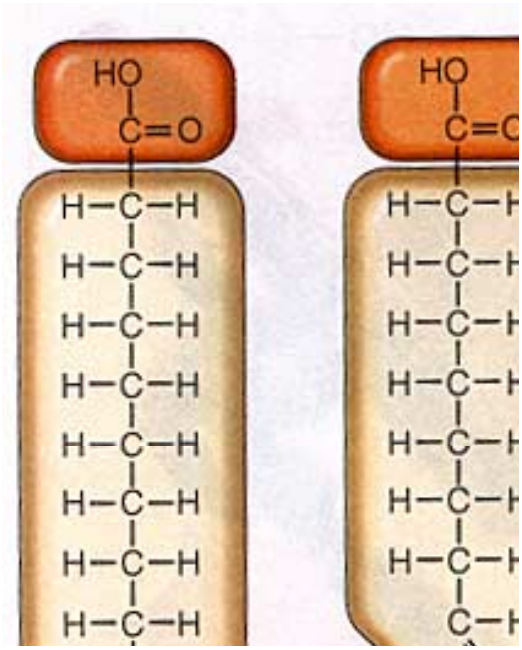
Hierarchical Structures and Biology

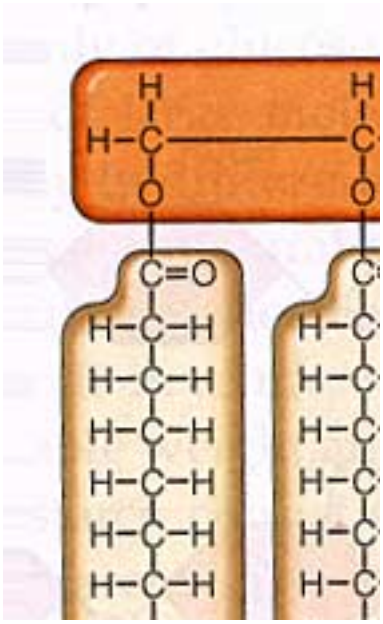
Main Types of Biological Molecules

1. Lipids (fats)

<u>Fatty acids</u> have a backbone of up to 36 carbon atoms and end with a –COOH group. The carbon chains can have unsaturated bonds as well as saturated.



<u>Triglycerides</u> such as butter and lard, are the most abundant fats in the body and are its richest energy source. They consist of 3 fatty acid tails attached to a glycerol molecule. Again chains can be saturated or unsaturated.



<u>Phospholipids</u> also have a glycerol 'backbone', but the third attachment to the glycerol is a hydrophilic head

consisting of a phosphate plus another hydrophilic group.

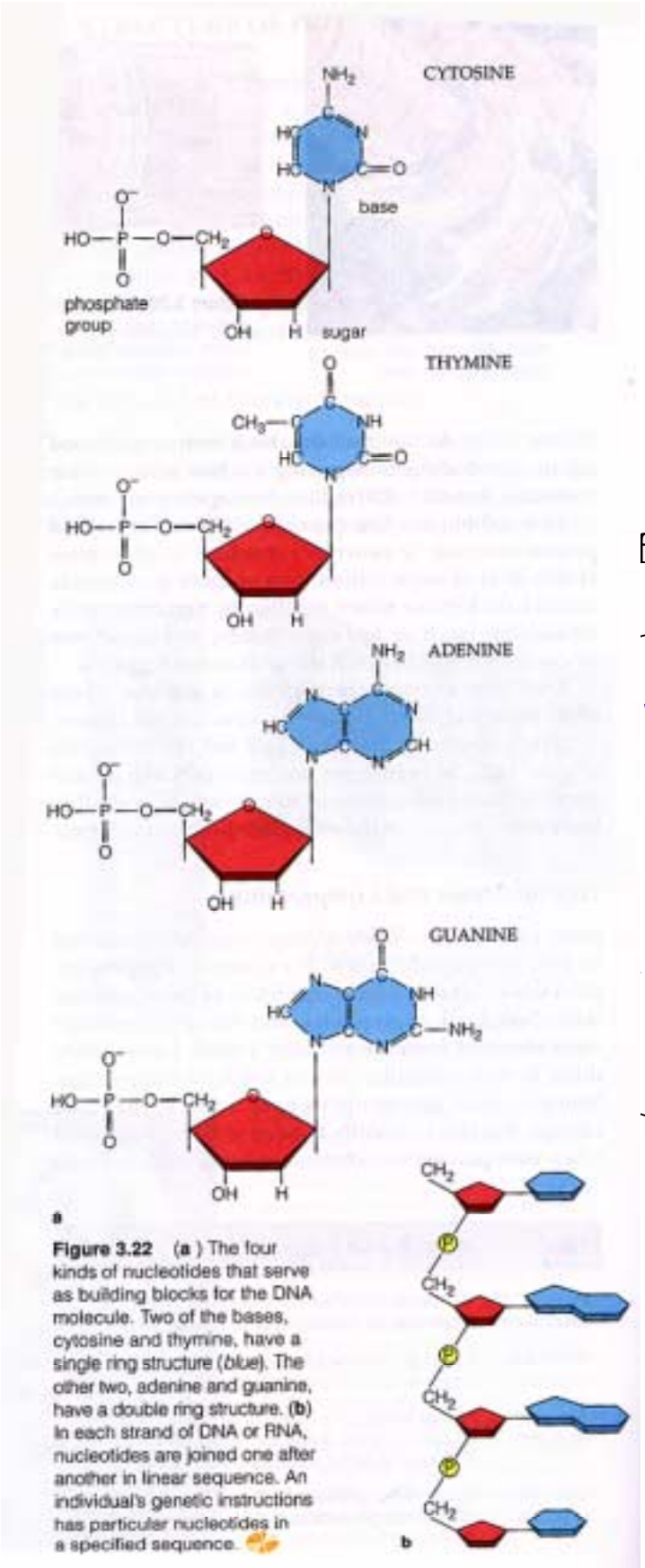
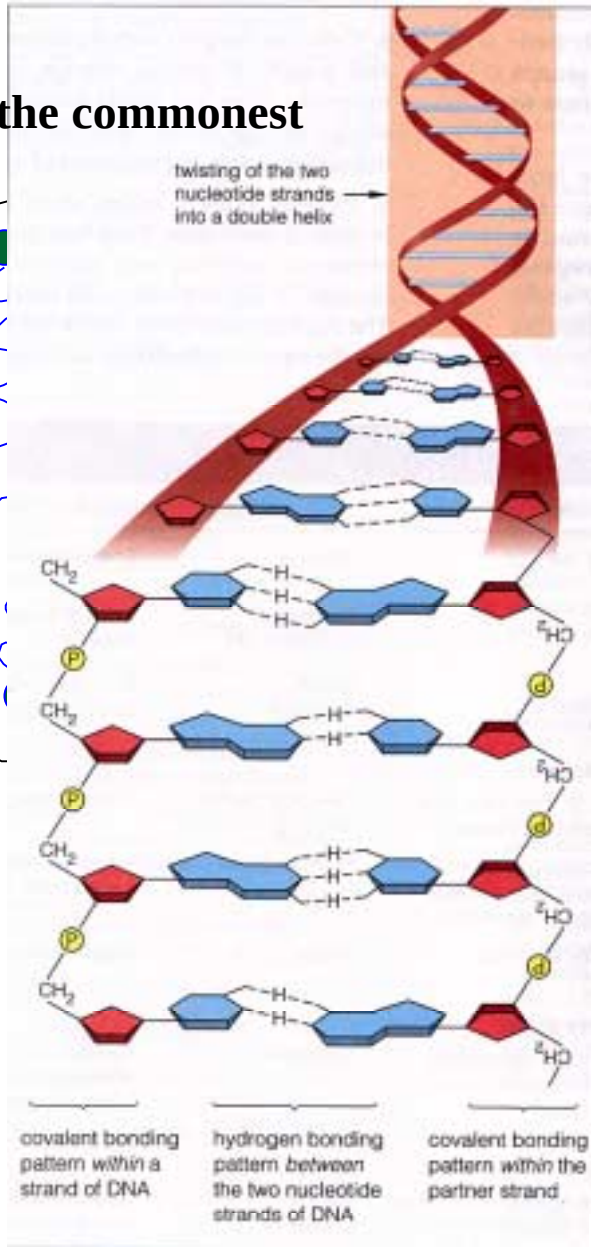


Figure 3.22 (**a**) The four kinds of nucleotides that serve as building blocks for the DNA molecule. Two of the bases, cytosine and thymine, have a single ring structure (*blue*). The other two, adenine and guanine, have a double ring structure. (**b**) In each strand of DNA or RNA, nucleotides are joined one after another in linear sequence. An individual's genetic instructions has particular nucleotides in a specified sequence.

f the commonest



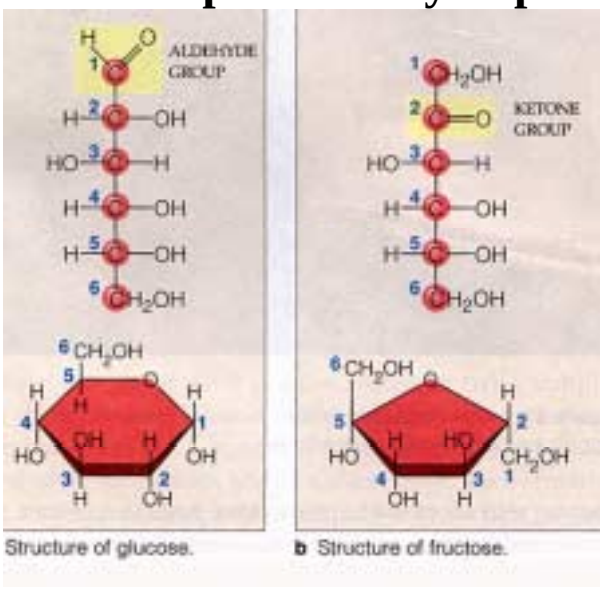
Bonding is always A-T and C-G (base pairing), and the pairs are linked through a sugar phosphate backbone..

RNA has uracil in place of thymine.

3 Polysaccharides

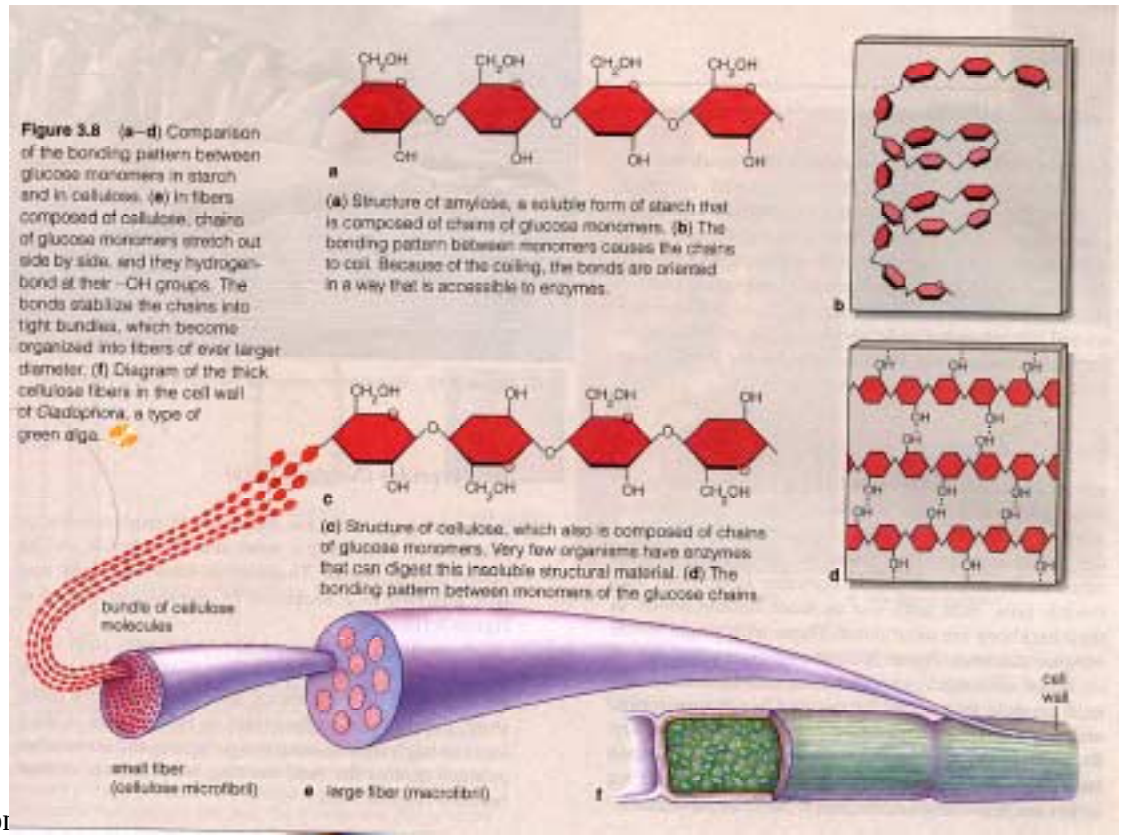
Polysaccharides are long chains of simple sugar molecules. Sugars are 5 or 6 membered saturated carbon rings.

Polysaccharides are particularly important in plants.

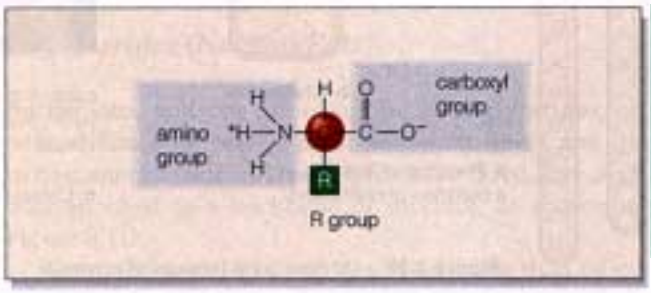


Structure of glucose. b Structure of fructose.

Examples include starch and cellulose.



4 Proteins



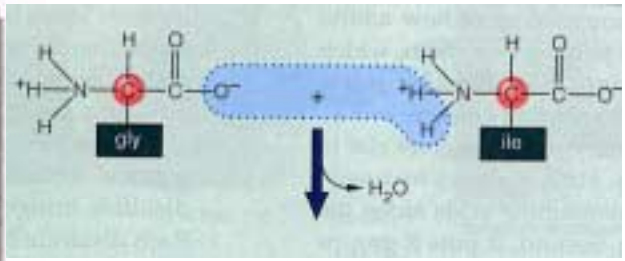
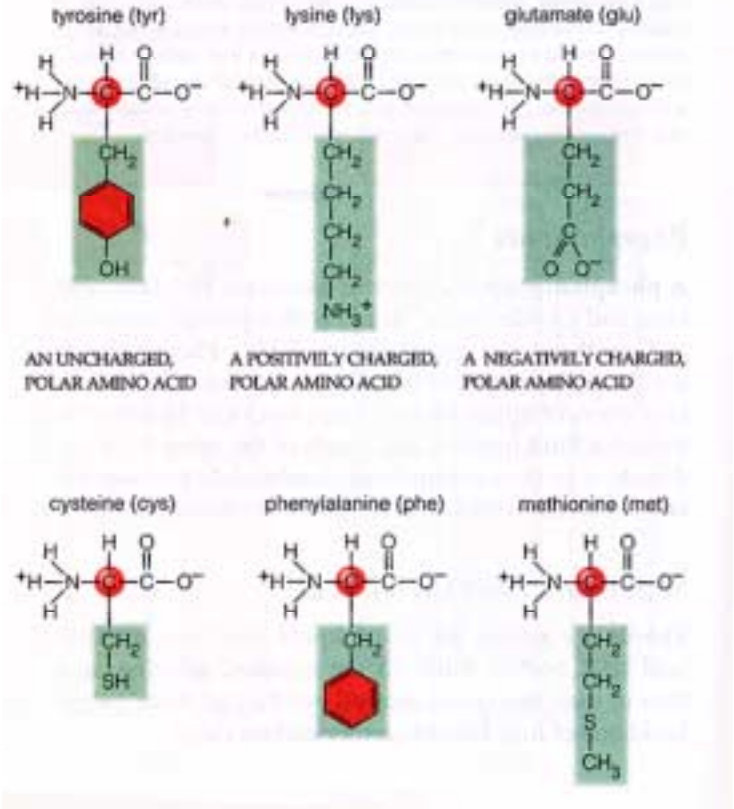


Figure 3.14 Generalized structural formula for the amino acids.

Peptide bond forms with release of water.



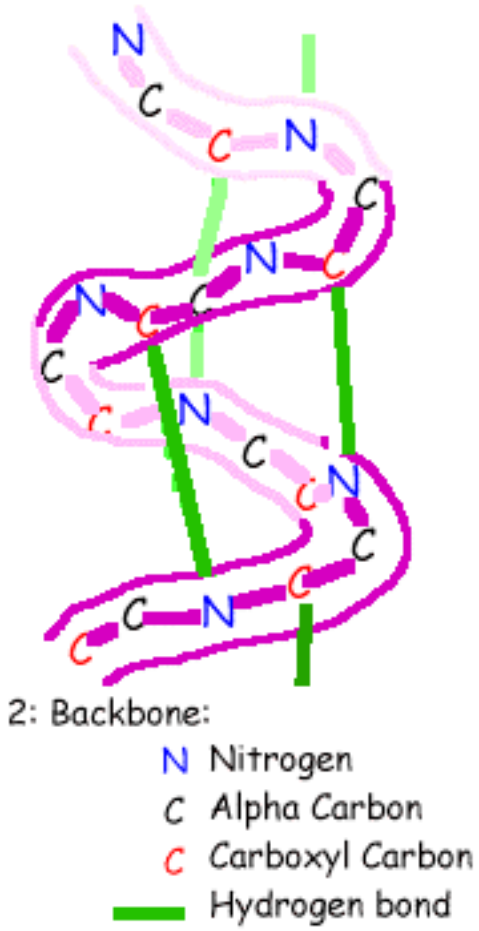
Proteins vary hugely in size i.e. how many amino acids are strung together.

Proteins are <u>not</u> random coils. They have very precise secondary structure, and this is vital for their function.

Protein Secondary Structure

Two commonly repeating motifs:

α helix



This is the most abundant type of secondary structure in proteins.

The helix has an average of 3.6 amino acids per turn with
a h **ıps**
ab

Av
β s

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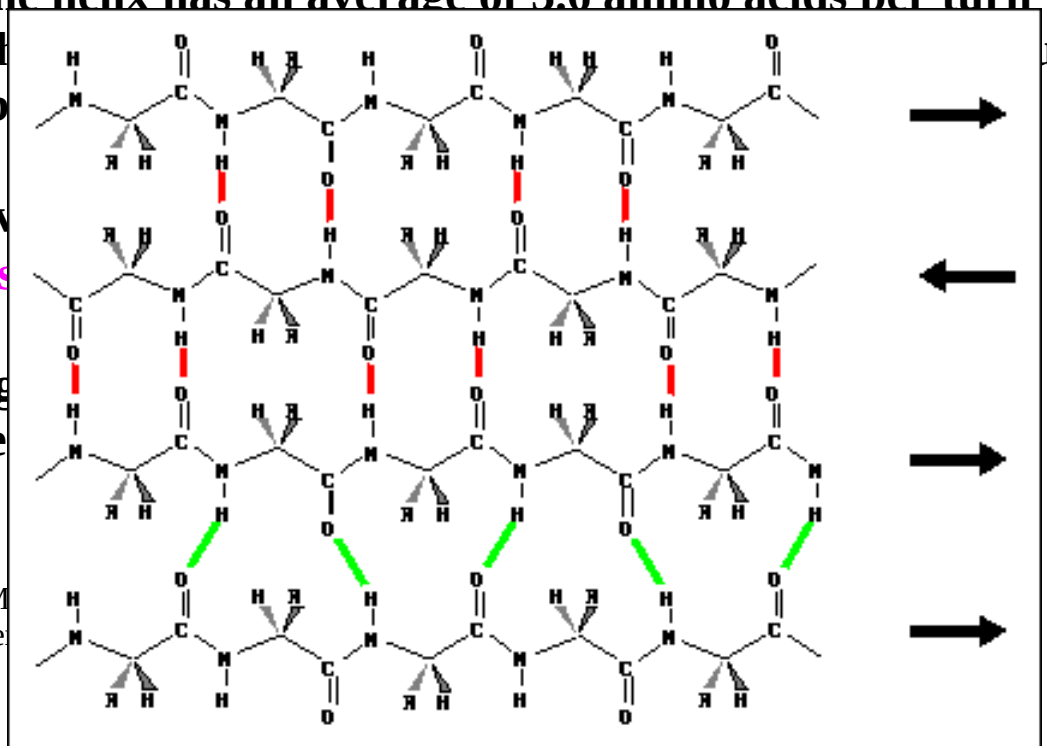
ne



AM
Hie

Hydrogen bonding forms between an average of 5-10 consecutive amino acids in one portion of the chain with another 5-10 further down the chain.

The interacting regions may be adjacent, with a short loop in between or far apart with other structures in between.

The tertiary shape of a protein is determined by the location of these standard motifs and how the chains pack in between.
Shape determines function