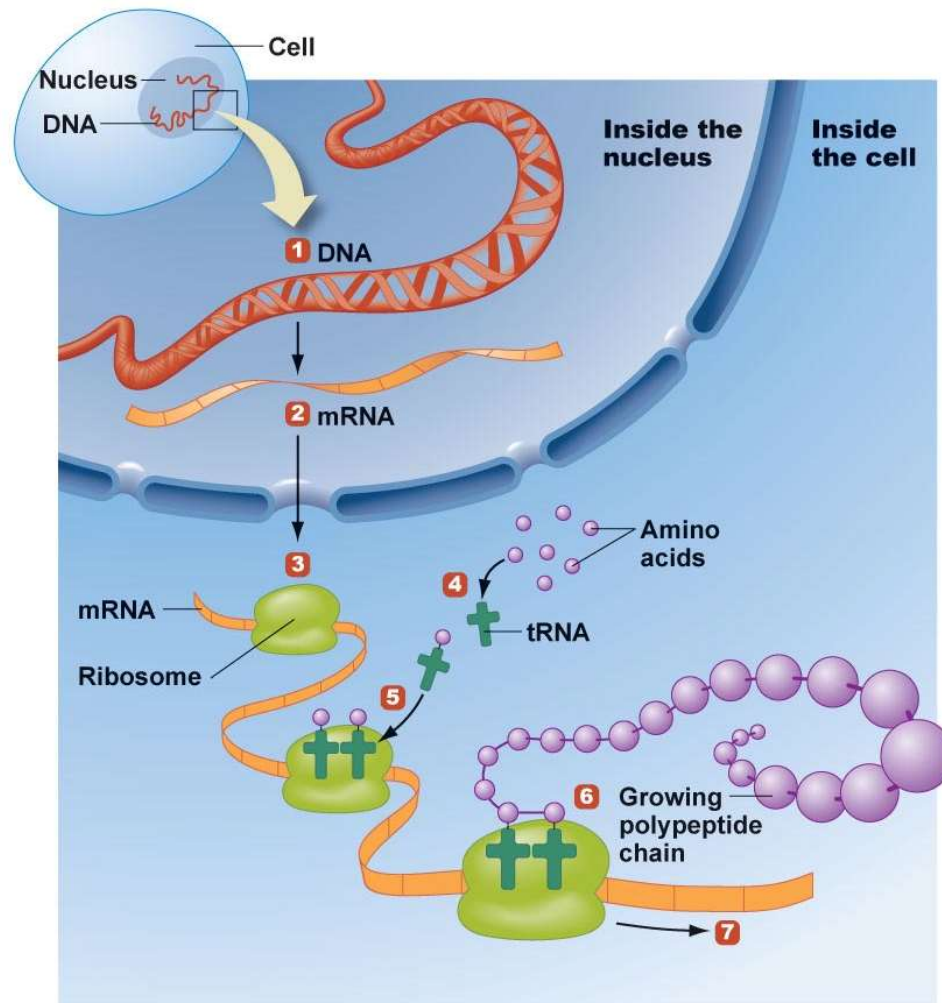


Proteins

Proteins



What Are Proteins?

- Large molecules (macromolecules), Made up of chains of amino acids
- Are found in every cell in the body and involved in most of the body's functions and life processes

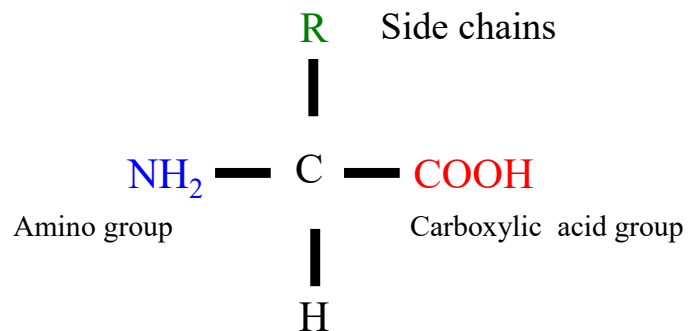
Types of amino acids:

- **Essential amino acids:** histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine
- **Nonessential amino acids:** alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, proline, serine, and tyrosine

Length of proteins

- **Peptides:** <50 amino acids
Dipeptides: 2 amino acids; Tripeptides: 3 amino acids
- **Proteins:** >50 amino acids (typically 100-10,000)

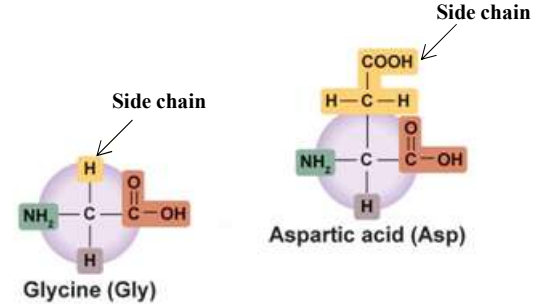
Amino acid: Basic unit of protein



An amino acid

Amino acids are composed of carbon, hydrogen, oxygen, nitrogen, sulphur

There are 20 side chains and 20 unique amino acids



Different amino acids, showing their unique side chains

Amino acids	Abbreviations
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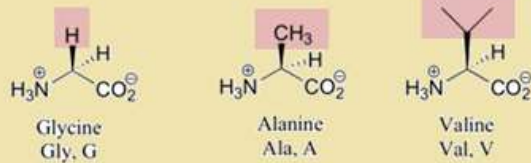
Alanine	Ala	A
Cysteine	Cys	C
Aspartic acid	Asp	D
Glutamic acid	Glu	E
Phenylalanine	Phe	F
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Lysine	Lys	K
Leucine	Leu	L
Methionine	Met	M
Asparagine	Asn	N
Proline	Pro	P
Glutamine	Gln	Q
Arginine	Arg	R
Serine	Ser	S
Threonine	Thr	T
Valine	Val	V
Tryptophan	Trp	W
Tyrosine	Tyr	Y

Types of Amino Acids

Polar amino acids have hydrophilic side chains, which means they're actually attracted to water and participate in hydrogen bonding with the highly polar water molecules.

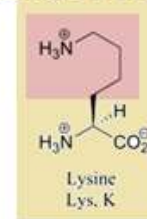
Non-polar

aliphatic side groups



Polar

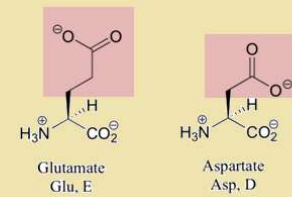
Positively charged side groups



Aromatic side groups



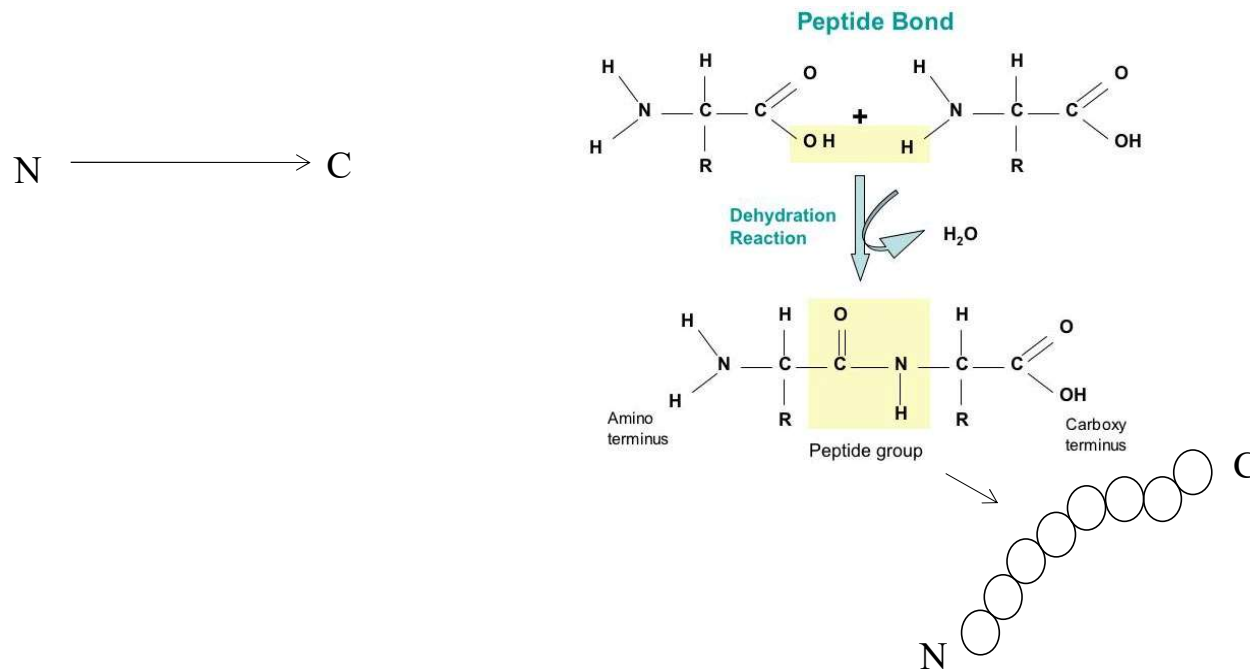
Negatively charged side groups



Non-polar amino acids tend to be found in the centre of the molecule (stabilise the structure) Polar amino acids tend to be located on the protein surface (capable of interacting with water molecules)

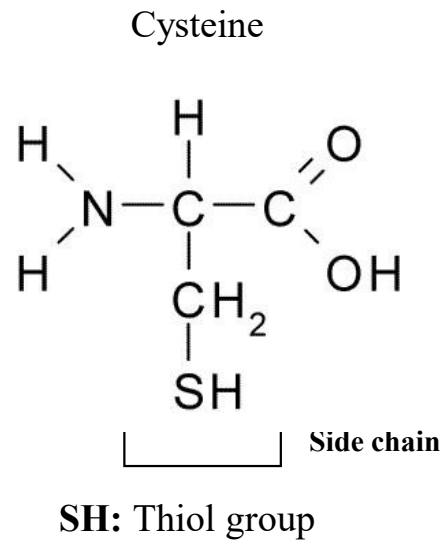
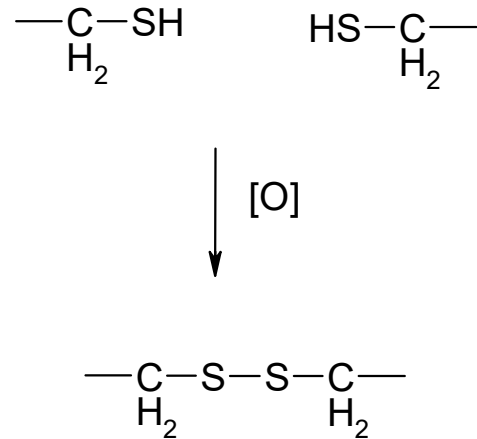
Peptide Bonds

- Carboxyl group + amino group form a strong covalent bond releasing water in the process = a **condensation reaction**
- Amino acids join together in a long chain: **N** terminal end to **C** terminal end



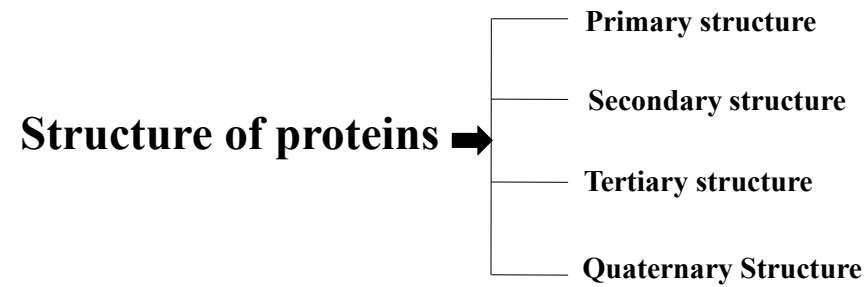
Disulfide Bonds

- The thiol groups of two Cysteine molecules form these types of bonds under oxidizing conditions
- Intermolecular or intramolecular cross-link (covalent bond)
- It helps the protein to stabilize and maintain its distinct three dimensional form.



Proteins classified by function

- **Catalytic:** enzymes (eg proteases)
- **Communication:** hormones (eg insulin)
- **Protective/Assist the immune system:** eg antibody
- **Structural and mechanical support:** eg actin, myosin
- **Pigments:** eg rhodopsin
- **Transport nutrients:** eg hemoglobin
- **Toxins:** eg snake venom



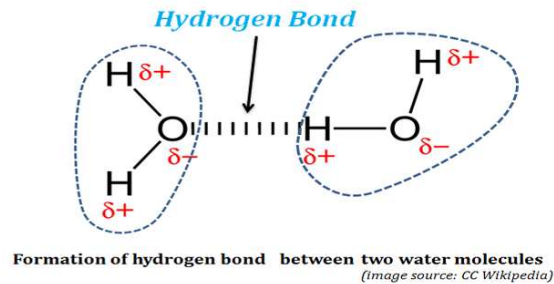
Primary structure



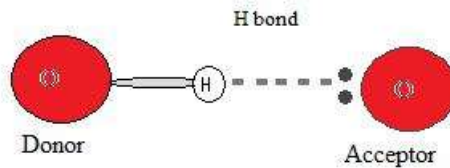
Primary Structure

- ✓ There are 20 different standard amino acids used by cells for protein construction.
- ✓ Amino acids, as their name indicates, contain both a basic amino group and an acidic carboxyl group.
- ✓ The individual amino acid join together in a long chain by forming peptide bonds between the -NH₂ of one amino acid and the -COOH of another.
- ✓ Sequences with fewer than 50 amino acids are generally referred to as peptides, while the terms protein or polypeptide are used for longer sequences.
- ✓ The N-terminus describes the end of the sequence with a free amino group. The end of the protein sequence with a free carboxyl group is called the C-terminus.

Hydrogen bond



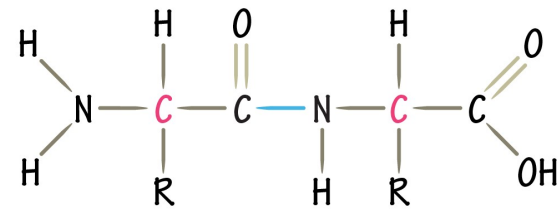
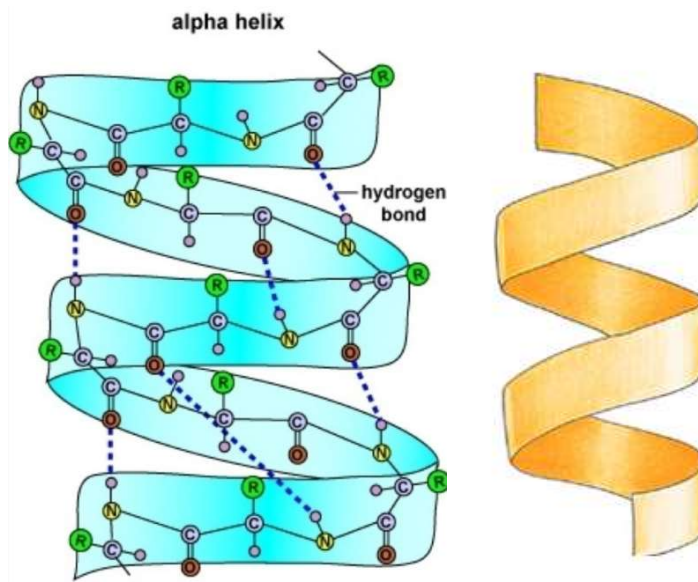
A hydrogen bond is a primarily electrostatic attraction between a hydrogen (H) atom which is covalently bound to a more electronegative atom (nitrogen, oxygen, or fluorine) and another electronegative atom bearing a lone pair of electrons.



Secondary structure

Local sub-structure on the actual polypeptide backbone chain

Alpha helix

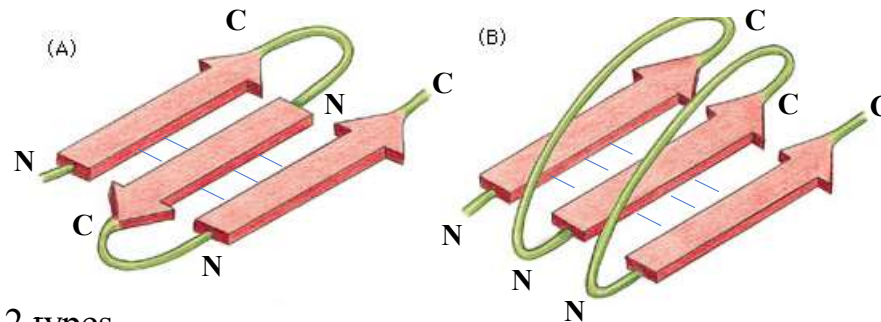
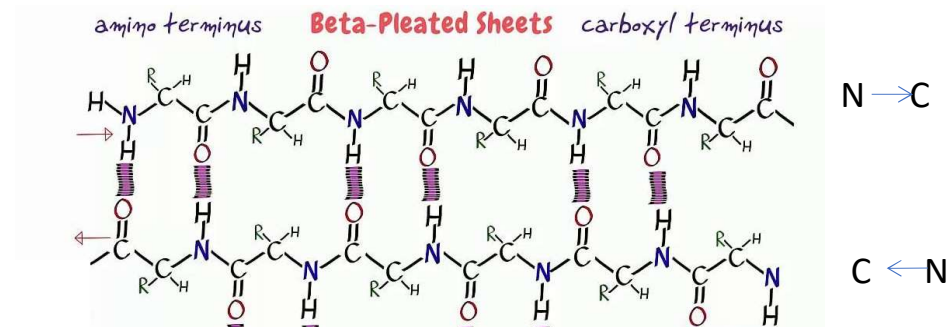


The folding of the N-C-C backbone of the polypeptide chain using weak hydrogen bonds

Intra-strand hydrogen bonding

Beta pleated sheet

Inter-strand hydrogen bonding



- Can be of 2 types
 - Anti-parallel – run in an opposite direction of its neighbor (A)
 - Parallel – run in the same direction (B)

Secondary Structure:

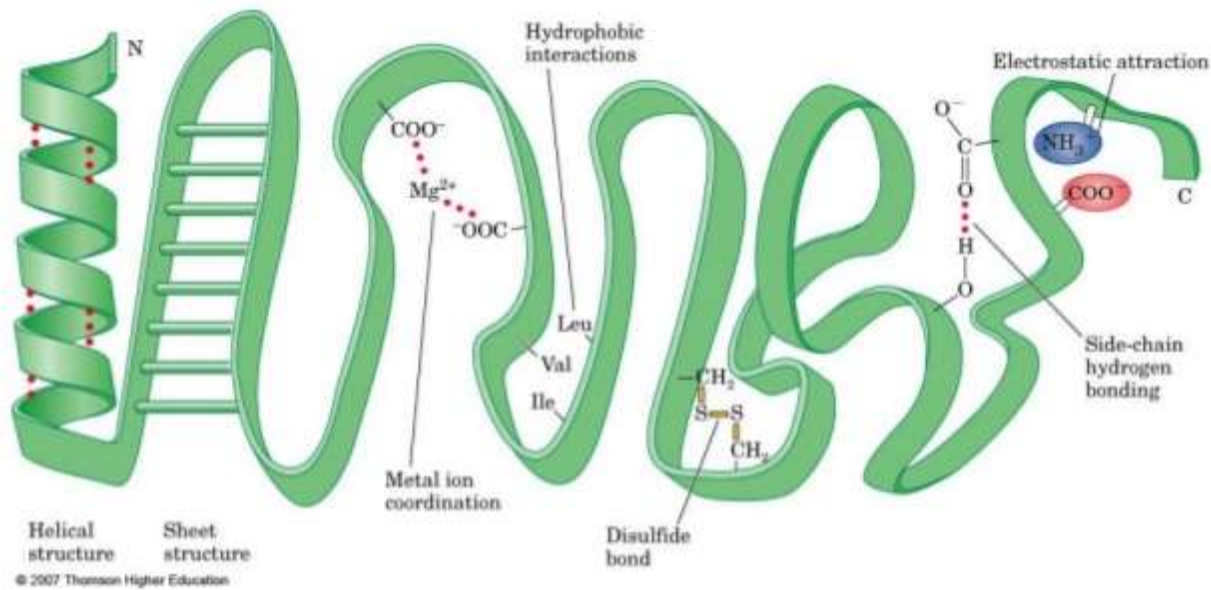
It refers to the folding of a polypeptide chain and a local sub-structure on the actual polypeptide backbone chain. There are two types of secondary structures observed in proteins.

One type is the alpha (α) helix structure. The α -helix is a right hand-coiled (helix) in which backbone N-H group forms a hydrogen bond to the backbone C=O group of the amino acid located 3-4 amino acids along the protein sequence. The hydrogen bonds make this structure especially stable.

The hydrogen bonding in a β -sheet is between strands (inter-strand) rather than within strands (intra-strand). The sheet conformation consists of pairs of strands lying side-by side. The two strands can be either parallel or anti-parallel depending on whether the strand directions (N-terminus to C-terminus) are the same or opposite.

Tertiary structure (Forces that stabilise the three dimensional structure)

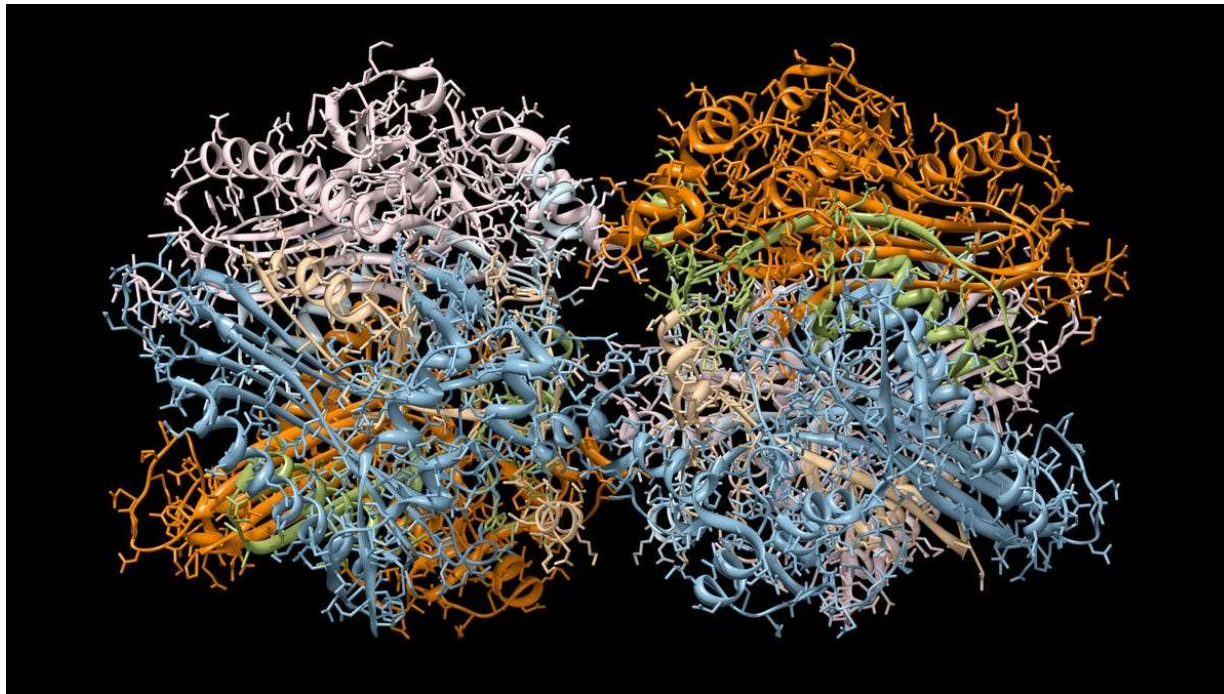
The overall three-dimensional shape of an entire protein molecule is the tertiary structure. The protein molecule will bend and twist in such a way as to achieve maximum stability. Although the three-dimensional shape of a protein may seem irregular and random, it is fashioned by many stabilizing forces due to bonding interactions between the side-chain groups of the amino acids.

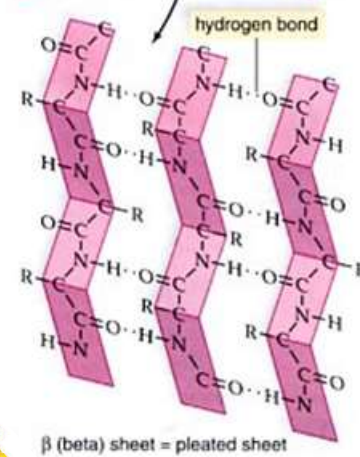
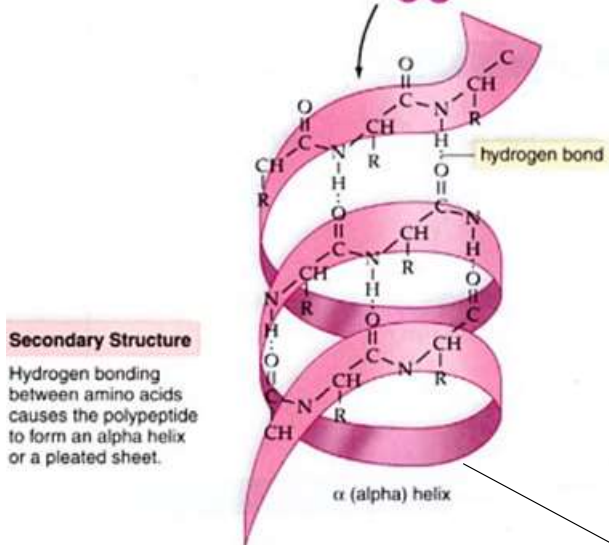
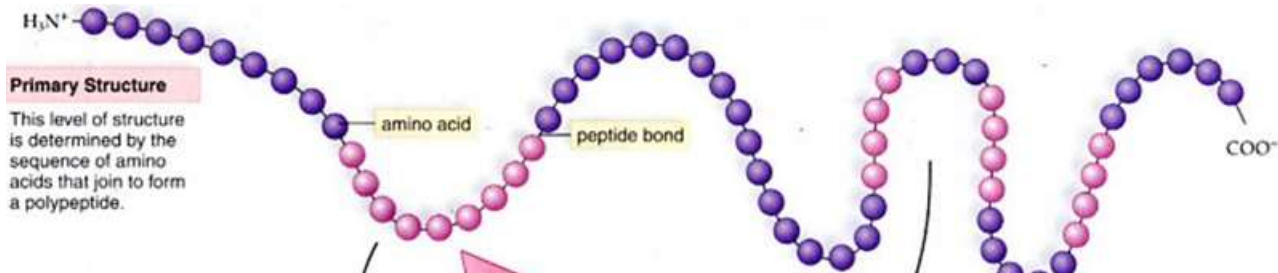


Tertiary Structure:

1. Under physiologic conditions, the "R" group of the amino acid is either hydrophobic or hydrophilic. The amino acids with hydrophilic "R" groups will seek contact with their aqueous environment, while amino acids with hydrophobic "R" groups will seek to avoid water and position themselves towards the center of the protein. Acidic or basic amino acid side-chains will generally be exposed on the surface of the protein as they are hydrophilic.
2. The formation of disulfide bridges by oxidation of the thiol groups on cysteine is an important aspect of the stabilization of protein tertiary structure, allowing different parts of the protein chain to be held together covalently.
3. Hydrogen bonds may form between different side-chain groups. Like disulfide bridges, these hydrogen bonds can bring together two parts of a chain that are some distance away in terms of sequence.
4. Electrostatic interactions between positively and negatively charged sites on amino acid side chains also help to stabilize the tertiary structure of a protein.
5. It is shown that the binding of metal ions can stabilize proteins (Metal ion coordination).

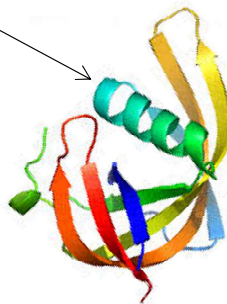
3D Structure of Nearly Every Protein Known to Science



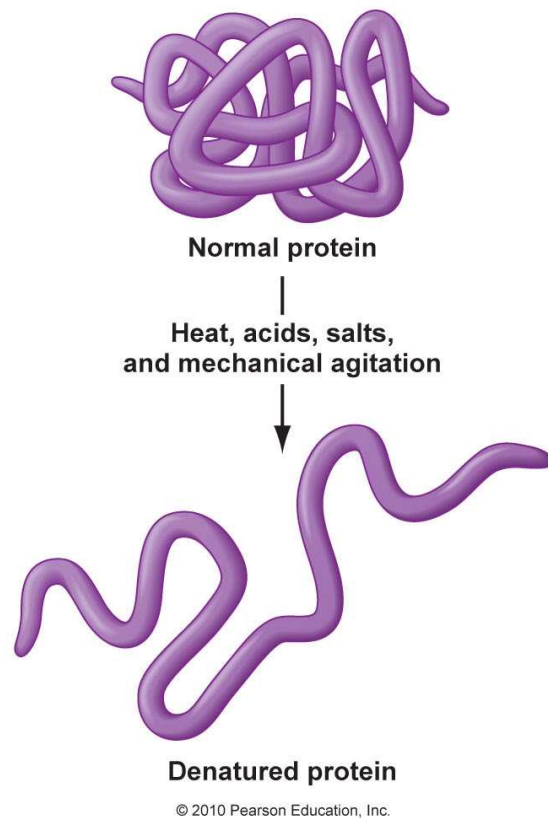


Tertiary Structure

Due in part to covalent bonding between *R* groups the polypeptide folds and twists giving it a characteristic globular shape.



Denaturing a Protein



Attractions and interactions between the side chains cause the proteins to fold into precise three-dimensional shapes

- Alteration of the protein's shape and thus functions as well
- Primary structure is unchanged by denaturing