

BIOCHEMISTRY KEY TERMS AND CONCEPTS

Biochemistry- the study of the chemistry of living organisms, especially the structure and function of their chemical component.

Living Organisms differ from inanimate objects

- Reproduction- self replication
- evolve
- far from equilibrium
- sense & response to change in environment
- much more complex mixtures of thousands of chemical molecules that are highly organized.

Three Unifying Principles of Life

1. ALL living organisms are comprised of molecules built from the same kinds of monomeric units
2. In ALL living organisms, the function of a macromolecule is determined by its structure/sequence
3. Living organisms differ from each other due to their unique set of macromolecules

Water and Life

- Water is one of the essential molecules for life
- without water, there can be no life as we understand it
- water makes up ~70% of the mass of the human body
- solvent for most molecules in living organisms
- drives the arrangement of biological macromolecules into structures critical for their function
- most biochemical reactions occur in an aqueous environment
- water participates in many biochemical reactions

Structure of Water

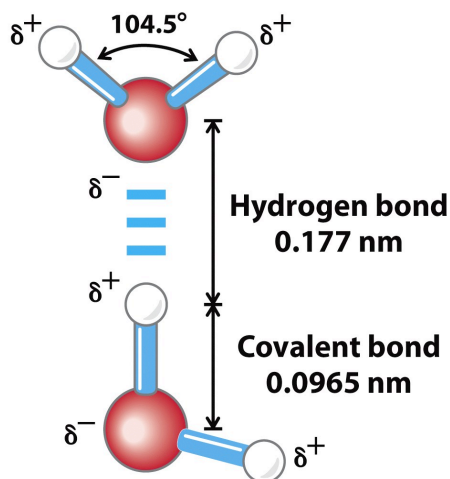


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109 degrees--> tetrahedron but not quite

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How liquid water differs from solid water

- solid water (ice) is a crystal of water molecules oriented tetrahedrally to maximize the # of H-bonds
- each water molecule H-bonds 4 molecules
- creates an open structure less dense than liquid water.
- water expands when frozen
- liquid water consists of small networks of H-bonded molecules
- networks are irregular and varied
- each water molecule H-bonds on average 3.4 other molecules and bonds are distorted
- networks are constantly forming and reforming in liquid water

Water as a solvent

universal solvent- dissolves more types of molecules to a greater concentration than any other solvent.

- solutes are hydrophilic (water-loving)

Solvating Ions

- dipoles on water orient around ions to form a hydration shell
- dipole interactions are weaker and separate ionic bonds since they partially neutralize the ionic charge on the ions.
- dissolved ions acquire greater freedom of motion (entropy)

Hydrophobic molecules in water

- oil and water don't mix
- non-polar molecules are usually insoluble in water

-molecules minimize their contact with water by:

i) caging the molecules

- water molecules form an ordered network around non-polar groups to maximize H-Bonds.

--molecules minimize their contact with water by:

- forming molecular aggregates of non-polar molecules

Amphipathic molecules in water:

Amphipathic- a molecule that contains both polar(hydrophilic) and non polar(hydrophobic) regions

- these molecules folds itself until all hydrophobic bits are exposed inside and hydrophilic bits on the outside. IE: DNA is a amphipathic molecule

Hydrophobic effect- the tendency of water to minimize its contacts with non polar substances, thereby inducing the substances to aggregate or fold in on itself.

- this is the driving force for assembly of membranes in most proteins and other biomolecules

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Bond energies in bio-molecules:

- covalent (sharing of valence electrons) ~ 400kJ/mol
- ionic (between opposite charges) ~ 86kJ/mol
- H-bonds 23 kJ/mol
- dipole-dipole 9.3 kJ/mol
- London dispersion forces *0.3kJ/mol

Bases- a purine or a pyrimidine component of a nucleoside, nucleotide or nucleic acid
ex: Adenine

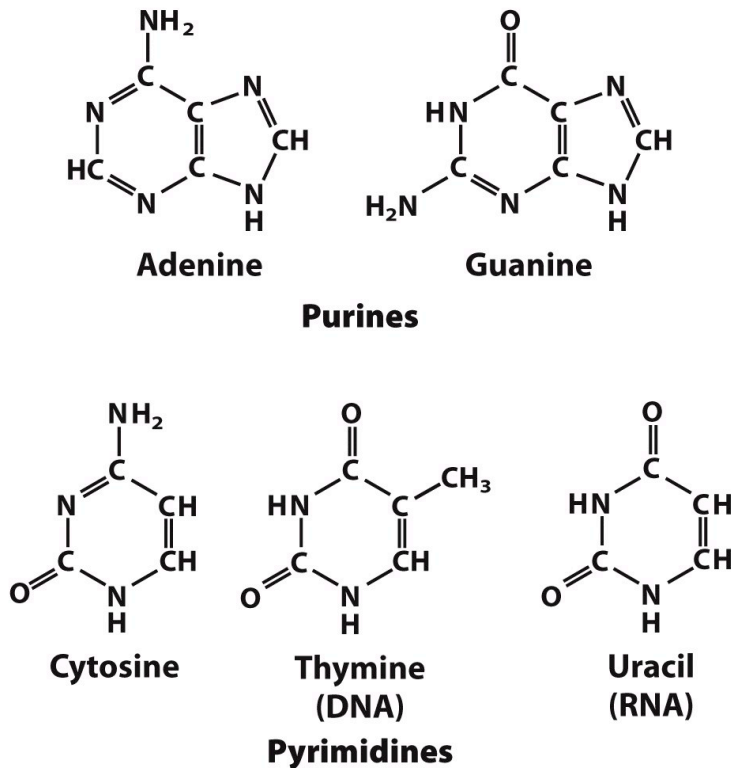
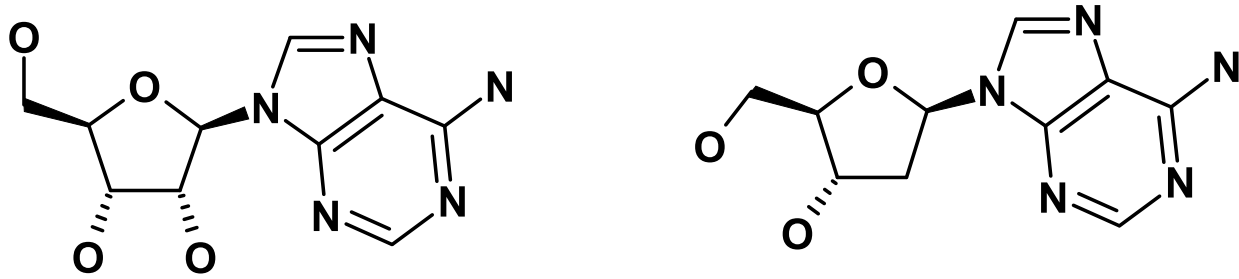


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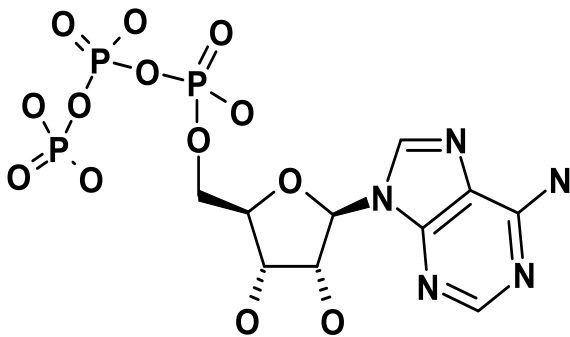
Nucleosides-an organic compound consisting of a nitrogen-containing purine or pyrimidine base linked to a sugar (ribose or dexoyribose)

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ex: adenosine or deoxyadenosine



Nucleotide- an organic compound consisting of nitrogen- containing purine or pyrimidine base linked to a sugar (either a ribose or deoxyribose and linked to a phosphate group).



EX: ATP

Functions of nucleotides:

- building blocks of nucleic acids
- participate in oxidation
- energy transfer
- intracellular signaling
- biosynthetic reactions
- building blocks of enzyme cofactors

Nucleic Acid: a polymer of nucleotide residues

example : DNA and RNA

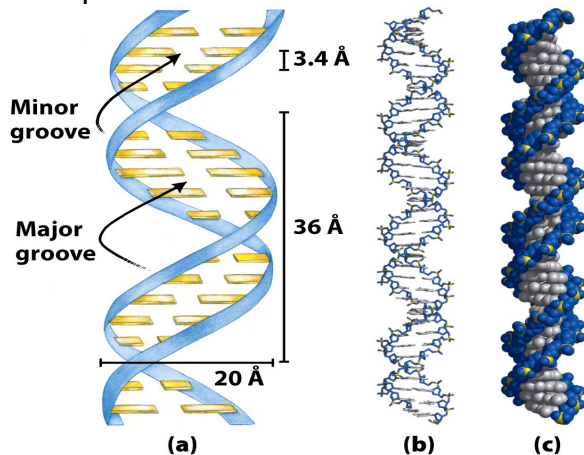


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Functions of nucleic acids: store and decode genetic info

- DNA codes the sequence of amino acids in proteins
- RNA carries a copy of the code to the sites where proteins make.
- Proteins are assembled using machinery containing RNA

Many scientists believe that the earliest forms of life made use of RNA for most functions many which are performed today

- not all gene, proteins just a lot more and more stable

Physio-chemical features of bases:

- planar – ie flat
- aromatic -contains 6 membered benzene-like ring with alternating double bonds
- heterocyclic - the rings have N instead of C at some corners
- poorly water soluble (ie relatively non-polar)
- capable of forming H-bonds
- N-1 of pyrimidines and N-9 of purines is covalently bound to a pentose sugar on nucleosides and nucleotides

Sugars

- either ribose or deoxyribose
- pentoses - have 5-membered rings
- carbons are labelled with a "prime"
- bonded to bases at the 1' carbon

phosphate

- can have monophosphate, diphosphate, triphosphate
- bonded to 5'C of the sugar on nucleotides
- absent on nucleosides
- highly water-soluble
- under physiological conditions, phosphates are deprotonated
- Mg²⁺ in cells usually associate the with negative charges on the phosphates of nucleotides

DNA double helix Structures

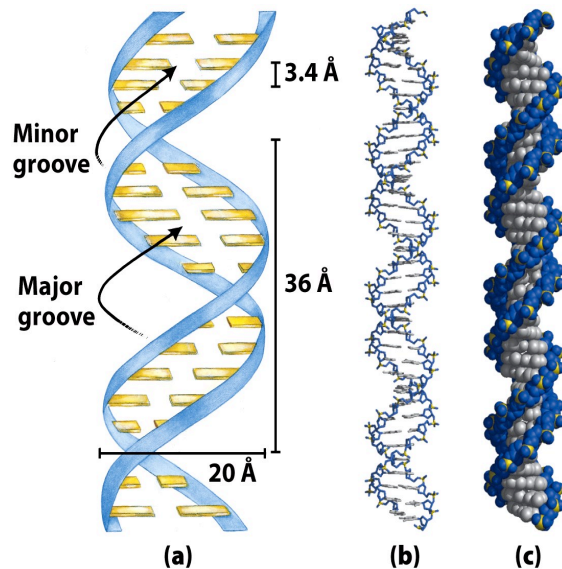


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Right handed helix called DNA-b it has 10 base pairs per turn
-the bases of DNA are point inward
A-T with 2 H-bonds
G-C with 3 H-Bonds

- non-polar bases are only exposed to the solvent at the edges
- bases stack one on top of the next with the plane of the rings parallel
- allows for London dispersion forces and dipole dipole interactions
- the folding of the DNA into this structure is driven by the hydrophobic effect

hydrophobic effect: the tendency, of water to minimize its contact with non-polar substances.

- sugar-phosphate backbone exposed on the outside
- highly polar
- minimize repulsions between charged phosphate groups.
- charged phosphates form ionic bonds with aqueous cations eg. Mg^{2+}

d) RNA structures

-RNA can form many different structures

- each structure is stabilized by the same forces as those stabilizing the DNA double helix
- ionic interactions--> phosphates on backbone can form ionic bonds with solvent cations

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- London dispersion, and dipole-dipole
- Between bases stacked
- Hydrogen bonds between bases + sugar phosphate backbone with water

The presence of the OH group on ribose makes it much more susceptible to base-catalyzed hydrolysis than deoxyribose.

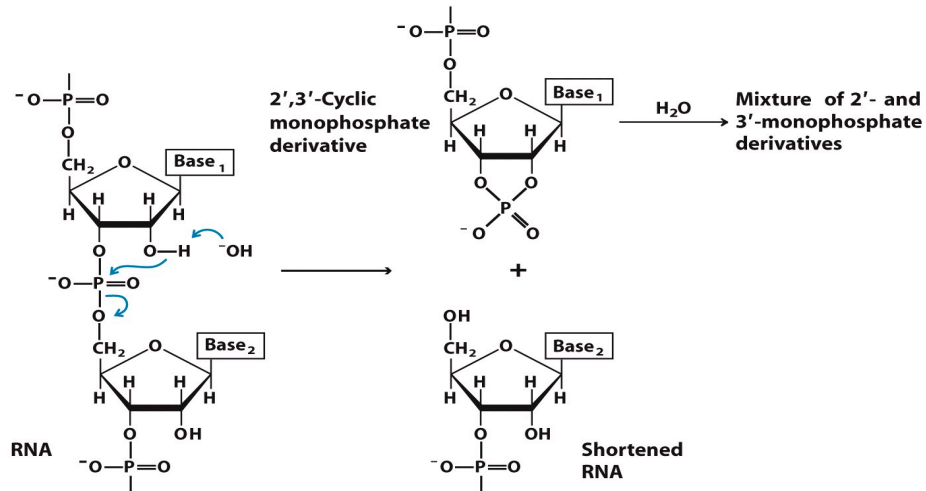


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Nucleic Acid Denaturation

denaturation defn:

- partial or complete unfolding of the specific native conformation resulting in loss of function
- heat and extremes of pH can denature DNA and RNA
- process is reversible

Polymerase Chain Reaction (PCR)

- target DNA is denatured
- short DNA stretches complementary to the ends of the region of interest (primers) anneal to the target
- DNA polymerase elongates the primers making a new copy of the target

REPEAT

AMINO ACIDS and PROTEINS

- ▀ proteins are linear polymers of amino acids
- usually 100 to 10 000 amino acids/protein
- 20 different standard amino acids available
- the structure and function of a protein is dictated by the linear sequence of its component amino acids
- branching does not occur

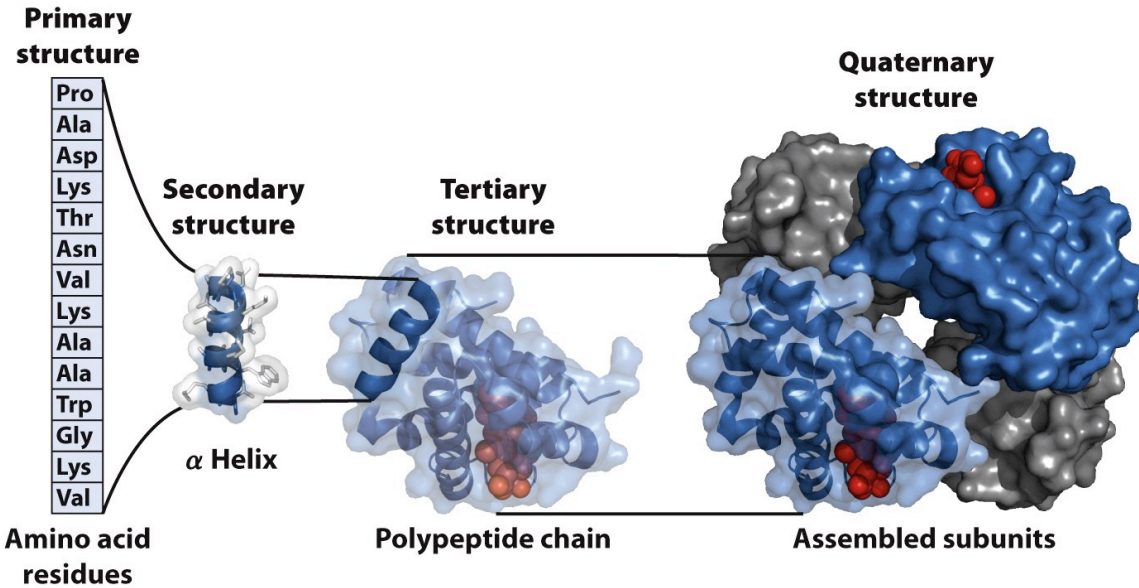


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- some proteins are monomeric, they have one protein chain and no 4^o structure
- many proteins are polymeric, they are assembled from more than one polypeptide chain and have a 4^o structure

Functions of proteins

-

AMINO ACIDS

- the centre carbon is chiral
- two configurations possible

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-only the L-amino acids found in Earth proteins

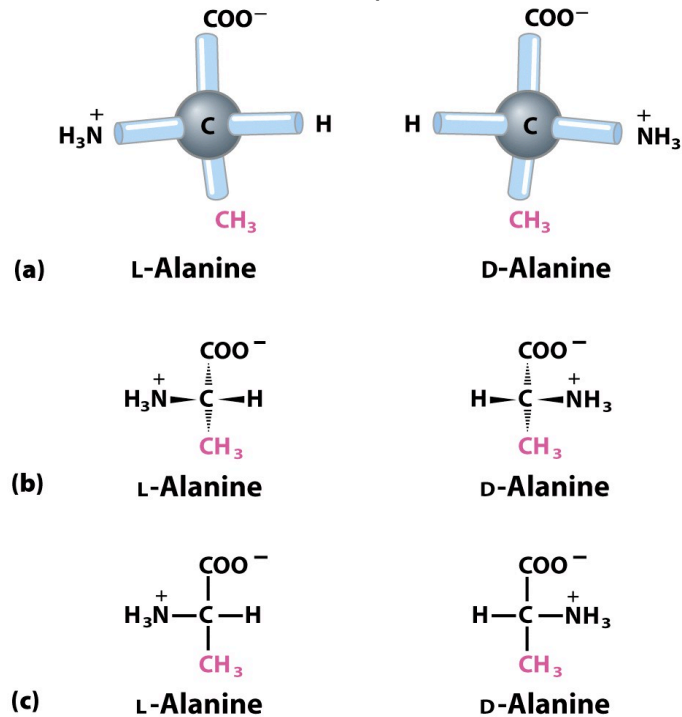


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we can classify amino acid side chains based on their chemical properties

non-polar, aliphatic amino acids

- i) Glycine [G] (Gly)
- ii) Alanine [A] (Ala)
- iii) Valine [V] (Val)
- iv) Leucine [L] (Leu)
- v) Isoleucine [I] (Ile)
- vi) Proline [P] (Pro)
- vii) Methionine [M] (Met)

aromatic amino acids

- viii) Phenylalanine [F] (Phe)
- ix) Tyrosine [Y] (Tyr)
- x) Tryptophan [W] (Trp)

polar, uncharged amino acids

- xi) Serine [S] (Ser)
- xii) Threonine [T] (Thr)
- xiii) Cysteine [C] (Cys)
- xiv) Asparagine [N] (Asp)
- xv) Glutamine [Q] (Gln)

polar, acidic amino acids

- xvi) Aspartic acid [D] (Asp)
- xvii) Glutamic acid [E] (Glu)

polar, basic amino acids

- xviii) Lysine [K] (Lys)
- xix) Arginine [R] (Arg)
- xx) Histidine [H] (His)

Acid-base properties of amino acids

-the amino and carboxylic acid groups on free amino acids readily ionize

-pKa (carboxylic acid group) ~2.2

-pKa (amino group) ~ 9.4

- at pH 7.4 (physiological)

A zwitterion is an amino acid that has both groups ionized can act as an acid or base.

- side chains are also readily ionizable

-will ionize but only under very basic conditions (high pKa)

-the actual pKa of a group depends on the local environment

-eg pKa of histidine is 6.04 in solution

-if surrounded by positive charges, the pKa will be

-if surrounded by negative charges, the pKa will be

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peptide bonds

- amino acids are joined together by peptide bonds
- peptide bond
- amide linkage (CO-NH)
- formed by a condensation reaction with loss of a water molecule

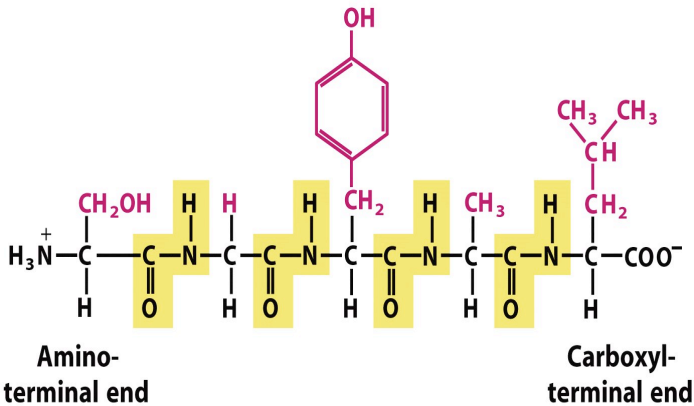


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▣disulfide bonds can covalently link two polypeptide chains or distant sites on the same chain

-formed when the thiol groups on two cysteine residues are oxidized

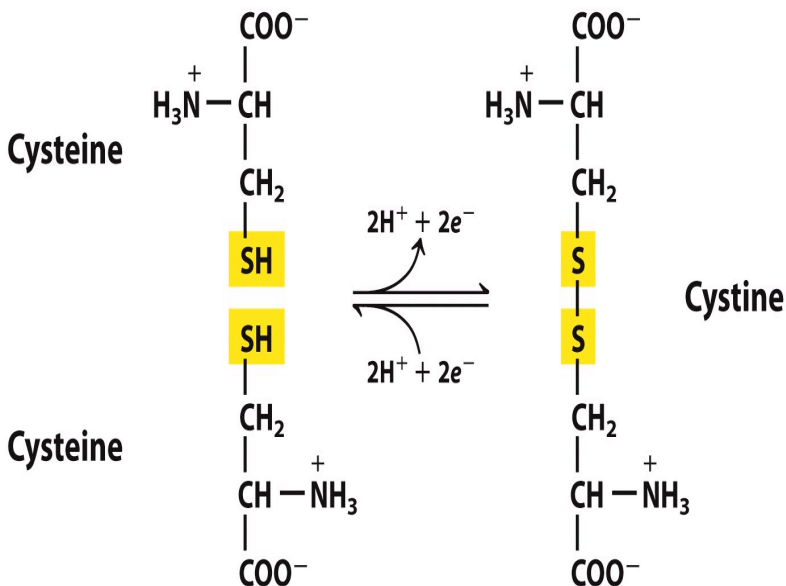


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-reducing agents such as dithiothreitol (DTT) will break disulfide bonds

-disulfide bonds link the side chains only and do not involve the peptide bonds

polypeptide defn– polymer of amino acids, generally less than 100

protein defn– polymer of amino acids

Primary Protein Structure

-linear sequence of amino acids

-a protein's 3D structure is determined by the linear sequence

-the sequence of amino acid residues help drive the folding process

-changes in amino acid sequence can cause drastic effects, ie sickle cell anemia

Secondary Protein Structure

-Secondary protein structure: the local spatial arrangement of the protein backbone without regard to the conformations of the side chains.

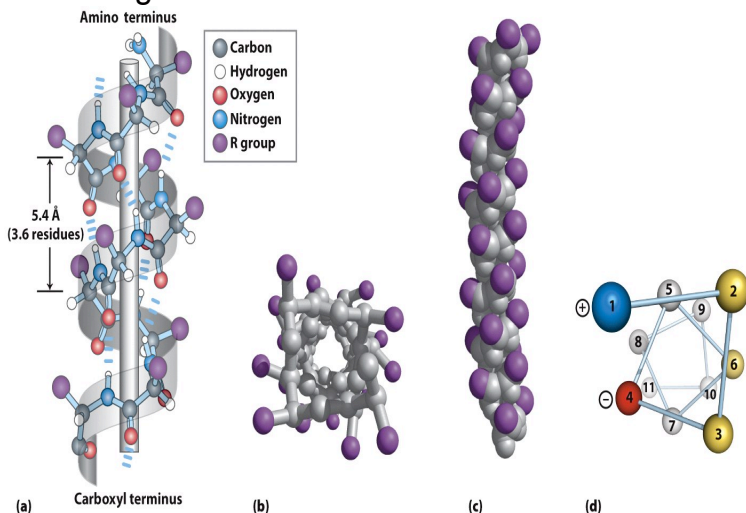


Figure 4-4
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-the backbone of a protein consists of:

-N-C α -C-N-C α -C-...

N – from the amino group

C α - covalently bound to the R group

C – carbonyl carbon (C=O)

-C-N is the peptide bond linking two amino acid residues

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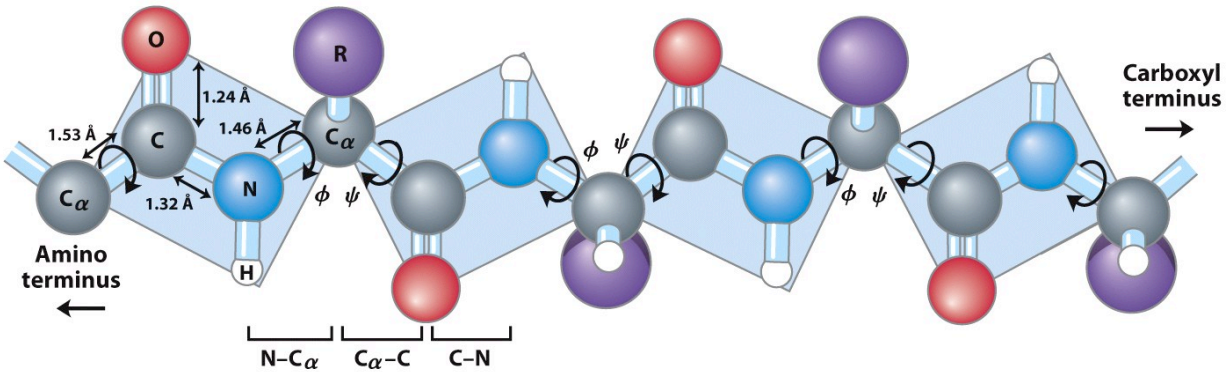


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-the peptide bond adopts a planar, rigid structure

-due to partial double bond characteristics

-resonance stabilized with the carbonyl oxygen

-double bond has trans configuration

– ensures that successive R groups are on opposite sides of the backbone and do not clash sterically

-flexibility of the peptide backbone therefore due to conformations around the $C\alpha$ atom

-defined by the torsion angles

-Ramachandran plot depicts the sterically allowed Φ and Ψ angles

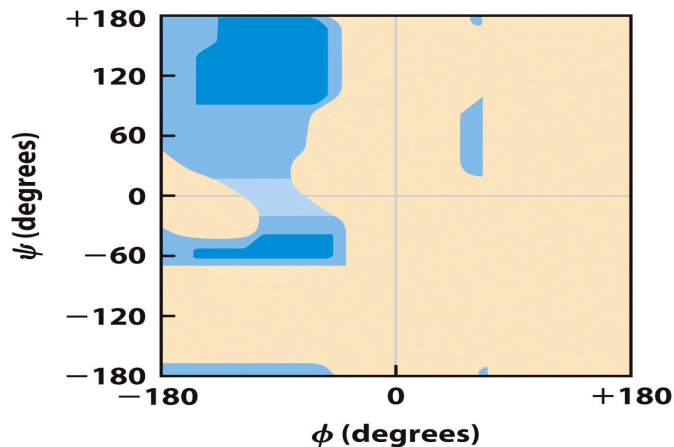


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-each amino acid is capable of adopting the Φ and Ψ bond angles of many structures

-however, some amino acids are more likely than others to be found in α -helices or β -sheets

-this info used to predict 2^o structure from 1^o sequence

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- backbone arranged such that the R groups of the amino acid protrude out from the helical backbone
- these H-bonds help stabilize the helix
- all H-bond-forming groups in the helix backbone are H-bonded

d) β -sheets

- proposed in 1951 by Linus Pauling and Robert Corey

- backbone is stretched out into a zigzag structure with chains running side-by-side

several polypeptide

Antiparallel

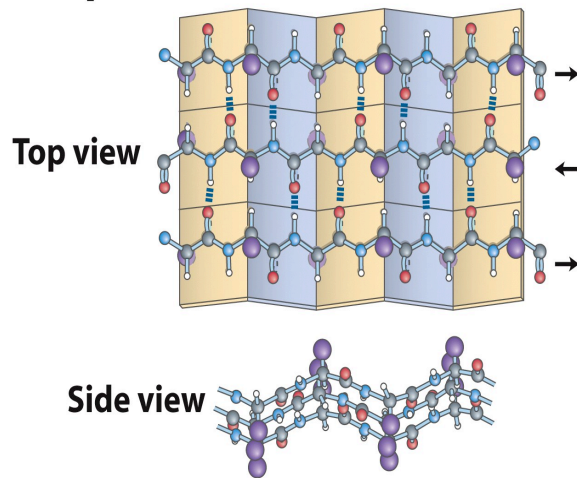


Figure 4-6a
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- a β sheet contains 2-22 β -strands (polypeptide chains)
 - avg 6
- each β -strand contains up to 15 residues
 - avg 6
- the backbone is slightly rippled (zigzag)
 - looks like a pleated sheet
- neighbouring chains H-bond each other
- all H-bond-forming groups in the helix backbone are H-bonded
- the H-bonds help stabilize the sheet

H-bonded

Parallel

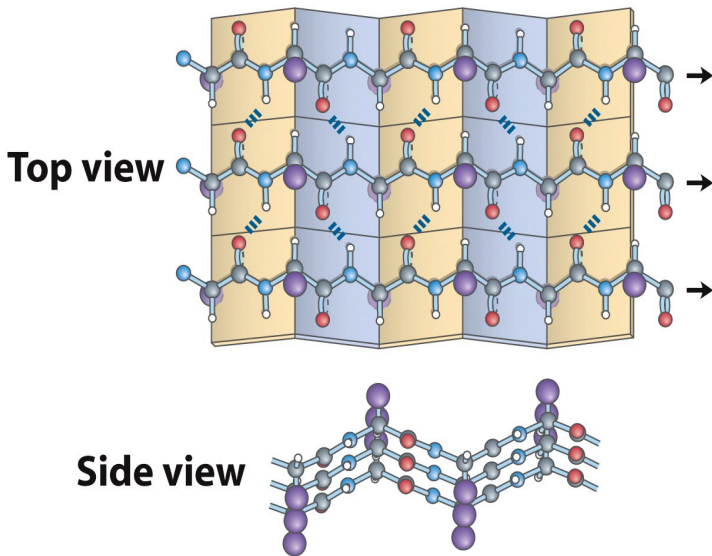


Figure 4-6b
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turns and loops

-the polypeptide backbone often has many bends that allow the protein to fold in on itself and form a compact shape eg to allow antiparallel Beta sheets

irregular structures

-most proteins have regions where successive residues do not have similar Φ and Ψ values

-form irregular structures

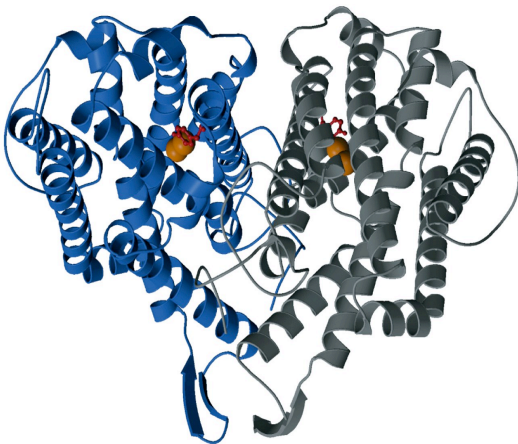


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