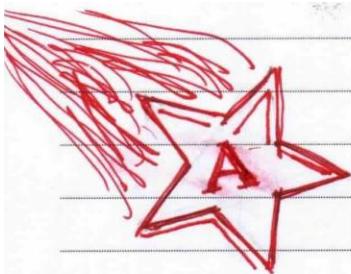


بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ



تلخیص  
صلادة

علوم الحياة  
Bio101

Campbell Biology

2011/2012

اعداد الطالبة

أسيل الزغول

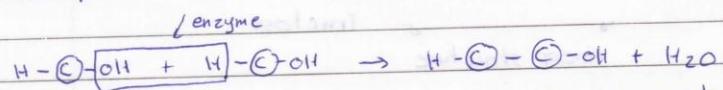
سنة أولى طب

## Chapter 5 (Biological macro molecules).

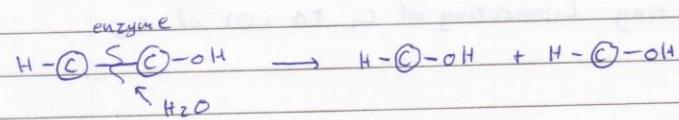
\* monomer :- small building unit  $\xrightarrow{\text{identical}}$   
\* polymer : group of monomers  $\xrightarrow{\text{similar}}$

\* macromolecules :- 1) carbohydrates (polymers) 2) proteins (polymers)  
3) lipids (not polymers) 4) nucleic acid (polymers)

+ cells produce all these 4 substances by syntheses reaction :-



condensations reaction = dehydration reaction (produce water)



breakdown = hydrolyses reaction

1] carbohydrates (sugar)  $\rightarrow$  monosaccharide = monomers 3-7 carbon  
 $\rightarrow$  disaccharide  
 $\rightarrow$  polysaccharide

\* function of monosaccharide 1] Fuel for cells, 2] building molecules

C : H : O

1 : 2 : 1

\* classification :-

1] numbers of C :-

Hexoses (6c) :- Fructose, Glucose / Pentose (5c)

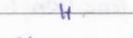
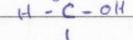
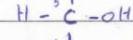
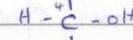
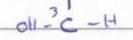
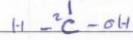
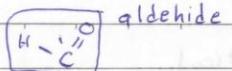
Triose (3c).

2] The carbonyl group :-

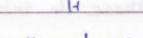
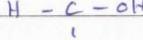
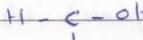
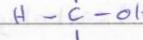
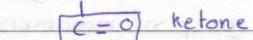
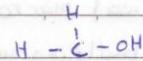
Glucose :- aldose  $\Rightarrow$  aldehyde

Fructose :- ketose  $\Rightarrow$  ketone.

(e.g. Glucose and galactose)  $\leftarrow$  3] arrangement of substances around the same (C)



Glucose

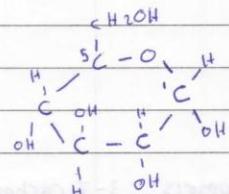


Fructose

linear structure

\* in water = ring structure

Glucose: linear  $\rightarrow$  ring (connecting of C<sub>1</sub> to (O) of C<sub>5</sub>)

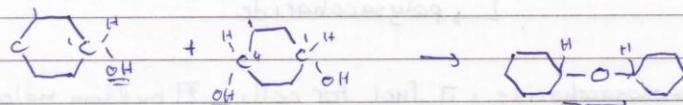


$\alpha$  Glucose when (OH) of C<sub>1</sub> is down

$\beta$  glucose when (OH) of C<sub>1</sub> is up

\* disaccharides -

Glucose      Glucose      maltose



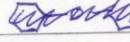
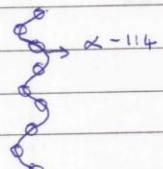
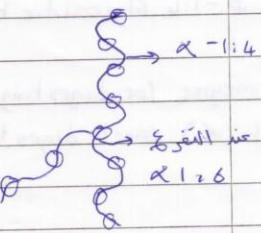
we omit one(H) and (OH)

$\alpha$  1:4 Glycosidic bond

covalent bond

Glucose + Fructose  $\rightarrow$  sucrose

" + galactose  $\rightarrow$  lactose

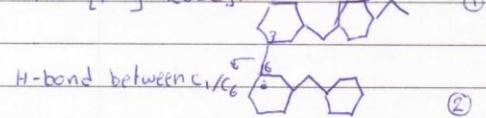
Polysaccharides (depend on position of glycosidic linkage)		
storage	structure	sugar monomers
Monomers =	monomers =	e.g. cellulose (plant) chitin (insects)
$(\alpha\text{-glucose})_n$ (100-1000)	$(\beta\text{-glucose})_n$	
e.g. storage starch : polysaccharide in plants		
Glycogen : storage polysaccharide in animals (in liver and muscles cells)		
* starch bond : $\alpha-1:4$ glycosidic		الرابطة الرابطة
* cellulose bond : $\beta-1:4$ "		الرابطة الرابطة
* starch	<ul style="list-style-type: none"> <li>simple (unbranched)</li> <li>complex (branched)</li> </ul>	
	$\alpha-1:4$	
Amylose (simple) helical shape 25% in plants		
	$\alpha-1:4$ $\alpha-1:6$	
		الرابطة الرابطة
		Amylopectin (complex) 75% in plants

\* Glycogen :- more branched than amylopectin and every thing else is the same.

\* structural polysaccharide :-

i) cellulose :- is available in cell wall of plants

unit :-  $[\beta\text{-glucose}]_n$



shape : linear / unbranched

\* microfibrils :- group of cellulose which are grouped (give strong building to plants).

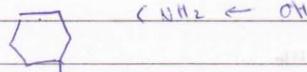
\* paper / cotton is made of cellulose

\* in food package it's called - insoluble Fibre

ii) Chitine :- i] in exoskeleton of arthropods ii] cell wall of fungi

unit :-  $[\beta\text{-Glucosamine}]_n$

bond :-  $\beta\text{-1:4}$  Glycosidic bond



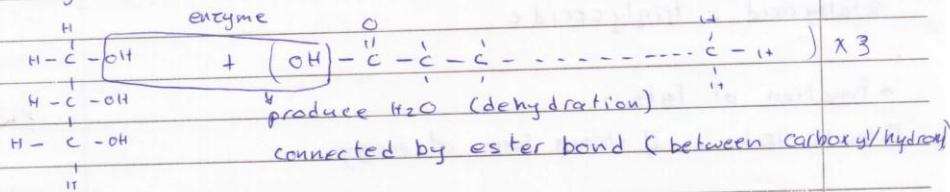
\* The enzyme for digesting starch ( $\alpha$ ) can't digest cellulose ( $\beta$ )

lipids ~~not~~ polar because they consist a lot of C-H

\* lipids are diverse, the common thing of all lipids that they are hydrophobic

fats and oil :: made of two component  $\xrightarrow{\text{Glycerol}}$   
 $\xrightarrow{\text{3 fatty acid}}$

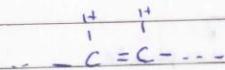
Glycerol



\* number of carbon could be as long as 24 carbon / usually (16-18) carbons

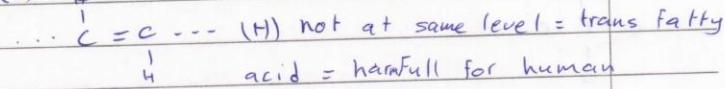
\* fatty acid is saturated = all bonds are single (linear shape)

\* .. unsaturated = at least there is one double bond

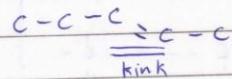


(H) in same level = cis-fatty acid = useful

(H)



\* when double bond is available abinding ~~back~~ = kink



\* cis / trans are Geometric isomer ~~نقطة موجة الـcis على الرابطة~~

\* cis is changed into trans by heat

\* group of fatty acid which are saturated = solid at room temp.  
= fat = poly saturated fat = in animals

\* oil = at least one unsaturated fat = liquid at room temp.  
= in plants and Fish

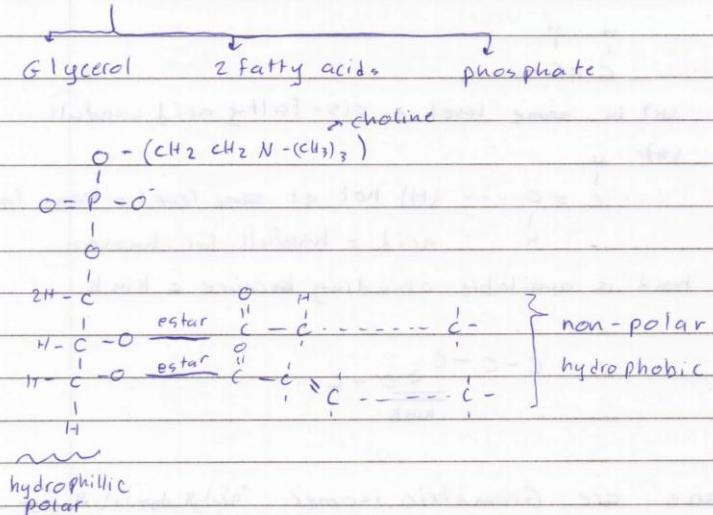
3 fatty acid = triglyceride

\* Function of fats :-

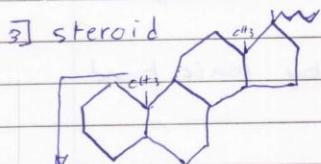
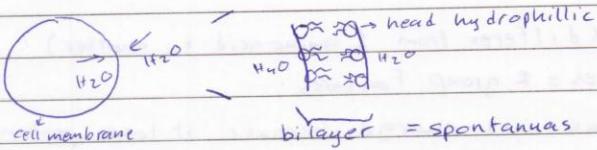
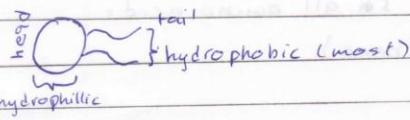
1] build lipids 2] strong form of energy

\* Fatty acids differ in length / location of double bond

2] Phospholipids :- (cell membrane)



\* symbol of phospholipids:



cholesterol : used to make sex hormones  
(estrogen / testosterone)

\* Proteins = polymer = amino acid monomers = 50%. Dry mass of cell  
are must in any living system / vital

\* Function: 1] make some enzymes (digestive enzyme)

2] work as hormones e.g.: ansolyn

3] work as receptors

↳ structural protein (support) e.g.: <sup>①</sup> collagen

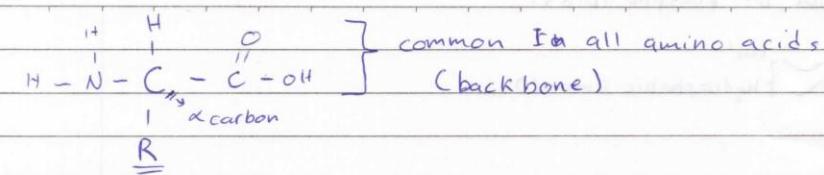
② keratin hair  
- nail  
Feather

5] transport eg:- hemoglobin

6] Contractile egs: actin / myosin

## 7] defence (anti bodies)

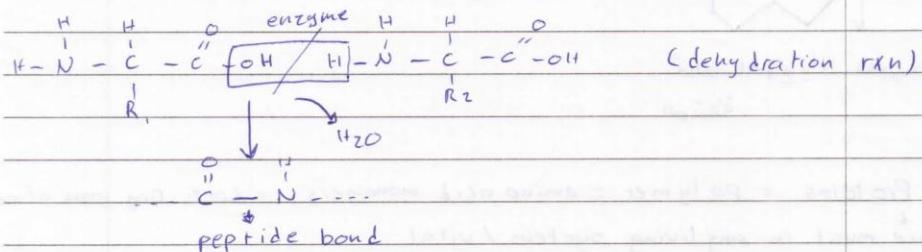
8] storage eg: protein of milks



Side group chain (differs from 1 amino acid to another)

amino acid Features = R group Features

- \* acidic amino acid has (-) charge because it loses proton
- \* Basic " " " (+) " " " gains "
- \* both are charged = hydrophilic
- \* they could be connected together by ionic bond

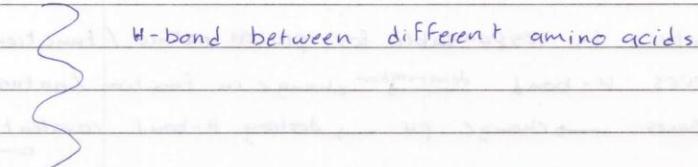


- \* protein = polypeptide
- \* protein always has two ends amino end (N-terminus) carboxyl end (C-terminus)

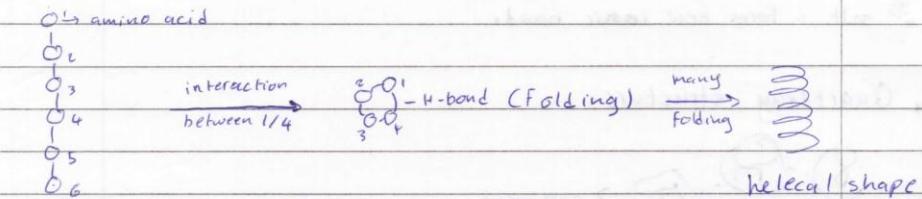
- \* every protein has specific amino acid sequence = primary structure  
determines the 3D structure
- protein will have

- \* peptide bond stabilize the primary structure of protein
- \* Frederick Sanger determined the amino acid sequence

\* primary structure (amino acid sequence)



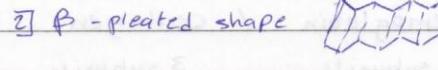
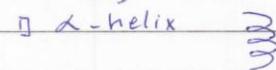
\* secondary structure :-



\* interactions happen between backbone of different amino acid.

\* H-bond stabilize the secondary structure

\* secondary structures:-

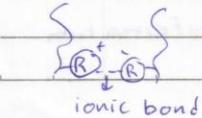


\* secondary structure because of H-bond between different backbone of amino group

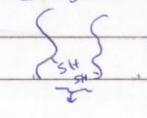
\* proteins don't stay at secondary structure because R-group is able to interact.

\* R-group interactions :-

1] ionic bond



2] disulfide bridge



3] hydrophobic interaction

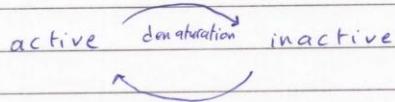
4] H-bond

(2) R-group interactions → Tertiary structure = the final shape if the protein was made of one-polypeptide

\* The final structure is responsible for protein nature / Function

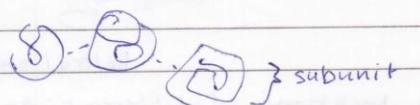
\* Heat → removes H-bond denaturation change in function / nature

\* strong acids / bases → change pH → destroy H-bond, covalent bond



\* salt : form new ionic bonds

\* Quaternary structure :-



3 subunits

interactions (H-bond / ionic bond) between

backbone or (R) group

eg: Hemoglobin / collagen

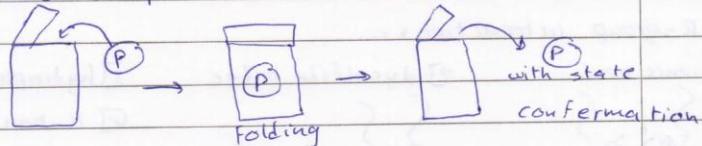
4 subunits

3 subunits

Globular

Fibrous

\* If folding happens in cell (pH / solute), different conformation will occur. (so folding must happen in static environment which is called chaperonins (has si lender))



Nucleic Acids = polymers = Nucleotide monomers (polynucleotide strand)

DNA carries the genetic information

one type

made of double strand

RNA

many types

made of one strand

\* nucleotide → ribose sugar (pentose)

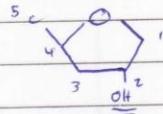
    |

    nitrogen base

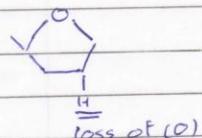
    |

    PO<sub>4</sub> group

\* ribose:- it makes RNA

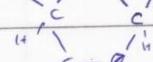


\* deoxyribose (DNA)



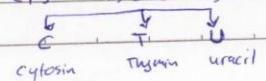
\* nucleotide:-

(P<sub>2</sub>O<sub>7</sub>)<sub>2</sub>C<sub>10</sub>H<sub>16</sub>O<sub>4</sub> N-Base (full of NH or NH<sub>2</sub>)



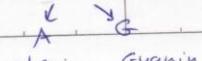
\* N-Bases that make RNA, DNA are ring structure

(pyrimidine) one ring



cytosin      Thymine      uracil

two ring (Purine)



adenin      Guanin

\* A, C, G, are common in RNA and DNA

\* T → DNA

\* U → RNA

\* the differences between RNA, DNA :-

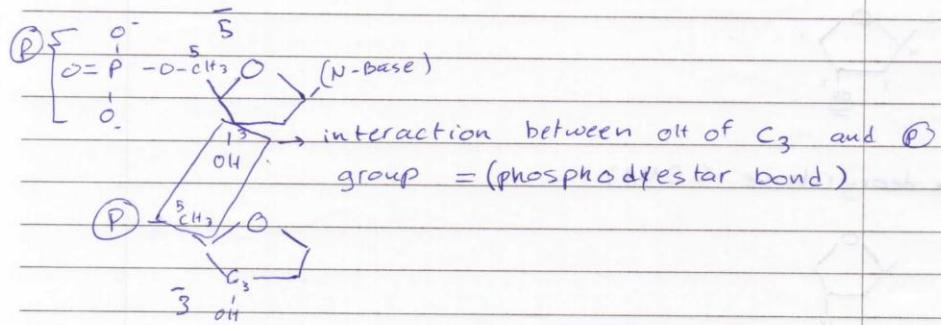
1] N-base

2] sugar ring

3] strand number

\* Nucleotide = sugar + (P) + N-Base

\* Nucleoside = sugar + N-Base



(sugar + PO<sub>4</sub>) are common between all DNA or RNA

= Back bone

\* They differ in Base sequence

\* every DNA has specific base sequence