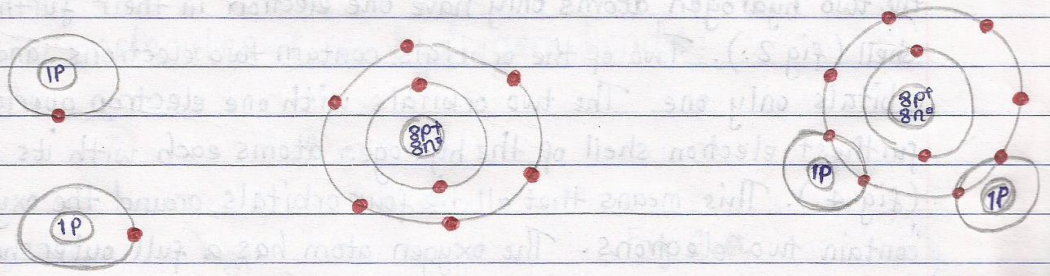
In order to appreciate why water is important to living organisms, it is first necessary to know some characteristics of H_2O molecules.

States of Water

Water has three states. Below freezing, water is solid (ice) or snow flakes. Between freezing and boiling, water is a liquid. And above its boiling point, water is a gas.
Water is found on earth in all its three forms.
There are words scientists use to describe water changing from one state to another. These are as follows:

(i) Solid to liquid is called melting.
(ii) Liquid to gas is called evaporation.
(iii) Liquid to solid is called freezing.
(iv) Gas to liquid is called condensation.
(v) Gas to solid is called frost.
(vi) Solid to gas is called sublimation.

Water Structure and its Shape.



Hydrogen atoms Oxygen atom Water molecule

Fig2: The electron in the first shell is in a single orbital.

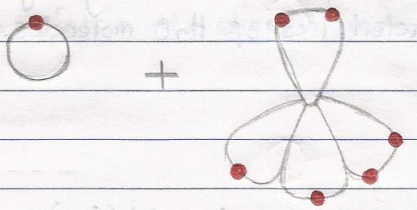
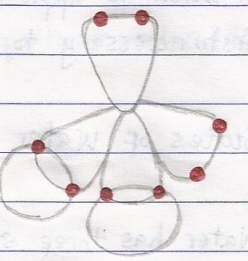


Fig 3: The electrons in the second shell are arranged in four (4) orbitals.

Figure one 4 :



Here, the orbitals overlap forming covalent bonds.

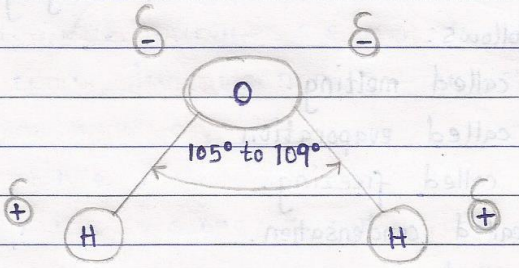


Fig 5 : The water molecule (H_2O)

The oxygen atom in water is arranged as shown in figure 1 while the two hydrogen atoms only have one electron in their furthest electron shell (fig 2.). Two of the orbitals contain two electrons and two of the orbitals only one. The two orbitals with one electron overlap with the furthest electron shell of the hydrogen atoms each with its one electron (fig 4.). This means that all the four orbitals around the oxygen atom now contain two electrons. The oxygen atom has a full outer shell and then each hydrogen has a full outershell. Then the molecule is stable.

The two covalent bonds are where the orbitals from two atoms overlap. If the bonds are represented by lines or solid lines and the orbitals are not drawn, the water molecule looks like it is drawn in fig 5.

The water molecule is bent because of

1. the arrangement of the orbitals around the nucleus of the oxygen atom.

2. and also because the unshared pairs of electrons in the oxygen atom repel the shared pairs of electrons so that the hydrogen nuclei are pushed towards one another as a consequence the molecule is bent.

The angle made between the oxygen and the two hydrogen atoms is in the range between 105° and 109°. As the water molecule is bent and the charge distribution across the molecule is unequal, their is a positive and negative end to the molecule. A molecule with a positive and negative end is a Polar Molecule.
Having determined that the shape and the charge distribution of the water molecule are due to the atoms involved, it is possible to examine how the properties of water are due to the shape and the charge distribution of the individual water molecule. The importance of water to life on earth in large parts depends on its unusual properties.

PROPERTIES OF WATER (H_2O)

1. Water molecules form hydrogen bonds.

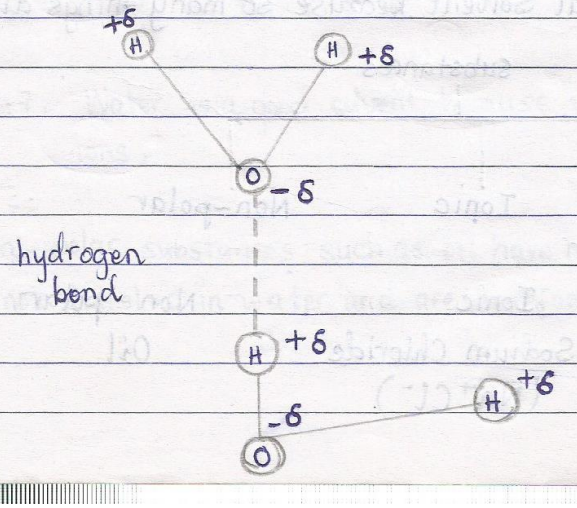


Fig 6.a.

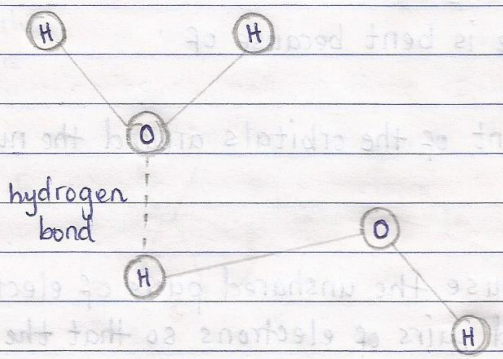


Fig 6.b.

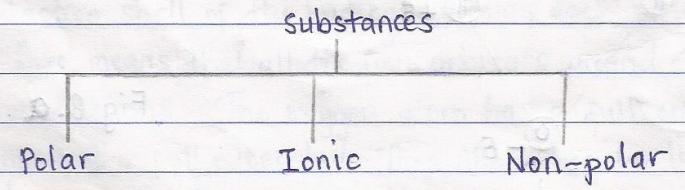
water molecule (H_2O)

The positively charged end of one water molecule is attracted to the negatively charged end of another water molecule. The force of attraction between the water molecules are very strong and this force is called the Hydrogen Bond. The attraction is at its strongest when oxygen, a hydrogen atom and an oxygen atom again are in a straight line as shown in the fig. 6.c but not in figure 6.b.

Hydrogen bonds are about 20 times weaker than most covalent bonds. A hydrogen bond can also form between a nitrogen atom in a molecule and a hydrogen atom in another molecule.

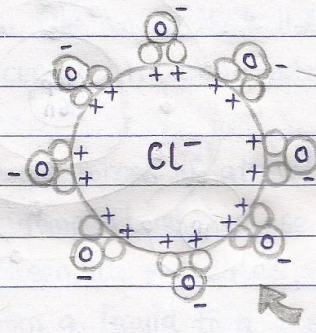
2. Water is the Universal Solvent

The dipolar molecules make water an excellent solvent, in fact water is often called the Universal Solvent because so many things dissolve in it.



Polar	Ionic	Non-polar
Sugar	Sodium Chloride (Na^+Cl^-)	Oil

- Polar and Ionic substances have an electrostatic charge so they are attracted to the charges on water molecules. They dissolve in water, they are therefore called Hydrophilic (water loving). When a salt (an ionic compound) dissolves in water the ions separate and layers of water molecules form around the ions. These layers of water molecules prevent ions or polar molecules from clumping together and therefore keep the particles in solution.



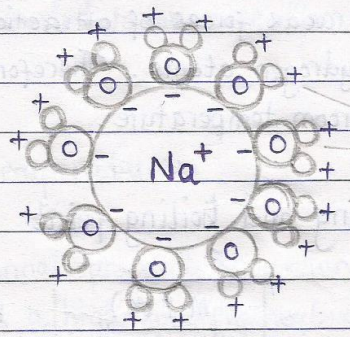
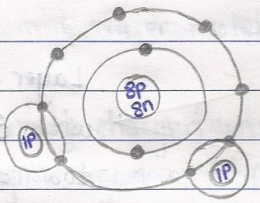


Fig.7. Water is a good solvent because its molecules form a layer around ions.

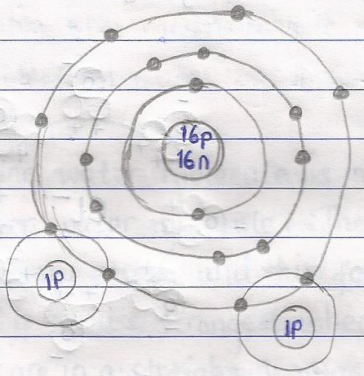
- Non-polar substances such as oil have no charge on their molecules. They do not dissolve in water and are therefore called Hydrophobic (water hating).

3. Water is a liquid at room temperature.

Compounds with molecules as small as those of H_2O e.g HS_2 are usually gases at room temperature. Water is a liquid at r.t.p because of hydrogen bonding. One H_2O molecule can form hydrogen bonds with up to four other H_2O molecules.



H_2O
is liquid at room temperature



H_2S
is a gas at room temperature

The hydrogen sulphide has weak forces of attraction between its protons and the electrons of the hydrogen atoms. Therefore, it forms no hydrogen bonds and hence it is a gas at room temperature.

4. Water has a high melting and boiling point

Substance	Molecular mass	M.P (°c)	B.P (°c)	Liquid over	State at 0°C and at 25°C
Water (H_2O)	18	0°	100°	100°c	Liquid
Hydrogen Sulphide (H_2S)	34	-85°	-61°	24	Gas
Ammonia (NH_3)	17	-78°	-33°	45	Gas
Methane (CH_4)	16	-182°	-164°	18	Gas
Carbon Monoxide (CO)	28	-199°	-19°	18	Gas

Water melts at 0° C and boils at 100°C. These are very unusual melting and boiling points for a substance made up of small molecules.
The table on the previous page shows the melting and boiling points of substances made up of molecules that are of a similar size to water.

As can be seen from the table, the substances except water would be gases at 0°C, so none of them would make a very good solvent for biologically important molecules. The reason that H_2O has a high m.p and b.p is that there are strong forces of attraction between the molecules. These attractions are hydrogen bonds.
Substances with weak forces of attraction between the molecules melt and boil at much lower temperatures because less energy is needed to overcome the weak forces between the molecules, thus allowing the molecules to move more and change from a liquid to a gas or vice-versa. Water also remains a liquid over a very wide range of temperature - a much larger range than any other substance made from such small molecules.
The forces of attraction between the molecules of liquid H_2O are very strong. So, a lot of energy is needed to overcome them and allow the molecules to escape to form a gas.

5. Water and Temperature

An important thermal property of water is its ability to resist temperature changes. H_2O has a high specific heat capacity. It needs to gain a lot of heat energy to raise its temperature. Conversely, it needs to lose a lot of heat energy to lower its temperature. Liquid water does not heat up or cool down quickly. It takes a lot of energy to raise the temperature of 1 kg of water by 1°C and a lot of energy is given out before the temperature of 1 kg of H_2O falls by 1°C of temperature. As a result, we say that liquid H_2O has a high specific capacity for heat.

5.1 Specific heat capacity of Water

If energy is supplied to a substance, the molecules will have more kinetic energy and the temperature of the substance will rise.
In liquid H_2O some of the energy goes into breaking the hydrogen bonds that hold the molecules together, and only part of the energy goes into increasing the temperature of the liquid. This is why it requires a lot of energy to raise the temperature of 1 kg of water by 1°C.

The table below shows the comparative specific heats among compounds.
(The quantity of heat in calories required to raise the temperatures of 1 gram through 1°C.)

Substance	Specific Heat (calories)
Water	1.00
Ethyl alcohol (Ethanol)	0.6
Sugar (Sucrose)	0.3
Iron	0.1
Satt (NaCl)	0.21

One Calory is defined as the amount of heat that will raise the temperature of one gram of water by 1°C.
The specific heat of water is about twice the specific heat of an alcohol, as shown in the table, and it is approximately 0.5 calories will raise the temperature of 1 g of an alcohol by 1°C. It is ten times that of Iron.

The high specific heat of water is a consequence of hydrogen bonding. The H-bonds in water tend to restrict the movement of the molecules in order for the kinetic energy of water molecules to increase sufficiently for the temperature to rise by 1°C it is necessary first to break a number of the H-bonds holding the molecules together.

What does the high specific heat of water mean in biological terms?

It means that the temperature of water will rise more slowly than the temperature of almost any other material. In contrast, the temperature will drop more slowly as heat is removed. As a result, organisms that live in oceans or large bodies of fresh water live in an environment where the temperature of water is relatively constant.
Also, the high water content of plants and animals helps them to maintain a relatively constant internal temperature.

5.2 Vaporization or Water has a high latent heat of vaporisation.

A lot of heat energy is needed to evaporate water. When water evaporates from a surface, it draws heat energy out of the material underneath creating a cooling effect.
Vaporization or evaporation is the change from a liquid to a gas. Water has a high heat of vaporization.

The table below shows the comparative heats of vaporization.
(The quantity of heat in calories required to convert 1 gram of liquid to 1 gram of gas.)

Liquid	Heat required (in calories)
Water at 0°C	596
Water at 100°C	540
Ammonia	295
Ether	9.4

At water's boiling point it takes 540 calories to change one gram of liquid water into vapour, almost 60 times as for ether and twice as much as for ammonia.

Hydrogen bonding is also responsible for water's high heat of vaporization. In order for a water molecule to break from its fellow molecules, the H-bonds have to be broken. This requires heat energy. As a consequence, when water evaporates as from the surface of your skin or leaf of a plant the escaping molecules carry a great deal of heat away with them. Thus, evaporation has a cooling effect.

Evaporation from the surface of a plant or animal is one of the principle ways in which these organisms has evolved a mechanism for lowering the body temperature. For example, sweating in mammals.

6. Density and Freezing Properties of Water

Weight = Volume × Density

10 grams = 10 × 1 (for liquid)
10 grams = 20 × 0.5 (for ice)

Temperature has an effect on the amount of bonding between H_2O molecules. At 0°C, the freezing point of water, the molecules are arranged in a regular hexagonal crystalline network in which each water molecule is hydrogen-bonded to four others.

At the temperatures just above 0°C some of the bonds are broken producing clusters of molecules which fit together more compactly than the spaced H_2O molecules in ice. This is why liquid water is denser than ice.

Water is most dense at 4°C, Changes in the density of water is important for the survival of many aquatic organisms.

The temperature of an ~~body of~~ open body of water such as a pond, lake or river is affected by the temperature of the air above the water.

Very cold air causes the body of water to pool from the surface downward. When the temperature of the upper layers falls to 4°C, the dense water sinks bringing warmer water to the surface. Convection currency of this sort delays the freezing of the body of water. Ultimately a point may be reached where the water near the surface freezes. The ice so formed being less dense than the water beneath floats on the surface where it insulates the water from further heat loss. Consequently, liquid water in which aquatic life can survive. This explains how fish, bacteria and other aquatic organisms live in frozen bodies of water. They actually live in the water which remains liquid below the ice.

7. Cohesion and Adhesion of Water Molecules

The attration between molecules of similar substances is called Cohesion. Hydrogen bonding gives water considerable cohesive properties, thus water molecules stick together because the polarity of water causes it to be attracted to other polar molecules.

The attraction between molecules of different substances is called Adhesion. Thus, water molecules also stick to other surfaces such as the sides of its glass container.

The cohesion of liquid water is responsible for its surface tension. Water molecules have a much stronger attraction to other water molecules than to molecules in the air. An air-interface (waterface)

At an air-water interface, e.g on the surface of a pond, a water molecule on the surface forms hydrogen bonds with other water molecules around and

below it but not with air molecules above it.

The unequal distribution of hydrogen bonds produces a force called surface-tension. All of the hydrogen bonds in water at the surface and downward resulting the molecules of the water to cling or stick together forming a tough fill of elastic skin that is difficult to break. The result is that some aquatic organisms can walk in water and can remain suspended from the underside of the skin.
The cohesion of liquid water, as a result, is responsible for its surface-tension. Water has a greater surface-tension than other liquids.

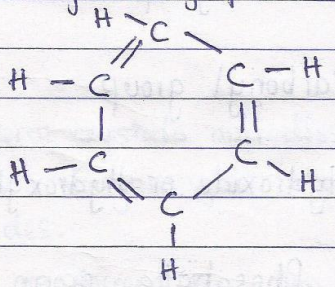
The adhesion of liquid water to other substances such as glass is responsible for capillary action. If a glass tube with a narrow diameter is placed into a beaker of water, the water will rise in the tube above the level of water in the beaker because the adhesion of water to the glass surface drawing it upward is stronger than the force of gravity which is drawing it down. The narrower the tube, the greater the electrostatic forces between the water and the glass, and the higher the water rises.
Capillarity of water is one of the forces which allow high trees to transport water from their roots to their leaves.

* Polarity is an uneven charge distribution within a molecule. In water, one part, or pole, of the molecule is slightly positive and slightly negative on the other.

Organic Molecules

Organic molecules or organic compounds
Compounds that contain the element carbon are classified as Organic, and all others as inorganic. The human body contains both. Cells contain organic molecules.

Carbon has four electrons in its outermost shell and this allows it to bond with as many as four other atoms. Moreover, because these bonds are covalent, they are quite strong. Usually, carbon bonds to nitrogen, oxygen hydrogen or another carbon atom. The ability of carbon to bond with other carbon atoms makes carbon chains of various lengths and shapes possible. Long chains containing ~~long~~ 50 or more carbon atoms are usually found in living systems. Carbon to carbon bonding sometimes results in ring compounds of biological significance.



Ring compound (Benzene).

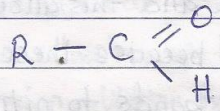
Small molecules have functional groups

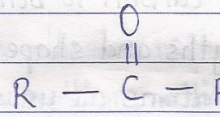
The small organic molecules in living organisms such as sugars, amino acids, fatty acids, and nucleotides all have a carbon backbone but in addition their functional groups such as the hydroxyl, carboxyl, phosphate groups. These functional groups determine the characteristics of small organic molecules. One characteristic of some organic mdecule of some importance is whether it is hydrophilic or hydrophobic.

Monomers

Each of the small organic molecules already mentioned can be a unit of a large organic molecule.
A unit is called a monomer, and the macromolecule is called a polymer.
Simple sugars such as glucose is the monomer of polysaccharides.

The functional groups of some common monomers e.g glucose, la·

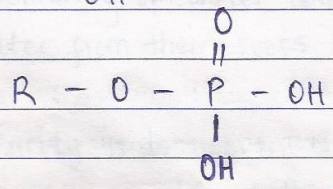
1.  Aldehyde group

2.  Ketone group

3. $R - OH$ Alcohol group

4. $C = O$ Carbonyl group

5. $- OH$ Hydroxide or Hydroxyl group

6.  Phosphate group

- Hydrophilic molecules have OH.

CARBOHYDRATES

Carbohydrates are widely distributed in plants and animals where they fulfil both structural and metabolic roles.
Glucose is synthesized from carbon dioxide and water in plants, and

$$CO_2 + H_2O \xrightarrow[\text{sunlight}]{\text{chlorophyll}} C_6H_{12}O_6 + O_2$$

stored as starch.
Animals can synthesize some carbohydrates from fats and proteins. But the bulk of animal carbohydrates is derived from plants.

Biomedical Importance

The sugar (glucose) is the most important carbohydrate, e.g the brain needs carbohydrates. It is absorbed into the blood because it is also a major fuel of the foetus of mammals.

Sugars

Solid sugar form crystals and dissolve in water to form a sweet-tasting solution. Sugars fall into two groups namely monossacharides and dissacharides.
Dissacharides are formed from two monossacharide molecules by a condensation reaction (where water is eliminated or dehydration).

Glucose + Glucose ⟶ Maltose
Glucose + Fructose ⟶ Sucrose
Glucose + Galactose ⟶ Lactose

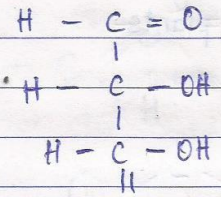
Sugars are one form of carbohydrates. The other form is polyssacharides.
- Carbohydrates are divided into three main classes namely, monosaccharides, disaccharides and polysaccharides.

Classification of Carbohydrates

They are classified as follows:

Monossacharides

These are carbohydrates that cannot be hydrolysed into simpler carbohydr... However, they can be sub-divided into trioses (with 3 carbon atoms),



The functional group

tetroses (4 carbon atoms), pentoses (5 carbon atoms), hexoses (6), heptoses (7) and octases (8), depending on the number of carbon atoms they possess.

Dissacharides

These produce two molecules of monossacharides when hydrolysed. For example, maltose yields glucose and glucose.

Oligossacharides

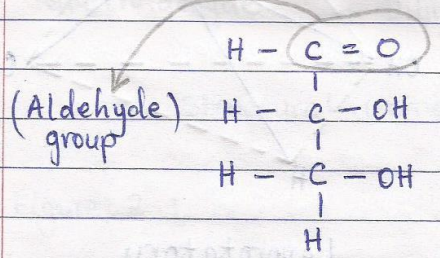
These yield two to ten monossacharide units when hydrolysed. For example, maltotriose.

Polyssacharides

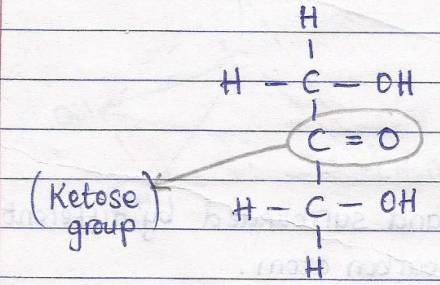
These yield more than ten molecules of monossacharides when hydrolysed. For example, starch.

Monossacharides contain only carbon, hydrogen and oxygen in the ratio of one carbon, two hydrogen and one oxygen (1C : 2H : 1O). Their empirical formular is $(CH_2O)_n$, where n = the number of carbon atoms.
Monossacharides also have certain reactive groups present. To be a monossacharide, the molecule must contain a carbonyl group (C=O), and atleast two hydroxyl groups (OH).
All monossacharides have names that end in -ose.
All monosaccharides are reducing sugars
Monossacharides can exist as chains or rings.

The simplest form of monossacharides is a triose.



Glyceraldehyde or
2,3 dihydroxy propanol.

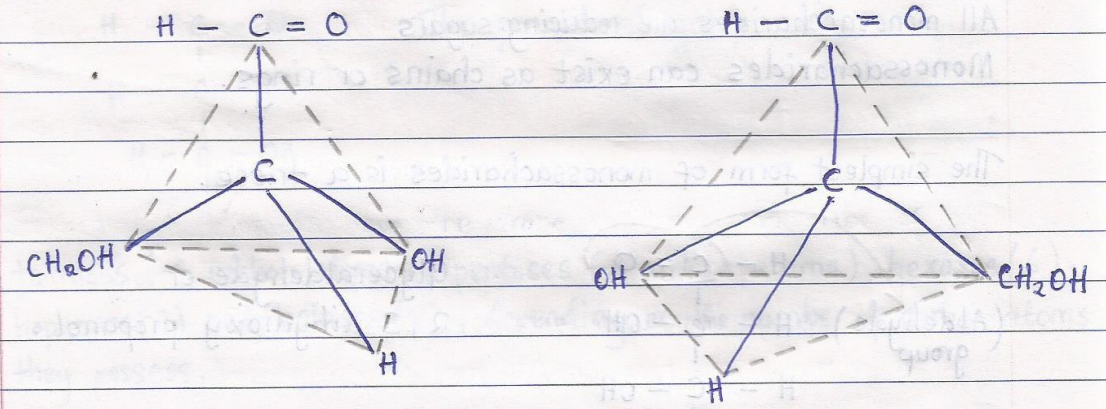


Dihydroxy acetone or
1,3 dihydroxy propanone.

A Triose contains three carbons. Trioses have a backbone of three carbons, a carbonyl group and two hydroxyl groups.
The structures above show two important trioses: glyceraldehyde and dihydroxyacetone. They are structural isomers of each other.
As can be seen from the structures, glyceraldehyde has a carboxyl group at the end of the molecule. This makes it an Aldose.
A sugar with an aldehyde group is called an Aldose.

A sugar with a ketone group is called a Ketose.

Trioses exist only as chains ; they are too short to form rings.
Dihydroxyacetone has a carboxyl group away from the end of the molecule
This makes it a ketose.



Dextrorotatory
or D - Glyceraldehyde

Levorotatory
or L - Glyceraldehyde

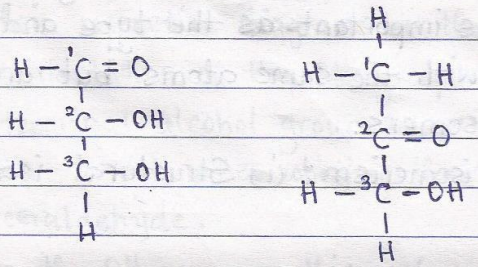
Stereoisomers

* When a carbon atom is connected to and surrounded by different formula units, it is called an Asymmetric carbon atom.
* As a matter of fact, a carbon atom that is connected or bonded with less than four different groups (formula units) is called a Non-Asymmetric carbon atom.
- In monosaccharides, all the carbon atoms except one have a hydroxyl group attached. The remaining carbon atom is either part of an aldehyde group in which case the monosaccharide is called an aldo sugar, or is part of a keto group, when it is called a keto sugar.

Types of Isomerism

1. Structural Isomerism

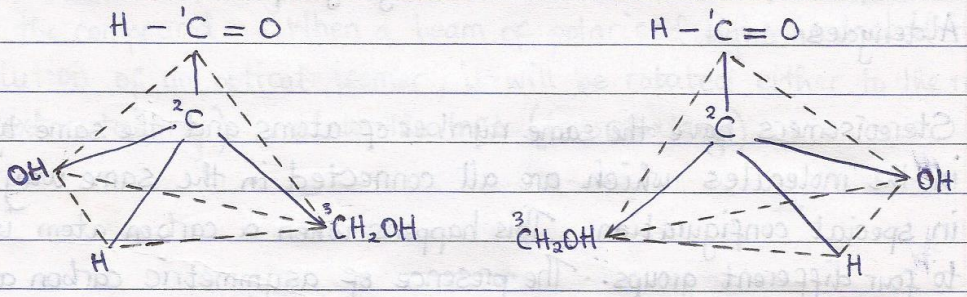
2. Stereoisomerism



Glyceraldehyde Dihydroxyacetane

Structural isomers

Figure 2.1



Levorotatory - Glyceraldehyde or L - Glyceraldehyde

Dextrorotatory - Glyceraldehyde or D - Glyceraldehyde

Stereoisomers

* Number of isomers in any compound = 2^{n-2}, where n = is the number of carbon atoms in the same compound (aldehyde compounds).

* In Ketones, the number of isomers is given by 2^{n-3}.

Sugars exhibit various forms of Isomerism.

As the shape of an organic molecule is crucial, the way the atoms are arranged in the molecules is as important as the type and the number of atoms present. Molecules with the same atoms but arranged in different ways are called Isomers.
There are two main types of isomerism: (i) Structural isomerism, and (ii) Stereo isomerism.

Structural isomers have the same number and type of atoms but the atoms are connected differently. One example of this is two molecules with the formula $C_3H_6O_3$ in which the carbonyl group is at a different place in the two molecules and they react differently with molecules with carbonyl groups that are away from the end of the molecules, called Ketones. Molecules with the carbonyl group at the end are called Aldehydes.

Stereoisomers have the same number of atoms and the same type of atoms in the molecules which are all connected in the same way but differ in special configuration. This happens when a carbon atom is connected to four different groups. The presence of asymmetric carbon atoms between allows the formation of stereoisomers.
The number of possible stereoisomers of a compound depends upon the number of the carbon atoms in the molecules.
For aldehyde compounds, the number of isomers is given by 2^{n-2}.
For Ketones, the number of isomers is given by 2^{n-3}. The 'n' is the number of carbon atoms in the molecules.

1. D and L Isomerism.

The designation of a sugar isomer as a D or its mirror image as the L form is determined by its special relationship to the parent compound of the carbohydrate family. The L and D forms of this sugar are shown in their respective diagrams on the previous page Figure 2.1.

The orientation of the OH group around the carbon atom adjacent to the terminal alcohol group, or primary alcohol atom, for example: carbon - 2 determines whether the sugar belongs to the D or L isomer in glyceraldehyde.

When the OH group on this carbon is on the right, the sugar is a member of the D - isomer; when it is on the left, it is a member of the L - isomer,

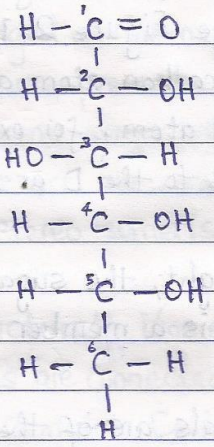
Most of the monossacharides occuring in mammals are of the D - isomer and enzymes responsible for their metabolism are specific for this configuration.

The presence of asymmetric carbon atoms also confers optical activity on the compound. When a beam of polarised light is passed through a solution of an optical isomer, it will be rotated either to the right (dextorotatory) or to the left (levorotatory).

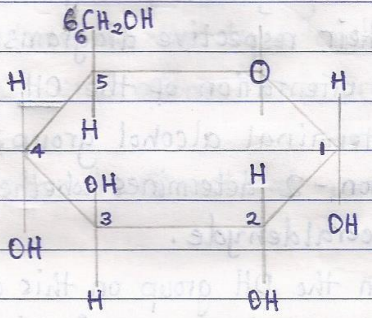
Hexoses

The structure of Glucose can be represented in 3 ways: ($C_6H_{12}O_6$)

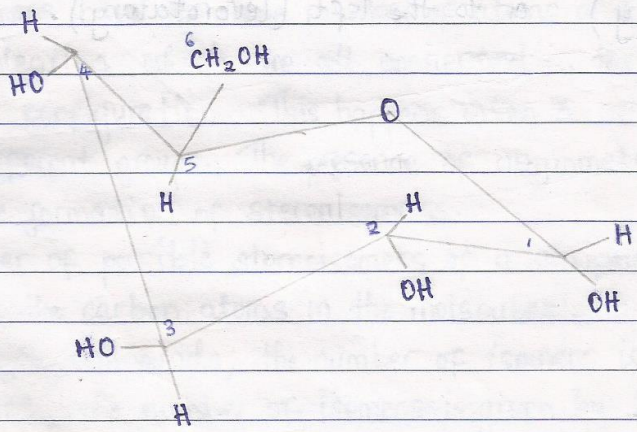
1. Straight chain



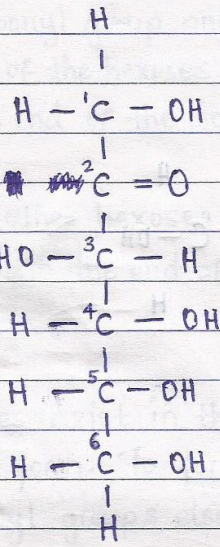
2. Ring form



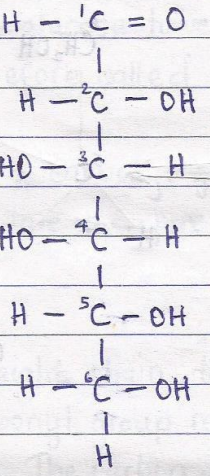
3. Chain form



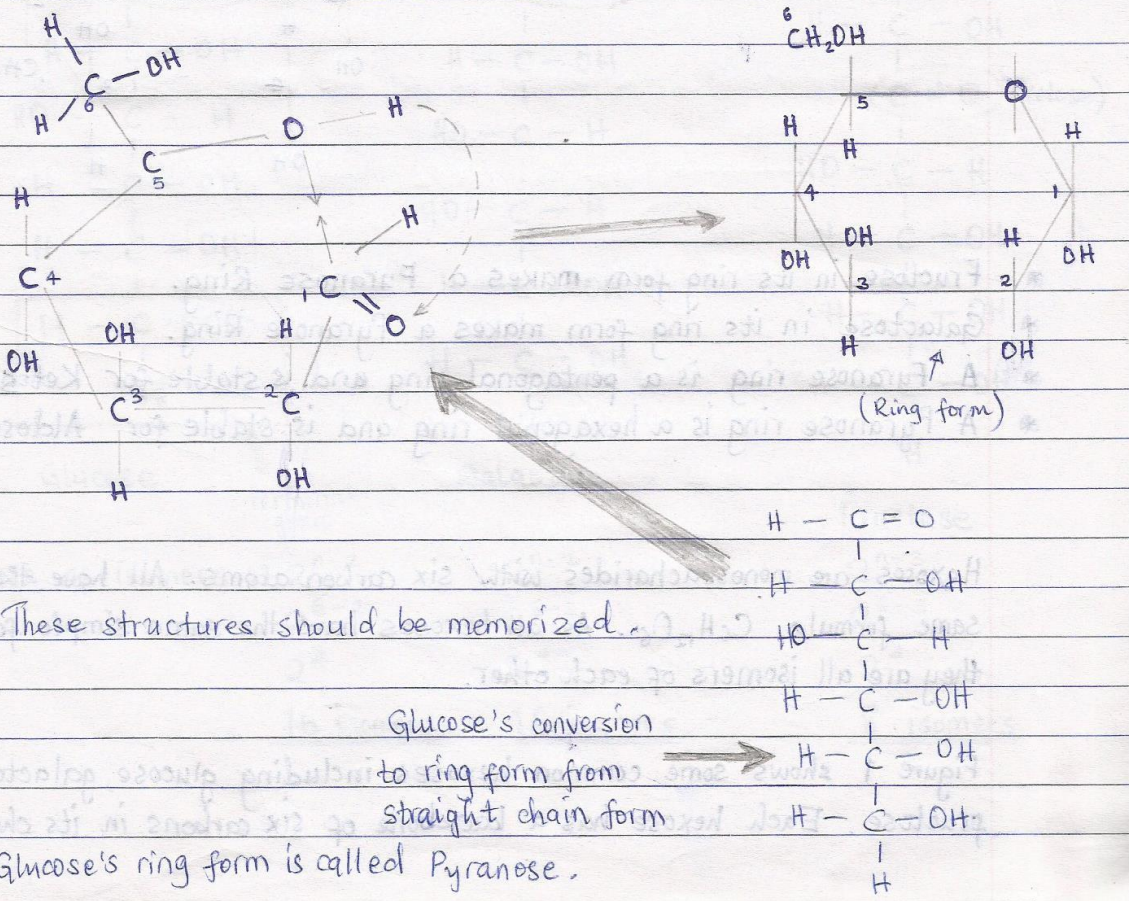
More straight chains



Fructose
(Ketose)



Galactose
(Aldose)

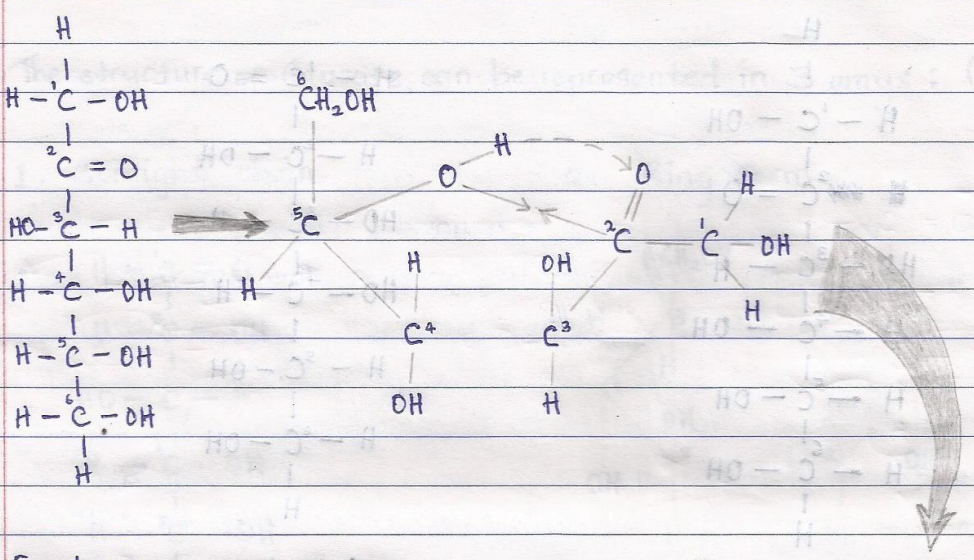


* These structures should be memorized.

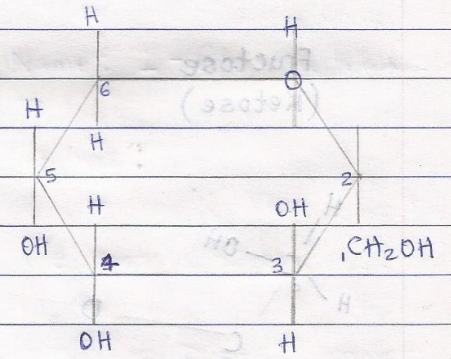
Glucose's conversion to ring form from straight chain form

* Glucose's ring form is called Pyranose.

* In water, chains bend to produce a ring form.



Fructose (straight) chain



* Fructose in its ring form makes a Furanose Ring.
* Galactose in its ring form makes a Pyranose Ring.
* A Furanose ring is a pentagonal ring and is stable for Ketoses.
* A Pyranose ring is a hexagonal ring and is stable for Aldoses.

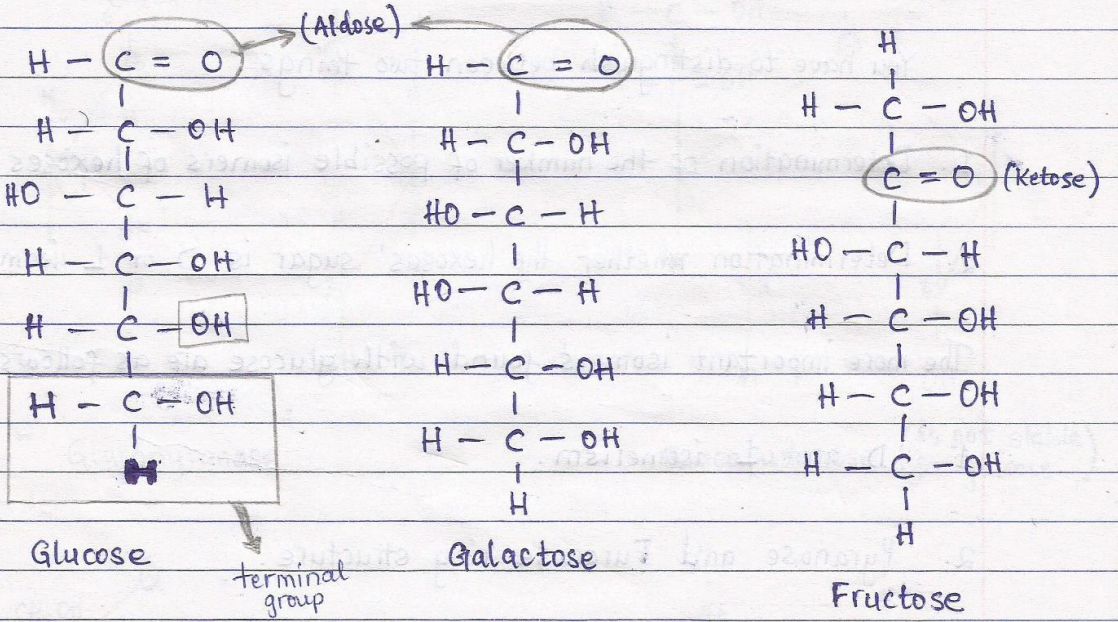
Hexoses are monossacharides with six carbon atoms. All have the simple same formula $C_6H_{12}O_6$. As all hexoses have the same simple formular, they are all isomers of each other.

Figure 1 shows some common hexoses including glucose, galactose and fructose. Each hexose has a backbone of six carbons in its chain,

a carbonyl group and atleast two hydroxyl groups (OH).
Some of the hexoses e.g galactose and glucose have a carbonyl group at the end of the molecule, and are therefore called Aldoses.

While other hexoses e.g fructose have a carbonyl group on carbon-2 away from the end of the molecule, and are therefore called Ketoses.

Hexoses exist in three forms, the straight chain, the ring form and a chain form. To form the link, a carbonyl group reacts with one of the hydroxyl groups elsewhere in the chain. The carbon are still numbered as they were in the straight chain form. The carbon one (1) is always drawn on the right handside.

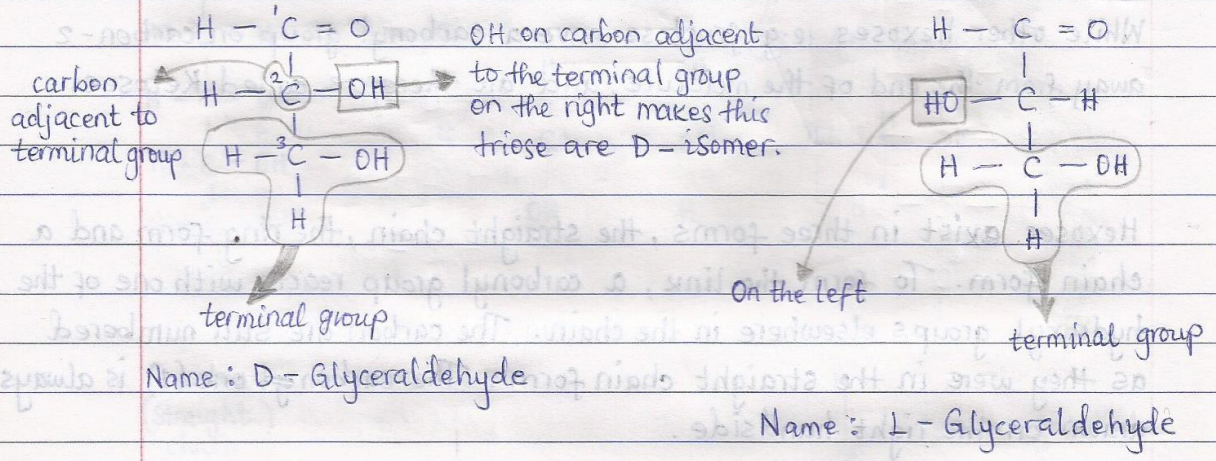


Glucose | Galactose | Fructose

	Glucose	Galactose	Fructose
No of isomers :	2^{n-2}	2^{n-2}	2^{n-3}
	2^{6-2}	2^{6-2}	2^{6-3}
	2^4	2^4	2^3
	16 isomers	16 isomers	8 isomers

Isomers of Hexoses

D and L isomers; these differ from the total number of isomers.



Name: D-Glyceraldehyde

Name: L-Glyceraldehyde

You have to distinguish between two things:

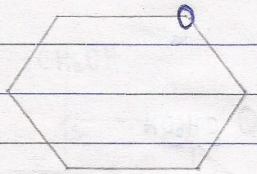
1. Determination of the number of possible isomers of hexoses.

2. Determination whether the hexoses' sugar is D or L isomer.

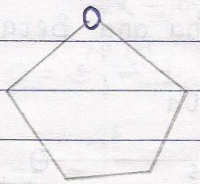
The more important isomers found with glucose are as follows:

1. D and L isomerism.

2. Pyranose and Furanose ring structure.



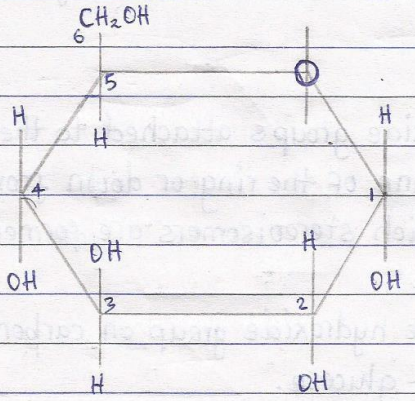
Pyranose (hexagon)



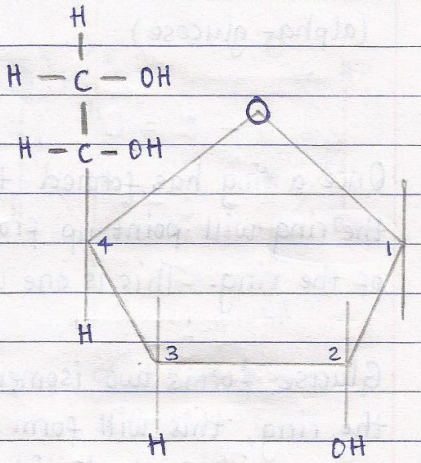
Furanose (pentagon)

Two types of rings can be formed. A ring of six atoms is called a Pyranose ring whereas a ring of five atoms is called a Furanose ring.

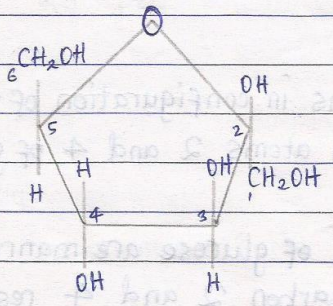
The pyranose ring is the more stable ring formed for aldoses (glucose and galactose) while the furanose ring is more stable for ketoses (fructose).



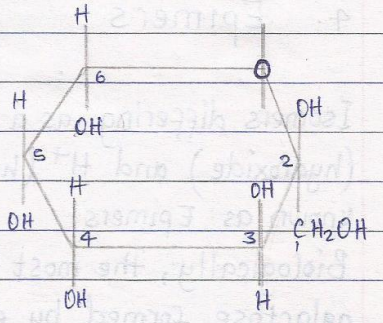
Glucopyranose



Glucofuranose (is not stable for glucose)

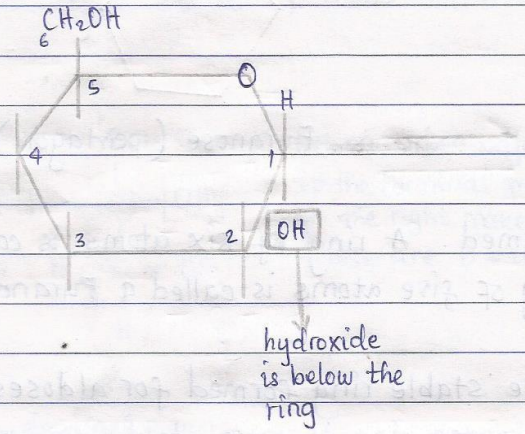


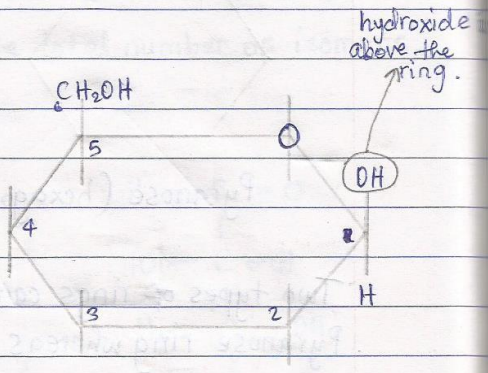
Fructofuranose



Fructo pyranose
(it is not stable)

3. Alpha and Beta (α and β)





α - Glucose
(alpha-glucose)

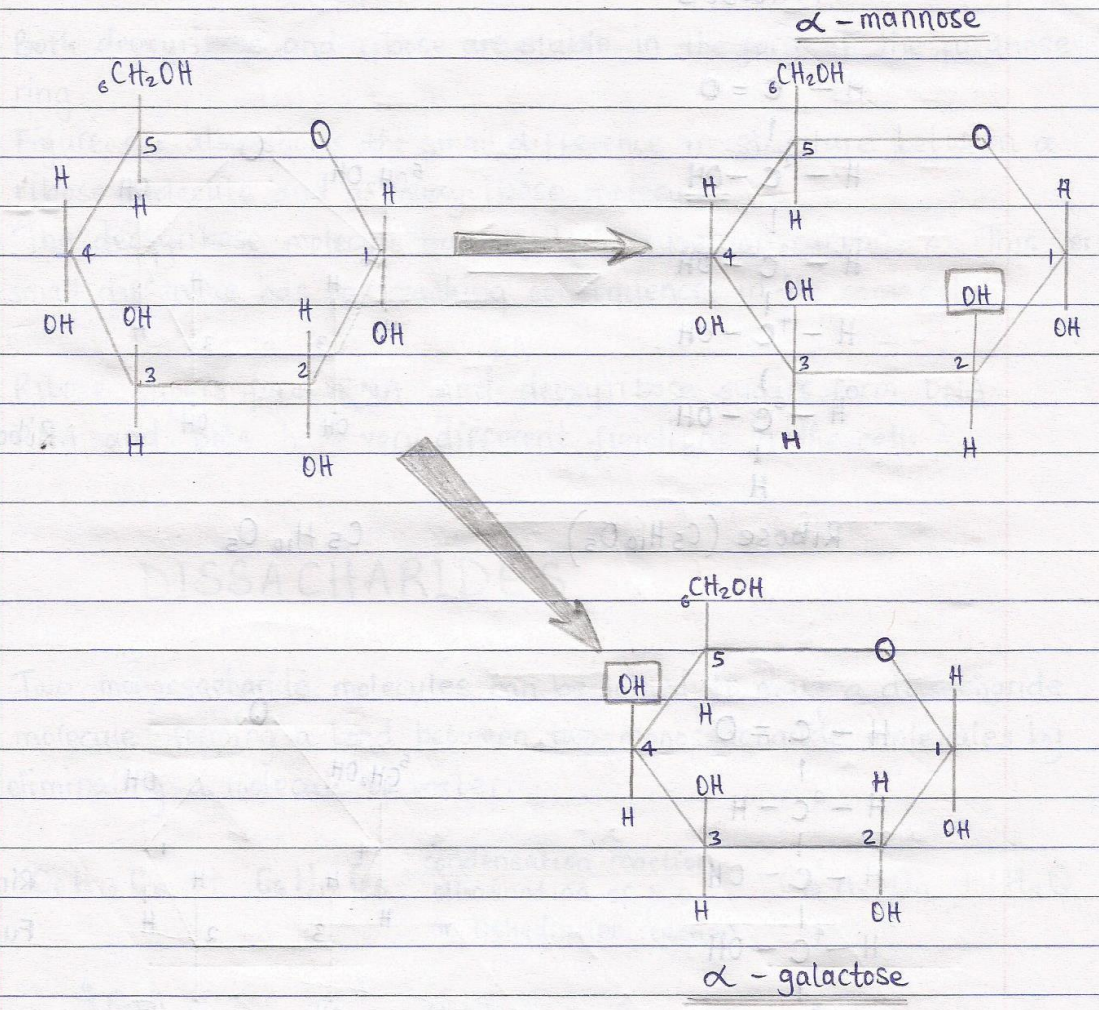
β - Glucose
(beta-glucose)

Once a ring has formed the hydroxide groups attached to the carbon in the ring will point up from the plane of the ring or down from the plane of the ring. This is one way in which stereoisomers are formed.

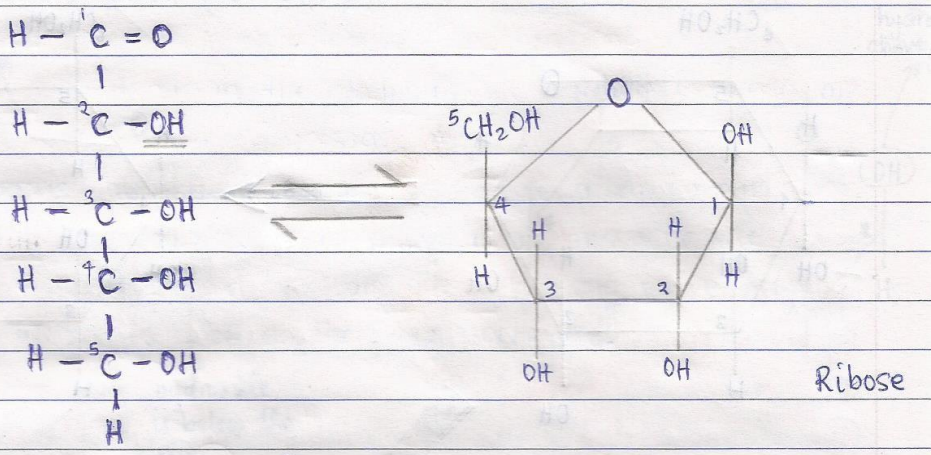
Glucose forms two isomers. If the hydroxide group on carbon-1 is below the ring, this will form an alpha-glucose.
However, if the hydroxide group on carbon - 1 is above the ring this will form a beta-glucose.

4. Epimers

Isomers differing as a resutt of variations in configuration of the OH^- (hydroxide) and H^+ (hydrogen) on carbon atoms 2 and 4 of glucose are known as Epimers.
Biologically, the most important epimers of glucose are mannose and galactose formed by epimerisation at carbon 2 and 4 respectively


α - mannose
α - galactose

Pentoses



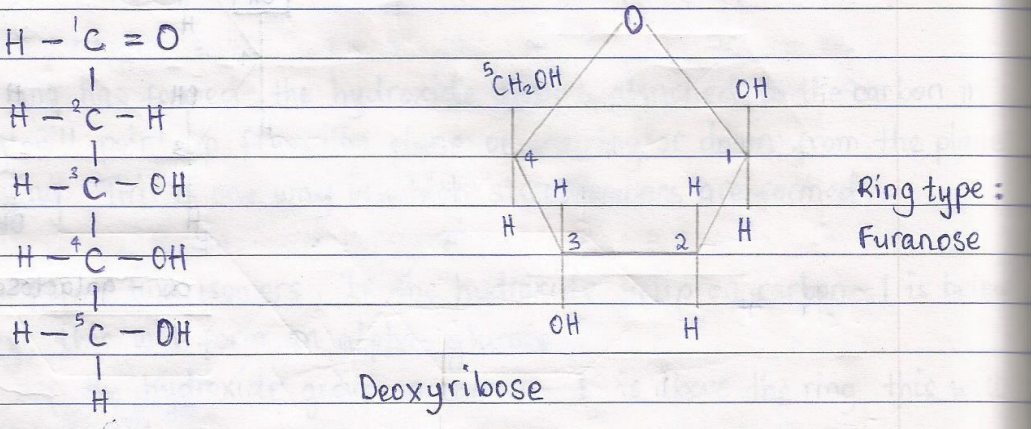


Fig 1: The structure of two common pentoses shown above.

Pentoses are monossacharides with five carbon atoms. They have the simple formular $C_5H_{10}O_5$, carbonyl group and atleast two hydroxide group. Pentoses exists in both chain and ring form.

Figure one (1) shows the structural formular of two important pentose ribose and deoxy-ribose in both the straight chain and ring form.

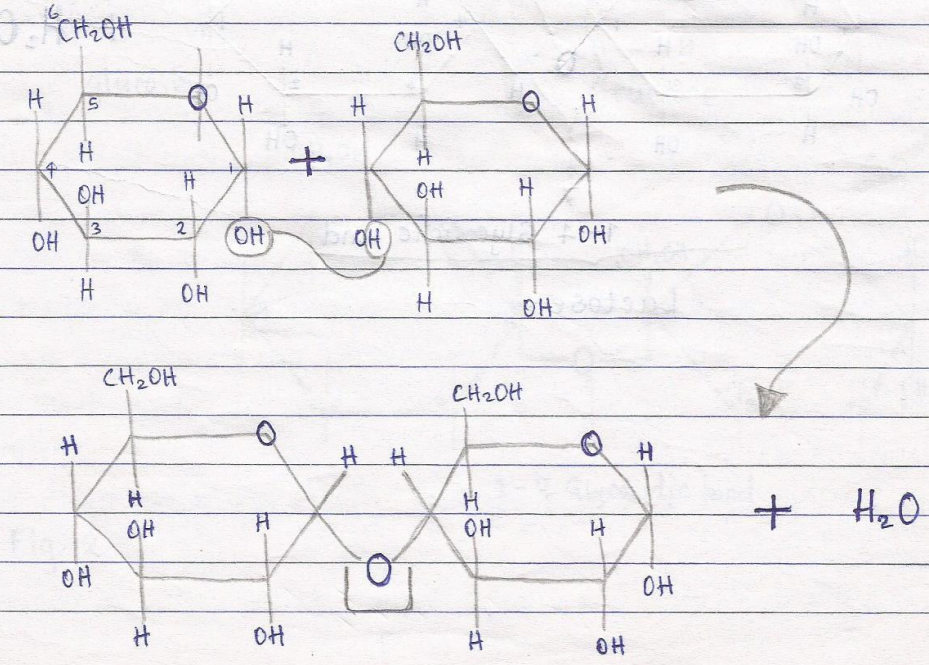
Both deoxyribose and ribose are stable in the form of the furanose ring.
Figure one also shows the small difference in structure between a ribose molecule and a deoxyribose molecule.
The deoxyribose molecule has one less oxygen on carbon - 2. This very small difference has far reaching consequences in the ~~same~~ cell.

Ribose sugars form RNA and deoxyribose sugars form DNA.
RNA and DNA have very different functions in the cell.

DISSACHARIDES

Two monossacharide molecules can be joined to make a dissacharide molecule: forming a bond between two monossacharide molecules by eliminating a molecule of water.

$$C_6H_{12}O_6 + C_6H_{12}O_6 \xrightarrow[\text{elimination of } H_2O \text{ or Dehydration reaction}]{\text{condensation reaction}} C_{12}H_{22}O_{11} + H_2O$$

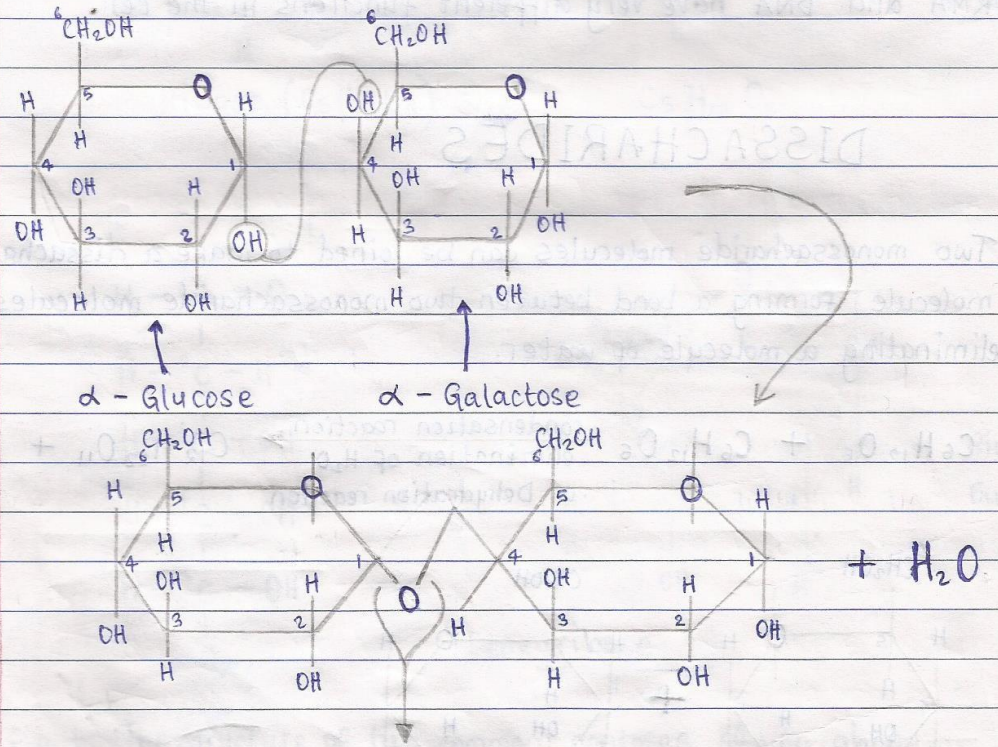


This type of reaction where a bond is formed by the elimination of a water (H_2O) molecule is called a Condensation.

The bond formed during the condensation reaction between monossacharide molecules is called a Glycosidic Bond.

This bond is formed between the carbonyl group on one monossaccharide molecule and a hydroxide group on another monossacharide.

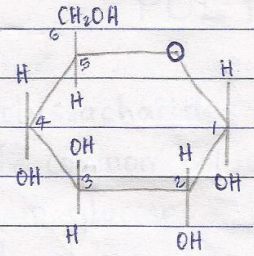
A 1-4 Glycosidic bond is from one-carbon-one of one monossacharide ~~and~~ to carbon four of another monossacharide.



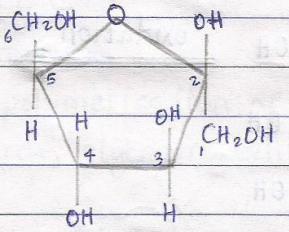
Lactose

Sucruose

While a 1 - 2 is from the carbon atom 1 of a monossacharide to carbon-2 of the second monosaccharide.

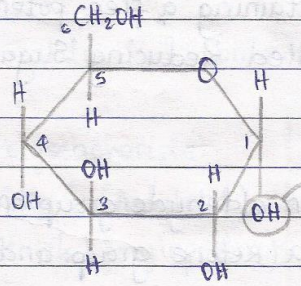


α - glucose

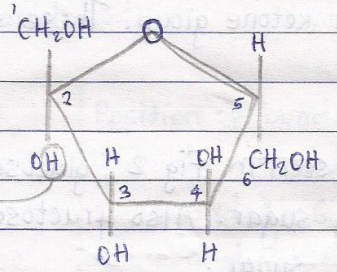


β - fructose

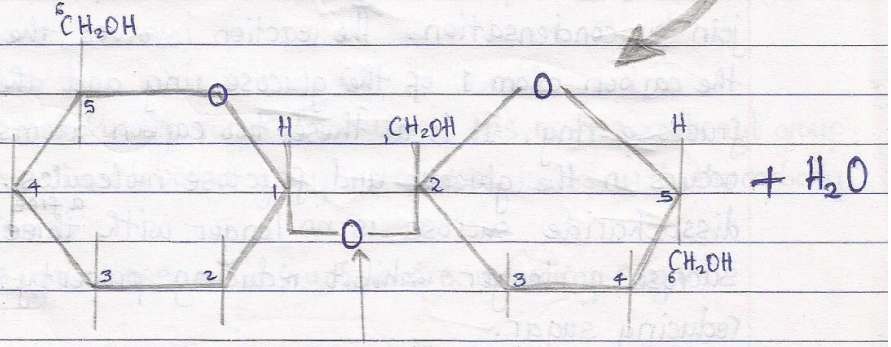
turning 180° and inverting itself



glucose



fructose

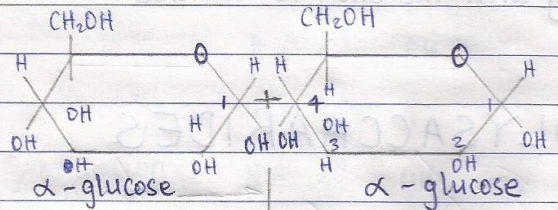


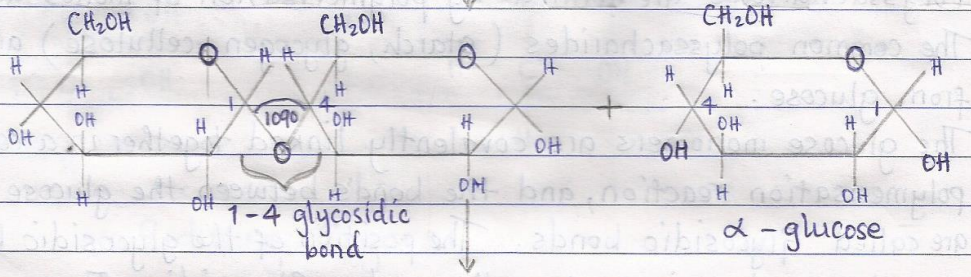
1 - 2 Glycosidic bond

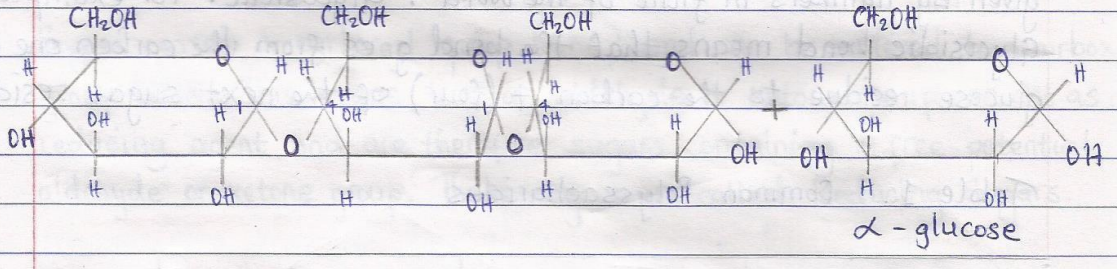
Fig. 2

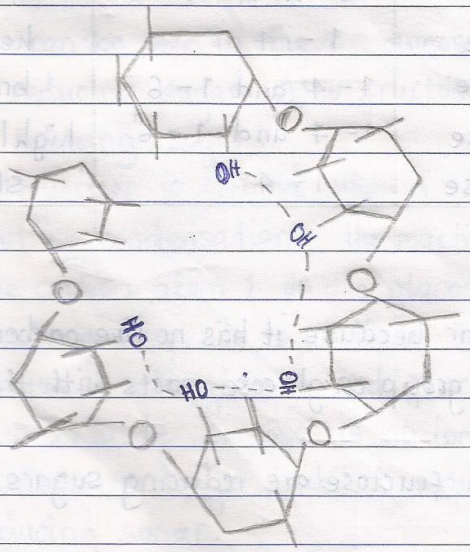
Starch

1. Amylose









* The hydrogen bond stabilizes the helical shape of the Amylose.

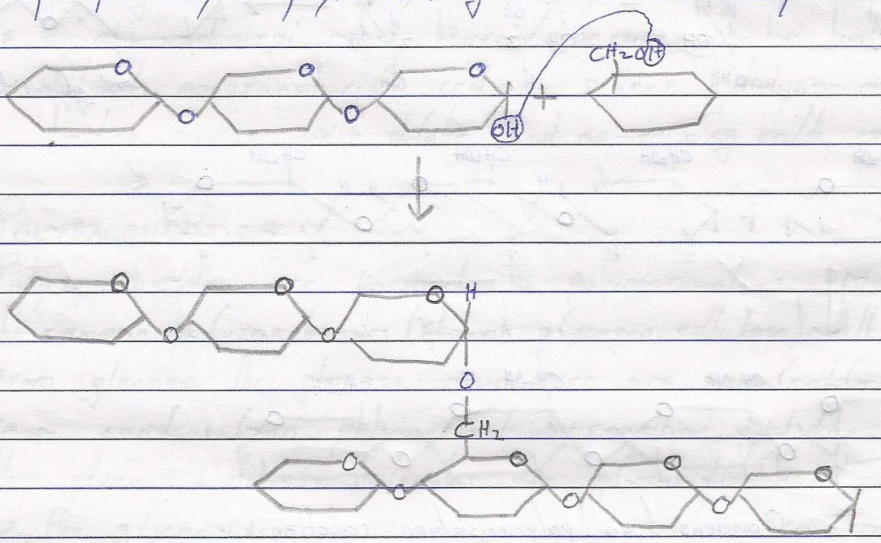
Starch is found in two forms, both formed from α-glucose residues. Starch is a polymer formed from α-glucose monomers. Starch can exist in two forms: a coiled polymer or a helical shape without branches and it is called Amylose. It has another form called Amylopectin.

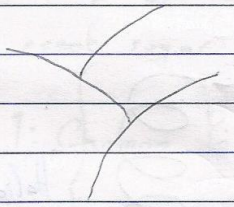
1. In amylose, the alpha glucose molecules are joined by 1-4 glycosidic bonds. The angle formed between the C-O-C bonds, ~~or~~ between the rings is similar to the angle of water molecules, about 109°. This angle means that the polymer is twisted into a helix (a shape like spiral staircase). The hydroxide group on the carbon-2 of each glucose residue projects into the middle of the spiral. This hydroxide groups form hydrogen bonds whith each other which stabilizes the shape of the amylose polymer, holding it in its helical shape.

2. Amylopectin

In amynopectin, the alpha-glucose monomers are joined by 1-4 glycosidic bonds, and 1-6 glycosidic bonds, each time there is a 1-6 glycosidic bond, a branched point is put into the polymer. The branched point occurs every 24-30 residues making a multi-branched, compact polymer.

angle made between the ~~two~~ C-OC bonds between the ~~rings~~ is similar to the angle ~~on~~ of the water molecule of 109°. This angle means the the polymer is twisted into a helix (a shape like a ~~spiral~~ stair case). ~~The hy~~ The hydrozeyl ~~gg~~ group on Carbon-two(2) of each glucose projects into a sp These hydrozeyl groups form hydrogen bonds with each other which stabilise the shape of the amylose polymer holding it in its helical shape.





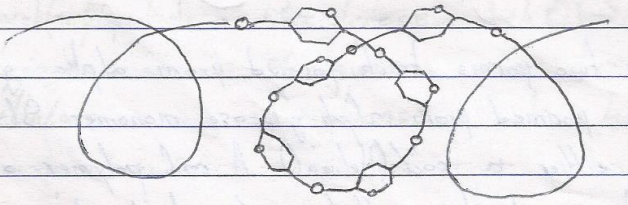
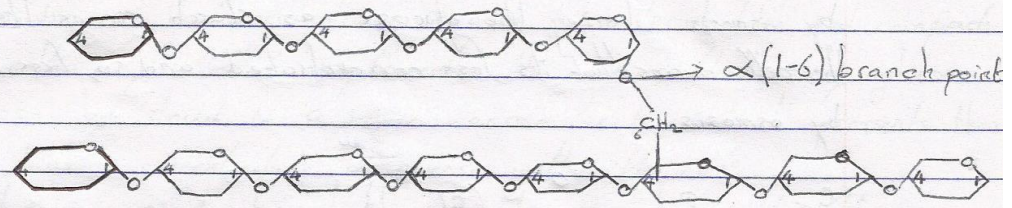
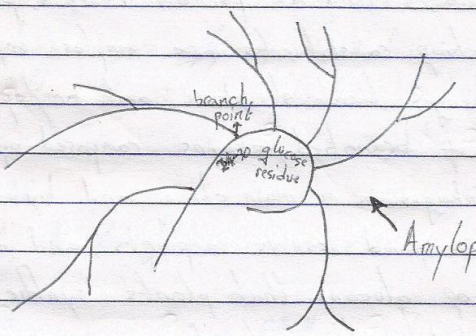


Fig 1: Structure of starch

A. Amylose (Forms a compact helical)



B. Amylopectin - Structure of two outer branches of amylopectin.
- the residue at the non-reducing ends are **bold**



Amylopectin forms a branched compact brush.

N.B. Starch (Amylose & Amylopectin) are is but found in legumes, potatoes, grains.

These hydroxyl group

In amylopectin, the alpha-glucose monomers are joined by 1-4 glycosidic and 1-6 glycosidic bond. Each time a 1-6 glycosidic bond is made, a branch point is put into the polymer. The branch points occur every 24-30 residues, making a multi-branched, compact polymer.

Both forms of starch are very compact. Amylose is coiled up into a compact helical shape and amylopectin is branched to form a closely compact brush shape. The function of starch is to act as an energy storage molecule in plant cells, and the compact shape means that many glucose residues can be stored in a volume within the cell aswell as saving space, converting the glucose molecules in ~~the~~ a polysaccharide reduces the number of small molecules in a cell. This is important because water enters the cell by osmosis, and the more molecules inside a cell, the more concentrated the solution in a cell and the more water that will enter

Both forms of starch are very compact. Amylose is coiled up into a compact helical shape and amylopectin is branched to form a closely packed brush shape.
The function of starch is to act as an energy storage molecule in plant cells and the compact shape means that many glucose residues can be stored in a small volume within the cell as well as saving space.
Converting the glucose molecules into a polysaccharide reduces the number of small molecules in the cell. This is important because water enters the cell by osmosis and the more ~~cells~~ molecules inside the cell, the more concentrated the solution inside the cell and the more water that will enter by osmosis.
Storing the glucose as starch means that the solution inside the cell is less concentrated and so, less water will enter by osmosis.

Storage Polysaccharide

1. Starch

Starch is formed of an alpha glycosidic chain and such a compound yielding only glucose on hydrolysis is called Glucan. It is the most important food source of carbohydrates and it is found in cereals, potatoes, legumes and other vegetables.
The two chief constituents of starch are amylose representing 15-20 percent which has a non branching helical structure and amylopectin representing 80-85% which consists of branched chains composed of 24-30 glucose residues, united by 1-4 linkages in the main chains and by 1-6 linkages at the branch points.

Starch is a food reserve in plants and a major nutrient for animals. It is a mixture of glucans that plants synthesize as their principle food reserve. It is deposited in the cytoplasm of plant cells as insoluble granules.

2. Glucagon (Glycogen)

Glycogen is also formed from alpha glucose residues. Glycogen is a polymer of alpha glucose monomers in which the residues are joined by 1-4 glycosidic bonds and 1-6 glycosidic bonds.

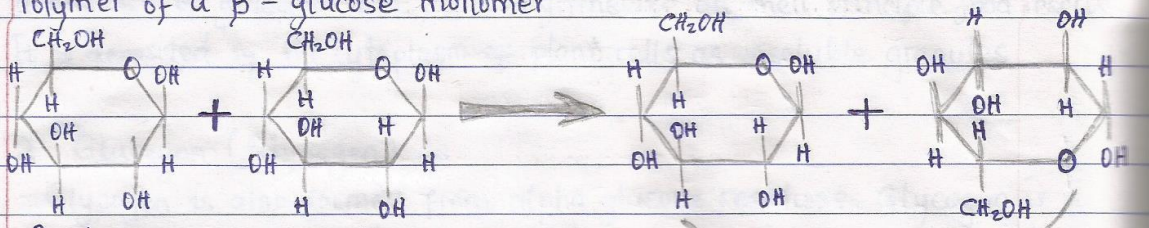
The glycogen polymer is branched like amylopectin, but the branch points in glycogen occur every 8-12 residues, so the macromolecule is even more brush-like and compact as with amylose and amylopectin. This means that many glucose molecules can be stored in a single macromolecule and it prevents them from being too high in concentration of glucose within the cells.

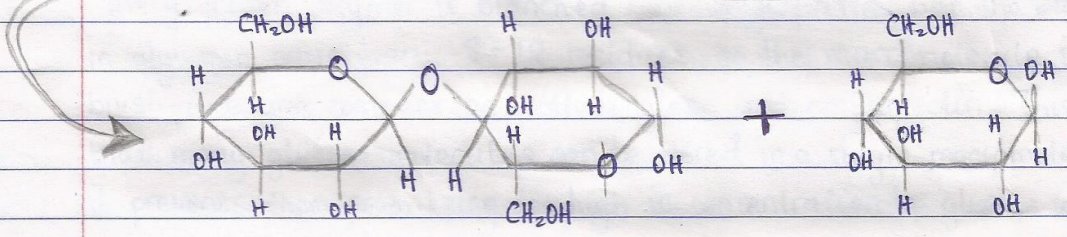
The structures of starch and glycogen differ only slightly. Glycogen is greatly characterized by many side branches which are chains of glucose that go off from the main chain. Animal cells store extra carbohydrates as glycogen which is sometimes called animal starch.

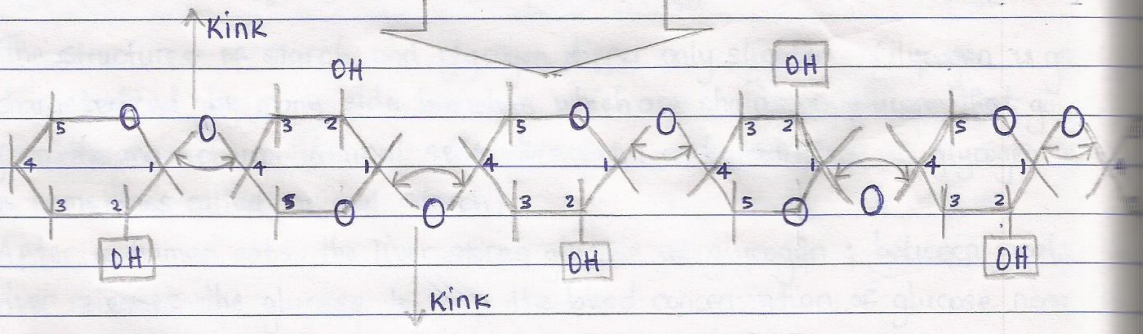
After a human eats, the liver stores glucose as glycogen; between meals, the liver releases the glucose to keep the blood concentration of glucose near the normal condition.

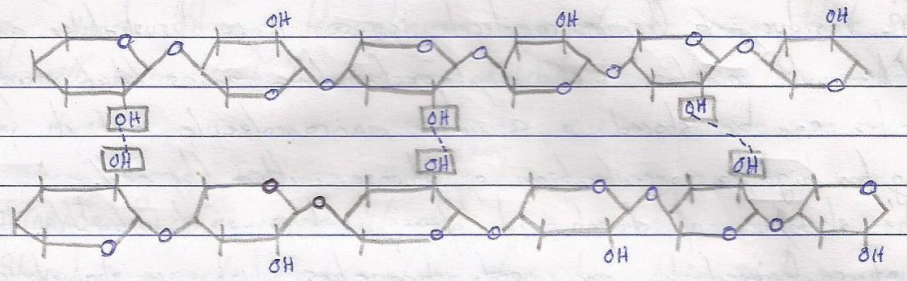
Cellulose

Polymer of a β-glucose monomer





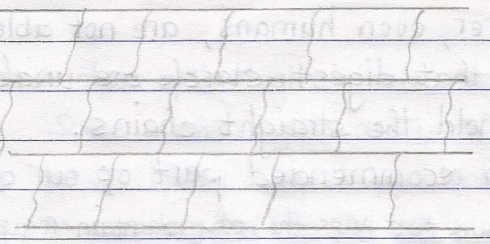




Cellulose is formed from beta-glucose polymonomers joined by 1-4 glycosidic bonds. In order to make a 1-4 glycosidic bond every second beta-glucose residue must be turned upside down. As every second residue is upside down, every kink that bends the polymer one way is cancelled out by the next kink which is in the opposite direction. This means that the polymer forms a straight chain. As there only 1-4 glycosidic bonds, there no branches in the polymer. These straight unbranched polymers pack closely together to form microfibrils. The polymers making up the microfibrils are held together by hydrogen bonds in the adjacent chains. The cellulose microfibrils are very strong when subjected to a pulling force along their length, and this strength makes them an excellent building material.

Humans have found many uses for cellulose. Cotton fibres are almost pure cellulose and we often wear cotton clothing. Furniture and buildings are made from wood which contains high percent of cellulose. Most animals including humans can't digest cellulose because the enzymes that can digest cellulose can't break the bet linkage between glucose molecules. Evenso, cellulose is a recommended part of our diet because it provides bulk or roughage that helps the body maintain regularity of ejection. For humans, plants are a source of starch and fibre. Cows and sheeps recieve nutrients from grass because they have special stomach where material can digest cellulose.

BLANK



Cellulose is formed from β-glucose monomers. It is a polymer of β-glucose monomers joined by 1-4 glycosidic bonds. In order to make the 1-4 glycosidic bonds, every second β-glucose residue must be turned upside down. As every second residue is upside down, every kink that bends the polymer one way is cancelled out by the next kink which is in the opposite direction. This means that a polymer forms a straight chain. As there are only 1-4 glycosidic bonds, there are no branches in the polymer. These straight unbranched polymers come together to form Microfibrils.

The polymers making up the microfibrils are held together by hydrogen bonds between adjacent chains.

The cellulose microfibrils are very strong when they are subjected to a pulling force along their length, and this strength makes them an excellent building material.

Humans have found many uses for cellulose. Cotton fibres are almost pure cellulose.

We often wear cotton clothing. Furniture and buildings are made from wood which contain cellulose, a high percentage of cellulose.

Most animals, however, even humans, are not able to digest cellulose because the enzymes that digest starch are unable to break the hydrogen bonds that hold the straight chains.
Even so, cellulose is a recommended part of our diet because it provides roughage or bulk that helps the body maintain regularity of elimination.
For humans, plants are a source of starch and fibre. Cows and sheep receive starch and nutrients from grass because they have special stomach where bacterial can digest cellulose.

LIPIDS

Lipids are a class of biological molecules that carry out multiple functions. Some such as fats are used as energy storage and heat insulation. However, the largest function of lipids in most cells are used to form membranes.
Some lipid function as vitamins (E) and others make up a large class of steroids hormones.
Lipids are extremely diverse group of molecules. Unlike polysaccharides lipids are not polymers rather they are quite small molecules that have strong dependency to associate through non-covalent forces.
Lipids are usually characterised by a kind of structure shown in Figure 1 below.

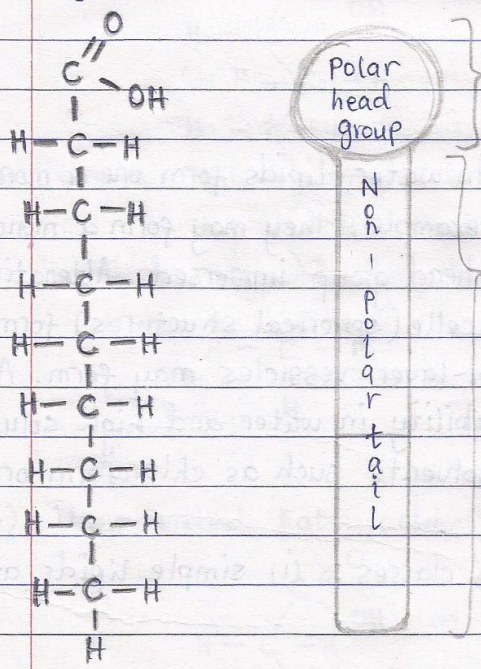


Fig 1. General lipid structure.

The structure consists of a polar hydrophilic head connected to a non-polar hydrophobic hydrocarbon tail.
Lipids are then examples of the molecules which are called Amphipathic.
* Amphipathic means the molecule has both a hydrophilic part and a non-hydrophilic or hydrophobic part.

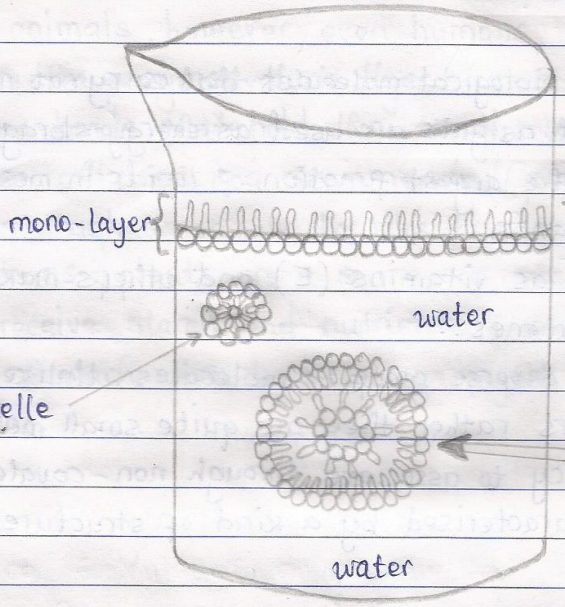


Fig 2.

When we attempt to dissolve lipids in water, lipids form one or more of the structure shown in figure 2. For example, they may form a mono-layer on the water surface with only the head group immersed. Alternatively, if the mixture is vigorously stirred, micelle (spherical structures) formed by the single layer of molecules or bi-layer vessicles may form. As a result, lipids defined by low solubility in water and high solubility in non-polar solvents or organic solvents such as chloroform or benzene.

Lipids can be classified into two classes: (i) simple lipids and (ii) complex lipids.

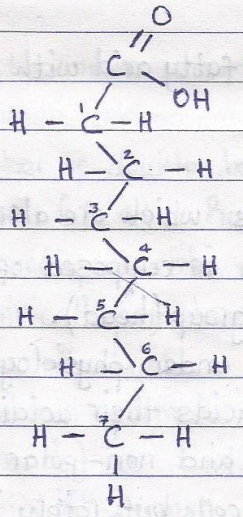
Simple Lipids -

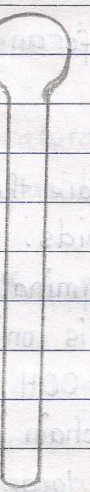
Simple lipids contain only carbon, oxygen and hydrogen. The most common are the fats, a combination of glycerol and fatty acids that are solid at room temperature.

Complex lipids contain four active ingredients namely (i) fatty acids (ii) glycerol (iii) phosphate group and (iv) polar molecules, or choline group.

FATTY ACIDS

(A) Saturated Fatty acid



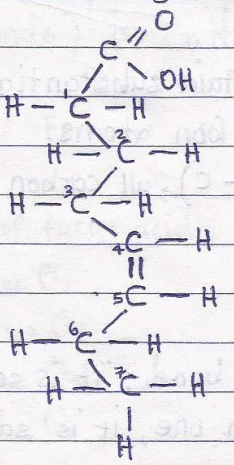


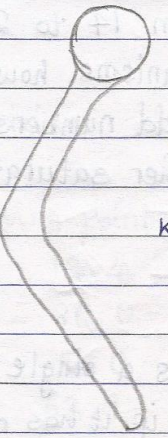
Empirical formula

$C_nH_{2n}O_2$

- $C_7H_{15}COOH$, or
- $C_8H_{16}O_2$

(B) Unsaturated Fatty acid





kink

Empirical formula for an un-saturated fatty acid with one double is $C_nH_{2n-2}O_2$.

- $C_7H_{13}COOH$, or
- $C_8H_{16-2}O_2$

$C_8H_{14}O_2$

- A double bond in the hydrocarbon tail introduces a kink, as shown in (B) on the previous page.
- In figure (A) on the previous page, the empirical formula for saturated fatty acids is given by $C_nH_{2n}O_2$. However, there is an extra hydrogen atom bonded with carbon-7 at the very tail of the fatty acid. As a result, an example of an empirical formula of a fatty acid is $C_7H_{15}COOH$ not $C_7H_{14}COOH$.
- Empirical formula for an un-saturated fatty acid with 2 double bonds is $C_nH_{2n-4}O_2$.
- Empirical formula for an un-saturated fatty acid with 3 double bonds is $C_nH_{2n-6}O_2$.
- Empirical formular for an un-saturated fatty acid with 4 double bonds is $C_nH_{2n-8}O_2$.

The simplest lipids are the fatty acids which are also constituents of many more complex lipids. A fatty acid is composed of a long hydrocarbon chain (tail) and a terminal carboxylic group (head).
The carboxyl group is ionised normally under physiological conditions.
The carboxyl group COH gives fatty acids their acidic properties.
The long hydrocarbon chain is uncharged and non-polar.
Fatty acids occur in large amounts in cells but rarely in a free uncomplex state. They are esterified to glycerol.
Most of the fatty acids found in nature have an even number of carbon atoms (usually from 14 to 24.).
Certain marine organisms however contain substantial amounts of fatty acids with odd numbers of carbon atoms.
Fatty acids are either saturated (C-C), all carbon to carbon chains are single bonds.

If a fatty acid has a single double bond, it is said to be mono-unsaturated. And if it has more than one, it is said to be poly-unsaturated.

Two common fatty acids are (i) Stearic acid ($C_{17}H_{35}COOH$) and (ii) Oleic acid ($C_{17}H_{33}COOH$).
The difference between stearic acid and oleic acid is the presence of one double bond in the hydrocarbon chain. As can be seen in figure (B), a kink introduced by a double bond makes the structure bent.

Unsaturated fatty acids are slightly more abundant in nature than saturated fatty acids

The most common unsaturated fatty acid is Oleic acid with one double bond between carbon-9 and carbon-10.
The number of double bonds in an unsaturated fatty acid varies from one to four (1-4). But in the fatty acids found in bacteria, this number rarely exceeds one.
The empirical formula for a saturated fatty acid (one with no double bond) is $C_nH_{2n}O_2$.
The empirical formula for an un-saturated fatty acid (one with one double bond) is $C_nH_{2n-2}O_2$.
The empirical formula for an un-saturated fatty acid (one with two double bonds) is $C_nH_{2n-4}O_2$.
The empirical formula for an un-saturated fatty acid (one with three double bonds) is $C_nH_{2n-6}O_2$.

Table 1: Formula of fatty acids

Formula of fatty acid	Melting Point (°C)
1. $C_{18}H_{34}O_2$	13.4
2. $C_{24}H_{48}O_2$	86.0
3. $C_{18}H_{32}O_2$	- 5.0
4. $C_{16}H_{32}O_2$	63.1

Long hydrocarbon chains of fatty acids are extra ordinary efficient of energy storage because they contain carbon in fully reduced form and will therefore yield a maximum amount of energy on oxidation. They are infact much more efficient energy storers than carbohydrates are. For this reason Lipids are used by many organisms including humans for Energy storage.

Triglycerides

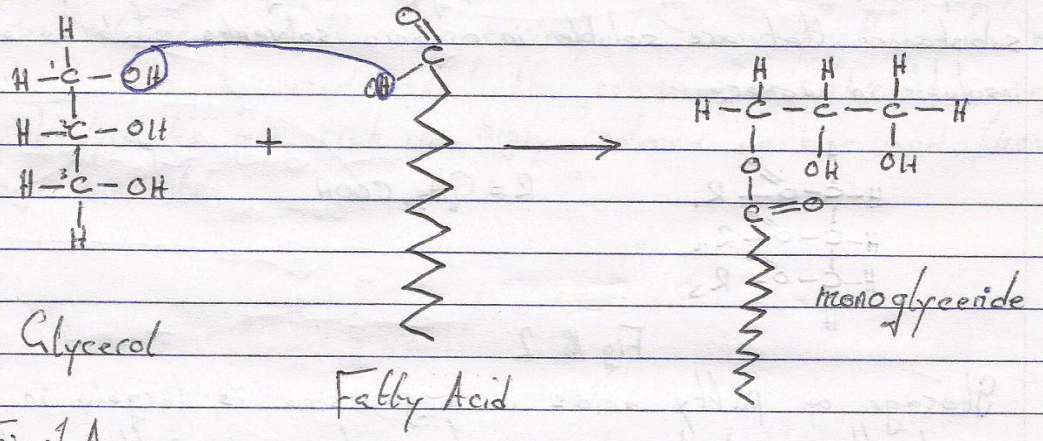


Fig: 1.A

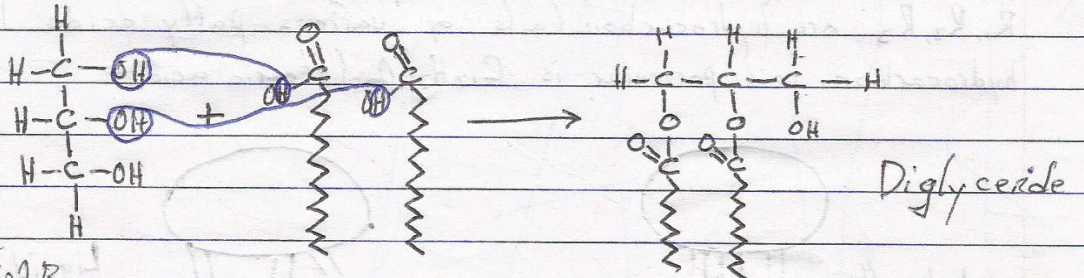


Fig 1.B

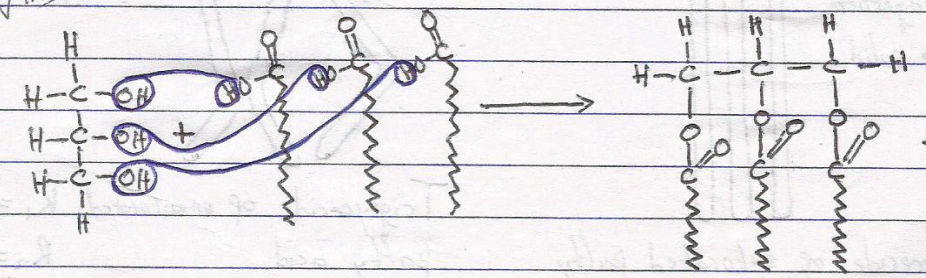
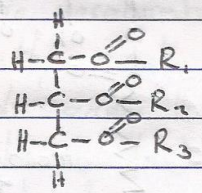


Fig 1.C

Fatty acids react with glycerol to form glyceride. Glycerol is a simple three carbon molecule with a hydroxy group on each carbon. The hydroxyl groups can react with carbonyl groups of fatty acids. The bond formed between these two molecules is called an ESTER BOND.

Each of the hydroxyl group on the glycerol molecule can react with the carbonyl group of fatty acids. If only one reacts with a fatty acid, a monoglyceride is formed. If two hydroxyl groups react with two fatty acid, a diglyceride is formed and if all three react, a triglyceride is formed.

Glyceride are also called ~~Acylglycerols~~ Aglyceroids. Lipids are substances that are soluble in organic solvents such as ethanol but insoluble in water.



$R = C_6H_{32}COOH$

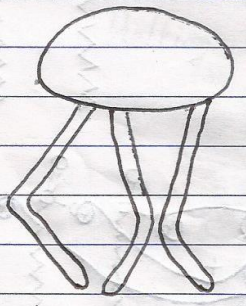
Fig B 2

Storage of fatty acids in organisms is largely in triglyceride or fats, these substances are tri-esters of fatty acids and glycerol. The general formula of triglycerides is shown in fig 2. where R_1, R_2, R_3 are hydrocarbon tails of various fatty acids. If the hydrocarbon tail formular is $C_{17}H_{35}O_2$ (stearic acid)



pack together to make solid

Triglyceride of saturated fatty acids $C_{17}H_{34}O_2$



Liquid

Triglyceride of unsaturated fatty acid

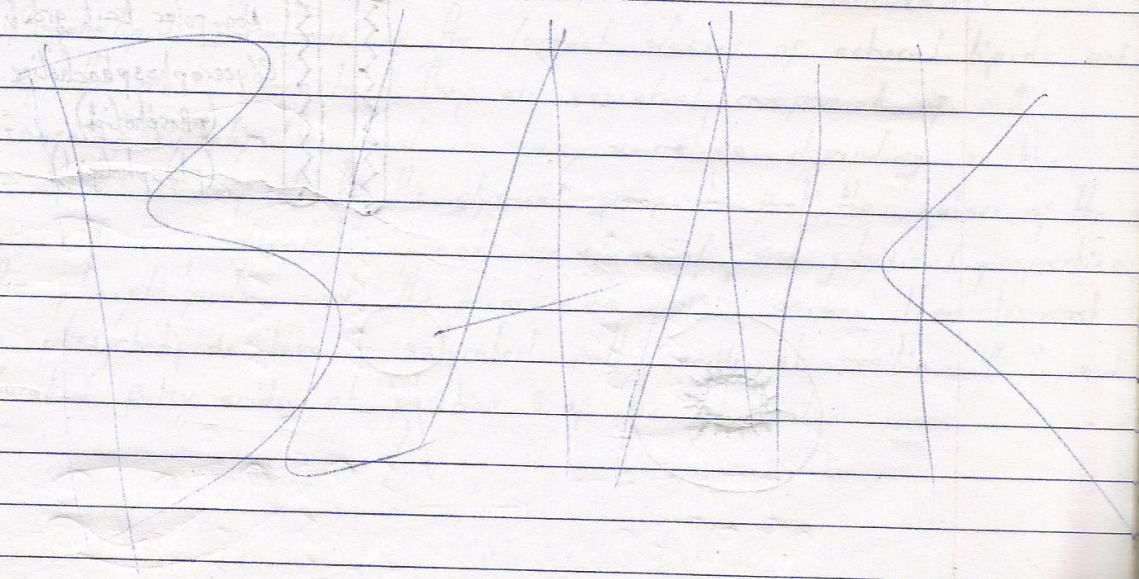
$R_1 = C_{17}H_{32}O_2$

$R_2 = C_{18}H_{32}O_2$

$R_3 = C_{16}H_{30}O_2$

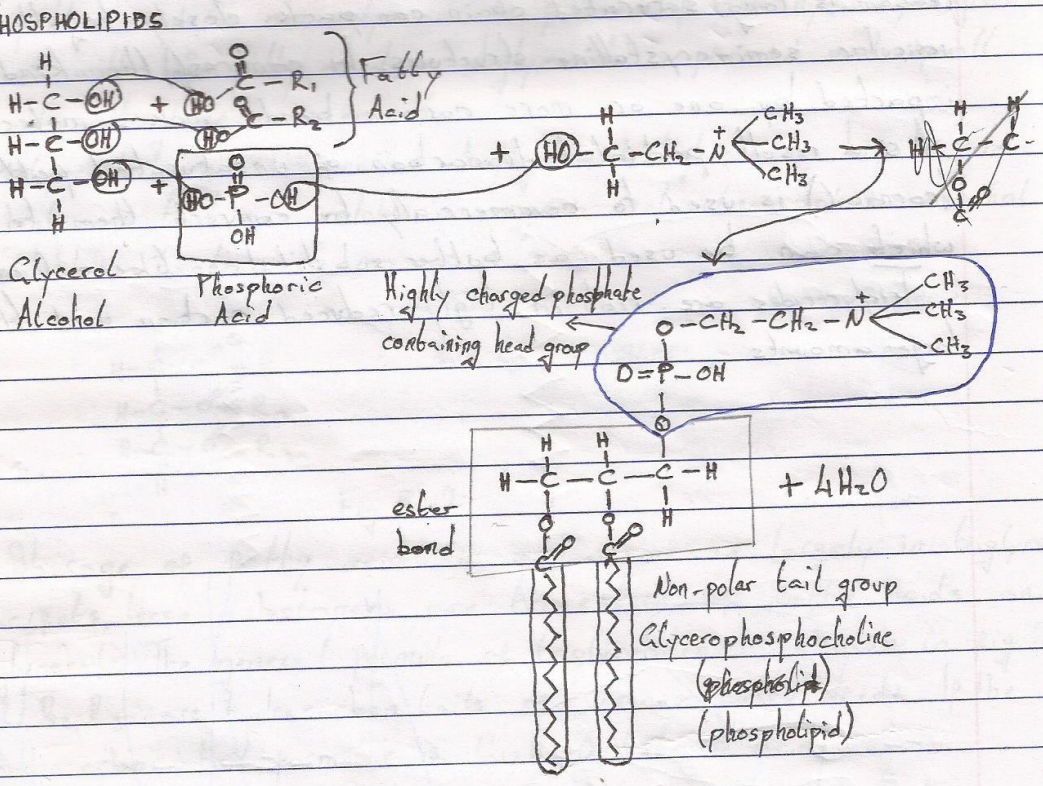
Most triglyceride however contain a mixture of fatty acids which often includes unsaturate ones. Fatty ~~acids~~ levels in fatty acids such as olive oil are liquid at room temperature whereas those with a high content like butter are solid. A wholly saturate fatty is quiteapirm solid especially if the hydrocarbon chain is long. This made clear from the melting point data in table 1, the reason is long saturated chain can pack closely together to form vesicular semi-crystalline structures. In contrast, the kind of bond imparted by one or more carbon bonds makes molecule dippicult As a result, partial hydrocarbon of unsaturated fatty oil like (corn oil) is used to commercially to convert them to solid pat which can be used as butter substitutes like oil morgarine.

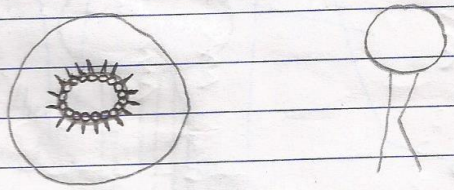
Triglycerides are rich in higly reduced carbon and thus yield large amounts



Lipids

Phospholipids





Phospholipids are complex molecules made from

1 Fatty acid group
2 Glycerol group
3 Phosphate
4 Large polar group

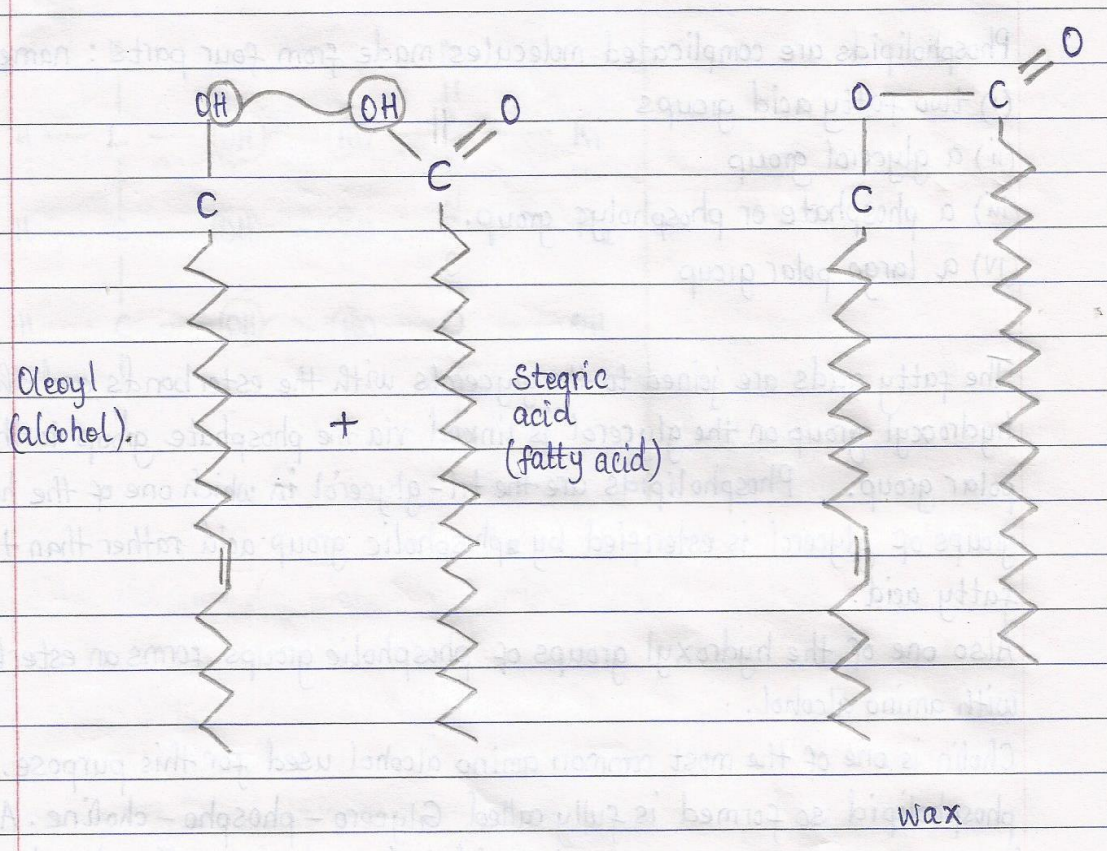
The fatty acids are joined to the glycerds by ester bond and then the third hydroxyl group on the third glycerol is linked through the phosphoric group to the polar group

Phospholipids are triacylglycerd in which on of the hydroxyl group in glycerol is esterified by phosphoric acid rather than by a fatty acid. Also one of the hydroxyl groups of the phosphoric acid forms an ester linkage with an amino alcohol. Choline is one of the most common amino alcohol used for this purpose. The phospholipid so formed is called as Glycerophosphocholine. An important property of a phospholipid is its polarity.

The phosphocholine head is charged and is therefore soluble in polar solvents such as water, while the tail of two hydrocarbon chain is non-polar. Phospholipid form the basis of all cellular membranes

Phospholipid form one of the largest classes of natural lipids and one of the most important. They are essential component of cell membranes, phospholipids exist in many varieties depending on the fatty acids esterified to the glycerol group. In fact, the nature of the fatty acids can greately appect the chemical and physical properties of the phospholipids and the membrane that contain them. In most cases, phospholipids have a saturated fatty acid at position # 1, and unsaturated fatty acids at position 3 of the glycerol.

WAXES



Waxes are esters of long chain alcohols with long chain fatty acids. The resulting molecule can be viewed as having a weak polar head group and a long non-polar tail.
Fatty acids found in waxes are usually saturated whereas the alcohols found in waxes may be saturated or unsaturated.

Waxes are highly insoluble due to the weak polar nature of the ester group. As a result, this class of molecules confers water repellant characteristic to animal skin, leaves of certain plants and to birds' feathers. The glossy surface of a polished apple results from a waxy coating.

PROTEINS

Proteins are very complex substances that contain the same three basic elements as carbohydrates and fats : carbon, hydrogen and oxygen. But in addition, proteins contain about 16% nitrogen (N). Sulphur is also present in many proteins, and other minerals such as Iron (Fe), copper Iodine (I) and Phosphorus (P) are present in smaller amounts.
Proteins make up a high percentage of the structure of living organisms, for example , about
Proteins also take part in the fundamental processes that make up life.

Every organism contains thousands of different kinds of proteins, each with its own unique three-dimensional structure which enables it to carry out a specific function.
Simple organisms such as bacteria have about 1000 different kinds of proteins molecules in their cells. Humans probably have between 50000 and 100 000 protein molecules.

FUNCTIONS OF PROTEINS

FUNCTION	CLASS OF PROTEIN	EXAMPLES	USE
Enzymes	Biological catalysts	Hydrolytic enzymes such as Amylase and Polymerase.	Biological catalysts
Defense	Antibodies	IgG (Immuno-globulin-Gamma) (an antibody)	To recognize foreign microbes and cancer cells.
Transport	Globular Protein	Haemoglobin	Carries oxygen (O_2) and Carbon dioxide (CO_2) in blood.
		Myoglobin	Carries oxygen (O_2) and carbon dioxide (CO_2) in muscles.

FUNCTION	CLASS OF PROTEIN	EXAMPLE	USE
Structural Proteins	Fibers	Collagen	Makes up tendons and ligaments.
		Keratin	Major components of hair and cells nails
		Fibrin	Blood clot
Motion	Muscle	Actin and Myosin	Involvement in movements. They enable muscles to move
Signal Proteins	~~Insulin~~ Hormones	Insulin	Involved in controlling glucose levels in the blood.
Regulation as osmotic regulation	Albumin	Serum albumin	Maintains osmotic concentration of blood.

Proteins are used as fuel especially during starvation and fasting, but their main function is as a source of amino acids. The amino acids are used to synthesize new proteins for growth and repair. 20 amino acids are needed by humans, 11 of which can be synthesized by the body and are termed as Non-essential Amino acids. The remaining 9 amino acids must be obtained from the diet and are called Essential Amino acids. One of these essential amino acids is called Histidine which is essential for infants, small children and adults.

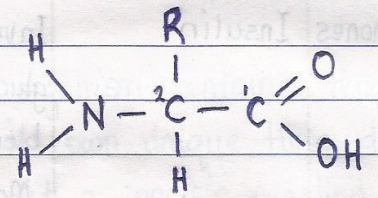
The body cannot store excess amino acids, so we needed a regular supply of proteins in our diet. However, the amount varies with age. Animal products such as meat, eggs, milk and cheese are a good source of proteins because they contain all the essential amino acids. These are called Complete amino acids.

* There is, and only should be, 120mg of glucose per $1mm^3$ of blood.

Most plant proteins are incomplete because they lack one or more essential amino acids. Nevertheless, all the amino acids can be obtained if a variety of plants foods is eaten.

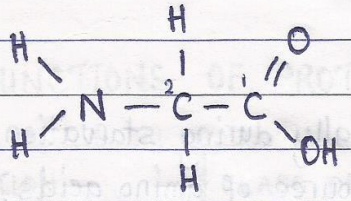
- Eating a mixture of beans and corn for example can obtain all the 9 essential amino acids.

AMINO ACIDS

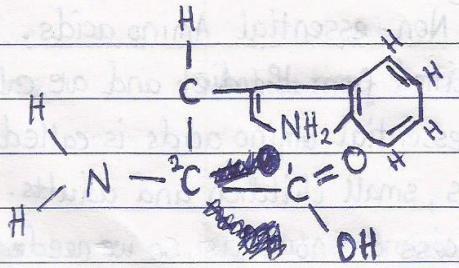


General formula of an amino acid

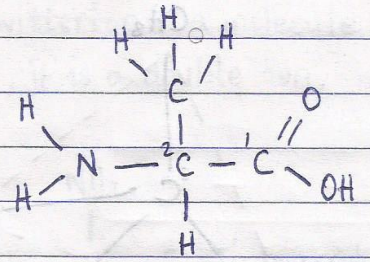
COOH = Carboxyl group (acidic)
NH_2 = Amine group (basic)
R = side chain group



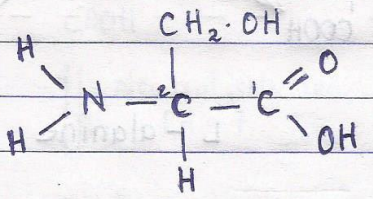
R = H
Glycine



Tryptophan



Alamine
(non-polar amino acid)

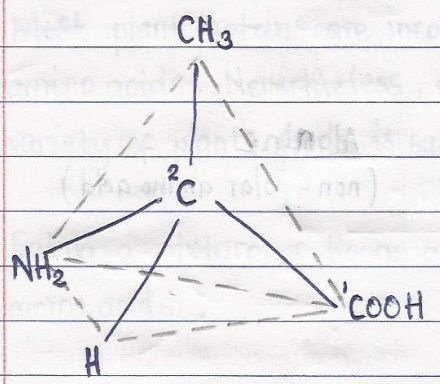


Serine
(Polar amino acid)

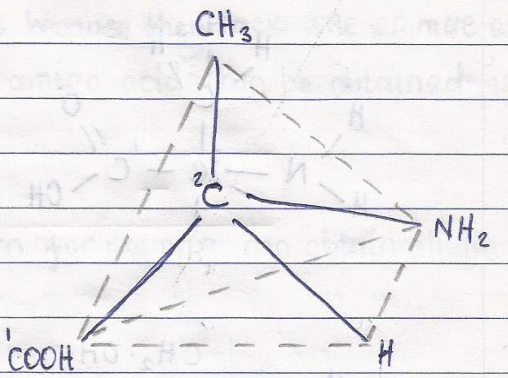
- A molecule that has a positive end and a negative end is called a Zwitterion.

A protein is a polymer containing up to 20 different amino acids. Amino acids are crystalline solids that are soluble in water. All amino acids contain two reactive groups and amine group and a carboxylic group. There are 20 common amino acids found in organisms, and these differ from one another by the composition of the other group attached to carbon-2 which is called the R-group.
The R-group varies in structure from a single hydrogen atom found in Glycine to CH_2OH as found in Serine, to CH_3 as found in Alamine to a complex ring structure called Tryptophan.

- Most bacteria form L-stereoisomers of amino acids, while



D - alanine



L - alanine

Carbon - 2 is joined to four different groups in amino acids except glycine. This means that all amino acids except glycine can make stereo-isomers.

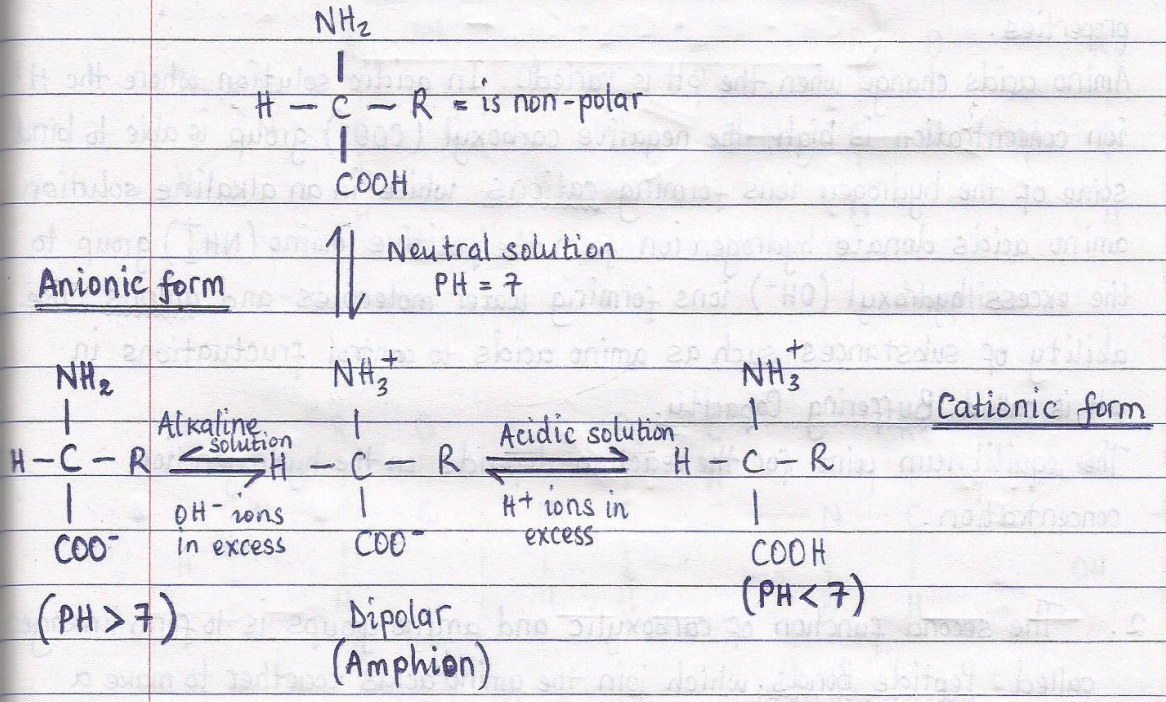
1. All common amino acids in mammalian organisms are L - amino acids rather than D - amino acids, but D - amino acids are found in the cell walls of bacteria.
2. All 20 amino acids have many properties in common. Each amino acid molecule contains an acidic group and a basic group, COOH and NH_2, respectively. This means that amino acids have the properties of an acid and properties of a base. Such substances are called Amphoteric At the PH of the cell about neutral, both the amine group and the carboxyl group are ionized.

$$-COOH \longrightarrow COO^- + H^+$$

$$-NH_2 + H^+ \longrightarrow NH_3^+$$

This means that each amino acid molecule is positively charged at one end and negatively charged at the other end, a strange type of ion called Zwitterion.

- A Zwitterion is a molecule with a positive group and a negative group, it is a double ion.



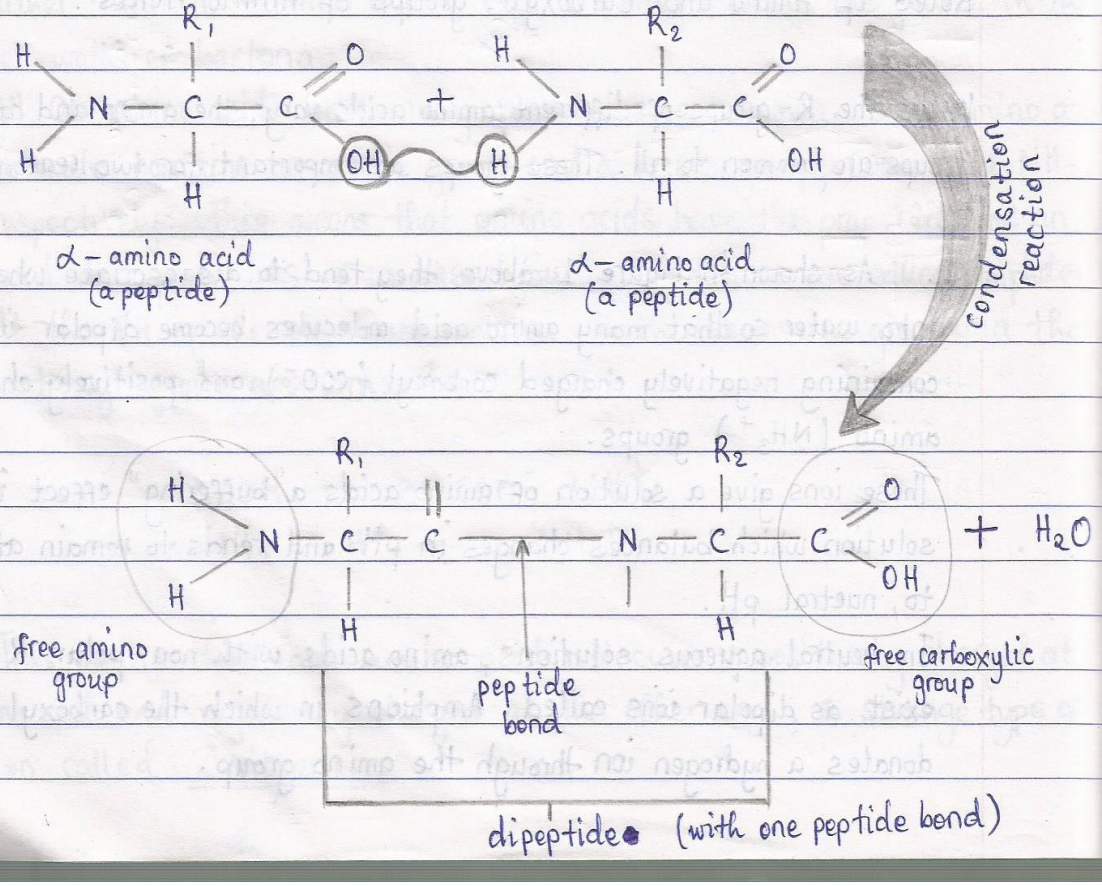
Roles of Amino and Carboxylic groups of Amino Acids.

While the R-groups of different amino acids vary, the amino and carboxylic groups are common to all. These groups are important for two reasons:

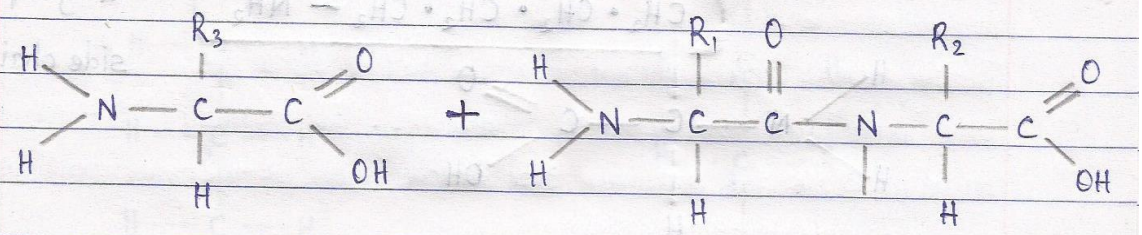
1. As shown in Figure 1 above, they tend to disassociate when dissolved into water so that many amino acid molecules become dipolar ions, each containing negatively charged carboxyl (COO^-) and positively charged amino (NH_3^+) groups.
These ions give a solution of amino acids a "buffering" effect i.e a solution which balances changes in pH and tends to remain at, or close to, nuetral pH.
In neutral aqueous solutions, amino acids with non-polar R-groups exist as dipolar ions called Amphions in which the carboxyl group donates a hydrogen ion through the amino group.

Amino acids can therefore act as donors and acceptors of hydrogen ions and are hence said to be Amphoteric.
An Amphoteric substance is a substance that has both acidic and basic properties.
Amino acids change when the pH is varied. In acidic solution where the H^+ ion concentration is high, the negative carboxyl (COO^-) group is able to bind some of the hydrogen ions forming cations while in an alkaline solution amino acids donate hydrogen ion from the positive amino (NH_3^+) group to the excess hydroxyl (OH^-) ions forming water molecules and anions. The ability of substances such as amino acids to control fructuations in pH is called Buffering Capacity.
The equilibrium point for the reaction depends on the hydrogen ion concentration.

2. The second function of carboxylic and amino groups is to form linkages called Peptide Bonds, which join the amino acids together to make a chain of peptides.

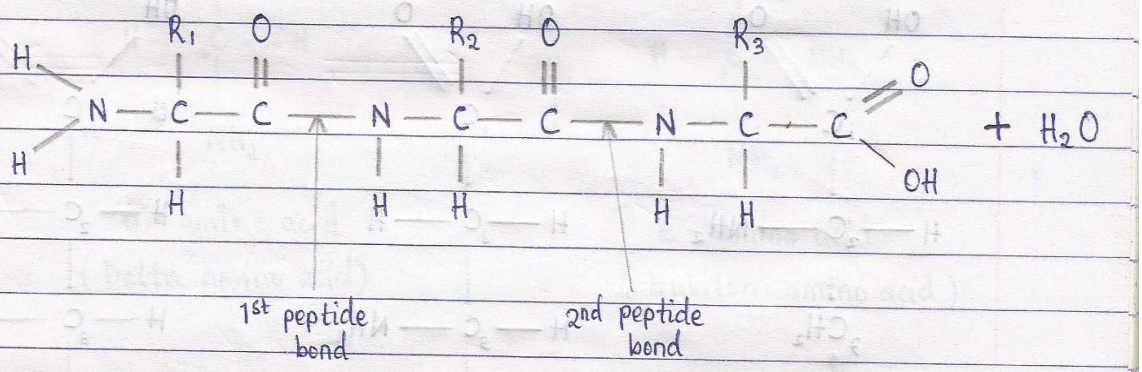


- Short chains have 9 amino acids e.g Hormones.
- Long chains can have ten thousands (10 000) of amino acids.



. α - amino acid

dipeptide



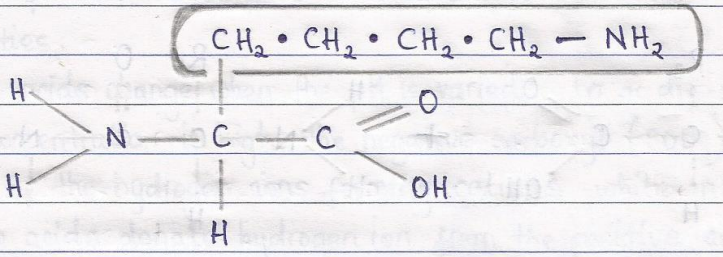
Hence: Tripeptides + amino acid ⟶ Polypeptide

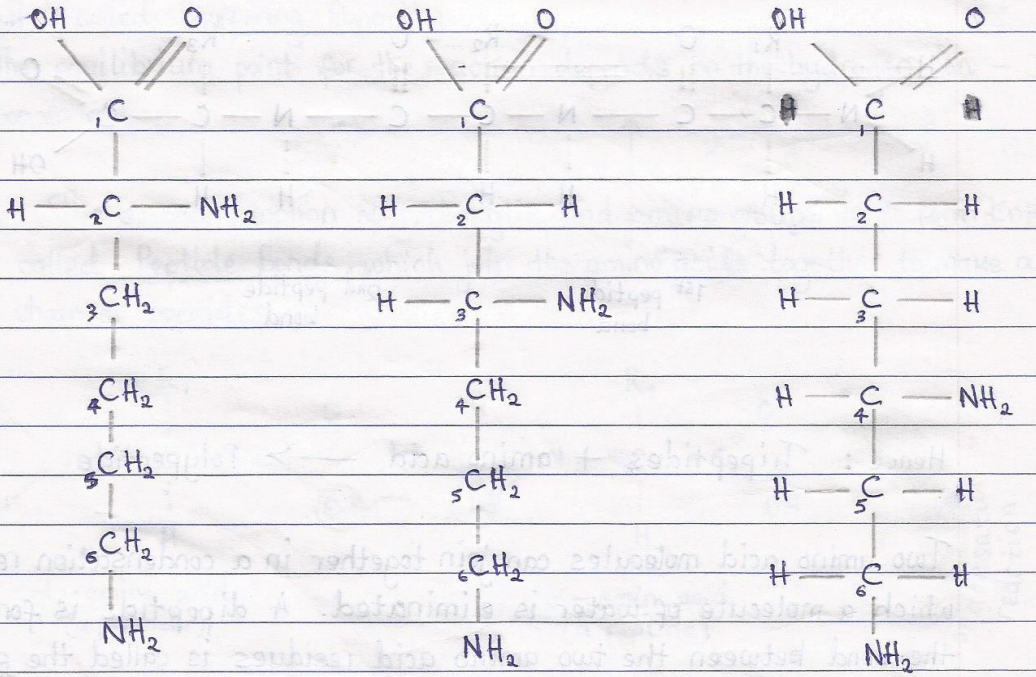
Two amino acid molecules can join together in a condensation reaction in which a molecule of water is eliminated. A dipeptide is formed and the bond between the two amino acid residues is called the peptide bond. Additional amino acids can react with a dipeptide to form first a tripeptide and then a polypeptide.

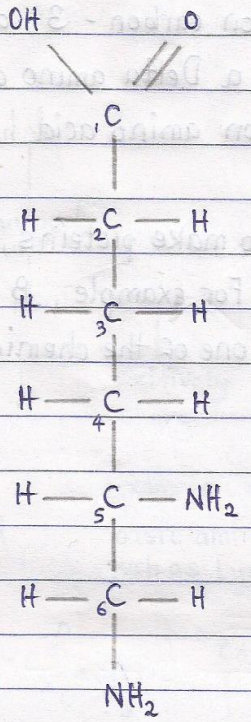
NOTE: When an amino group (NH_2) is joined to carbon-2, the amino acid is called α - amino acid (alpha amino acid).

ISOMERISM LYSINE

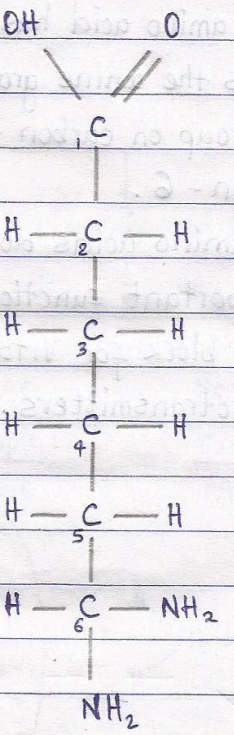
The chemical structure of Lysine and its isomerism.







δ - amino acid
(Delta amino acid)



E - amino acid
(Epsilon amino acid)

POSITION OF NH_2

Carbon - 2	Alpha (α)
Carbon - 3	Beta (β)
Carbon - 4	Gamma (γ)
Carbon - 5	Delta (δ)
Carbon - 6	Epsilon (ε)

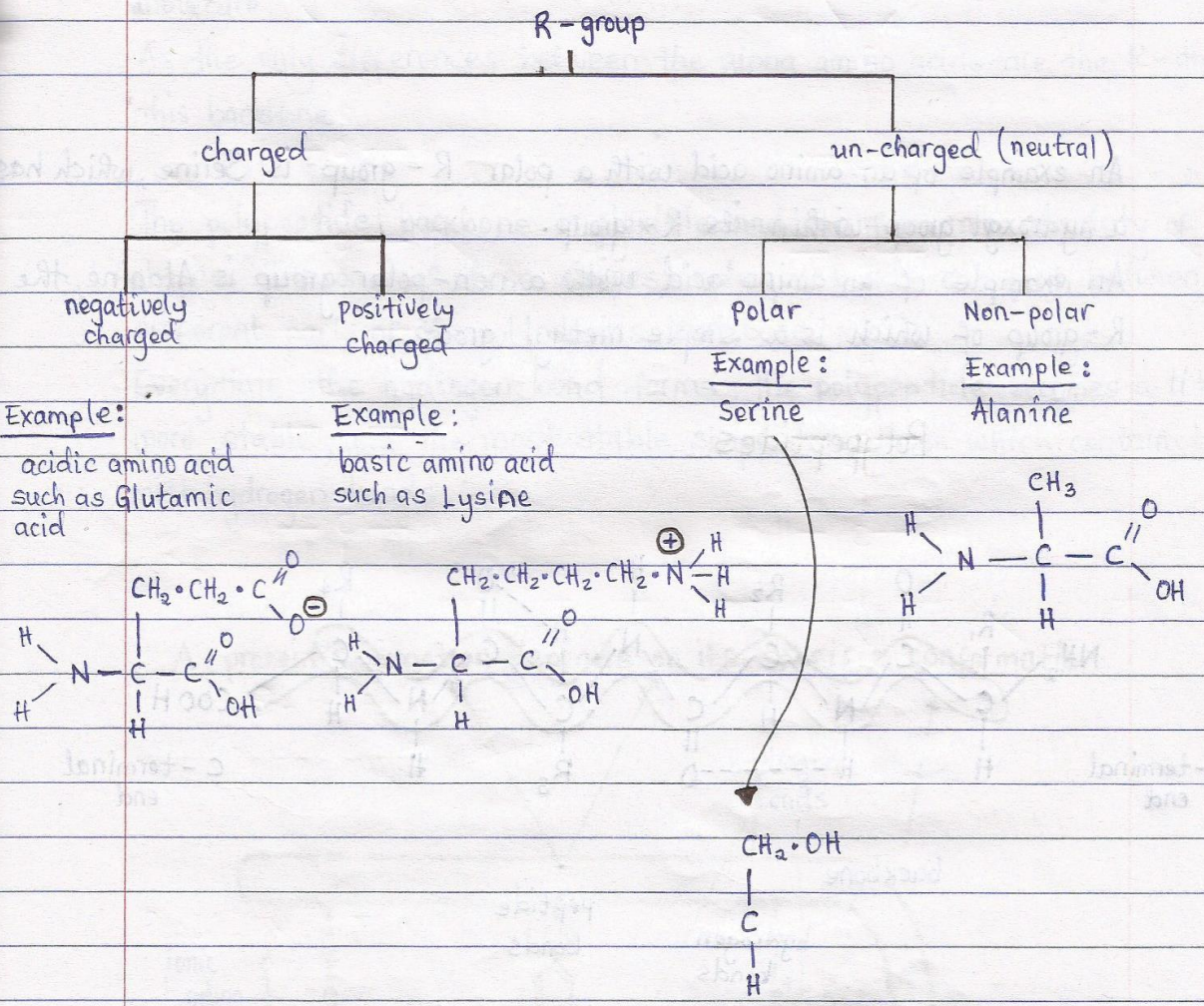
RARE AMINO ACIDS

Not all amino acids are alpha amino acids. Any molecule containing both a carboxylic group and an amine group is an Amino acid. Alpha amino acids have the amine group on carbon-2 but other amino acids have the amine group further away from the carbon-2.

A Beta amino acid has the amine group on carbon - 3, a Gamma amino acid has the amine group on carbon - 4, a Delta amino acid has the amine group on carbon - 5, and an Epsilon amino acid has the amine group on carbon - 6.

These amino acids do not join together to make proteins, but some of them have important functions in organisms. For example, β-alanine is the building block for Vitamin B5 which is one of the chemicals used by cells as neurotransmitters.

Classification of R-groups of amino acids



The different R-groups give each amino acid slightly different propertyes. These R-groups are very important because they are unaffected when the amino acids join to make a poly-peptide and contribute toward the properties of the poly-peptide.

The different R-groups can be classified according to whether they are charged or uncharged (neutral), uncharged polar or non-polar, as the PH of the cell.

Some of the R-groups will have a positive or negative charge as the PH of the cell. These are called charged groups.

An example of an amino acid with a polar R-group is Serine, which has a hydroxyl group within its R-group.
An example of an amino acid with a non-polar group is Alanine, the R-group of which is a simple methyl group.

Polypeptides

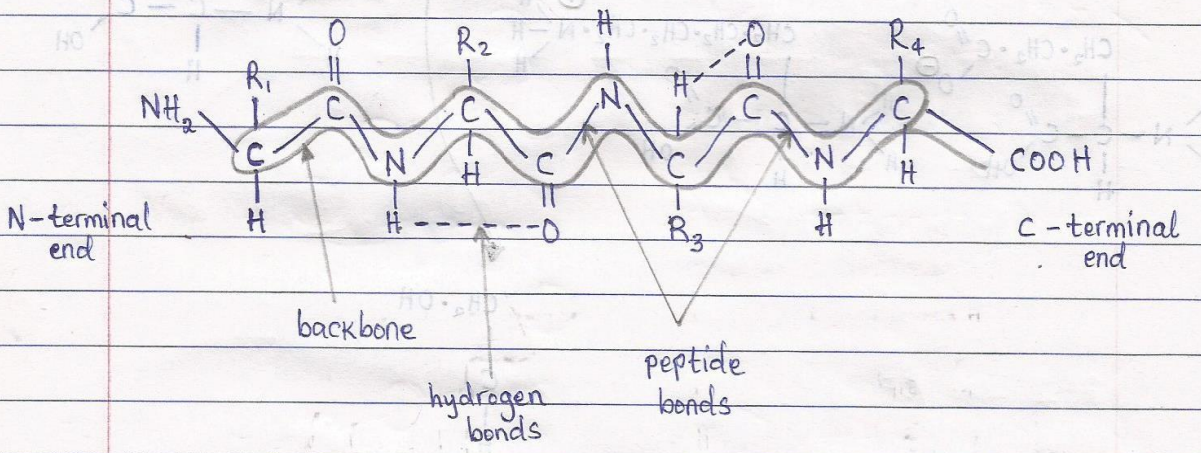


Fig 1 : All polypeptides have a similar backbone and R-groups that vary depending on the amino acid residues present

A chain of amino acid residues link together to form a polymer. This is referred to as a polypeptide. Proteins are polypeptides in their final form. Some proteins are just a single polypeptide chain folded into a certain shape, while others contain more than

The polypeptide has a backbone that runs the length of the macro-molecule.
As the only differences between the alpha amino acids are the R-groups this backbone

The polypeptide backbone is flexible and can form into a variety of shapes. In some of these shapes, hydrogen bonds can form between different parts of the polypeptide backbone.
Everytime the hydrogen bond forms, the polypeptide becomes a little more stable, and the most stable shapes are those which contain the most hydrogen bonds.

A protein's function depends on its specific conformation

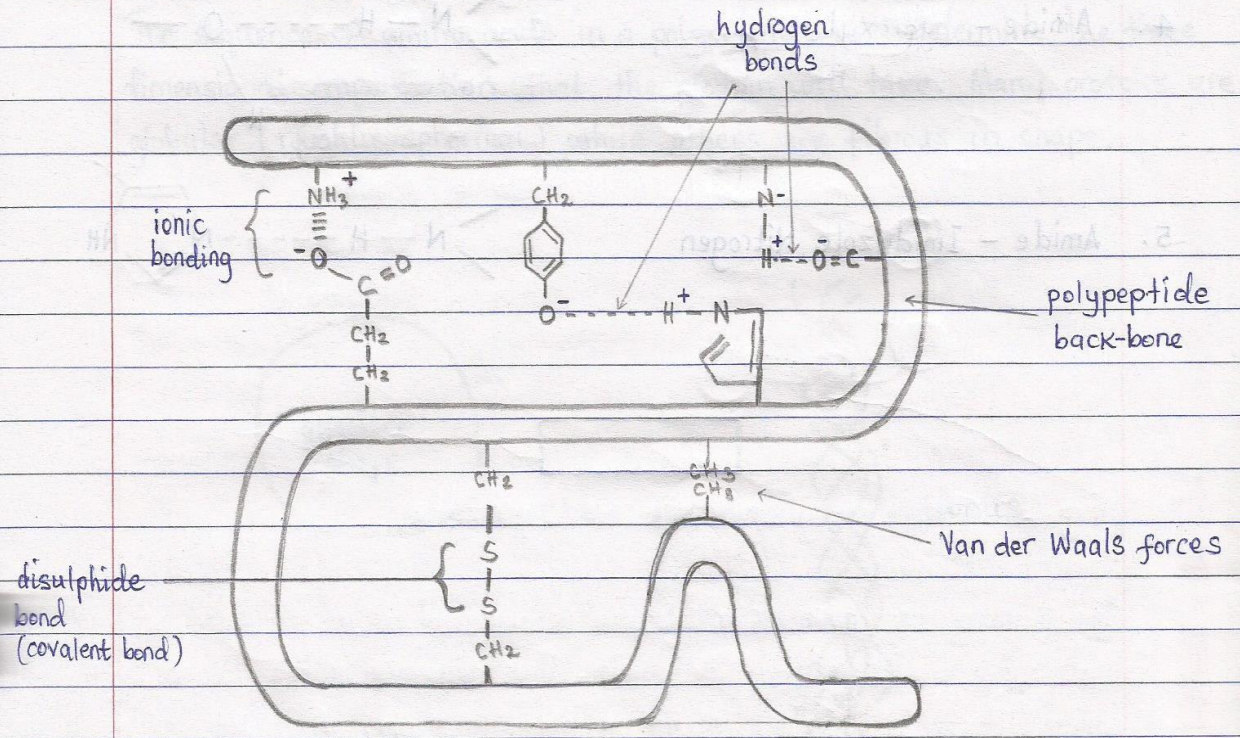
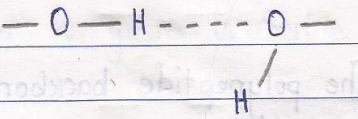


Fig 1 : Cross-linking within a polypeptide.

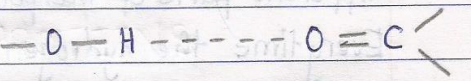
Examples of hydrogen bonds in Proteins

Type of hydrogen bond

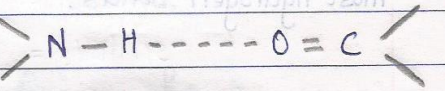
1. Hydroxyl - hydroxyl



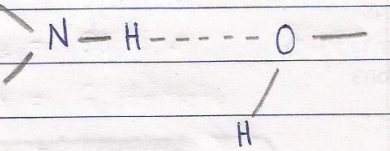
2. Hydroxyl - carbonyl



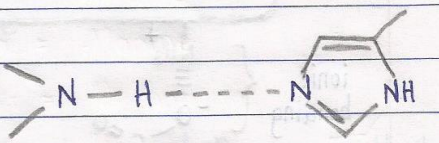
3. Amide - carbonyl



4. Amide - hydroxyl



5. Amide - Imidazole Nitrogen

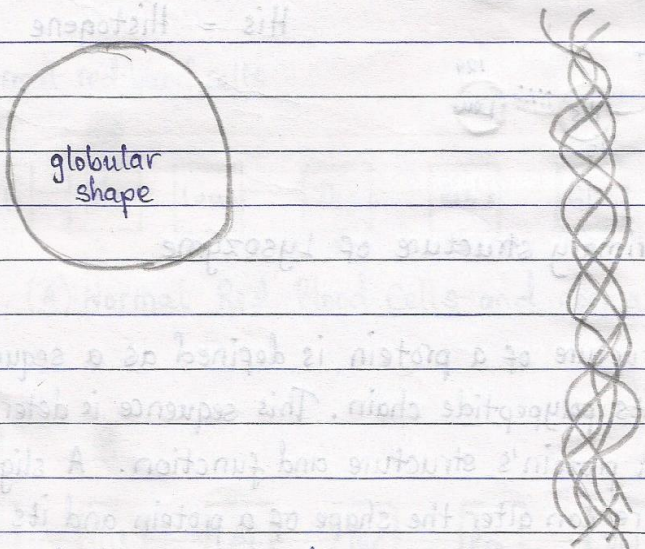


A protein can be described as a chain of amino acids joined by peptide bonds in a specific sequence, However, a functional protein is not just a polypeptide chain but one or more peptides are folded, twisted into compact shapes that contain coils, zigzags, turns and loops.

A number of factors constrain rotation around the covalent bonds in a polypeptide chain in its native conformation. These include the ~~naught~~ presence of weak chemical forces which are :

(i) Hydrogen bonds
(ii) Van der Waal's forces
(iii) Ionic bonds
(iv) Hydrophobic interactions, and
(v) Certain covalent bonds such as the disulphide bond formed between two Cystine amino acids.

The sequence of amino acids in a polypeptide will determine the three dimensional conformation that the protein will take. Many proteins are globular (roughly spherical) while others are fibrous in shape.



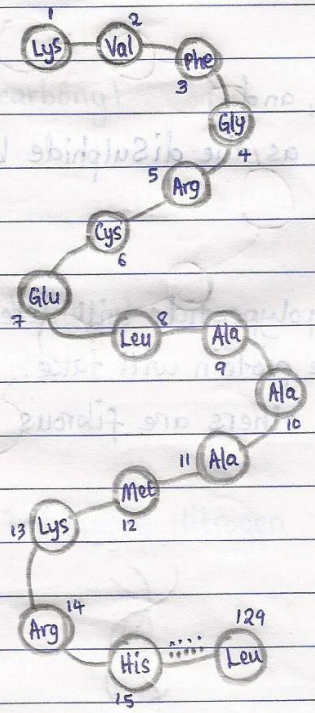
- However, within these broad categories countless variations are possible.

Levels of protein structure

There are four levels of protein structure ; namely,

(i) Primary structure
(ii) Secondary structure
(iii) Tertiary structure
(iv) Quatenary structure

PRIMARY STRUCTURE OF PROTEINS



Lys = Lysine
Val = Valine
Phe = Phenylalanine
Gly = Glycine
Arg = Arginine
Cys = Cystine
Glu = Glutamate
Leu = Leusine
Ala = Alanine
Met = Methaonine
His = Histogene

Fig. 1 : The primary structure of Lysozyme

The primary structure of a protein is defined as a sequence of amino acids that make up its polypeptide chain. This sequence is determined by the genes which dictate a protein's structure and function. A slight change in the primary structure can alter the shape of a protein and its ability to function. Because the R-groups that distinguish the various amino acids play no role in the peptide backbone of proteins, a protein can consist of any sequence

of amino acids. Thus, a protein containing 100 amino acids could form any of 20^{100} different amino acid sequences; that is, the same as 10^{130} or 1 followed by 130 zeroes more than the number of atoms known in the Universe. This is an important property of proteins, since it permits such great diverse.

The primary structure of a protein has its unique number and its sequence of amino acids. As an example, we will examine the primary structure of Lysozyme, the anti-bacteria illustrated in Fig.1. Lysozyme is a relatively small protein. Its single polypeptide chain is only from 1 - 9 amino acids. The primary structure is like the order of letters in a very long word. If left to chance, there will be 20^{129} different ways of arranging the amino acids into a polypeptide chain of its length. However, the precise primary structure of a protein is determined not by the random linking of amino acids but by inherited genetic information. Just a slight change in a primary structure can affect a protein's conformation and ability to function. For instance, the substitution of one amino acid for another at a particular position in the primary structure of Haemoglobin – the protein that carries oxygen in the red blood cells – causes the sickle cell anaemia disease, an inherited blood disorder.

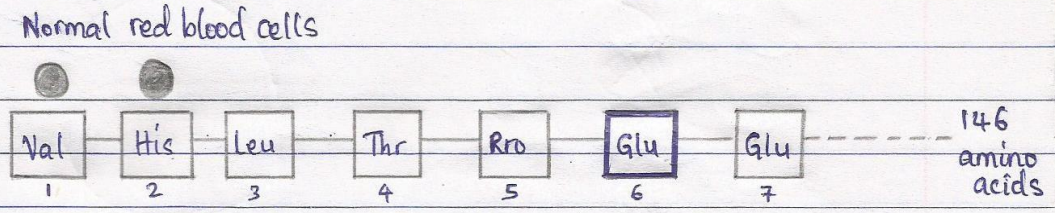


Fig. 2. (A): Normal Red Blood Cells and normal Haemoglobin

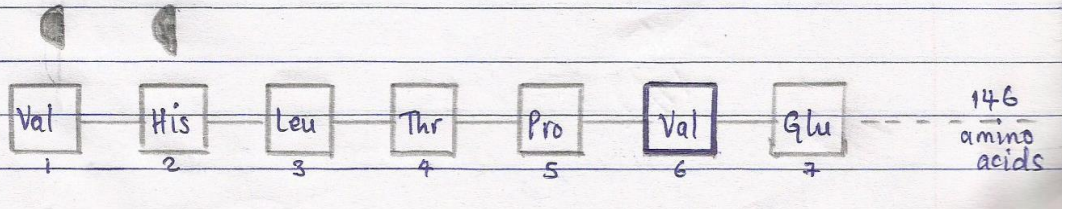
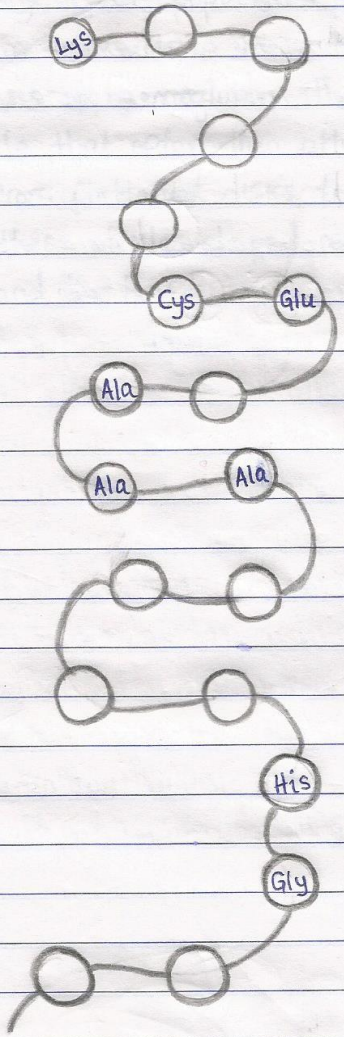
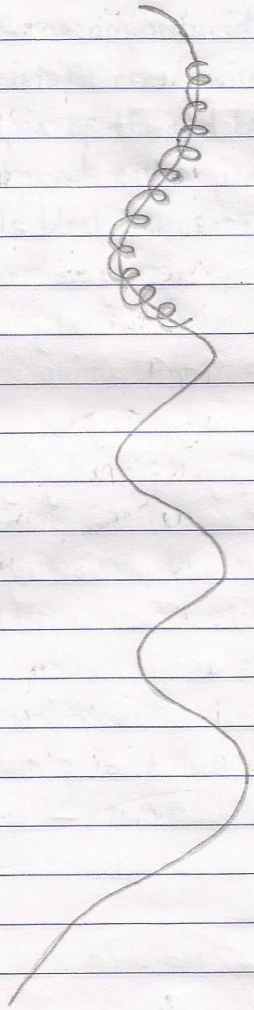


Fig. 2. (B): Sickle-cell Red Blood Cells and Sickle-celled Haemoglobin

The disease sickle-cell anaemia – an inherited blood disorder that primarily affects population in central Africa as well as 1 in 400 African American – results in the substitution of one amino acid by another during synthesis of haemoglobin. This single mistake creates a mishape haemoglobin molecule that often then alters the shapes of the red blood cells changing them from flattened disks to sickle-shaped cells. Death can result when these sickle-shaped red-blood cells block the tiny vessels of the brain and the heart.

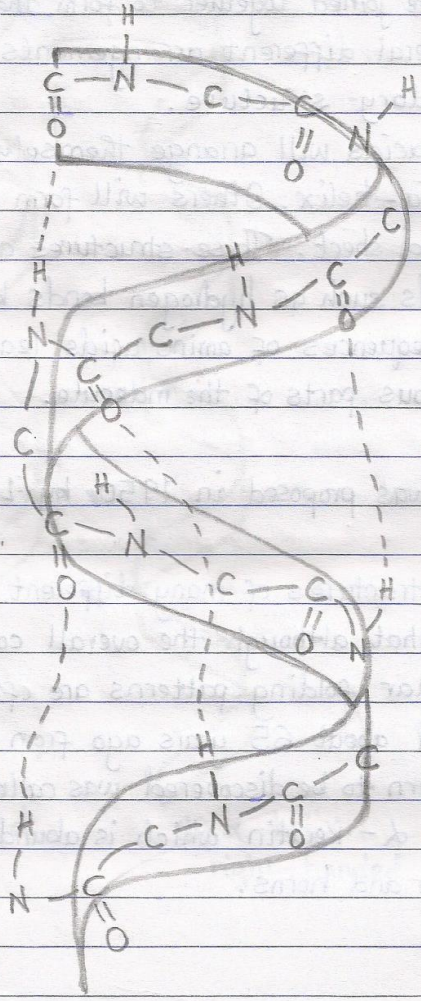
The Secondary Structure of Proteins

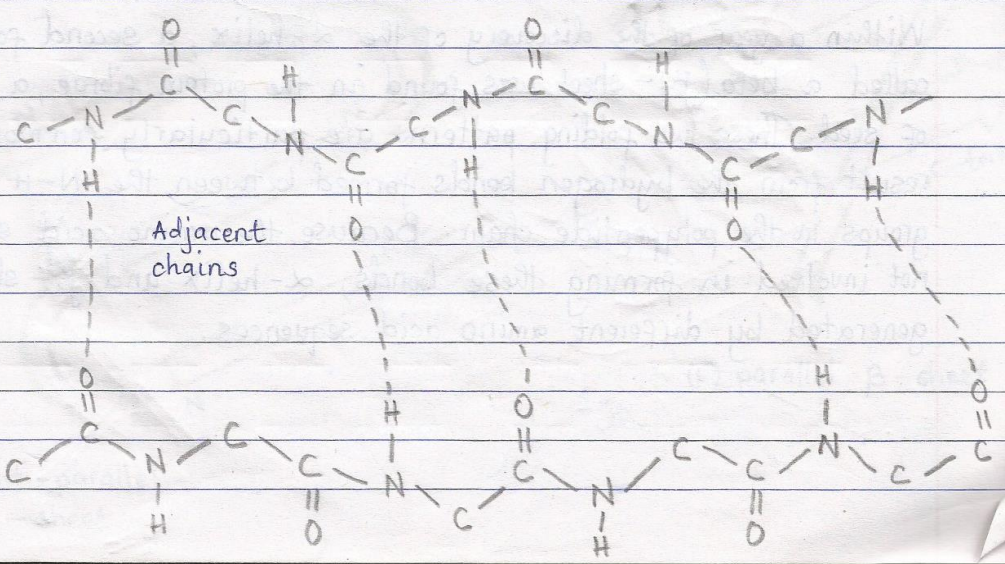




α-helix

Lysozyme
129 amino

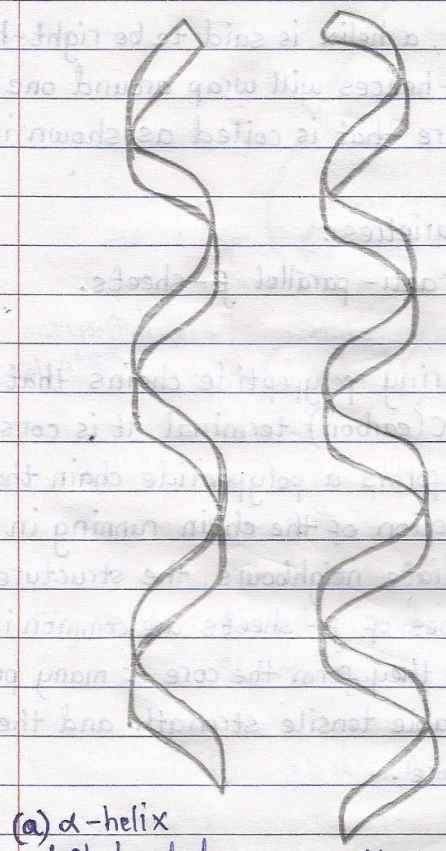

hydrogen
bonds


Adjacent
chains

Once the specific amino acids are joined together to form the primary structure, the amino acids will form several different arrangements within the protein. This is the protein's secondary structure.
Certain sequences of amino acids will arrange themselves into a helical structure termed an alpha-helix. Others will form a pleated structure termed as a beta-pleated sheet. These structures are formed when the amino acids form weak bonds such as hydrogen bonds between other amino acids. This is why certain sequences of amino acids lead to distinctive secondary structures in various parts of the molecule.

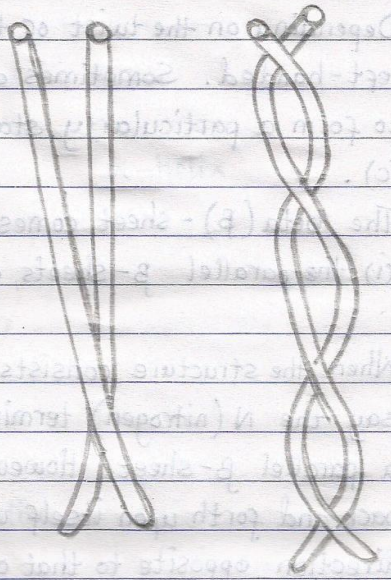
Alpha-helical conformation was proposed in 1950 by Linus Pauling and Robert Corey.
When the three-dimensional structures of many different protein molecules are compared, it becomes clear that although the overall conformation of each protein is unique, two regular folding patterns are often found in parts of them. Both were discovered about 65 years ago from studies on hair and silk. The first folding pattern to be discovered was called the α-helix and it was found in the protein α-keratin which is abundant in the skin and its derivatives such as hair and horns.

Within a year of the discovery of the α-helix, a second folded structure called a beta(β)-sheet was found in the protein fibrae, a major constituent of seed. These two folding patterns are particularly common because they result from the hydrogen bonds formed between the N-H and C=O groups in the polypeptide chain. Because the amino acid side chain are not involved in forming these bonds, α-helix and β-sheet can be generated by different amino acid sequences.

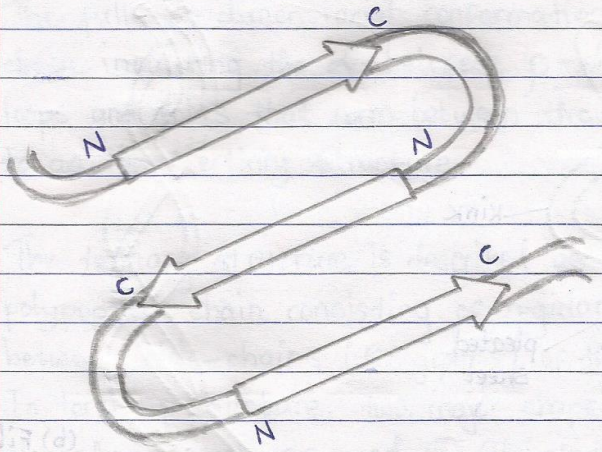


(a) α-helix
left-handed

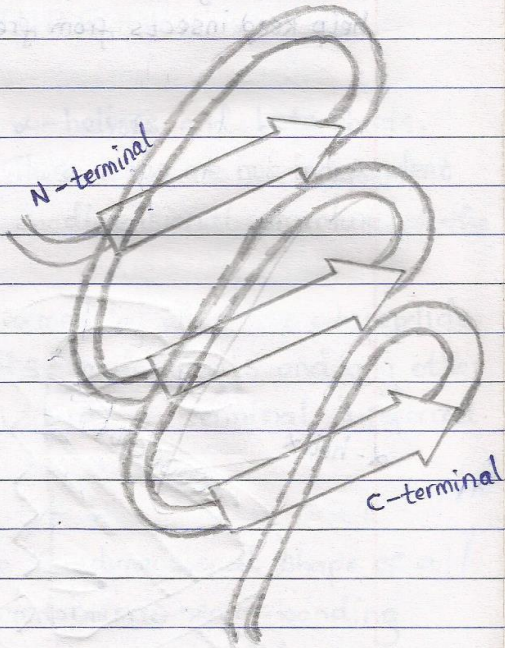
(b) α-helix
right-handed



(c) intertwined α-helices
can form a coiled-coil



(d) anti-parallel
β-sheet



(e) parallel β-sheet

Depending on the twist of the staircase, a helix is said to be right-handed or left-handed. Sometimes a pair of α-helices will wrap around one another to form a particularly stable structure that is coiled as shown in Fig. 1. (c).

The beta (β)-sheet comes into two varieties:
(i) the parallel β-sheets, and (ii) the anti-parallel β-sheets.

When the structure consists of neighbouring polypeptide chains that run from say the N (nitrogen) terminal to the C (carbon) terminal it is considered as a parallel β-sheet. However, when it forms a polypeptide chain that folds back and forth upon itself with each section of the chain running in the direction opposite to that of its immediate neighbours, the structure is called the anti-parallel β-sheets. Both types of β-sheets are common in protein and produce a very rigid structure and they form the core of many proteins. β-sheets give silk fibres their remarkable tensile strength and they can help keep insects from freezing in the core.

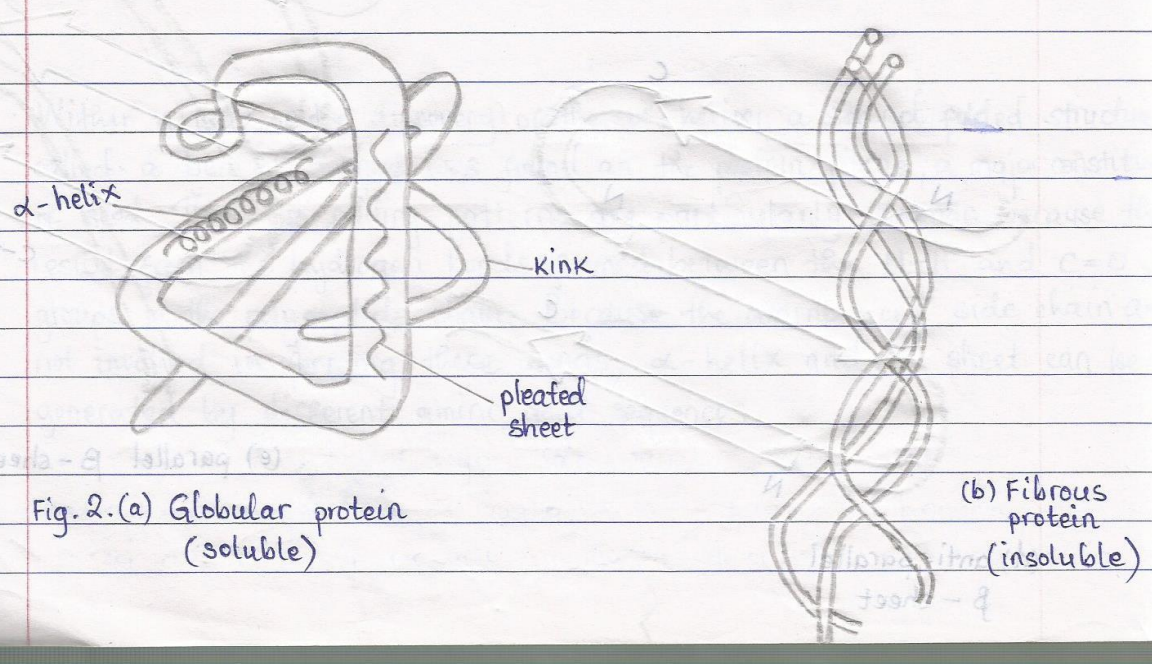


Fig. 2. (a) Globular protein (soluble)

(b) Fibrous protein (insoluble)

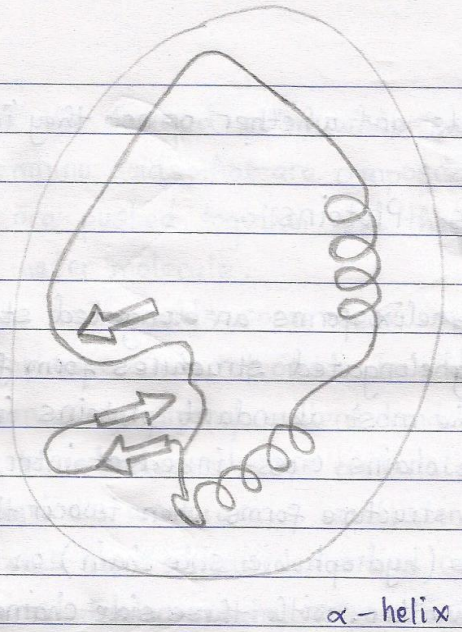


Figure 1 : Globular protein of a single polypeptide chain; Tertiary Structure.

THE TERTIARY STRUCTURE

A protein's structure does not end with α-helises and beta sheets. There are also higher levels of organisation. These levels are not independent but are built one up on the next until the 3-dimensional structure of the entire protein has been fully defined.
The full 3-dimensional conformation formed by an entire polypeptide chain including the α-helixes, β-sheets, random coils and any other loops and folds that form between the -N and -C terminal is referred to as the Tertiary Structure.

The tertiary structure is described as the 3-dimensional shape of a polypeptide chain consisting of regular contortions from bonding between side-chains (R-groups) of the various amino acids.
In tertiary structure, two major shapes exist : ① Fibrous, which have elongated structures and ② Globular, which tend to be spherical.
The shape of a tertiary structures are determined in large parts by the

sequence of amino acids and whether or not they interact with water.

Fibrous Proteins

An un-interrupted α-helix forms an elongated structure
Polypeptides with long elongated structures form fibrous protein. Fibrous proteins are the most abundant proteins in mammals. It consists of parallel polypeptide chains cross-linked at intervals to form long fibrous or sheets. This structure forms when two or three α-helices have most of their non-polar (hydrophobic side chain) on one side so that they can twist around each other, with these side chains facing inwards thereby minimizing their contact with water.

Fibrous proteins are usually insoluble in water and physically tough which suits them for their mainly structural functions, for example Collagen is a fibrous protein that has helical sub-units super-coiled into a larger triple helix. The super-coiled organisation of collagen which is similar to the construction of a rope gives the long fibres great strength. This suits collagen fibres to their function of connecting tissues to their tendons and ligaments.

An un-interrupted β-pleated sheets also form fibrous proteins.

Silk fibroin is the protein that makes up the silk secreated by silk-worms which is made almost entirely of β-pleated sheets.

Globular Proteins

In globular proteins the polypeptide chain is tightly folded to form a spherical shape. Hydrophilic amino acids that have charged polar groups are found outside of the globular protein molecule where they can

interact with the charged polar water molecules.
Hydrophobic amino acids that are composed largely of non-polar methyl (CH_3) groups are pushed together and they cluster inside the molecule to avoid the water molecule.
The non-polar amino acids form weak interactions with each other termed Hydrophobic interactions. In addition, to this weak bond, some amino acids can form strong covalent bonds between sulphur atoms in different cysteine molecule. The combination of strong and weak bonds between the various amino acids results in the tertiary structure of the protein. Proteins that contain extensive regions of sheets generally form globular proteins. Extensive helices are found in fibrous proteins. However, globular proteins can contain short stretches of helices.

Sometimes the R-groups projecting from the backbone of a polypeptide chain interfere with the folding pattern. The presence of certain amino acid residues can introduce a kink into a polypeptide. This can cause the polypeptide to fold up into a compact structure rather than forming an elongated, fibrous structure. Folded compact polypeptides form globular proteins. The structure of globular proteins consists of region of α-helix and region of β-pleated sheets joined together by length of polypeptide containing kinks. Globular proteins are soluble in water; this includes enzymes, antibodies and many hormones.

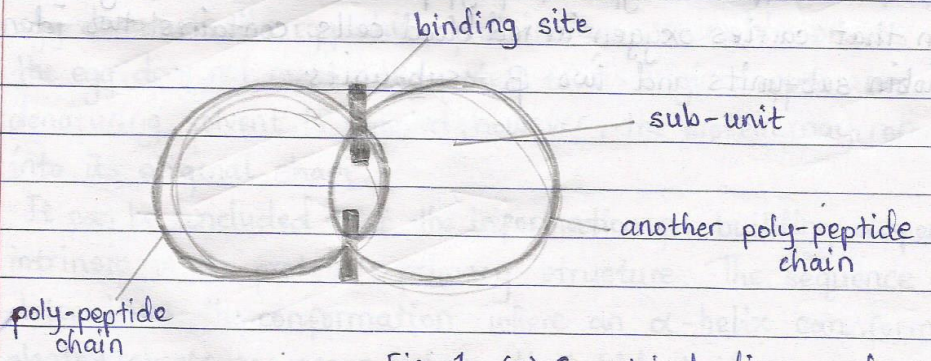


Fig. 1. (a) Symetrical dimer such as CAP proteins is found in bacteria cells.

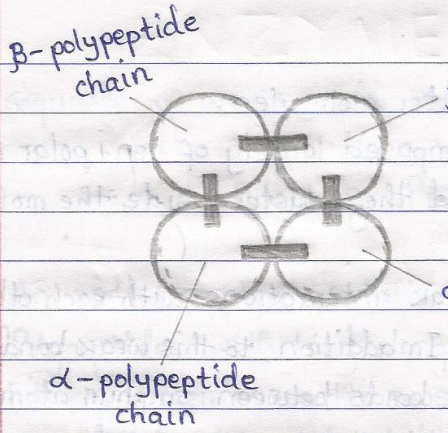


Fig. 1. (b) Asymetrical tetramer such as haemoglobin.

Large protein molecules often consists of more than one polypeptide chains held together by many weak non-covalent bonds that enable a polypeptide chain to form into a specific conformation, also allows proteins to bind to each other to produce larger substances, or structures in the cells.

Any region on a protein's surface that interacts with another molecule through sets of non-covalent bonds is termed as a Binding Site.

A protein can contain binding sites for a variety of molecules, both large and small. If a binding site recognizes the surface of a second protein, the tight binding of two folded polypeptide chains at this site will create a large protein molecule. Each polypeptide chain in such a protein is called a Sub-unit. These chains or sub-units may be identical or different. Such proteins that consist of more than one polypeptide chain, which has a specific shape are termed as the Quatenary structure. Other proteins contain more different types of polypeptide chains. Haemoglobin, the protein that carries oxygen in red blood cells contains two identical α-globin sub-units and two β-sub-units.

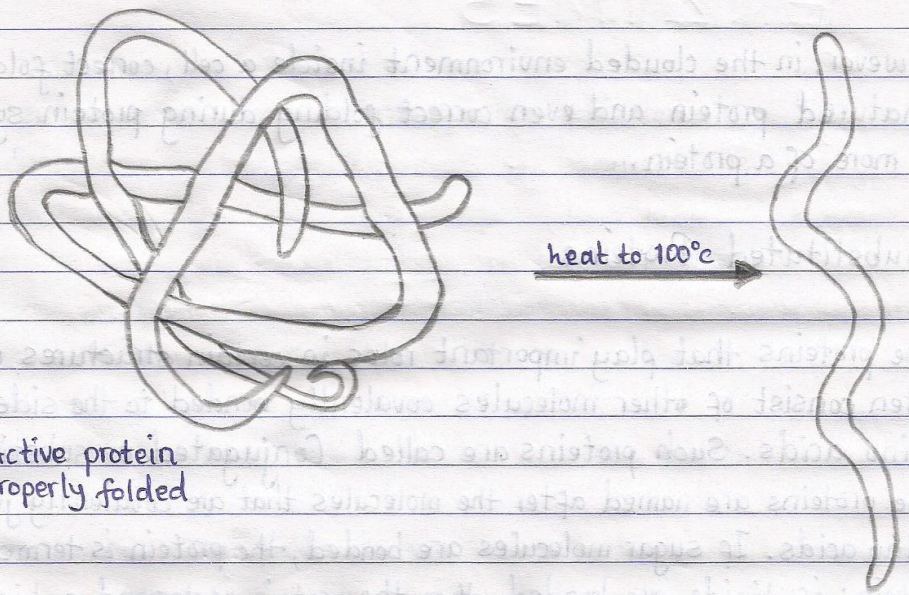


Fig 2 : Denaturation of a protein

A protein must have its proper shape to function. When proteins encounter different conditions such as high temperatures, high or low pH, or certain solvents, bonds within the proteins are broken and its shape changes (Fig. 2). The protein becomes denatured, and no longer functions.

Most bacteria cannot grow at high temperature because their enzymes are denatured by the heat. Denaturation may be reversible in some cases while in other cases it is irreversible. For example, boiling an egg denatures the egg white protein, an irreversible process since cooling the egg does not restore the protein to its original appearance. If a denaturing solvent is removed, however, the protein may reform spontaneously into its original shape.

It can be concluded that the information for building a specific shape is intrinsic in the protein's primary structure. The sequence of amino acids determines the conformation where an α-helix can form, where pleated sheets can occur, where disulphide bridges are located, where ionic bonds can form and so on.

However, in the clouded environment inside a cell, correct folding of a denatured protein and even correct folding during protein synthesis may be more of a protein.

Substituted Proteins

The proteins that play important roles in certain structures of the cell often consist of other molecules covalently bonded to the side chains of amino acids. Such proteins are called Conjugated or substituted proteins. The proteins are named after the molecules that are covalently joined to the amino acids. If sugar molecules are bonded, the protein is termed a Glyco-protein; if lipids are bonded, then the protein is termed a Lipoprotein.

ENZYMES

In living cells, hundreds of different biochemical reactions take place rapidly and simultaneously. The reactions go on at relatively low temp (4°-40°C) and normally controlled in such a way that useful products are made and wastes are removed at rates which satisfy the metabolic needs of cells. How can reactions take place so rapidly at such modest temperature?

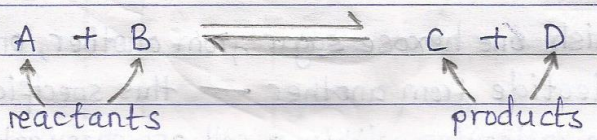
The answer to this question comes from a study of enzymes.

Enzymes were isolated almost accidentally in 1897 by Hans and Edward Buchner; they were interested in making extracts of yeast cells for a medical purpose. One of the problems they were facing was how to preserve the yeast juice. They tried various methods, one of which involved adding larger amounts of sucrose to the juice. To their surprise they found that the sugar was fermented eventhough there were no live yeast cells in the mixture. Up to this time, it was thought that fermentation could only take place in the presence of living organisms. The word "enzyme" meaning "in yeast" was used to describe the substance or substances in yeast juice which brought about the fermentation of sucrose.

THE STRUCTURE OF ENZYMES

Over 90 percent of enzymes are globular proteins; the remainder are conjugative proteins which have a non-protein fraction called a Prosthetic group. Most enzymes have relative molar masses between 50,000 to 200 000 (g/mol).
Enzymes are soluble in water and work in aqueous solutions in living cells.

A Catalyst is a substance which affects the rate of a chemical reaction. The biochemical reactions catalysed by enzymes are mainly reversible reactions.
An example of a reversible reaction is as follows:



At equilibrium, the rate at which A and B are converted to C is equal to the rate at which C is converted back to A and B. The position of the equilibrium depends on the energy difference between the reactants and the products. Enzymes do not change the direction of the reaction; they, however, speed up the rate at which equilibrium is reached.

All enzymes are proteins and such they have the properties of proteins:

(i) they are polymers of amino acid residues.
(ii) they are denatured by high temperatures and extremes in pH.
(iii) they have three dimensional structures that are unique to that particular protein.
(iv) their final shape is determined by the sequence of the amino acid residues.
(v) some enzymes require non-protein groups to function effectively.

Enzymes are different from other catalysts.

Most inorganic catalysts catalyse a series of reactions that are involved with similar substances. Enzymes, however, are very specific; they catalyse only one particular reaction.

An enzyme can distinguish one hexose sugar from another, one amino acid from another, one nucleotide from another — this specificity is very essential as many of the molecules within a cell are chemically very similar, differing from each other only by the position of one small group of atoms. Each enzyme has a specific substrate. The substrate is the substance that interacts with the enzyme and then reacts. All enzymes are catalysts and as such, they have properties of catalysts:

(i) they increase the rate of a reaction.
(ii) they do not change the outcome of the reaction.
(iii) the enzyme itself emerges unchanged from the reaction.

Most enzymes are named according to a system of rules given below:

(i) Enzymes' names end in — ase; example: amylase and hydrolase.
(ii) The second part of the name, the one that end in —ase describes the type of reactions that the enzyme catalyses; example: the enzyme oxidase oxidises substrates.
(iii) The first part of the name is the name of the enzyme's substrate; example: glucose phosphate isomerase rearranges the atoms in a glucose phosphate molecule.

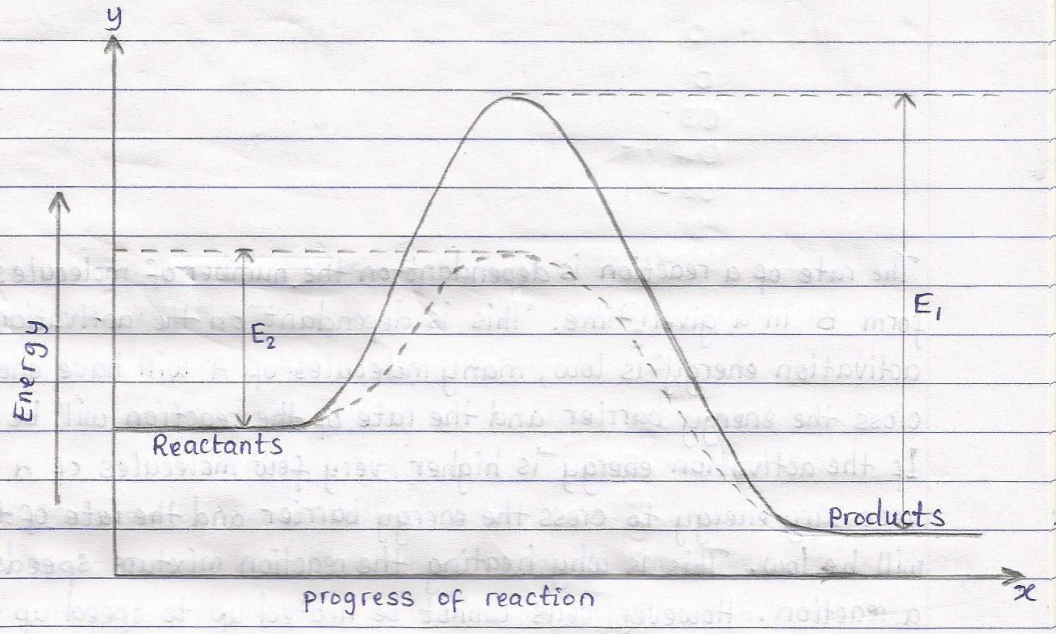


Fig. 1: Energy diagram showing a catalysed and uncatalysed chemical rxn.

The rate of a reaction (rxn) can be measured by monitoring how the concentration of the reactants decreases with time or the how the concentration of the products increases with time.
A simple reaction in which a reacting molecule 'A' gives a product 'B' can be modelled by the graph shown above in Fig. 1.

Enzyme Action.

Enzymes lower the barriers that block chemical reactions.

Catalysis and energy of activation.

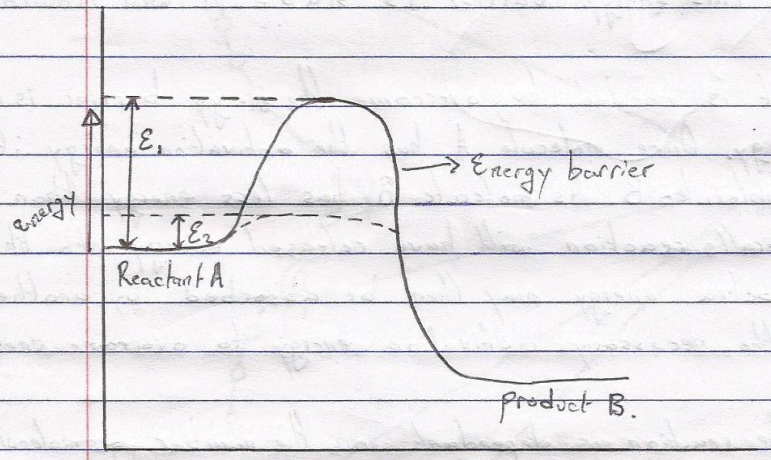


Fig 1: Energy diagram showing a catalysed and uncatalysed chemical reaction.

E_1 = Activation energy of un-catalysed reaction.

E_2 = Activation energy of catalysed reaction

———— uncatalysed reaction

– – – – – – catalysed reaction

The rate of the reaction can be measured by monitoring how the concentration of the reactants decreases with time or how the concentration of the ~~increases~~ product increases with time.

A simple reaction in which a reacting molecule A gives the product molecules B can be modelled by a graph ~~showing~~ shown in Fig 1.

In the reaction shown, molecule A has a certain amount of energy stored in it while molecule B has less energy stored in it.

Although molecule A has more energy stored in it than molecule B, it doesnot not automatically react to give molecule B, because in order

to start reacting, it needs extra energy. This is shown in figure 1 as a peak on the graph, we say that their is an energy barrier between molecule A and molecule B that most be crossed, before molecule A can react. Because of this energy barrier is stable, it will remain as it is.

The energy that is needed to overcome the energy barrier is called the activation energy. Once molecule A has the activation energy it will react to form molecule B. As molecule B has less energy than molecule A, the overall reaction will have released energy into the surrounding this extra energy may then be absorbed by another molecule giving it the necessary activation energy to overcome energy barrier.

The rate of the reaction is dependant on the number of molecules of A that form B in a given time. This is dependant on the activation energy. If the activation-energy is low, many molecules of A will be high If the activation energy is high, very few molecules of A will have the necessary energy to cross the energy barrier and the rate of the reaction will be low. This is why heating the mixture speeds up the rate of reaction, so the rate is increased by enzymes. Each enzyme binds tightly to 1 molecule of substrate and holds it in a way that greatly reduces the activation energy of a particular chemical reaction that the bound substrate can undergo. The substance that can lower the activation energy of a reaction is termed as a catalyst. Enzymes like all catalysts work by decreasing the activation energy of the reaction. Once the energy barrier has being lowered the molecules of A will need energy, in order to react to form molecule B. This means that more molecules of A will react so rate of reaction is increased.

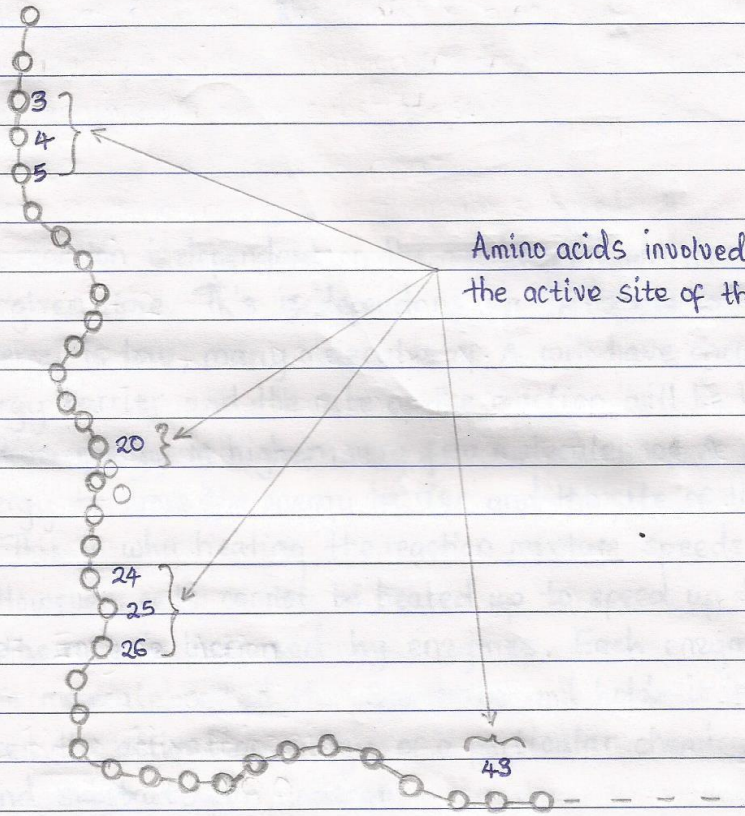


Fig. 1. (a) Position of the amino acids of the active site shown as the primary structure of the enzyme.

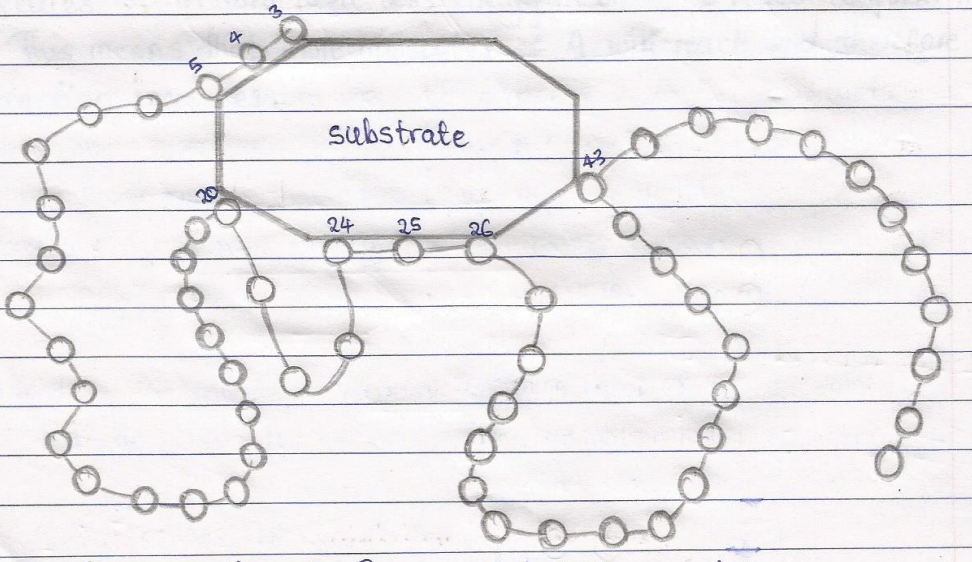


Fig. 1 (b) Representation of Enzyme - substrate complex

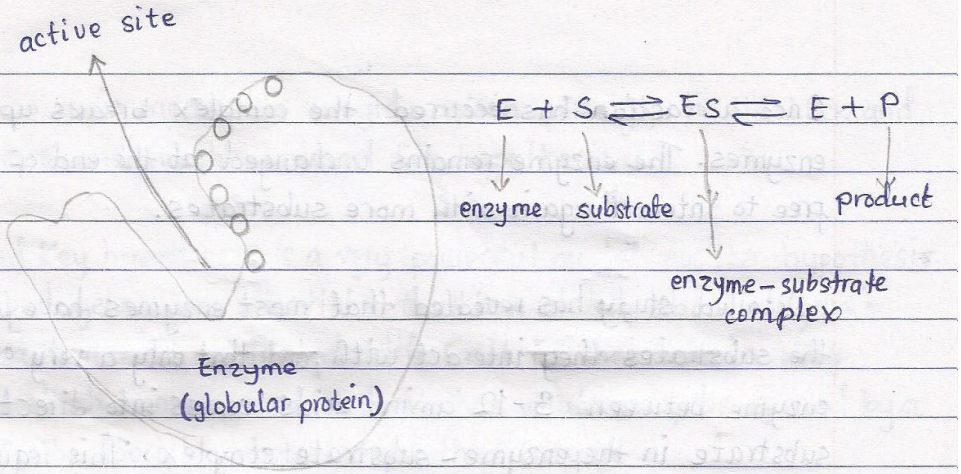


Fig. 2: There is a groove or pocket in the enzyme where the substance will bind the active site.

Certain terms are used to describe reactions that are catalysed by enzymes.

Thousands of scientists specialised in the study of enzymes and their properties. When many scientists study the same subject, they need a language that will help them communicate with each other so that when one scientist uses a certain word the other scientist interprets it in the right way.
The reactants in an enzyme-catalysed reaction are all called the Substrate, while the products are still referred to as Products.
Abbreviations are often used: E for enzymes, S for substrates, and P for products. Square brackets [ ] are used for concentration. [S] means concentration of substrate and [P] means the concentration of products.

Reactions catalysed by enzymes suggest that an enzyme binds with its substrate to form a short-lived Enzyme-Substrate complex.

$$E + S \rightleftharpoons ES \rightleftharpoons E + P$$

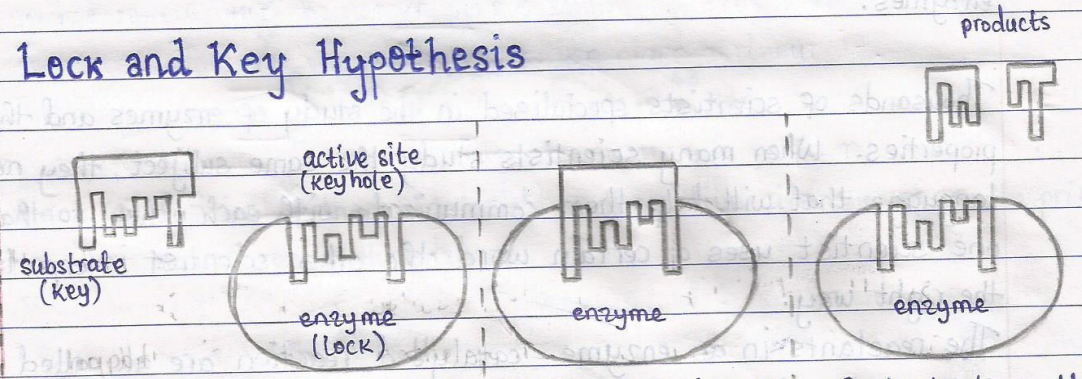
Enzyme — Substrate — Enzyme-Substrate Complex — Enzyme — Product

Once a reaction has occured, the complex breaks up into products and enzymes. The enzyme remains unchanged at the end of the reaction and is free to interact again with more substrates.

Detailed study has revealed that most enzymes have large molecules than the substrates they interact with, and that only a very small portion of the enzyme between 3-12 amino acids comes into direct contact with the substrate in the enzyme-substrate complex. This region is called the Active Site of the enzyme. It is here that binding of the substrate occurs. The remaining amino acids, which comprise the bulk of the enzyme, function to maintain the correct globular shape of the enzyme molecule.

Mechanism of Enzyme Action

1. Lock and Key Hypothesis



Substrate arrives at the active site of an enzyme. The enzyme has a hole that is exactly the right one shape to fit the substrate

Substrate fits into the active site where the rearrangement of the molecules occurs to form products. This is called Enzyme-Substrate Complex in which substrate binds the active site.

Products leave the active site.

Fig. 1 : Fischer's Lock and Key hypothesis.

There are two main models of enzyme action namely, (i) the Lock and Key hypothesis and (ii) the Induced Fit hypothesis.

The Lock and Key hypothesis is a very powerful model modern hypothesis that has helped generation scientists to think clearly about enzyme-catalysed reactions. It originated with Emil Fischer who in 1894 suggested that the enzyme was a lock that would only be opened by a certain key, the specific substrate ~~of~~ for that enzyme.
He further suggested that there is a keyhole in the enzyme that is specific with a fixed shape. The keyhole is called the active site.
The active site is where the substrate binds to that enzyme and where the reaction occurs. The active site is exactly the right shape to bind the substrate molecule. The substrate binds to the enzyme like a key fitting into a lock. Once the substrate has bound to the active site, the reaction occurs and products are released leaving the active site free to receive further substrate molecules.

2. The Induced Fit Hypothesis

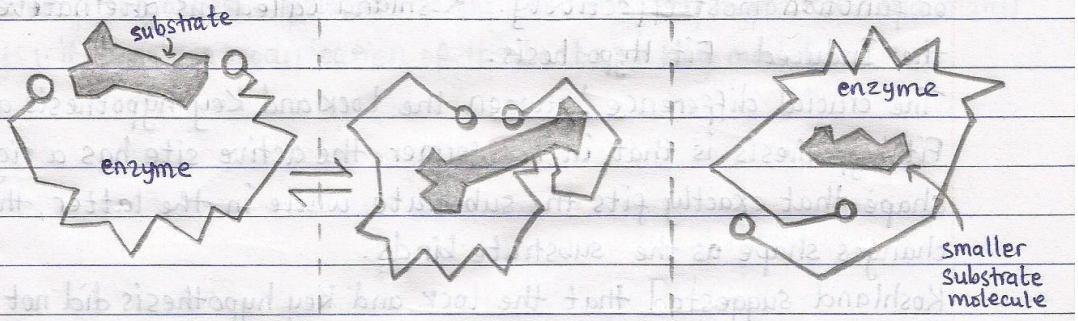
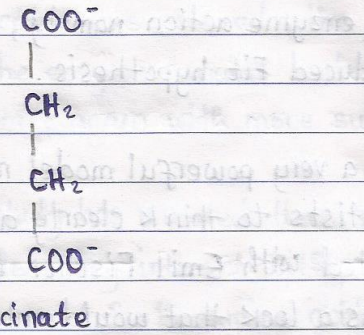


Fig. 2: Diagram to show Koshland's induced fit hypothesis.



In 1959, Koshland suggested a modification to the Lock and Key hypothesis. He suggested that enzymes and their active sites are basically more flexible structures than rigid or fixed structures. which were described by the Lock and Key hypothesis. Koshland proposed that a dynamic interaction occuring between enzymes and substrates occurs. When a substrate combines with an enzyme, it induces change in the enzyme structure so that the active site's shape changes and the change is so essential. The reaction would not take place without it.

The amino acid which constitutes the active site are moulded (changed) into a precise formation which enables the enzyme to perform its catalytic role or function most effectively. Koshland called his alternative modern model the Induced-Fit Hypothesis.

The crucial difference between the Lock and Key hypothesis and the Induced Fit hypothesis is that in the former, the active site has a rigid structure shape that exactly fits the substrate while in the latter, the active site changes shape as the substrate binds.

Koshland suggested that the Lock and Key hypothesis did not explain why enzymes do not catalyse reactions when a substrate is replaced by a smaller but chemically similar molecule. If the active site was precisely the correct shape to catalyse the reaction as the Lock and Key hypothesis suggested, the small molecules should be able to slip or glide into the site and undergo a reaction. This does not happen because only the substrate itself reacts. Koshland suggested that there was an extra step that had to happen before the reaction could take place and that this step required

the correct substrate. He further suggested that the R-groups necessary for the reaction were not in the right positions for the reaction to occur when the enzyme has no substrate bound.
When the small molecules enter the active site, they do not fit and the R-groups stay in the wrong position. However, when the correct substrate enters the active site of the shape, the whole protein changes to bring the R-groups into the correct position and the reaction goes ahead.

X-ray diffraction studies of the enzymes carboxylpeptidase, have provided evidence that the change in shape does occur when the substrate binds. Scientists have compared the shape of the enzyme carboxylpeptidase with a bound substrate molecule and results have shown that the enzyme does indeed have a different shape structure from the enzyme part to the enzyme-substrate complex. This X-ray diffraction data supported the idea that there is change in the three dimensional (3D) structure of the enzyme and it is what is called the Conformation change when the substrate binds. This indicates that the induced-fit hypothesis may be more accurate than the Lock and Key hypothesis. But it should be kept in mind that the induced fit hypothesis grew out of the Lock and Key hypothesis and many ways; it is only a modification of the Lock and Key model.

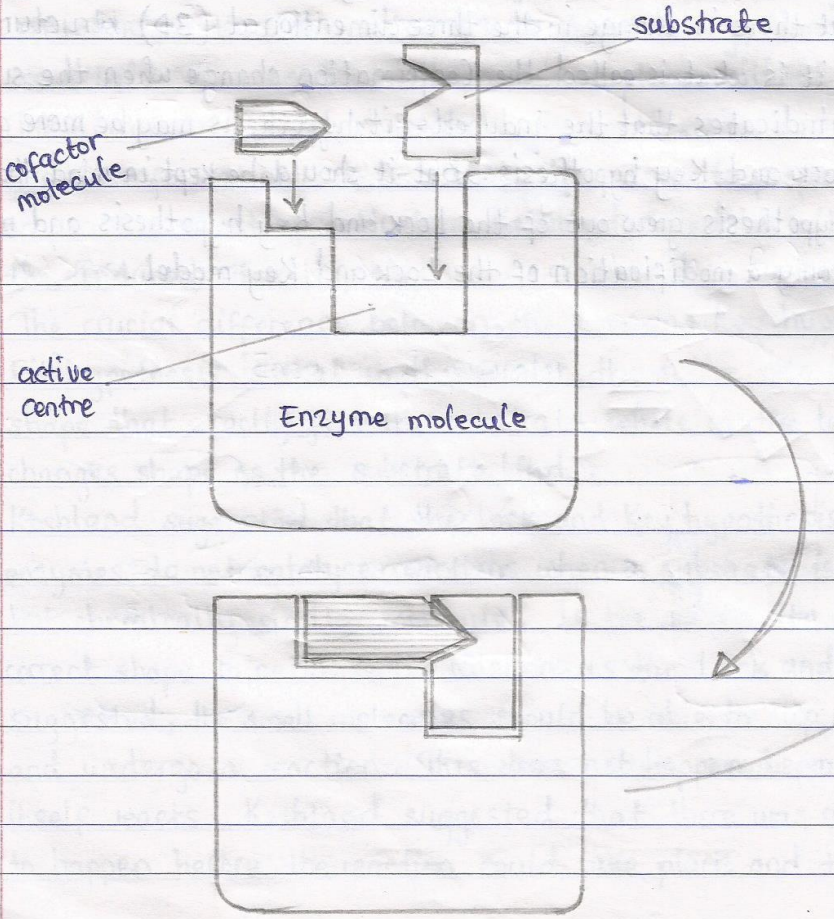
Enzyme Cofactors

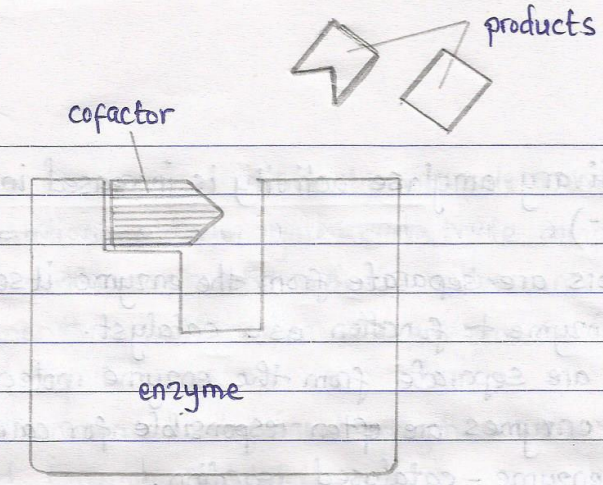
Many enzymes will not work correctly or efficiently unless the smaller non-protein substance called a Co-factor is present within the active centre.

Co-factors

- Inorganic ions
  - Zn^{2+}
  - Heam
- Organic molecules

The figure below, Fig





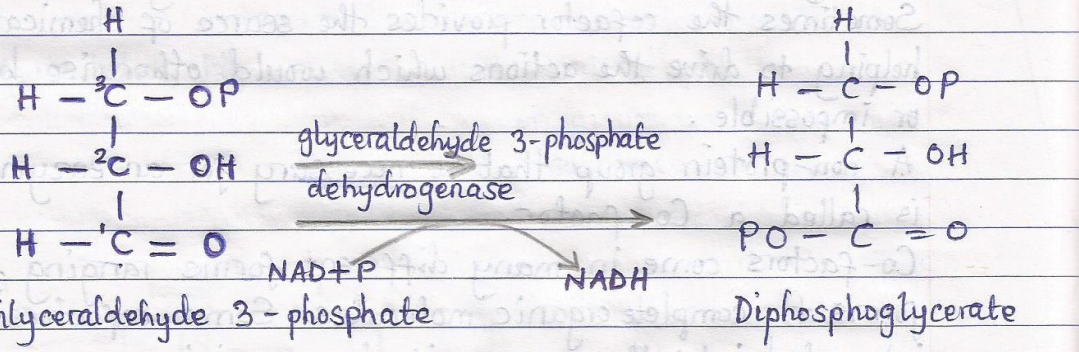
As shown in figure 1, the co-factor usually acts as a bridge between the enzyme and its substrate. Often it contributes directly to the chemical reactions which bring about
Sometimes the cofactor provides the source of chemical energy helping to drive the actions which would otherwise be difficult or impossible.
A non-protein group that is necessary for an enzyme to function is called a Co-factor.
Co-factors come in many different forms ranging from inorganic forms to complete organic molecules. Some cofactors are actually integrated into the enzyme itself, remaining as part of the enzyme molecule at all times. Zn^{2+} is a cofactor for the enzyme carboxypeptidase and the zinc ion is part of the structure of the enzyme molecule, held in place by the R-groups of the amino acid residues.
Another one, Heam, is a cofactor for a number of different enzymes including Cytochrome oxidase, and enzyme in respiration. These inorganic ions are thought to mould either enzyme or the substrate into a shape such that an enzyme substrate complex can be formed, hence increasing the chances of the reaction occuring between them, and therefore increasing the rate of reaction catalysed by that particular enzyme.

For example, salivary amylase activity is increased in the presence of chlorine ions (Cl^-).

Some cofactors are separate from the enzyme itself but still necessary for the enzyme to function as a catalyst.

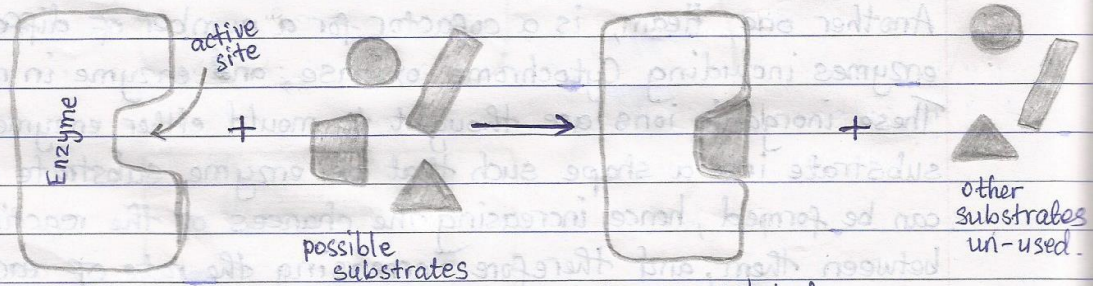
~~Co~~ factors that are separate from the enzyme molecule are called Co-enzymes. Co-enzymes are often responsible for carrying small atoms into or out of an enzyme-catalysed reaction.

For example, the Nicotinamide Adenine Dinucleotide (NAD) bring H hydrogen into a reaction or takes it away from the reaction, and therefore it is called a hydrogen-carrier.



NAD is derived from Nicotinic Acid (Vitamin B_3).

Enzyme Specificity



enzyme-substrate complex formed only with substrate having a complementary shape to active center of enzyme.

Because enzyme and substrate molecules are 3-dimensional structures, the formation of an enzyme-substrate complex requires that the shapes of the reactants and the active centers of the enzymes are complementary, otherwise the enzyme and the substrate cannot unite (Fig. 1.)

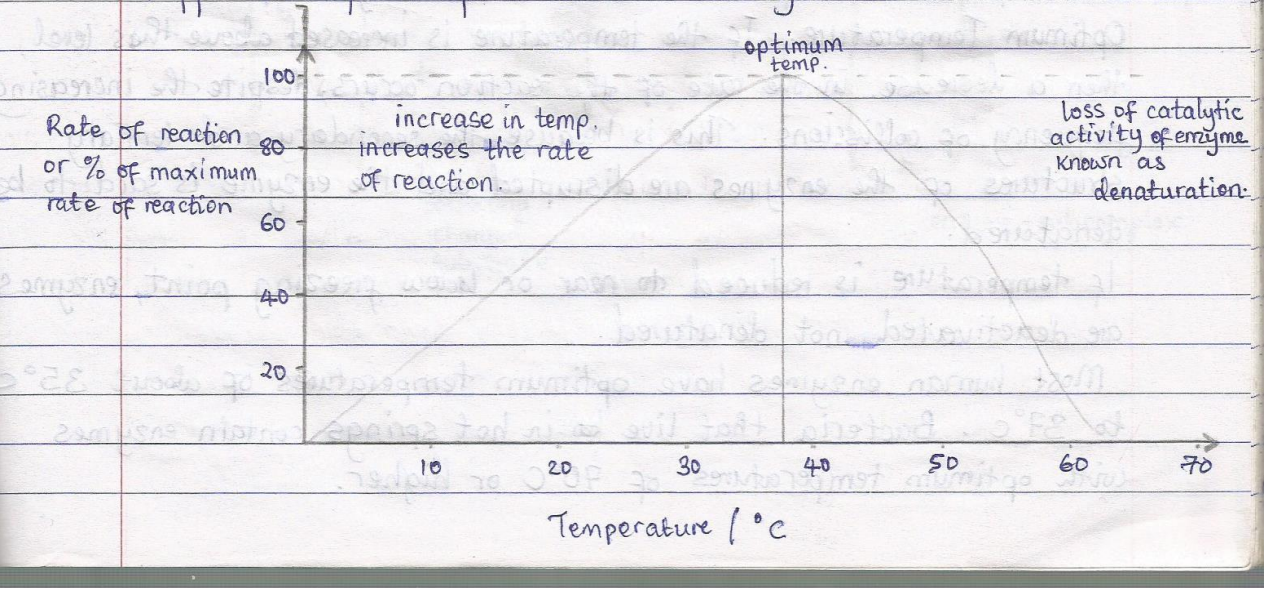
The phenomenon whereby most enzymes work with only one substrate is called Enzyme Specificity.

One of the systems used to name enzymes is based on the substrate with which the enzyme combines. For example, Lipases reacts with lipids

Factors affecting enzyme action

1. Enzyme concentration
2. Substrate concentration
3. Temperature
4. PH (Potential Hydrogen)
5. Co-factors
6. Inhibitors

1. Effects of temperature on Enzyme action



Temperature Coefficient (Q10) = $\frac{\text{rate of reaction at } t\,^{\circ}C + 10^{\circ}C}{\text{rate of reaction at } t\,^{\circ}C}$

The term (Q10) is used to express the effect of a 10°C rise in temperature between 4°C and the optimum temp (37°C) is equal to 2 or double activity.

When investigating the effect of a given factor on the rate of enzyme action, all other factors should be kept constant and at optimum levels whenever possible.

The effect of temperature on the rate of a reaction can be expressed as a temperature coefficient. The term 'temperature coefficient' is used to express the effect of a 10°C rise in temperature on the rate of a chemical reaction between 4°C and the optimum temperature (37°C).
The rate of an enzyme reaction is doubled for every rise of 10°C, meaning that Q10 equals two (2).
Heat increases molecular motion, thus the reactants move more quickly and chances of their collision into each other are increased. As a result, there is a greater probability of a reaction being caused.
The temperature that promotes maximum activity is referred to as the Optimum Temperature. If the temperature is increased above this level, then a decrease in the rate of the reaction occurs, despite the increasing frequency of collissions. This is because the secondary and tertiary structures of the enzymes are disrupted and the enzyme is said to be denatured.
If temperature is reduced to near or below freezing point, enzymes are deactivated, not denatured.
Most human enzymes have optimum temperatures of about 35°C to 37°C. Bacteria that live in hot springs contain enzymes with optimum temperatures of 70°C or higher.

2. The effect of pH on the rate of enzyme-catalysed reactions.

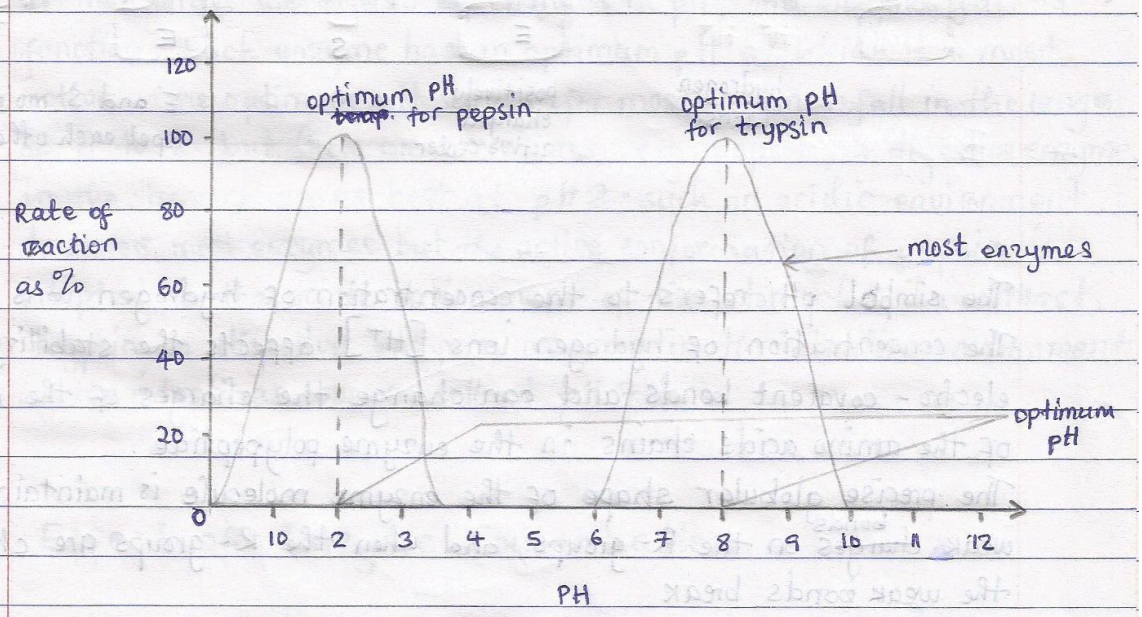
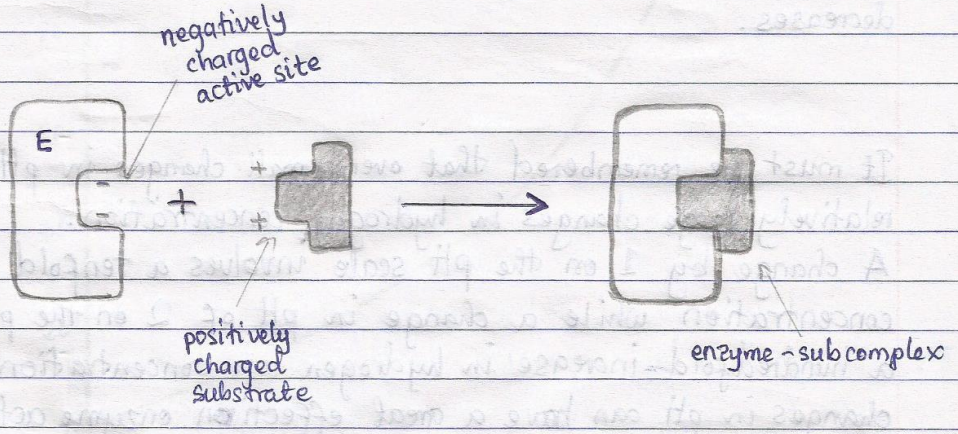
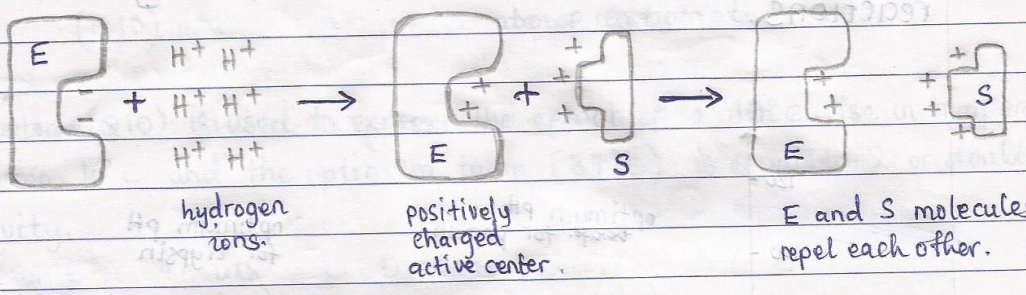


Fig. 2 : The effect of pH on the rates of enzyme reactions.





hydrogen ions.

positively charged active center.

E and S molecules repel each other.

The simbol pH refers to the concentration of hydrogen ions in solution. The concentration of hydrogen ions $[H^+]$ affects the stability of the electro-covalent bonds and can change the charges of the R-groups of the amino acids chains in the enzyme polypeptide.
The precise globular shape of the enzyme molecule is maintained by weak ~~charges~~ bonds on the R-groups, and when the R-groups are changed, the weak bonds break

Once the 3-dimensional shape of an enzyme molecule is altered, then the molecule as a catalyst is ineffective and the rate of reaction decreases.

It must be remembered that even small changes in pH mean high and relatively large changes in hydrogen concentration.
A change by 1 on the pH scale involves a tenfold change in hydrogen concentration while a change in pH of 2 on the pH scale represents a hundredfold increase in hydrogen ion concentration. Thus even small changes in pH can have a great effection enzyme activity.
Apart from the effect in denaturing enzymes, changes in hydrogen ion concentration can change the ionisation of the amino acid residues at the active centers of enzymes.

Ionisation of reactants can also be affected. The formation of enzyme-subcomplex sometimes depends on the

If the charges are altered by changes in pH, some enzymes fail to function. Each enzyme has an optimum pH at which it is most active. The optimum pH values for most enzymes fall in the range of 6 to 8 but there are exceptions .e.g pepsin, a digestive enzyme, in the stomach works best at pH 2; such an acidic environment denatures most enzymes but the active conformation of pepsin is adapted to the acidic environment of the stomach. In contrast, trypsin, a digestive enzyme, working in the alkaline environment of the intestines works well at pH 7.

3. Effect of Enzyme Concentration.

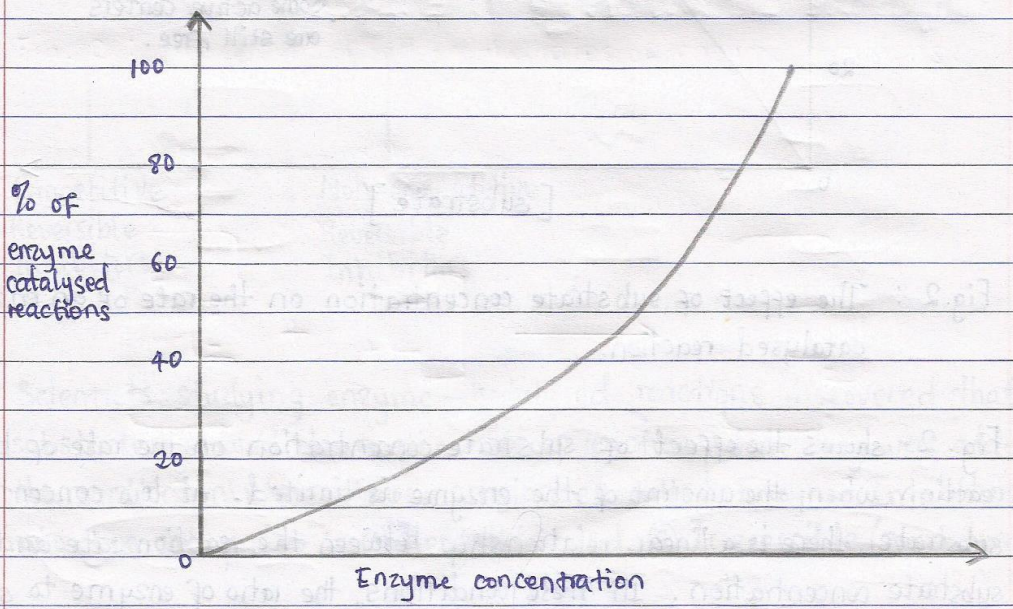


Fig. 1 : Relationship between enzyme concentration and the rate of enzyme reaction.

Provided that the substrate concentration is maintained at an high level and other conditions such as pH, temperature are kept constant, the rate of the reaction is proportional to the enzyme concentration. When the enzyme concentration is increased, the enzymatic reaction increases.

4 Effect of Substrate Concentration

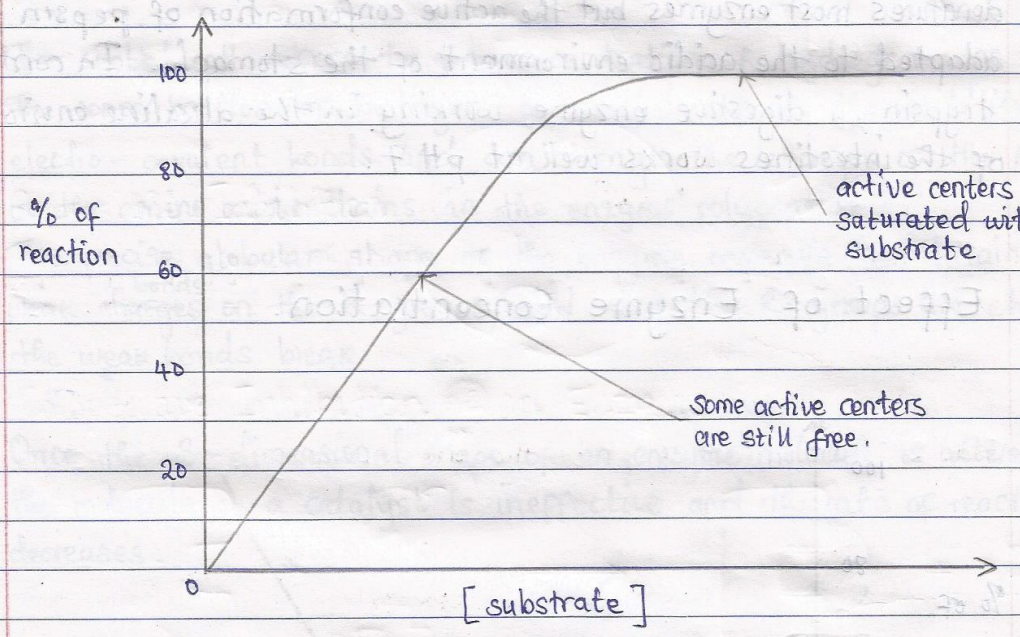
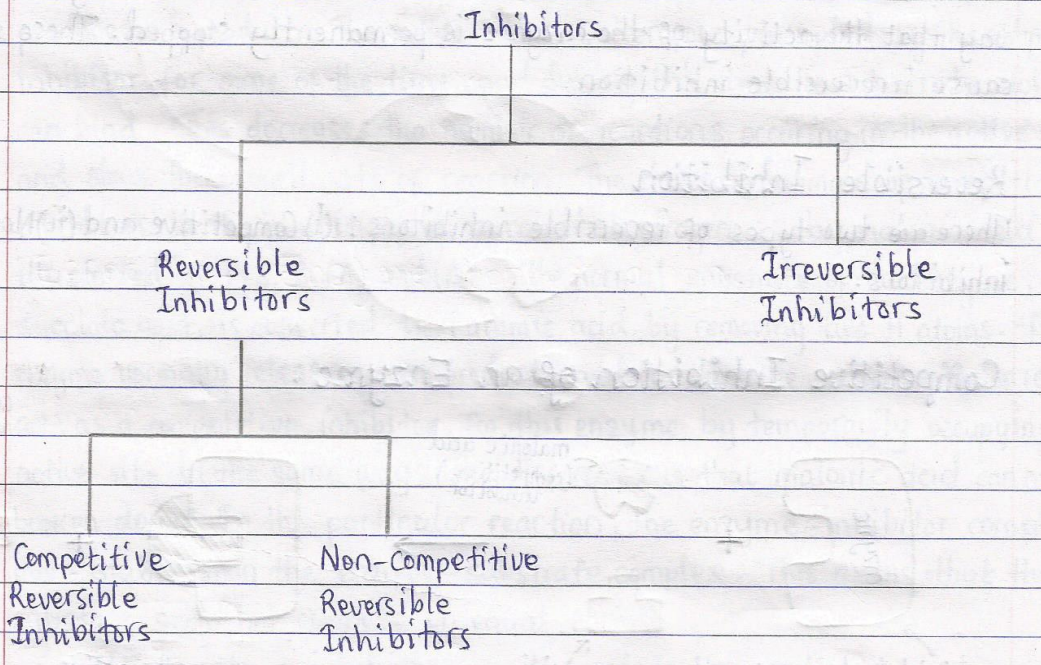


Fig. 2 : The effect of substrate concentration on the rate of an enzyme - catalysed reaction.

Fig. 2 shows the effect of substrate concentration on the rate of biochemical reaction when the amount of the enzyme is limited. At low concentration of substrate, there is a linear relationship between the reaction rate and the substrate concentration. In these conditions, the ratio of enzyme to substrate molecules is high. Consequently, some active centres of enzymes are always free for the reactants to bind with the enzyme. However, a point is reached when a further increase in substrate concentration does not produce significant

change in the reaction rate. This is because at high substrate concentration the active sites of the enzyme molecules at any given moment are saturated with substrates, thus any extra substrate has to wait until the enzyme-substrate complex has dissociated into products.

5. Effect of Enzyme Inhibitors



Scientists studying enzyme-catalysed reactions discovered that certain substrates slowed down the rate of reaction when they were added to the reaction mixture. These substances called Enzyme Inhibitors fall into two categories: ① Reversible and ② Irreversible (Non-reversible).

Reversible Inhibitors.

Reversible inhibitors are substances which prevent enzymes from combining with substrates. Activity of the enzyme is restored when the inhibitor is removed.

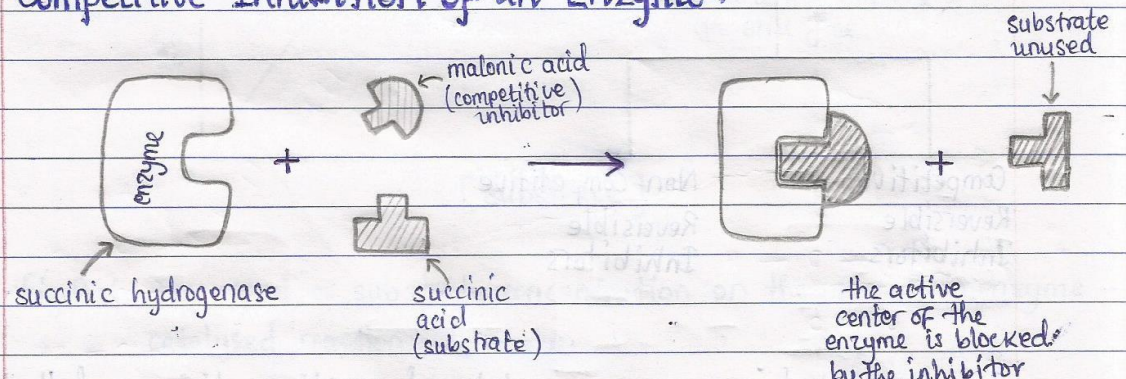
Non-Reversible Inhibitors

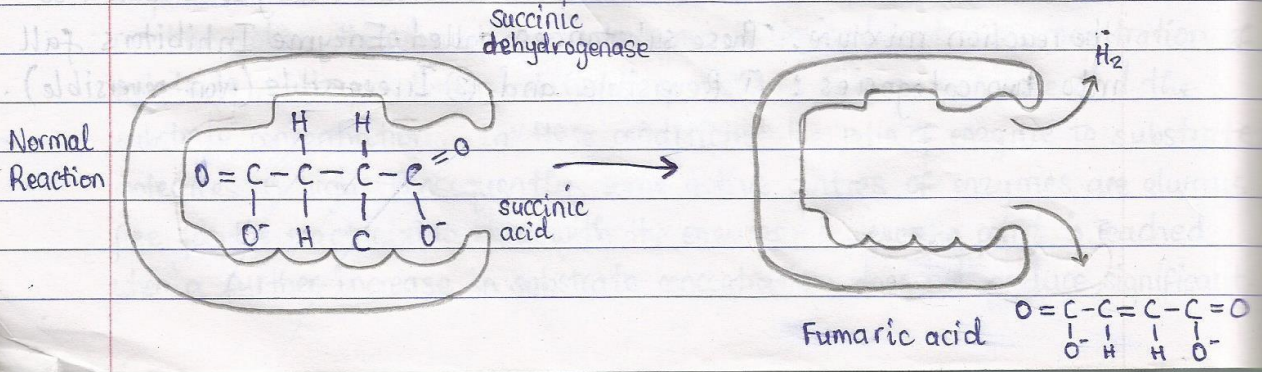
Non-reversible inhibitors are substances that bind with enzymes in such a way that the activity of the enzyme is permanently stopped. These substances cause irreversible inhibition.

Reversible Inhibition

There are two types of reversible inhibitors: (i) Competitive and (ii) Non-competitive inhibitors.

Competitive Inhibition of an Enzyme.





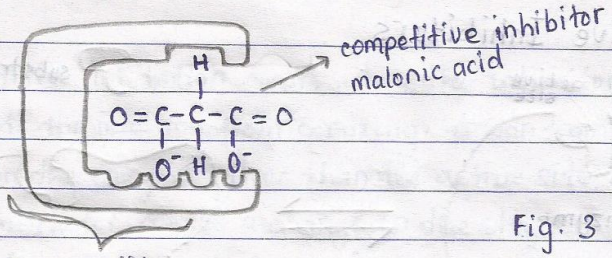


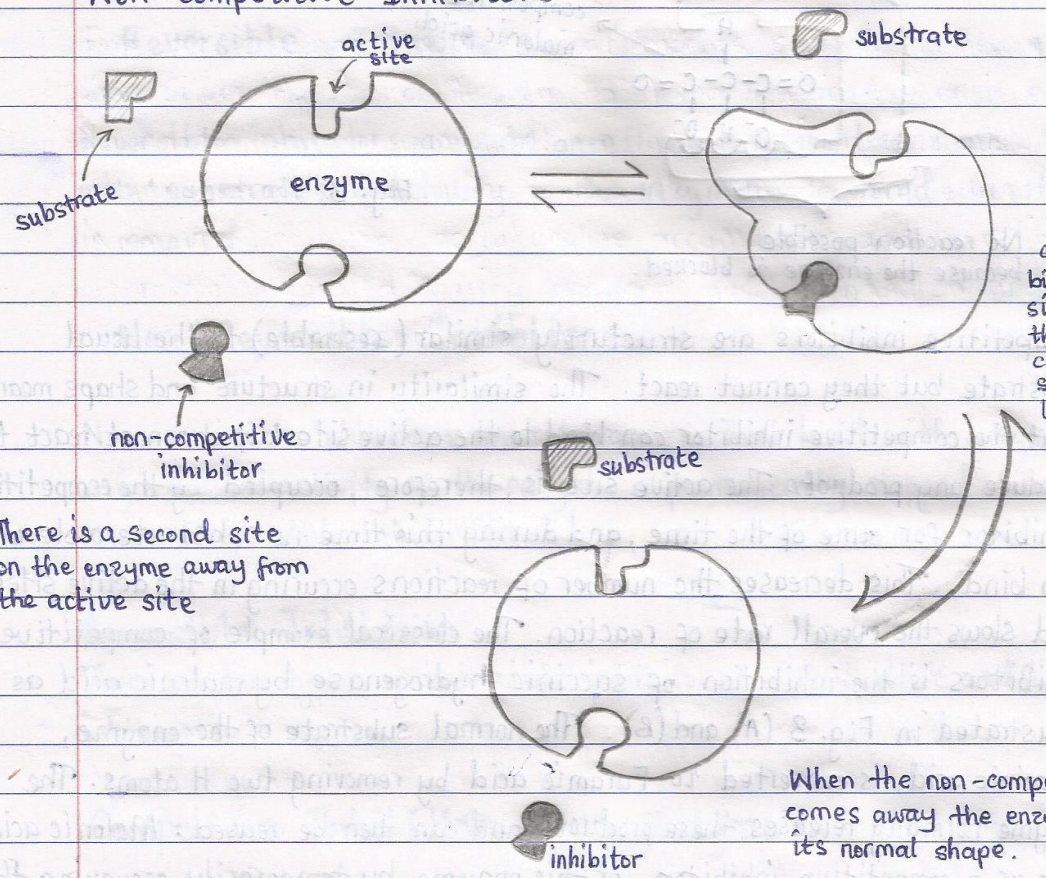
Fig. 3

No reaction possible
because the enzyme is blocked.

Competitive inhibitors are structurely similar (resemble) to the usual substrate but they cannot react. The similarity in structure and shape means that the competitive inhibitor can bind to the active site but it cannot react to produce any product. The active site is, therefore, occupied by the competitive inhibitor for some of the time, and during this time no substrate molecule can bind. This decreases the number of reactions occuring in the active sites and slows the overall rate of reaction. The classical example of competitive inhibitors is the inhibition of succinic hydrogenase by malonic acid as illustrated in Fig. 3 (A) and (B). The normal substrate of the enzyme, succinic acid, is converted to Furamic acid by removing two H atoms. The enzyme normally releases these products and can then be reused. Malonic acid acts as a competitive inhibitor for this enzyme by temporarily occupying the active site in the same way. The difference is that malonic acid cannot be broken down. In this particular reaction, the enzyme-inhibitor complex is more stable than the enzyme-substrate complex. This means that the two substances do not compete on equal terms.

Small amounts of inhibitors greatly reduce the reaction rates because the inhibitor molecules bind to the enzyme for longer. Competitive inhibitors have no permanent effect on the enzyme molecule and the inhibition they cause can be overcome either by increasing the concentration of substrates or by reducing the concentration of the inhibitor substance.

Non-competitive Inhibitors

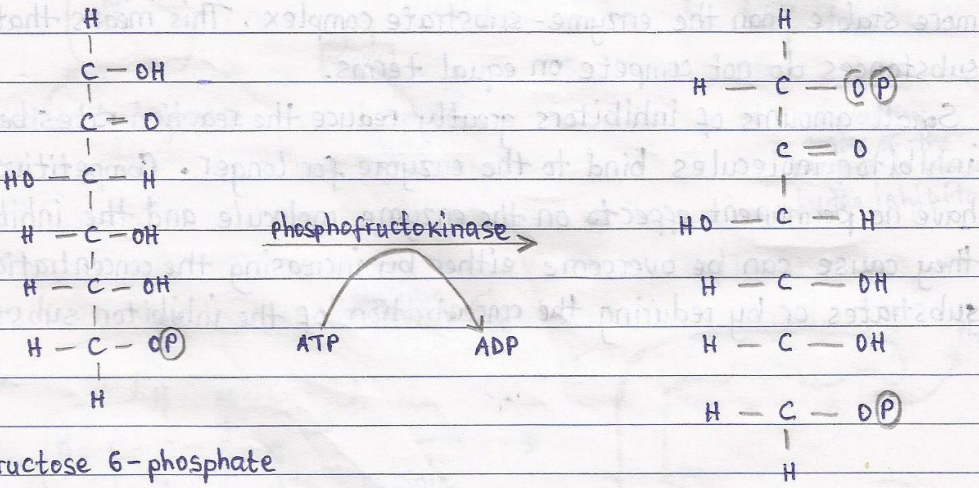


Enzyme-Inhibitor Complex:

When the non-competitive inhibitor binds to this second site, the shape of the enzyme is changed and the substrate can no longer bind.

There is a second site on the enzyme away from the active site

When the non-competitive inhibitor comes away the enzyme returns to its normal shape.



Fructose 6-phosphate

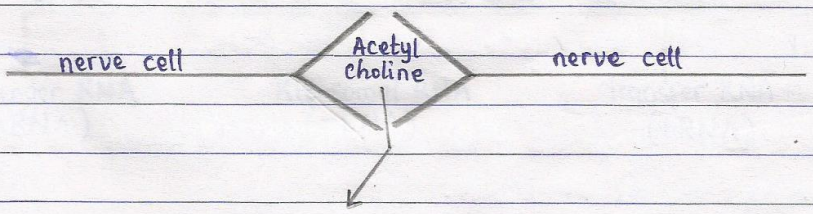
Non-competitive inhibition occurs when the inhibitor binds to the enzyme and prevents the reaction from occuring. A non-competitive inhibitor binds to a site on the enzyme other than the active site and it is thought that the inhibitor causes a change in the shape of the enzyme, preventing it from binding the substrate, so it cannot react.

The most important type of inhibition in cells is a form of non-competitive inhibition. Allosteric enzymes have two sites — they have the active site that binds the substrate and another

This other molecule can inhibit the enzyme, and as it is binding to the enzyme away from the active site this is the form of non-competitive inhibition. An example of an Allosteric enzyme is provided by the enzyme Phosphofructokinase, which catalyses the phosphorylation of fructose 6-phosphate to fructose 1,6-disphosphate. This reaction occurs during the glycolysis section of the respiratory pathway. When ATP is at high concentration, it inhibits the enzyme phosphofructokinase allosterically. However, when cell metabolism increases and more ATP is used up, the overall concentration of ATP decreases and the pathway once again comes into operation.

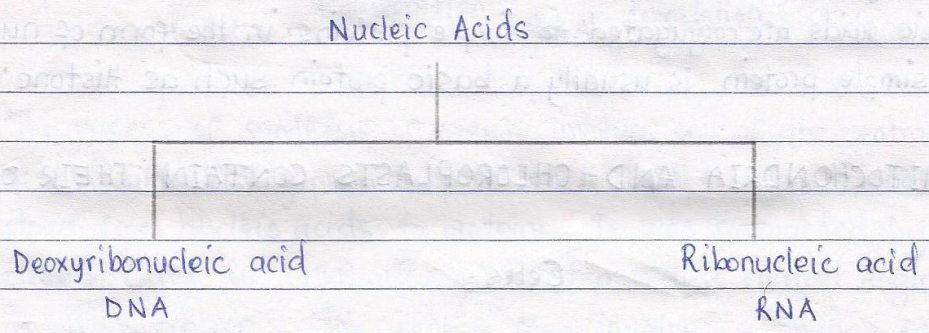
Irreversible Inhibition

Acetylcholine $\xrightarrow{\text{Cholinestrase}}$ Acetic acid + choline



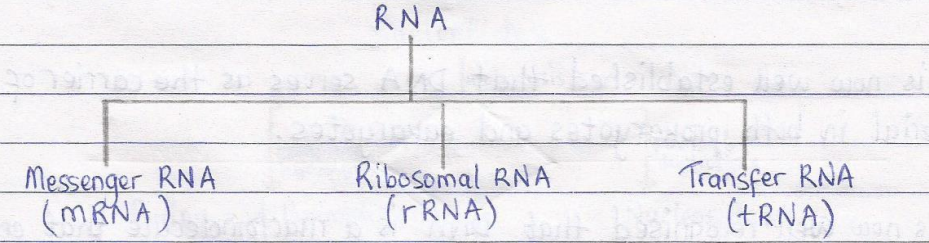
Very small concentrations of chemical reagents such as the heavy metal ions like Silver (Ag^{2+}) and Mercury (Hg^{2+}) and Arsenic (As) or insectides such as organophosphorus compounds e.g Parathim completely inhibits some enzymes because they combine permanently with the enzyme acetylcholinestrase When it is inhibited, acetyl choline accumulates and nerve impulses are constantly propagated causing prolonged muscle contraction and paralysis or death is the end result.

NUCLEIC ACIDS



There are two types of nucleic acids (i) Ribonucleic acid (RNA) and (ii) Deoxyribonucleic acid (DNA). Both DNA and RNA are major components of all cells, together making up from 5-15 % of their dry weight. Almost all the DNA of differentiated cells is present in the nucleus as chromatin which fills the entire nucleus of resting cells and is highly condensed into chromosomes as soon as the process of DNA replication is completed.

A small amount of DNA is present in mitochondria and chloroplast which is generally free of proteins. Scientists agree that DNA is a genetic material and that pure DNA is in the form of a double helix. However, DNA in the cell is not pure but is conjugated with a protein and coiled into structures called chromosomes.



RNA which is present in three different types: Messenger RNA (mRNA), Ribosomal RNA (rRNA) and Transfer RNA (tRNA).

RNA is present in both the nucleus and the cytoplasm of the cell, depending on its function.
Nucleic acids are conjugated to simple proteins in the form of nucleoproteins. The simple protein is usually a basic protein such as Histone or Protamine.

MITOCHONDRIA AND CHLOROPLASTS CONTAIN THEIR OWN DNA.

Cells

- Eukaryotic Cells (True cells)
- Prokaryotic Cells (Not true cells) [Bacterial]

Not all the genetic information of Eukaryotic cells is encoded by their nuclei-chromasomal DNA. Genetic studies discovered that mitochondria and chloroplasts have their own nucleic acids.
Mitochondria and chloroplasts' DNA molecule is relatively small, simple, double helix and is circular. The size of mitochondria genome is very much large in plants than it is in animals. DNA molecules from the mitochondria and chloroplasts are free from histone.

ROLE OF DNA

1. It is now well established that DNA serves as the carrier of genetic material in both prokaryotes and eukaryotes.

2. It is now well recognised that DNA is a macromolecule that controls every aspect of cell function.

DNA $\xrightarrow{\text{transcription}}$ RNA $\xrightarrow{\text{translation}}$ Proteins

This is done through protein sentences as suggested by the following sequence :

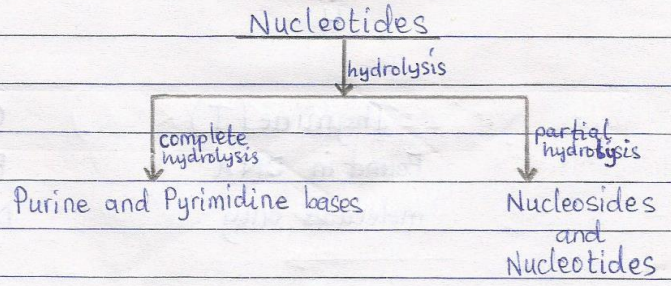
DNA $\xrightarrow{\text{transcription}}$ RNA $\xrightarrow{\text{translation}}$ Protein

The process of synthesis of protein involves one of the central dogma of molecular biology which postulates that the genetic material info flows from nucleic acids to proteins. It was forwarded by a scientist called Crick in 1958. The first step of this central dogma is known as Transcription. The second step involves a change from nucleotide sequences to amino acids sequences and it is called Translation.

DNA plays a very important role in hereditary. This is suggested by the fact that DNA is a replicon, a molecule that can undergo self-replication. It permits DNA to make copies of itself as the cell divides and these copies are given to daughter cells which can thus inherit each and every property and characteristic of the original cell. DNA is a molecule of unusual capacity that is able to encode a very large quantity of biological information.

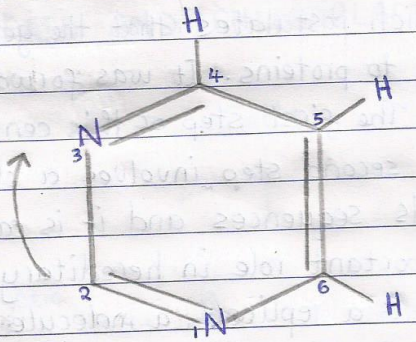
CHEMICAL STRUCTURE OF NUCLEIC ACIDS.

DNA and RNA are polymeric (they are polymers) molecules. monomeric units of DNA are called Deoxyribonucleotides and those for RNA are called Ribonucleotides.



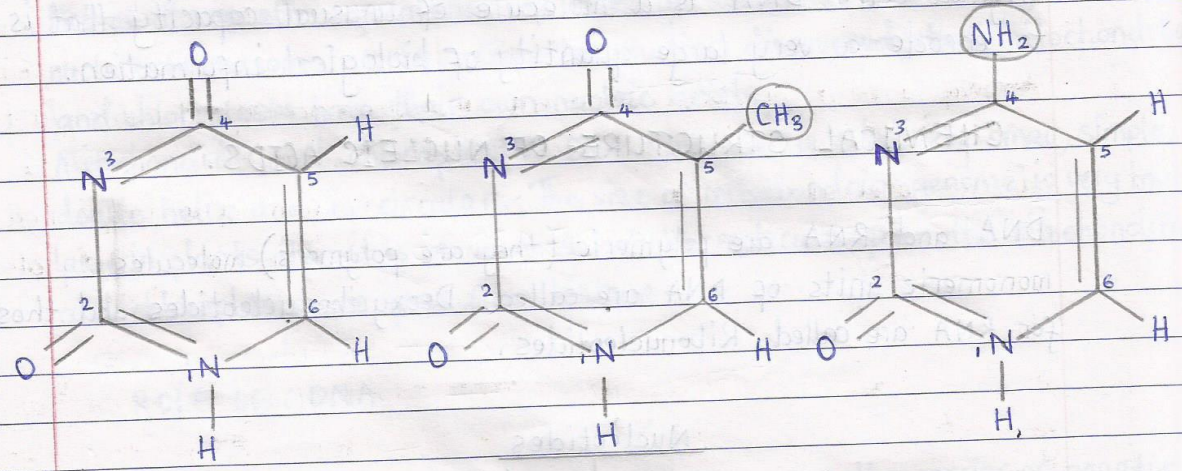
STRUCTURE OF BASES

These are nitrogenous heterocyclic bases which are derivatives of either pyrimidines or purines.



The pyrimidine base, the parent compound.

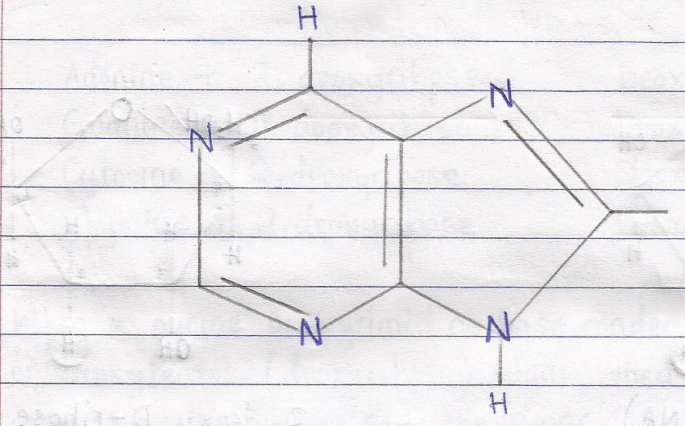
- There are three derivatives of pyrimidine bases



Uracil (U)
Found in RNA molecules only

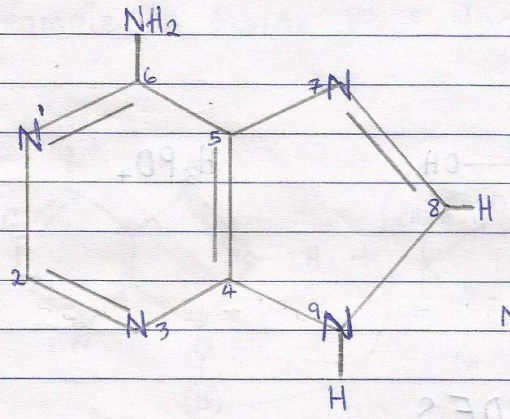
Thymine (T)
Found in DNA molecules only

Cytosine (C)
Found in both DNA and RNA

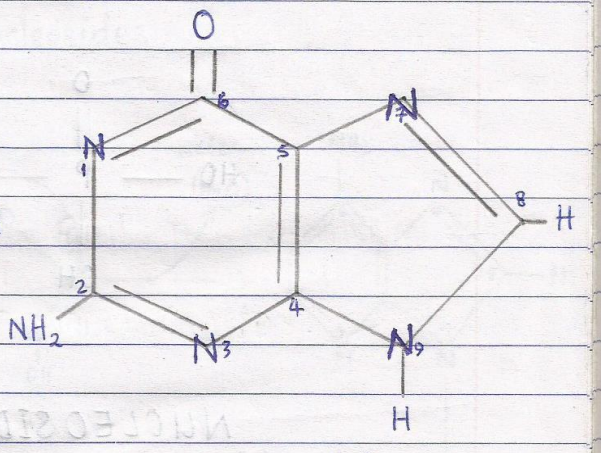


The Purine base, the parent compound.

There are 2 derivatives of purine bases.

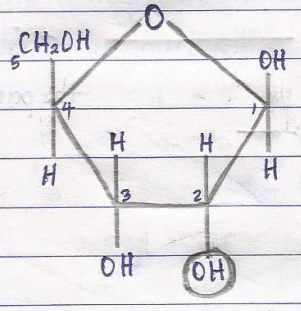


Adenine (A)
Found both in RNA and DNA.

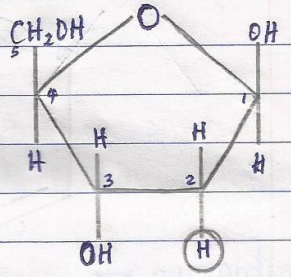


Guanine (G)
Found both in DNA and RNA.

RIBOSE SUGAR

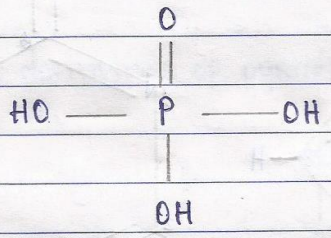


· D-Ribose (RNA).
Dextorotatory Ribose



2, deoxy D-ribose (DNA).
2, deoxy Dextorotatory Ribose

PHOSPHORIC ACID



H_3PO_4

NUCLEOSIDES

Purine nucleosides — Ribonucleosides
Pyrimidine nucleosides — Deoxyribonucleosides

RIBONUCLEOSIDES (RNA)

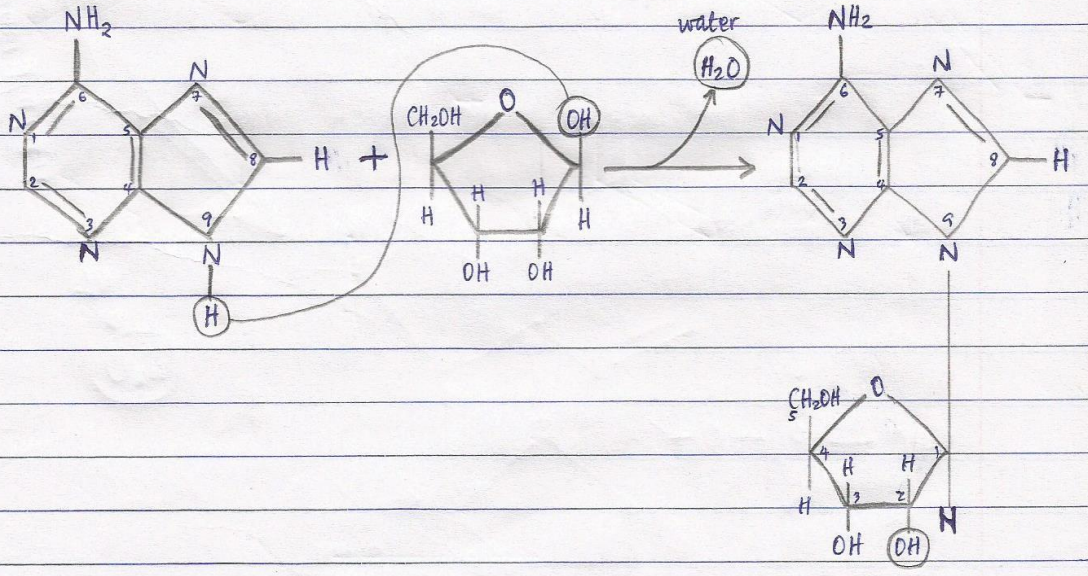
Adenine + Ribose ⟶ Adenosine } Purine
Guanine + Ribose ⟶ Guanosine }
Cytosine + Ribose ⟶ Cytidine } Pyrimidine
Uracil + Ribose ⟶ Uridine }

DEOXYRIBONUCLEOSIDES

Adenine + 2, deoxyribose	Deoxy adenosine	Purine
Guanine + 2, deoxyribose	Deoxy guanosine	Purine
Cytosine + 2, deoxyribose	Deoxy cytidine	Pyrimidine
Thymine + 2, deoxyribose	Deoxy thymidine	Pyrimidine

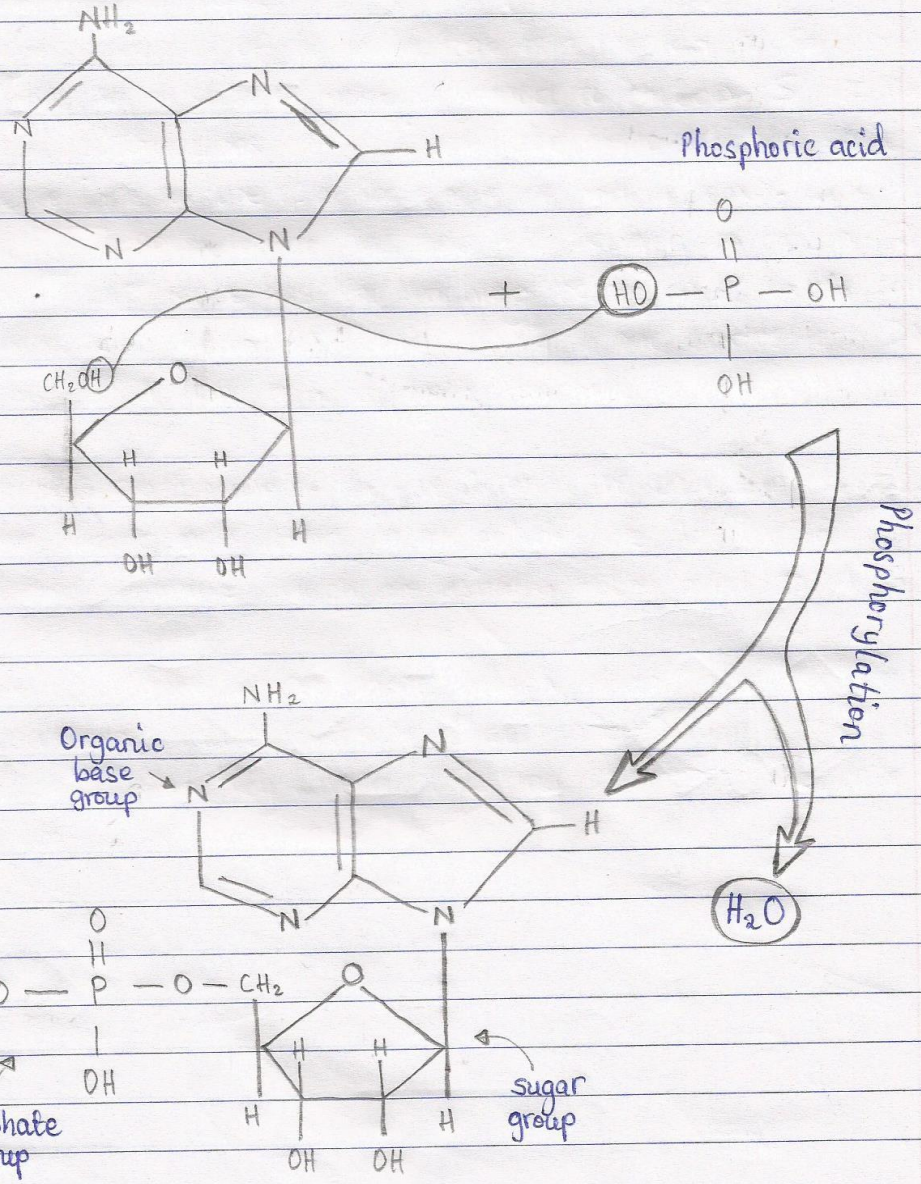
When a purine or pyrimidine base condenses with a Pentose (ribose) or DeoxyPentose (deoxyribose) sugar, they form a Nucleoside. In case of purine nucleosides, the sugar is attached to the Nitrogen-9 atom, while in pyrimidine nucleosides the sugar is attached to the Nitrogen-1 atom.

Example of Purine Base Nucleosides.

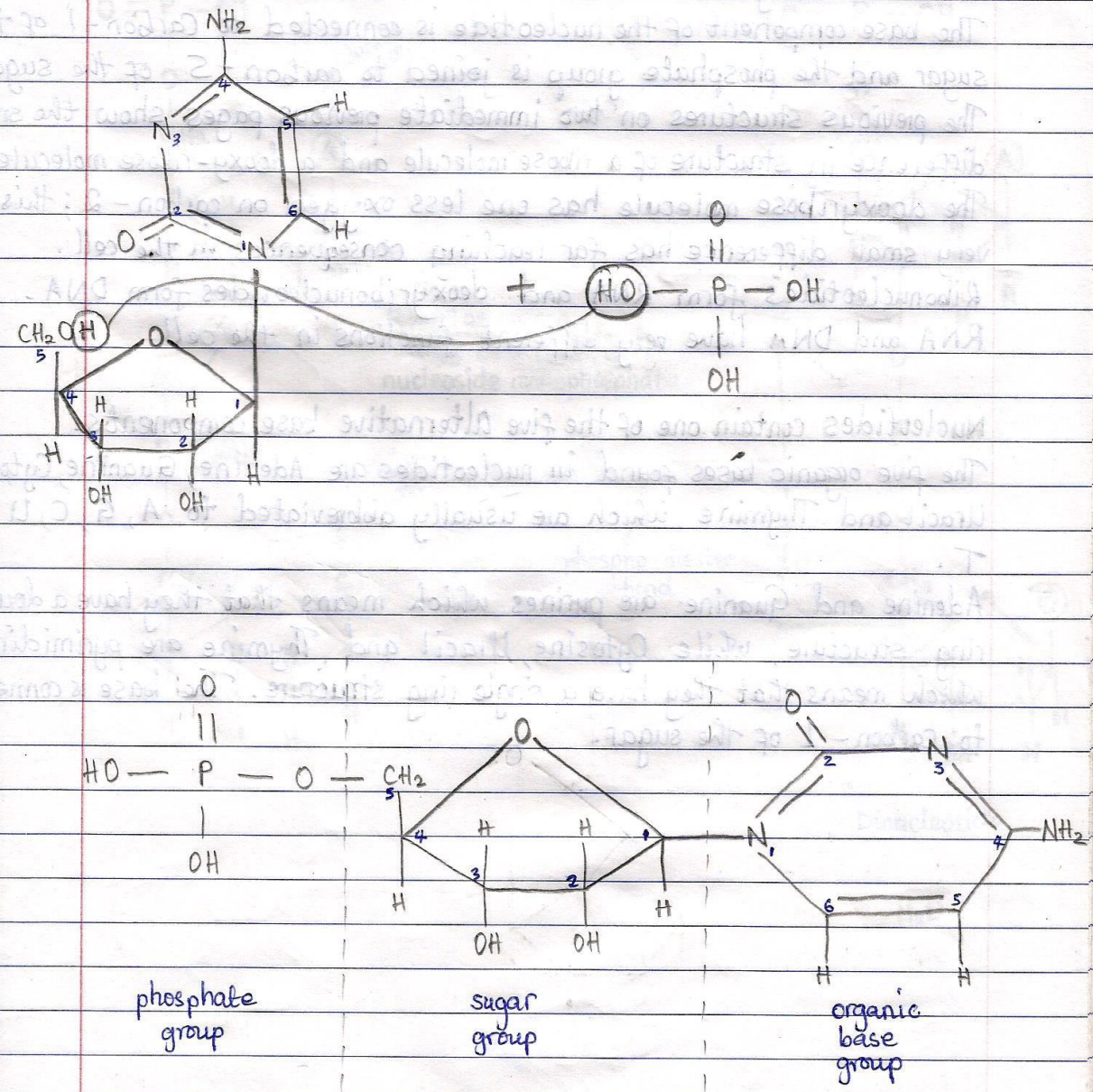


NUCLEOTIDES

Adenosine
(Ribonucleoside)



Adenosine 5' Monophosphate (AMP)
Phosphotic ester of a nucleoside

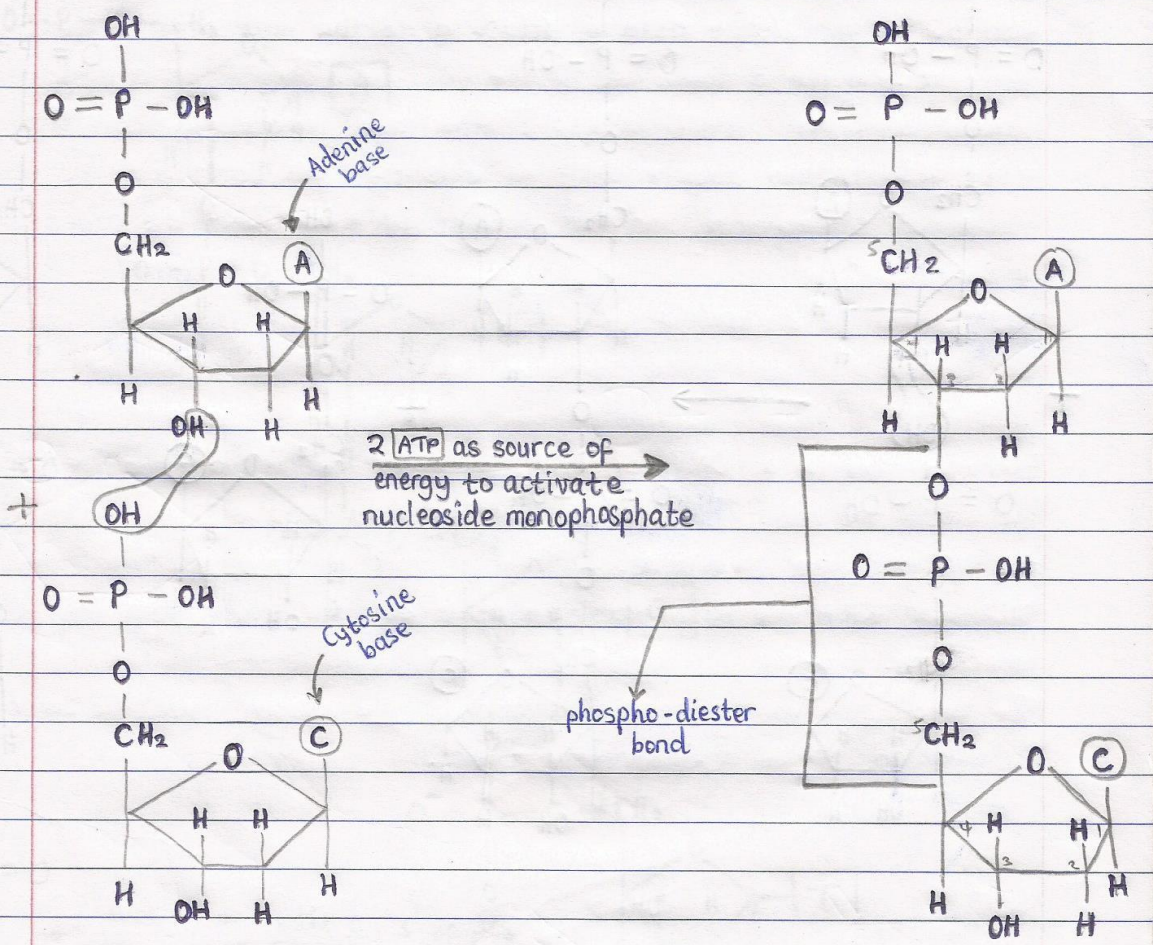


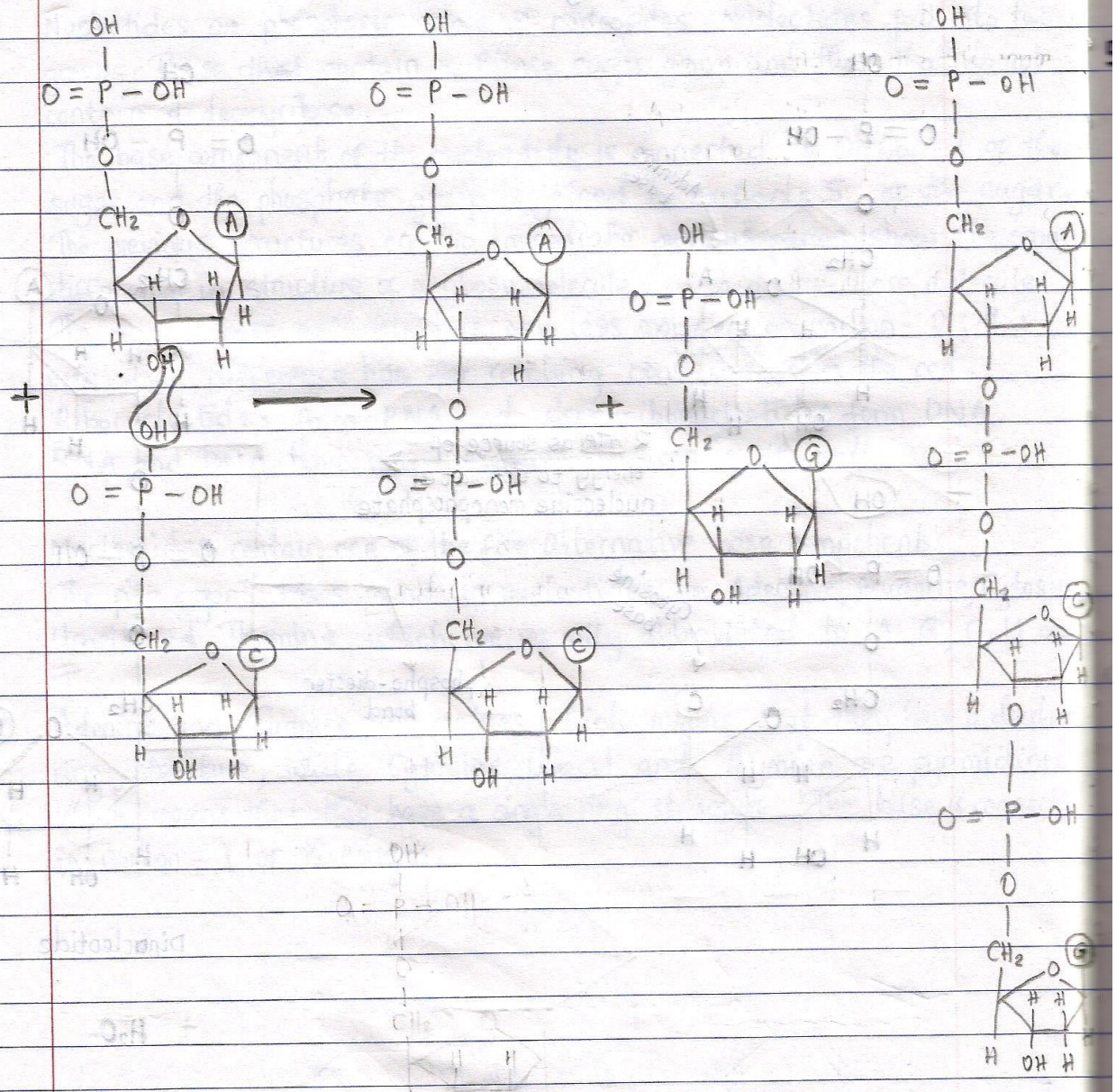
Cytidine 5'- Monophosphate
(A Ribonucleotide)

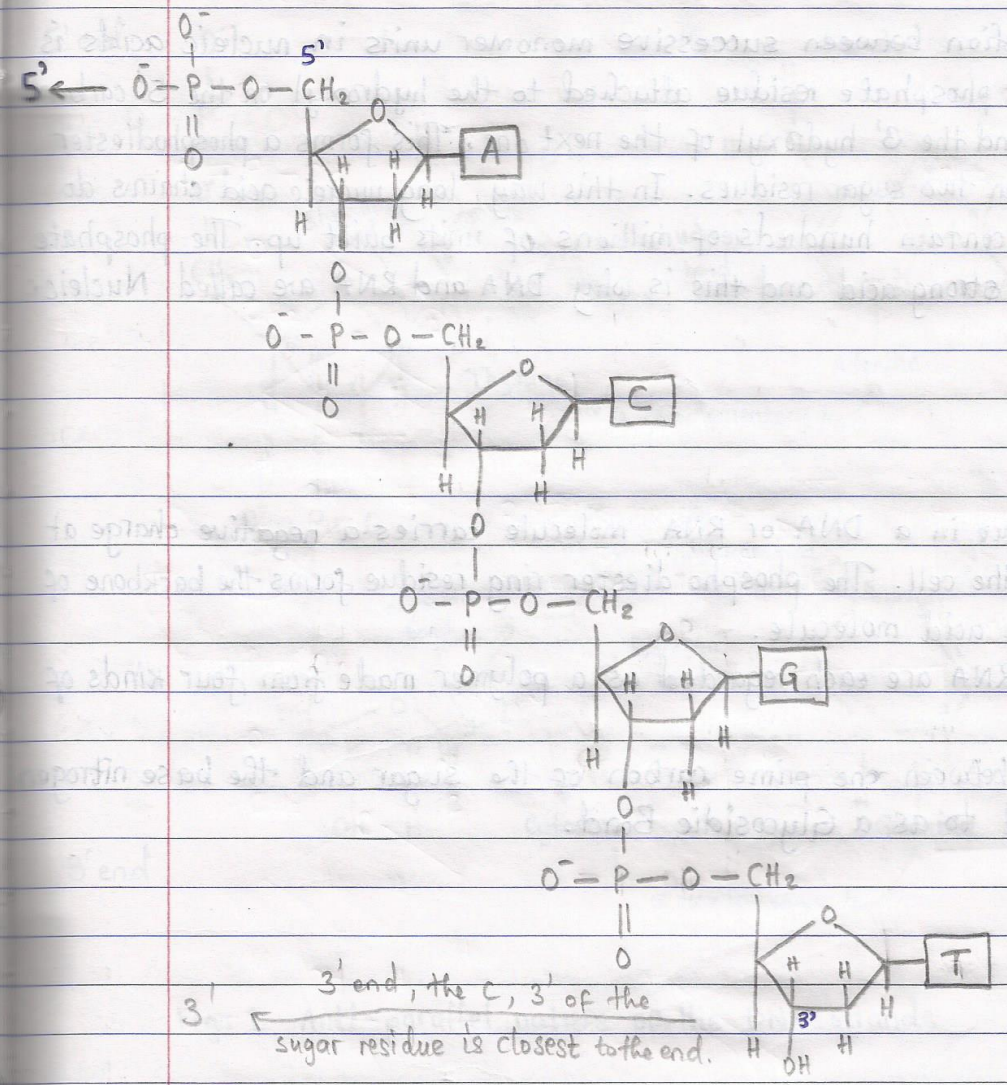
Nucleotides are phosphoric esters of nucleosides. Nucleotides fall into two groups. Those that contain a Ribose sugar group and those that do not contain a deoxyribose.
The base component of the nucleotide is connected to Carbon-1 of the sugar and the phosphate group is joined to carbon-5 of the sugar.
The previous structures on two immediate previous pages show the small difference in structure of a ribose molecule and a deoxy-ribose molecule.
The deoxyribose molecule has one less oxygen on carbon-2; this very small difference has far reaching consequences in the cell.
Ribonucleotides form RNA and deoxyribonucleotides form DNA.
RNA and DNA have very different functions in the cell.

Nucleotides contain one of the five alternative base components.
The five organic bases found in nucleotides are Adenine, Guanine, Cytosine Uracil and Thymine which are usually abbreviated to A, G, C, U and T.
Adenine and Guanine are purines which means that they have a double ring structure, while Cytosine, Uracil and Thymine are pyrimidines which means that they have a single ring structure. The base is connected to carbon-1 of the sugar.

Synthesis of a Polynucleotide, DNA or RNA







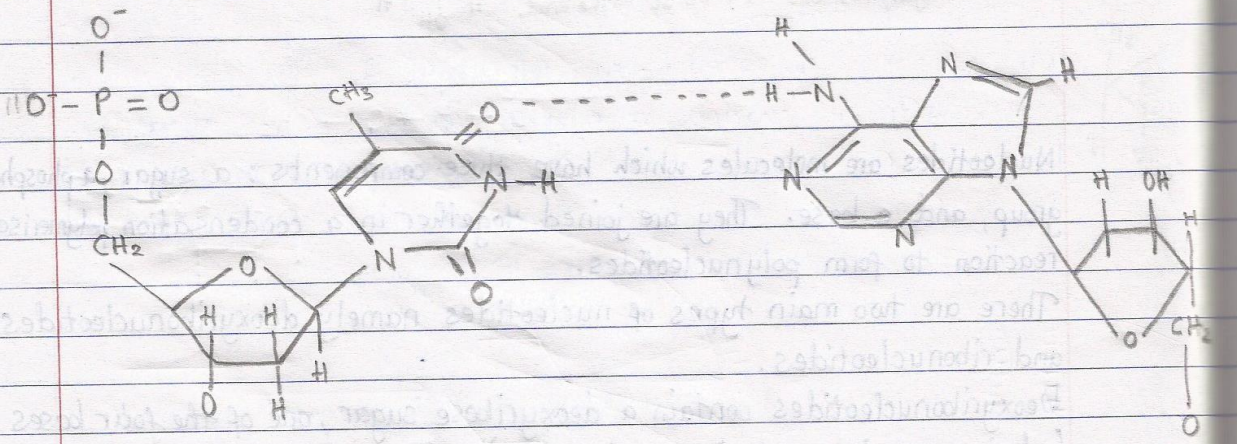
Nucleotides are molecules which have three components: a sugar, a phosphate group, and a base. They are joined together in a condensation polymerisation reaction to form polynucleotides.

There are two main types of nucleotides namely deoxyribonucleotides and ribonucleotides.

Deoxyribonucleotides contain a deoxyribose sugar, one of the four bases (adenine, guanine, cytosine or thymine) and one phosphate group. Ribonucleotides have a ribose sugar, one of the four bases (adenine, guanine, cytosine or uracil), and a phosphate group.

The connection between successive monomer units in nucleic acids is through a phosphate residue attached to the hydroxyl on the 5' carbon one unit and the 3' hydroxyl of the next one. This forms a phosphodiester link between two sugar residues. In this way, long nucleic acid chains do sometimes contain hundreds of millions of units built up. The phosphate group is a strong acid and this is why DNA and RNA are called Nucleic acids.

Every residue in a DNA or RNA molecule carries a negative charge at the pH of the cell. The phospho diester ring residue forms the backbone of the nucleic acid molecule.
DNA and RNA are each regarded as a polymer made from four kinds of monomers.
The bond between one prime carbon of the sugar and the base nitrogen is referred to as a Glycosidic Bond.



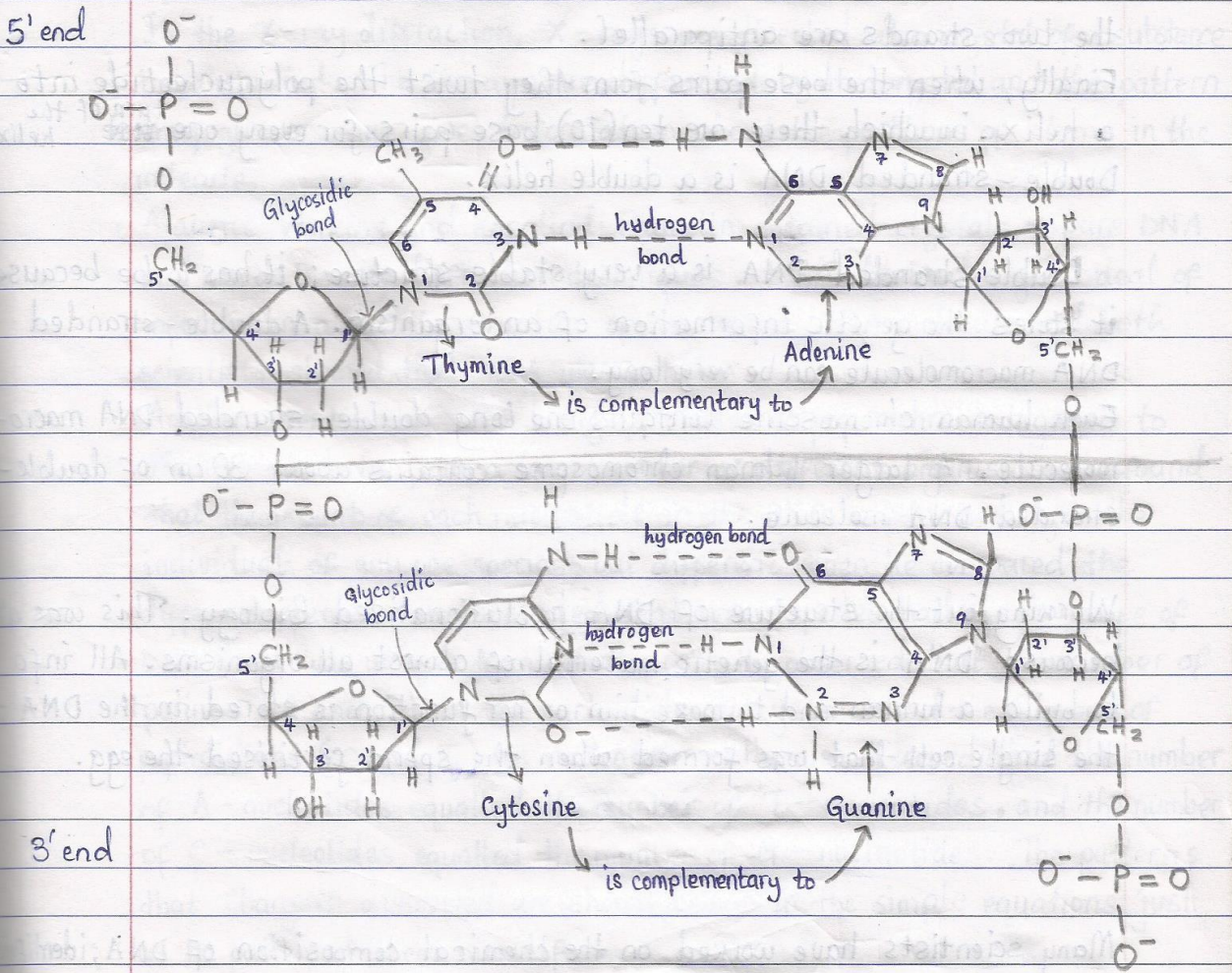


Fig. 1 Anti-parallel nature of the DNA strands

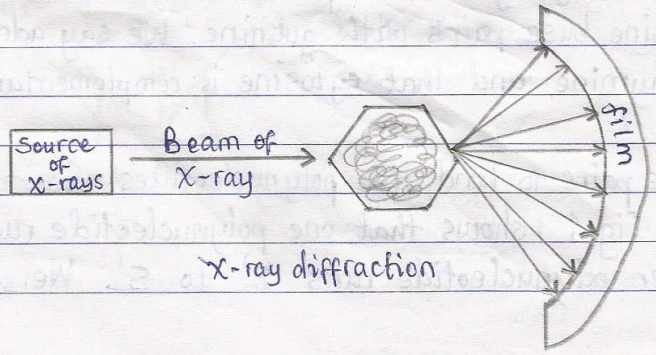
DNA is usually double-stranded, this means that there are two polynucleotide side by side held together by hydrogen bonds. The weak bonds are hydrogen bonds between the bases of the two nucleotides forming base pairs.
Only certain bases can hydrogen bond together : adenine base pairs with thymine, and cytosine base pairs with guanine. We say adenine is complementary to thymine and that cytosine is complementary to guanine.
In order for the base pairs to bond, the polynucleotides have to run in opposite directions. Fig. 1 shows that one polynucleotide runs 5' to 3' while the other polynucleotide runs 3' to 5'. We say that

the two strands are antiparallel.
Finally, when the base pairs form they twist the polynucleotide into a helix, in which there are ten (10) base pairs for every one turn of the helix.
Double-stranded DNA is a double helix.

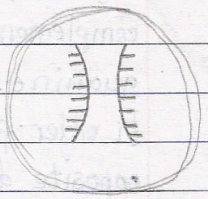
Double stranded DNA is a very stable structure; it has to be because it stores the genetic information of an organism. A double-stranded DNA macromolecule can be very long.
Each human chromosome contains one long double-stranded DNA macromolecule. A larger human chromosome contains about 30 cm of double-stranded DNA molecule.

Working out the structure of DNA revolutionalized Biology. This was all because DNA is the genetic material of almost all organisms. All info to build a human and to make him or her function is stored in the DNA of the single cell that was formed when the sperm fertilised the egg.

Many scientists have worked on the chemical composition of DNA, identifying the atoms that are present in the molecule and how they are joined together. Through the work of Biochemists, the nucleotide was established as the basic unit of DNA structure. Later on, scientists used the technique of X-ray diffraction throughout the 1940s to the 1950s to obtain accurate information about the position of individual atoms in the intact macromolecule.



X-ray diffraction


(1940-1950) DNA double helix
Photograph by Rosalind Franklin and Maurice Wilkins

In the X-ray diffraction, X-rays are directed at a crystal of a substance to be studied. The X-rays are diffracted by the crystal and the pattern they give or make gives information about the positions of atoms in the molecule.

Maurice Wilkins and Rosalind Franklin obtained crystals of pure DNA and used X-ray diffraction techniques. Both obtained a great deal of information about the structure of the intact DNA molecule and both scientists showed that DNA was a helix.

Another scientist, Erwin Chargaff, used a paper chromatograph to analyze the DNA from a large number of different organisms. He found that the amount of each nucleotide in the DNA was the same for the individual of any one species, but different when he compared the different species. He concluded that every species had its own type of DNA that was unique from all others'. He observed that the number of purines (A and G) in the nucleotide always equalled the number of pyrimidines (C and T) in nucleotides. He also observed that the number of A-nucleotides equalled the number of T-nucleotides, and the number of C-nucleotides equalled the number of G-nucleotides. The patterns that Chargaff discovered are shown below in the simple equations just as he patterned them himself:

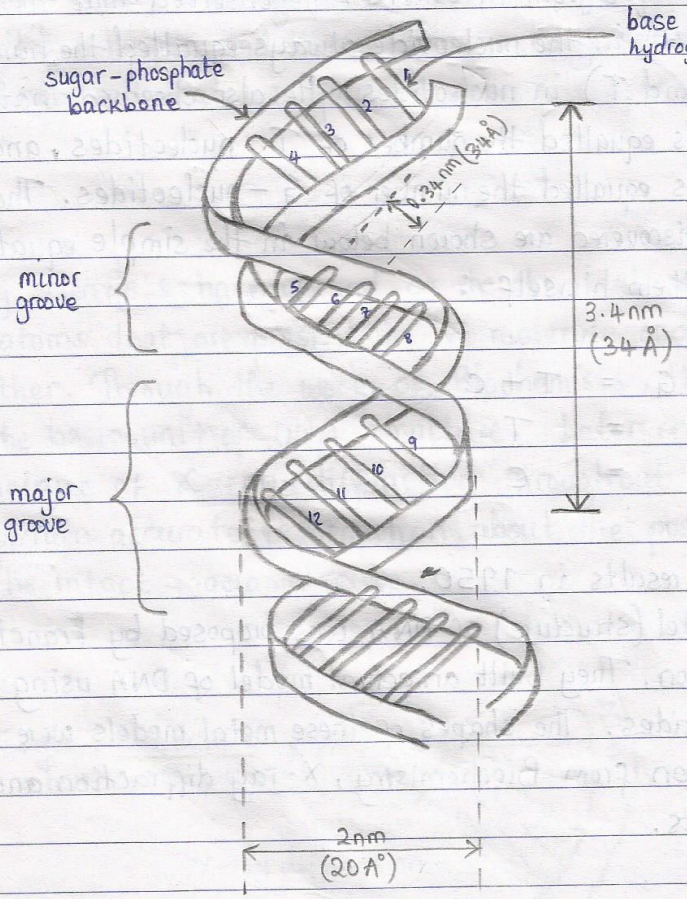
$$A + G = T + C$$
$$A = T$$
$$G = C$$

He published his results in 1950.

By 1951, a model (structure) of DNA was proposed by Francis Crick and James Watson. They built an actual model of DNA using metal shapes of nucleotides. The shapes of these metal models were based on all the information from Biochemistry, X-ray diffraction and from Chargaff's results.

Playing with the metal shapes provided their proposed DNA structure. Crick and Watson realised that an A- and T- side by side had the same dimensions as the G- and C- side by side. Further examination showed that Adenine (A) would bind to Thymine (T) with the formation of two hydrogen bonds and Guanine (G) would bond to Cytosine (C) with three hydrogen bonds. However, this hydrogen bond pairs would only form if one of the bases in each pair was upside down.

The hydrogen bonded base pairs gave Crick and Watson the starting point for resolving the list of the secrets of DNA. The crucial finding was that DNA has two polynucleotides and the two polynucleotides strands run in opposite directions. This meant that all the bases in one of the two strands were upside down and the base pairs could form between the bases projecting from one strand and the bases projecting from another strand.



Measurements

1. 1 metre (m) = 1000 or 10^3 milimetre (mm)
2. 1 milimetre (mm) = 1000 or 10^3 micrometer or mieron (μm)
3. 1 mieron (μm) = 1000 or 10^3 nanometer (nm)
4. 1 nanometer = 10 Angstron (Å)

Watson and Crick's Structural Model of DNA

According to Watson and Crick, DNA molecules contain two polynucleotide chains that are wrapped helically around each other with the sugar phosphate chain outside (forming ribbon-like coil backbone of double helix), and purines and pyrimidines on the inside of the double helix (projecting between two sugar phosphate groups as transverse bars). The distance between the two sides according to X-ray measurements is 2 (two) nanometers (nm). Two purines in combination would take up more than 2 nanometers, and two pyrimidines would not reach all the way across, but if a purine paired in each case with a pyrimidine, there would be a perfect-fit and the molecule would be the same width along its entire length.

The paired bases (rungs of the ladder) would therefore always be purine – pyrimidine combinations. Since a DNA molecule may be thousands of nucleotides long, there is a possibility of great variety in the sequence of bases and variety is one of the requirements for genetic materials.

The two polynucleotide strands are held together by hydrogen bonds between specific pairs of purines and pyrimidines. The H-bonds between purines and pyrimidines are such that adenine can bond only to thymine by two (2) H-bonds, and guanine can bond only to cytosine by three (3) H-bonds, and no other alternative is possible between them.

The specificity of the kind of H-bonds that can be formed assures that for every adenine in one chain there will be thymine in the other. For every guanine in the first chain, there will be a cytosine in the other, thus the two chains are complementary to each other; that is: the sequence of nucleotides in one chain dictates the sequence of nucleotides in the other. The two strands run anti-parallel to each other, that is to say: they have/run in opposite directions. One strand has phospho-diester linkage in 3' – 5' direction while other strands have phospho di-ester linkage in just the reverse of 5' – 3' direction.

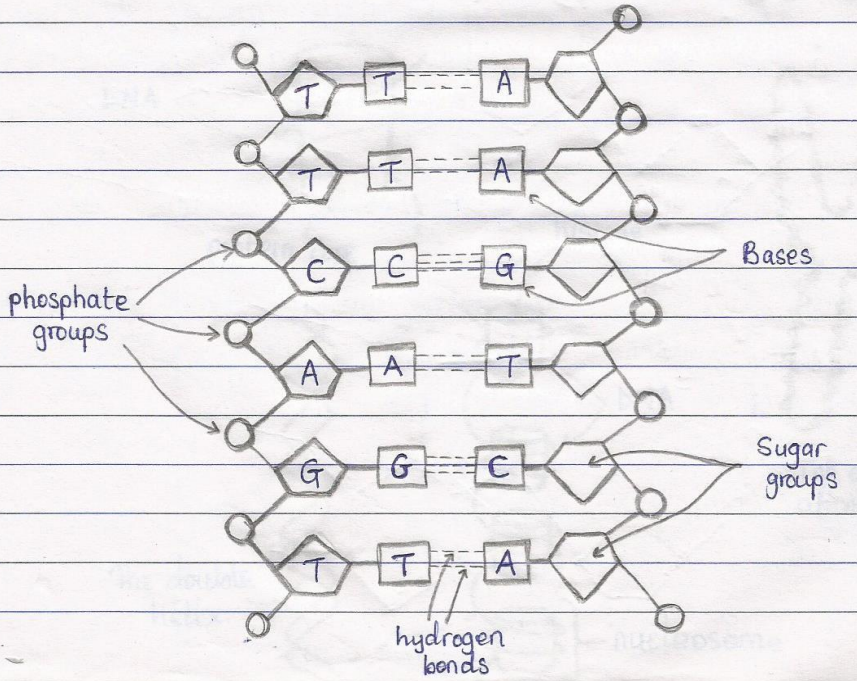
Further, four polynucleotide strands remain separated by 20 Angstrom (A°) distance.
The coiling of the double-helix is right-handed and the complete turn occurs every 34 Angstrom (A°).
Since each nucleotide occupies 3 – 4 A° distance along the length of the polynucleotide strand, 10 mononucleotides occur per complete turn.
The helix has two external grooves, the deep ~~white~~ wide one called major groove, and a shallow narrow one called minor groove. Both of these grooves are large enough to allow protein molecules to come in contact with the bases.

If one strand of DNA has the following sequence :

5'-TTCAGTACATTGCCA – 3

What is the complementary strand of this DNA?

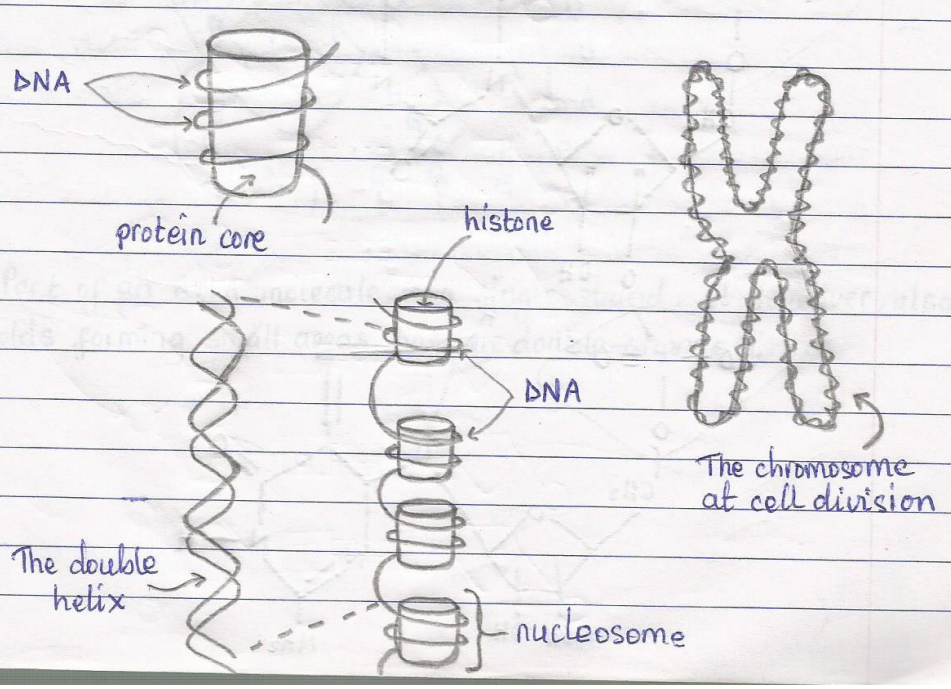
3'-AAGTCATGTAACGGT – 5'



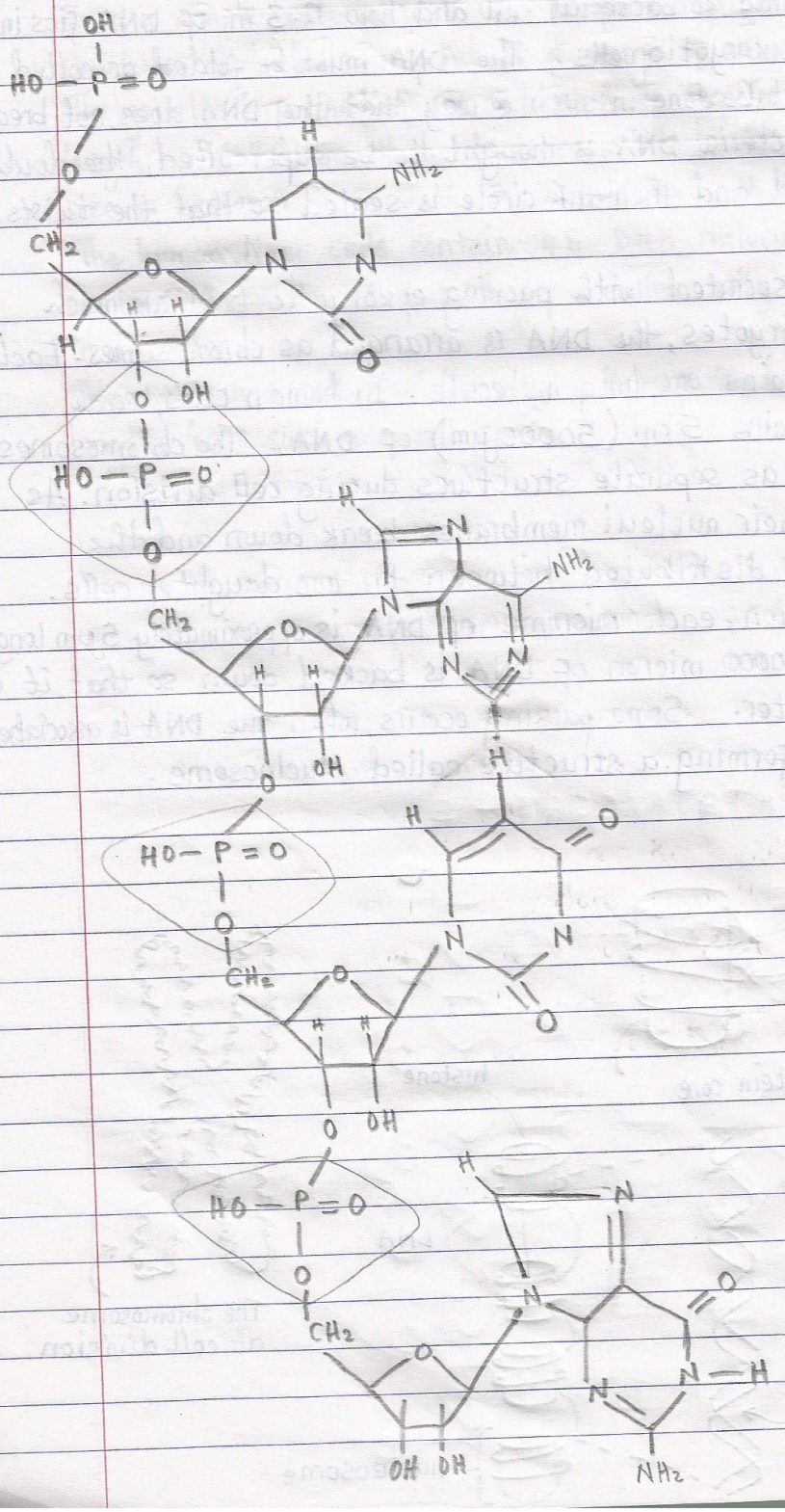
Even a simple bacterial cell is a complex organism filled with specialised structures and able to respond to a range of environmental factors.
The genetic information for a bacterium requires a circle of DNA with length of 1.36 mm that has to pack into a cell that is only 0.003 mm size of bacteria.
The human liver cells contain 46 DNA molecules whose total length is up to 2.2 metres, all packed into a nucleus only 10 μm = 0.000001 metres in diameter.
The DNA in a cell must be very well organised in order to pack these huge lengths into such a small space.

There is still a problem of understanding how a circle of DNA 1.36mm in length fits into a bacterial cell and how 2.3 m of DNA fits into the nucleus of eukaryotic cells. The DNA must be folded or coiled but the packing must be done in such a way that the DNA does not break. The circular bacteria DNA is thought to be supercoiled, the double helix is twisted and then the circle is sealed so that the twists do not go out.

The problems associated with packing eukaryotic DNA are much greater. In eukaryotes, the DNA is arranged as chromosomes. Each chromosome contains one long molecule. In human cells, each chromosome contains 5 cm (50000 μm) of DNA. The chromosomes are only visible as separate structures during cell division. As cells divide, their nucleui membranes break down and the chromosomes are distributed between the two daughter cells. During cell division, each microme of DNA is approximately 5 μm long. Somehow the 50000 micron of DNA is backed down so that it is 10000 times shorter. Some packing occurs when the DNA is associated with histones forming a structure called Nucleosome.



STRUCTURE OF RNA.



Molecules of RNA are built up from nucleotides containing the five-carbon sugar ribose and are always single stranded, Although the strand may be folded back on itself to give an apparently double-stranded structure. All cells contain three important types of RNA.

The structure of RNA is similar to that of DNA but it differs in several ways. First, RNA contains the pyrimide Uracil in place of thymine and the sugar ribose in place of deoxyribose. Also whereas DNA is a double-stranded molecule, RNA is considerably short and exists as a single chain of nucleotide. RNA is also much less stable than DNA. RNA needs to be less stable as it acts as a short-term functional molecule in the cell, while DNA needs to be extremely stable because it is the store of genetic information.

RNA is present in all cells and fulfills the number of very important functions

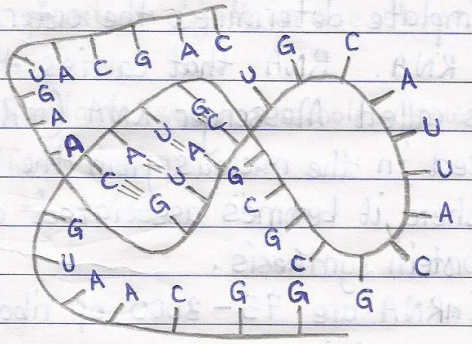
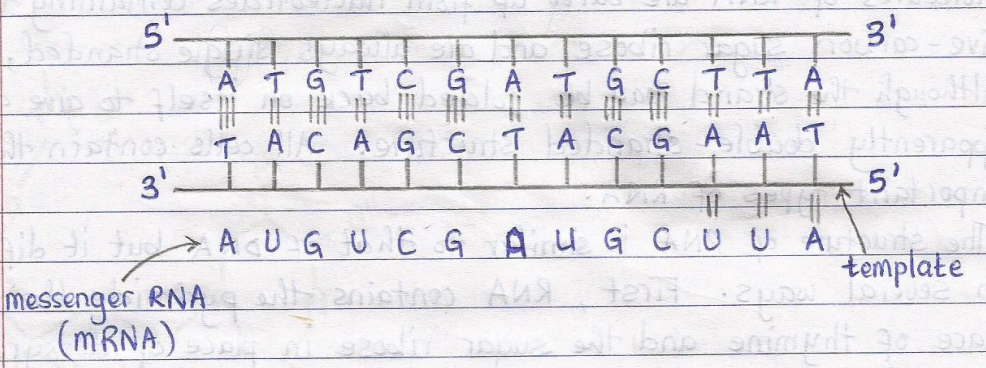
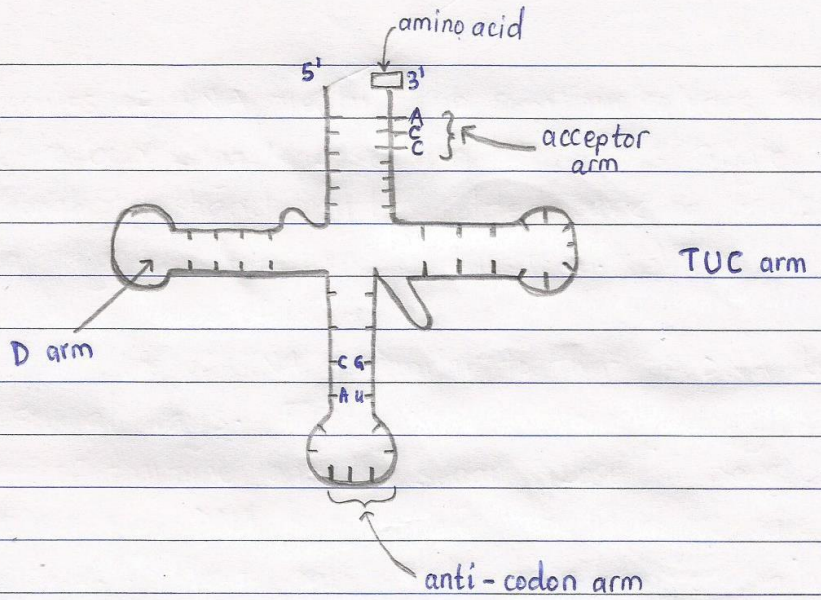


Fig 1: Part of an RNA molecule is a single strand. It, however, also folds forming small areas that are double-stranded.



1. MESSENGER - RNA (mRNA).

When the information stored in the DNA is needed for use in the cell, a copy of the information must be made. Scientists say that the info is transcribed, and the process is called Transcription.
Transcription uses DNA as a template for the synthesis of an RNA molecule. The template determines the order of the ribonucleotide residues in the RNA. RNA that carries the genetic information out from the DNA, is called Messenger RNA (mRNA), into the cell.
mRNA is produced in the nucleus from the DNA and then it passes into the cytoplasm where it becomes associated with ribosomes and starts the process of protein synthesis.
Molecules in the mRNA are 75 - 3000 of ribonucleotides long and are not folded in any special way.
The DNA polynucleotide in a chromosome may contain 300 million nucleotide residues



* A Codon is a sequence of three adjacent nucleotides which encode for a specific amino acid during protein synthesis or translation.
* Three special codons, called "stop codons", signal protein synthesis to terminate.
* A Heterocycle is a compound that has one or more atoms other than carbon in atleast one of its rings.
* A Template is a physical object whose shape is used as a guide to make other objects.
  In Biology, a template is a macromolecule which provides a pattern for the synthesis of another molecule.