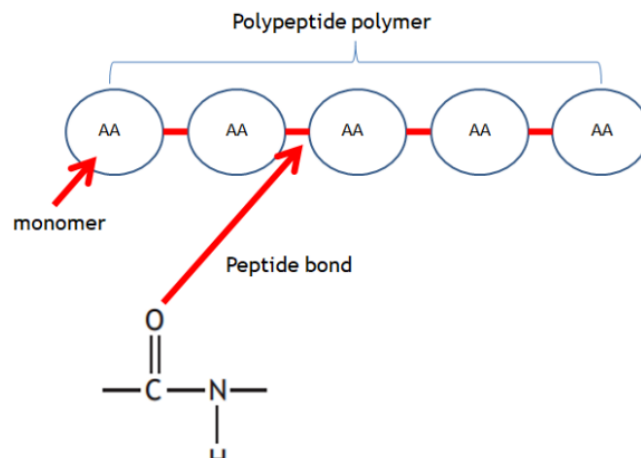


1.2 Amino Acids & Peptide bonds

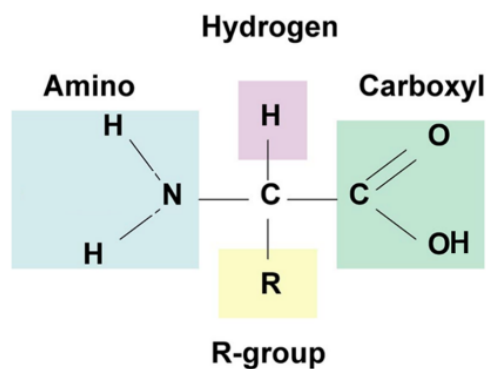
Proteins

Polymers of amino acid monomers joined by peptide bonds to form polypeptide chains.



Amino Acid Structure

Amino acids have the same basic structure of a central carbon with a COOH, NH₂, H atom & R group.

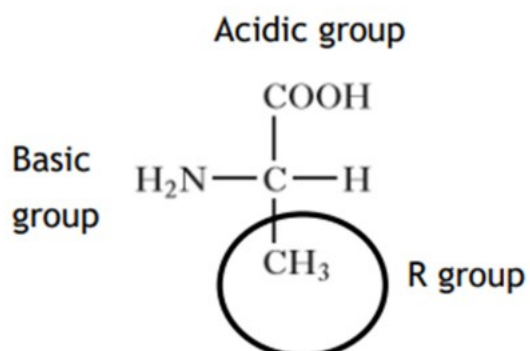


Amino acids ONLY differ in terms of their R group.

The wide range of functions carried out by proteins results from the diversity of R groups

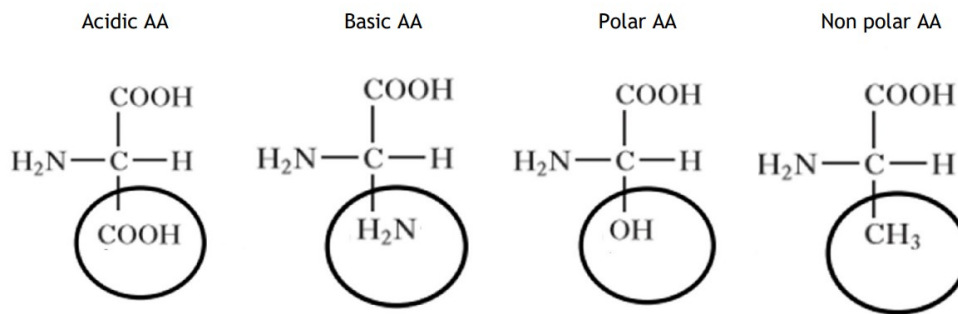
Differences in R groups

1. Size
2. Shape
3. Charge
4. Hydrogen Bonding capacity
5. Chemical reactivity



1.2 Amino Acid Classification

Amino acid classification

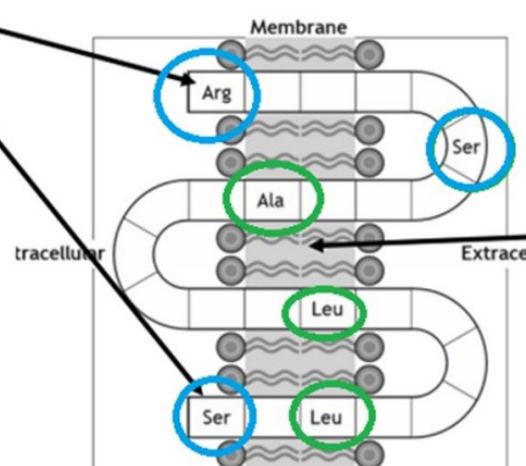


Type of Amino Acid	Hydrophilic/Hydrophobic	R group
Basic	Hydrophilic (+ve charge)	NH_3^+ group
Acidic	Hydrophilic (-ve charge)	COO^- group
Polar	Hydrophilic	OH group
Non Polar	Hydrophobic (no charge)	CH_3 group

Location of protein R groups

Hydrophilic R groups

SURFACE of
soluble protein



Hydrophobic R groups
centre of protein

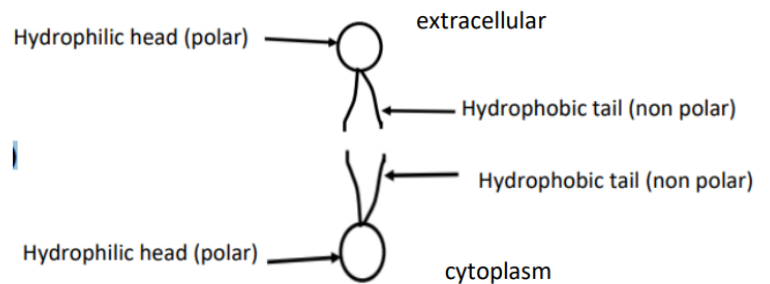
1.2 Integral & Peripheral Proteins

Membrane

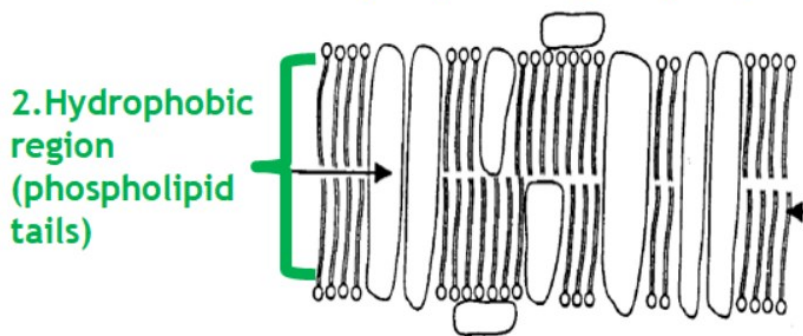
The Cell membrane

Phospholipid bilayer

1. Hydrophilic head (extracellular/cytoplasm)
2. Hydrophobic tail (middle of membrane)

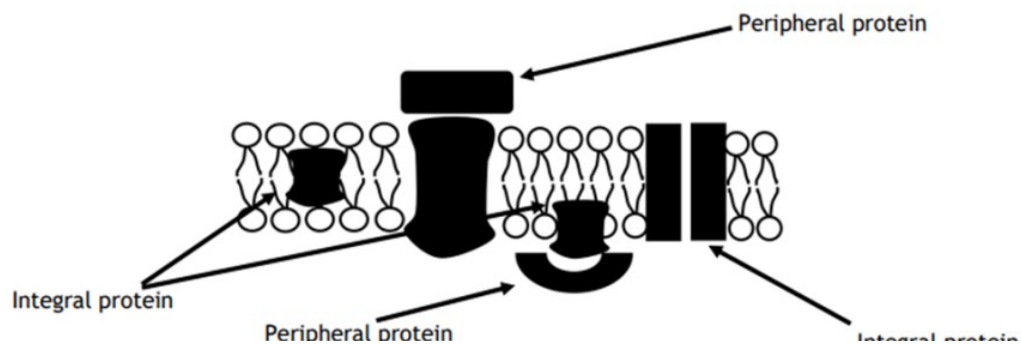


1. Hydrophilic region (phospholipid heads)



1. Hydrophilic phospholipid heads

Membrane proteins



1. Integral proteins

Held **within** the phospholipid bilayer due to regions of **hydrophobic R groups** enabling strong **hydrophobic interactions**

Integral proteins can be **transmembrane** & contain hydrophilic & hydrophobic R groups.

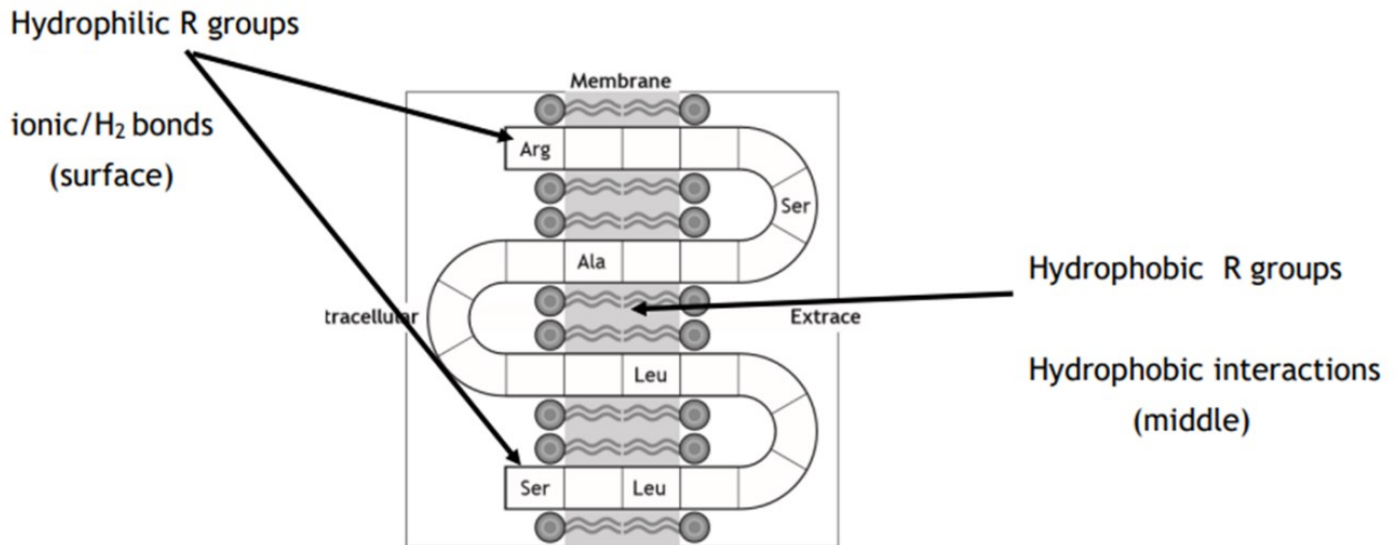
2. Peripheral proteins

Bound to the surface of membranes due to **hydrophilic R groups** on its **surface** by **ionic/hydrogen** bonds.

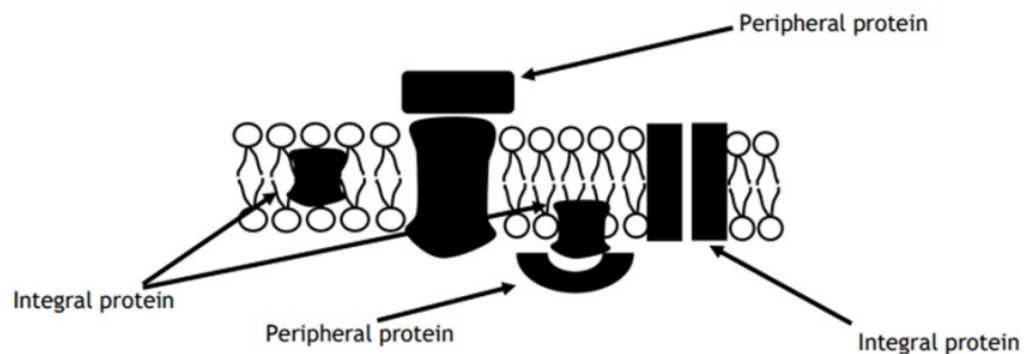
Contain many hydrophilic R groups & much fewer hydrophobic R groups.

1.2 Integral & Peripheral Proteins

Integral Proteins



Membrane proteins



Type of Membrane protein	Description	Type of R groups on protein	Type of interactions
Integral	Held within the phospholipid bilayer Some are transmembrane	Hydrophobic R groups in middle of protein	Strong hydrophobic interactions
Peripheral	Bound to surface of membrane	Hydrophilic R groups at surface	Ionic or hydrogen bonds

1.2 Protein Structure

Primary Structure

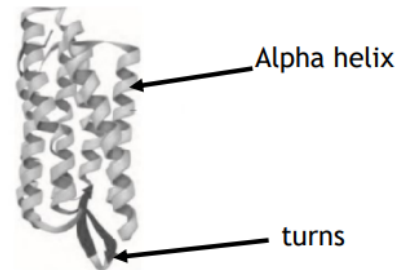
Sequence of amino acids in the polypeptide

Secondary Structure

Hydrogen bonding along the backbone of the protein strand results in secondary structure

Types of Secondary Structure

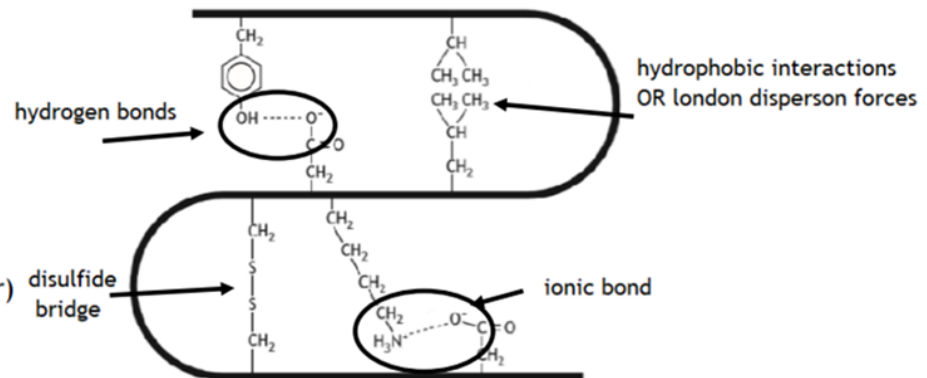
1. Alpha helices
2. Beta-pleated sheets (parallel/antiparallel)
3. Turns



Tertiary Structure

Folding of polypeptide chain into 3D structure due to interactions between R groups

1. Hydrophobic interactions
2. Ionic bonds
3. London dispersion forces
4. Hydrogen bonds
5. Disulfide bridges (covalent bond between R groups containing Sulfur)



Interactions of the R groups (tertiary level) can be influenced by temperature and pH.

1. Increasing temperature

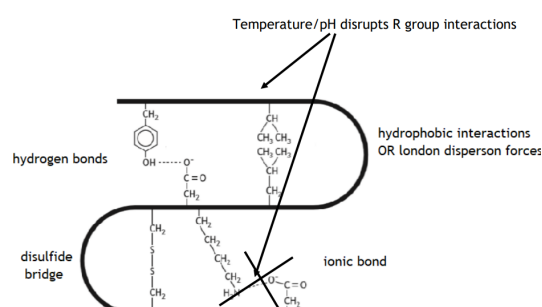
This disrupts the interactions that hold the protein in shape; the protein begins to unfold, eventually becoming denatured.

2. Altered pH from optimum

As pH increases or decreases from the optimum, ionic interactions between charged

groups are lost, which gradually changes the conformation of the protein until it

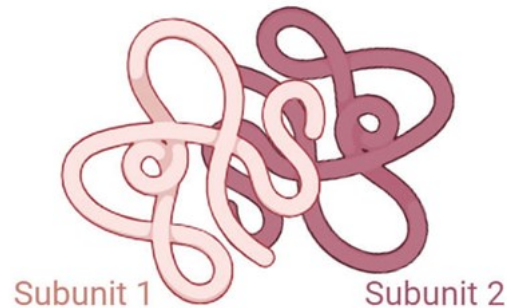
becomes denatured



1.2 Protein Structure

Quaternary structure

The spatial arrangement of the subunits in proteins with at least two connected polypeptide subunits

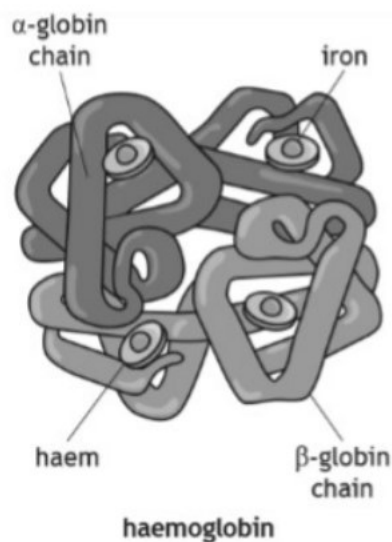


A prosthetic group

A non-protein unit tightly bound to a protein and necessary for its function

Example

Haemoglobin has 4 polypeptide sub-units with a prosthetic iron group required for oxygen binding to haemoglobin sub-units



1.2 Allosteric Proteins

Allosteric Proteins

Allosteric interactions between **spatially distinct sites** in proteins with **multi sub-units**.

Allosteric proteins show **co-operativity** where by changes in binding at one subunit alters the affinity of the remaining subunits.

Example

Irons binds to 1 subunit of haemoglobin which causes a conformational change in the other 3 sub units increasing their affinity to bind iron.

Allosteric Enzymes

The binding of a substrate molecule to one active site of an allosteric enzyme increases the affinity of other active sites for binding of substrate molecules.

The activity of allosteric enzymes can vary greatly with small changes in substrate concentration.

1.2 Allosteric Proteins

Factors lowering affinity of haemoglobin for oxygen (rightward shift on graph)

1. Lower pH
2. Higher temperature

This promotes increased oxygen delivery to tissues.

