ORGANIC CHEMICALS INVOLVED IN LIFE PROCESSES

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Contents

Summary

Organic compounds are complex molecules that are responsible for the continued existence of living matter. Organic compounds are those in which the main chemical bonds join carbon atoms to carbon or hydrogen atoms. Thus carbon dioxide (CO_2) is not an organic compound as the main chemical bonds join the carbon atom to two oxygen atoms, however propane (CH_3-CH_2-CH_3) is an organic compound as there are carbon-

carbon and carbon-hydrogen bonds. Every cell contains hundreds of organic compounds that vary in any number of conceivable ways. Of all the various organic compounds, four types are found in all cells and form the basis of living matter. The four are:

- Proteins
- Carbohydrates
- Lipids
- Nucleic acids

Each of the four types of organic compounds can be identified by their functional groups. The functional groups determine the properties of the organic compound.

1. Proteins

Proteins are far more complex than lipids and carbohydrates, controlling the majority of the structural and functional aspects of living cells. Proteins are the most abundant biological macromolecules that exist in cells. Amino acids are the building blocks of proteins, and are the molecules that cause proteins to differ in their functions in living systems. For example, proteins can function as enzymes, antibodies, structural molecules and hormones to mention but a few. The most varied and specialized of the proteins are the enzymes, which catalyze nearly all cellular reactions.

1.1. Amino Acids

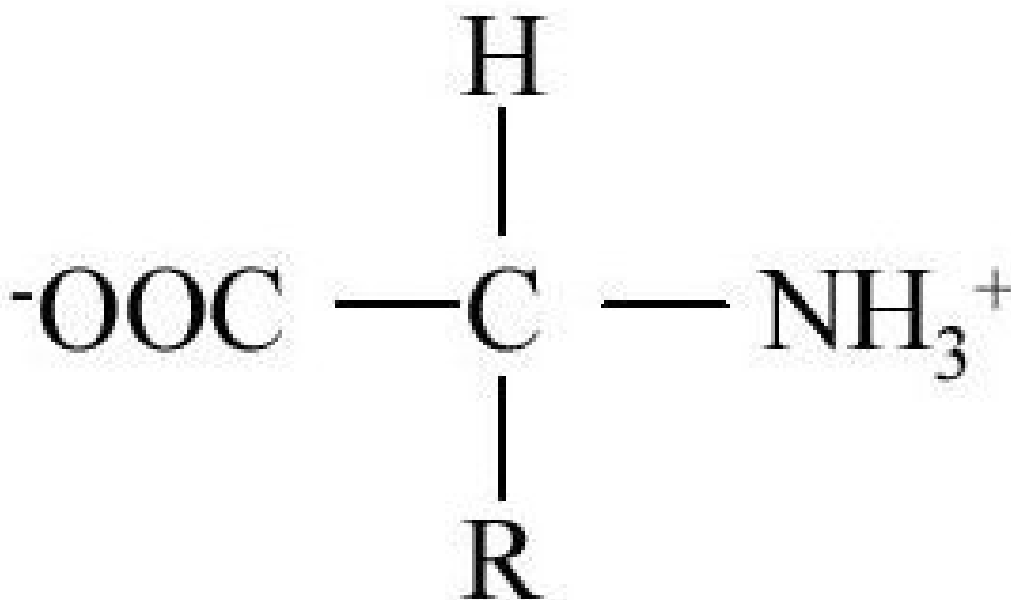$$^-OOC - \underset{\underset{R}{|}}{\overset{\overset{H}{|}}{C}} - NH_3^+$$

Figure 1. General structure of amino acids at pH 7.0.

Amino acids are the building blocks of proteins. The structure of an amino acid is shown in Figure 1, where this is the general structure of an amino acid at pH 7.0 and

where R- is the side chain, which is specific for each amino acid. NH_2- is an amino group and COOH- is a carboxyl group. The side chain (R) group of amino acids varies greatly depending on the type of amino acid. The R group can be simple, such as a hydrogen atom as is found in glycine, or more complex such as tryptophan where cyclic structures are prominent. There are 20 common amino acids found in proteins. The R group of the amino acids influence the nature of the protein produced. Some amino acids are non-polar at pH 6.5 to 7, some are polar and others are electrically charged (ionic). Figure 2 shows a structural view of the 20 amino acids as they would appear at pH 7.
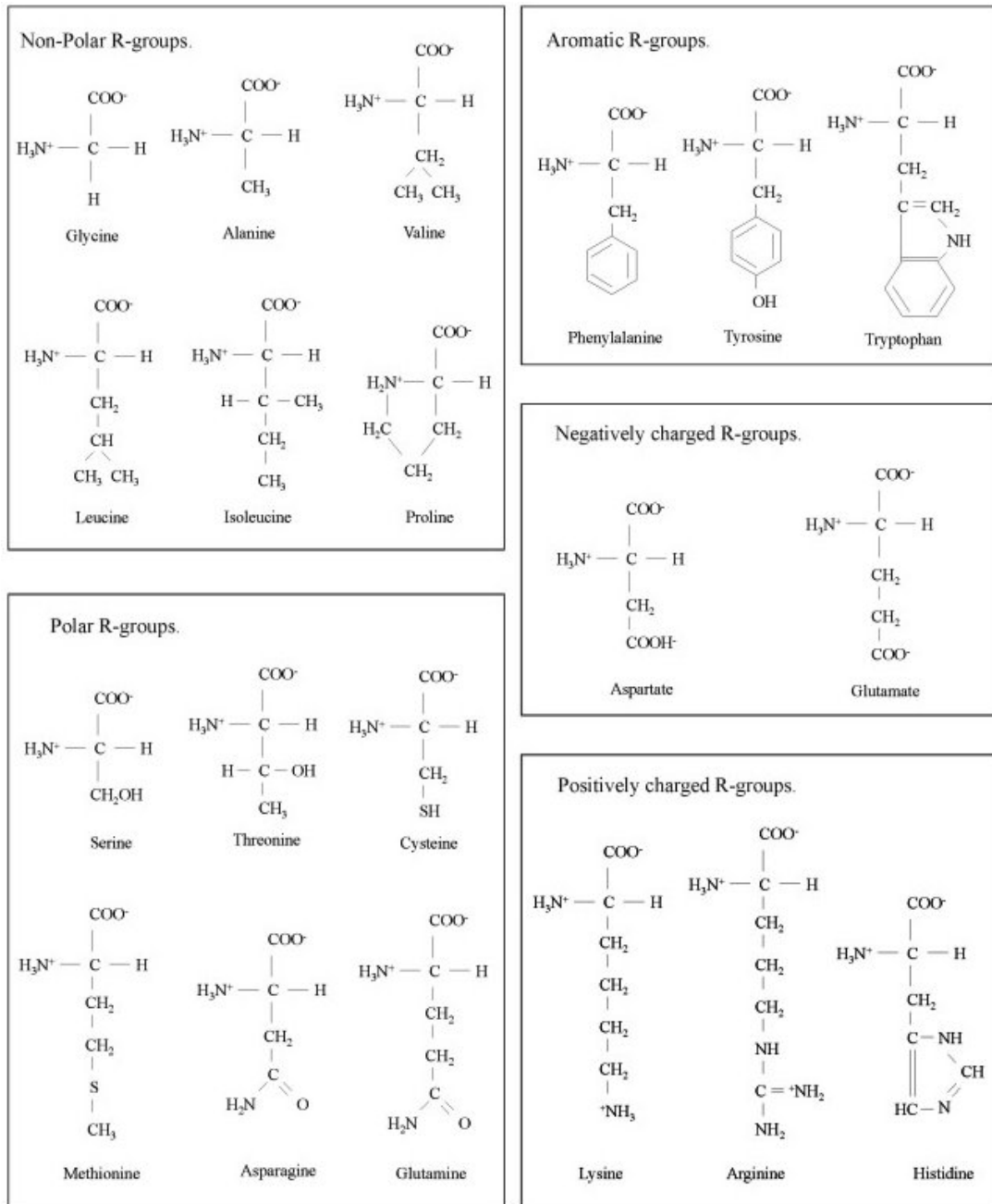

Figure 2. A structural view of the 20 amino acids as they would appear at pH 7.

1.2. Polypeptide chains

Polypeptides are formed by adjacent amino acids forming a covalent bond called a peptide bond. The peptide bond is formed when the amino group of one amino acid binds to the adjacent carboxyl group during a dehydration reaction. The resulting peptide bond (-NH-CO-) forms a dipeptide. If continuous polymerization occurs, the resulting complex is called a polypeptide. The polypeptide formed can vary completely from the next polypeptide synthesized. Features of polypeptides are:

- A sequence can contain any of the 20 amino acids

- A sequence can contain any number of one type of amino acid

- The sequence in which the amino acids join to form the polypeptide chain is unlimited

- The chains can be folded into a number of different conformations.

All these factors play an important role in the production of the vast variety of proteins.

1.3. Primary structure

The polypeptide chains synthesized from amino acids and peptide bonds represent the primary structure of a protein.

1.4. Secondary structure

A skeletal representation of the polypeptide chain would be in the form of a spiral (like a twisted elastic band). The spirals can either be 'right handed' (α-helix) or 'left handed' (β-helix). The hydroxyl and R groups of the amino acids project outwards from the spiral. In the majority of the proteins the spirals are similar with regard to their geometric properties. Hydrogen bonds form between the hydrogen atom of an amino group and the oxygen atom of the carboxyl group of amino acids three residues away. All the amino and carboxyl groups of amino acids in a polypeptide chain are linked by these hydrogen bonds. The hydrogen bonds that form greatly enhance the stability of the polypeptide spiral. The spiral formation of the polypeptide chain and the formation of the hydrogen bonds between amino acids form the secondary structure of a protein.

1.5. Tertiary structure

The tertiary structure of a protein is the structure of the protein after the polypeptide chain has been folded into its specific three dimensional conformation. Each protein has a particular conformation that differs from other proteins. During protein folding, the hydrophobic side chains of amino acids are buried within the interior of the protein. The protein folds into a highly specific conformation, forming sites that are able to recognize particular molecules during metabolism. If long coils of the polypeptide chains remain, the protein is said to be fibrous. When the polypeptide chains are looped, turned, and folded back on themselves, the protein is said to be globular.

1.6. Quaternary structure

Some proteins contain several polypeptide chains bonded together forming a bundle, this forms the quaternary structure. Proteins lacking quaternary structure are called monomeric, as they contain only one polypeptide chain. Proteins possessing the quaternary structure are classified according to the number of polypeptide chains they posses: dimeric proteins contain two polypeptide chains; trimeric contain three polypeptide chains; tetrameric contain four polypeptide chains and so forth. If the protein consists of a number of identical polypeptide chains it is classified as a homomeric protein. If different polypeptide chains making up the quaternary structure of a protein, it is classified as a heteromeric protein.

1.7. Enzymes

Virtually all enzymes are proteins with the exception of a few catalytic RNAs. Enzymes catalyze almost every biochemical reaction in the cell, and are extremely efficient catalysts, increasing reaction rates by 10^7 to 10^{14} fold. Most enzymes require co-factors to operate adequately. These co-factors may be simple such as Na^+, which bind to a critical site on the enzyme. The co-factors function by assisting in the binding of the substrate(s) [S] to the enzyme [E] to form the enzyme–substrate complex [ES]. More complex co-factors are called co-enzymes and assist the enzyme in reactions where portions of a substrate need to be transferred to another compound. In these reactions the enzyme catalyses the reaction and the co-enzyme carries out the transfer. Co-enzymes include some derivatives of vitamins and nucleic acids.

Enzymes are classified according to the reactions they catalyze: proteinases catalyse reactions involving proteins; carbohydrases and lipases catalyse reactions involving carbohydrates and lipids respectively and so on. The suffix –ase always identifies an enzyme.

Enzyme catalysed reactions are characterized by the formation of an enzyme–substrate complex [ES]. The substrate is a compound on which the enzyme will act, accelerating the reaction to produce the required product. The substrate will bind to a specific site on the enzyme called the binding site. The binding site contains the active site which promotes the required reaction. If the enzyme is denatured it will remain catalytically active only if the active and binding sites remain constant. The function of enzymes is to lower the activation energy for the specific reaction and thereby increase the rate of the reaction.

Enzymes are flexible molecules that can be induced by their specific substrate to mould themselves around the substrate. The "induced fit" increases the reactivity of the enzyme with the substrate, due to the enhanced interaction between the enzyme and substrate. Enzymes are, however, highly specific and only form ES complexes with their specific substrate(s), this reaction can be compared to a lock and key. Only a specific key will open a certain lock and the same theory holds true for enzymes and their substrate(s), only specific substrate(s) will interact with a certain enzyme. Figure 3 shows a graphical display of enzyme–substrate specificity.

(a) Substrates 1 and 2 attempting to enter the active site of the enzyme.

(b) Substrate 1 fits into the binding site of the enzyme while substrate 2 is excluded due

to it having the incorrect conformation to fit into the binding site.

(c) Substrate 1 is catalyzed by the enzyme to produce the required products.

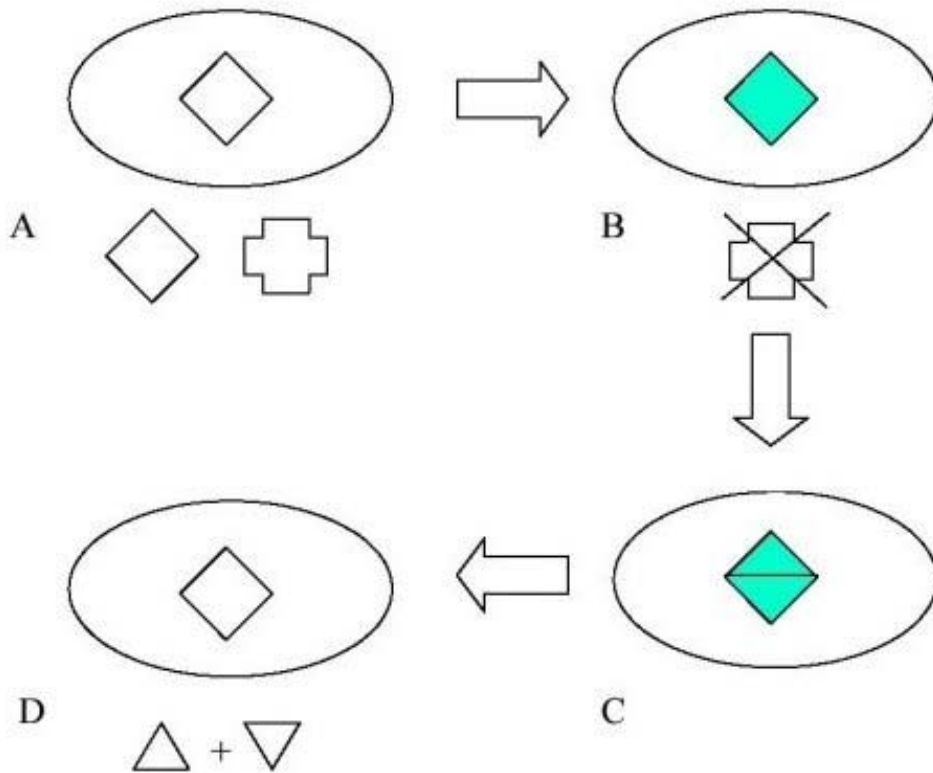(d) The enzyme releases the products, and is now ready to bind the next substrate.

Figure 3. A graphical display of the enzyme - substrate specificity.
Enzyme - ◯, substrate 1 - ◇, and substrate 2 - ✚

A) Substrates 1 and 2 attempting to enter the active site of the enzyme.
B) Substrate 1 fits into the binding site of the enzyme while substrate 2 is excluded due to it having the incorrect conformation to fit into the binding site.
C) Substrate 1 is catalysed by the enzyme to produce the required products.
D) The enzyme releases the products, and is now ready for the next substrate.

Enzymes are extremely sensitive to changes in the external environment. Temperature and pH play a vital role in controlling the rates of catalysis by enzymes. A large increase or decrease in temperature or pH causes the denaturing of the enzyme. When an enzyme is denatured it loses all its catalytic ability due to the bonds holding the enzyme together in a specific conformation being broken. A temperature and pH value exists where the enzyme activity is at its highest; this is called the optimal enzymatic conditions. The optimum temperature and pH values differ for different enzymes.

2. Carbohydrates

Carbohydrates are the most abundant biomolecules on earth, found widely distributed in

nature. Fifty to eighty percent of the dry weight of plants is composed of carbohydrates, including cellulose, starch and pectin which are important structural components. The term 'carbohydrate' is derived from the French 'hydrate de carbone'. Carbon and water constitute the principal components of carbohydrates. There are three major groups of carbohydrates that exist, separated by differences in size.

Monosaccharides are also-called "simple sugars" and are the smallest of the three groups, consisting of a single polyhydroxy aldehyde or ketone. Disaccharides consist of a short chain containing two monosaccharides joined together through glycosidic linkages. The most abundant of the disaccharides is sucrose, consisting of one glucose and one fructose unit joined covalently to each other through a glycosidic linkage. Polysaccharides are the largest in size of the three groups consisting of hundreds of monosaccharides bound covalently to each other through glycosidic linkages. Carbohydrates form the basis of many natural fermentations such as beer, wine and vinegar. Carbohydrates are also a valuable source for the production of cotton cloth, paper and antibiotics, as well as a valuable source of fuels.

2.1. Monosaccarides

There are several classes of monosaccharides that exist, being distinguished from each other by the number of carbons present. Monosaccharides that consist of three carbons (C_3) are called trioses, C_4 sugars are tetroses, C_5 sugars are pentoses and C_6 sugars are hexoses.

2.1.1. Stereo-isomerization

Every monosaccharide that has a hydroxyl group positioned to the right of its highest numbered asymmetric carbon atom, according to the Fischer projection formulas, is assigned the prefix D-. Their enantiomers are assigned the prefix L- when the hydroxyl group is positioned to the left. Figure 4 shows the stereoisomers (mirror images) of glyceraldehydes shown as their Fischer projection formulae. Two sugars that differ only in their conformational state around one of their carbon atoms are called epimers. D-Glucose and D-galactose are epimers as there is a conformational change around the fourth carbon. Figure 5 shows D-glucose and its epimer D-galactose.
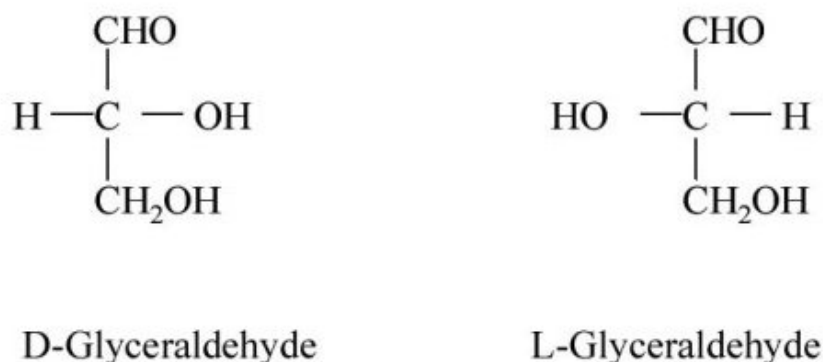

Figure 4. Stereoisomers (mirror images) of glyceraldehydes shown in the Fischer projection formulae.
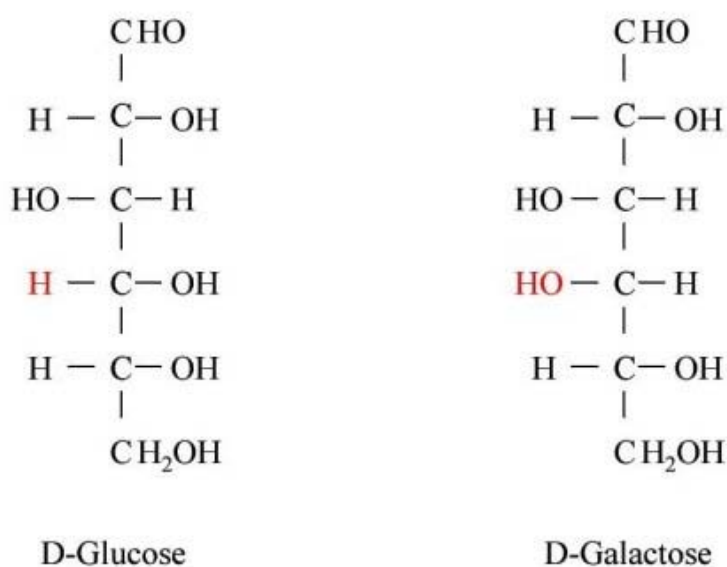
Figure 5. D-glucose and its epimer D-galactose

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Biographical Sketch

Bret Pletschke was born in 1968 and obtained his BSc (1989), BSc Hons(Biochemistry) (1990), MSc (Biochemistry) (1992) and PhD (Biochemistry) (1996) at the University of Port Elizabeth, South Africa. During his under- and postgraduate training he was awarded several NRF, MRC and UPE bursaries, as well as a Van Der Biji Scholarship (ESKOM). During his postgraduate training he was also appointed as a

Supplementary Instruction Leader (Feb 1993 to Nov 1993) and as a Lecturer (contract) in the Department of Biochemistry and Microbiology (July 1995 to Sept 1996). He worked at The Ludwig Maximilians University in the Surgical Clinic and Policlinic, Munich, Germany during October 1996, and was then appointed as a Postdoctoral Fellow/Chief Scientific Officer in the Departments of Chemical Pathology and Biochemistry at The University of Cape Town, South Africa from June 1997 to Dec 1999. In January 2000 he was appointed to the post of Lecturer in Biochemistry at the Department of Biochemistry, Microbiology and Biotechnology at Rhodes University, Grahamstown, South Africa. His research interests are in the field of Environmental Enzymology and Bioremediation- He is currently actively involved in conducting research on enzymes involved in the anaerobic digestion of wastewater sludges, the teaching of undergraduate students and supervision of postgraduate students.